Anhang

Kapitel 4

4.5.1 Protokoll-Verdauroboter

Protokoll des Trypsinverdaus mittels Verdauroboter

1. 60µl 50% ACN/50 mM NH_4HCO_3 zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
2. 60 µl 50 mM NH_4HCO_3 zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
3. 60 µl ACN zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
4. 30 µl 10 mM DTT/50 mM NH_4HCO_3 zugeben, 20 min bei 60°C inkubieren, Flüssigkeit entfernen
5. 30µl 55 mM IAA/50 mM NH_4HCO_3 zugeben, 15 min bei RT inkubieren, Flüssigkeit entfernen
6. 60 µl 50 mM NH_4HCO_3 zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
7. 60 µl 25 mM NH_4HCO_3 zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
8. 60 µl ACN zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
9. 60 µl ACN zugeben, 10 min bei RT inkubieren, Flüssigkeit entfernen
10. Flüssigkeit entfernen, 10 min trocknen
11. 15 µl 10 ng/µl Trypsin/ 25 mM NH_4HCO_3 zugeben, 2 h bei 37°C inkubieren
12. 10 µl H2O zugeben, 2 h bei 37°C inkubieren
13. 10 µl 5% (v/v) Ameisensäure zugeben

Elution

14. 20 µl 25 mM NH_4HCO_3 zugeben, 20 min bei RT inkubieren
15. 20 µl ACN zugeben, 20 min inkubieren
16. Elution mit 60µl Luft, 10 min inkubieren

4.5.5 Python-Skripte

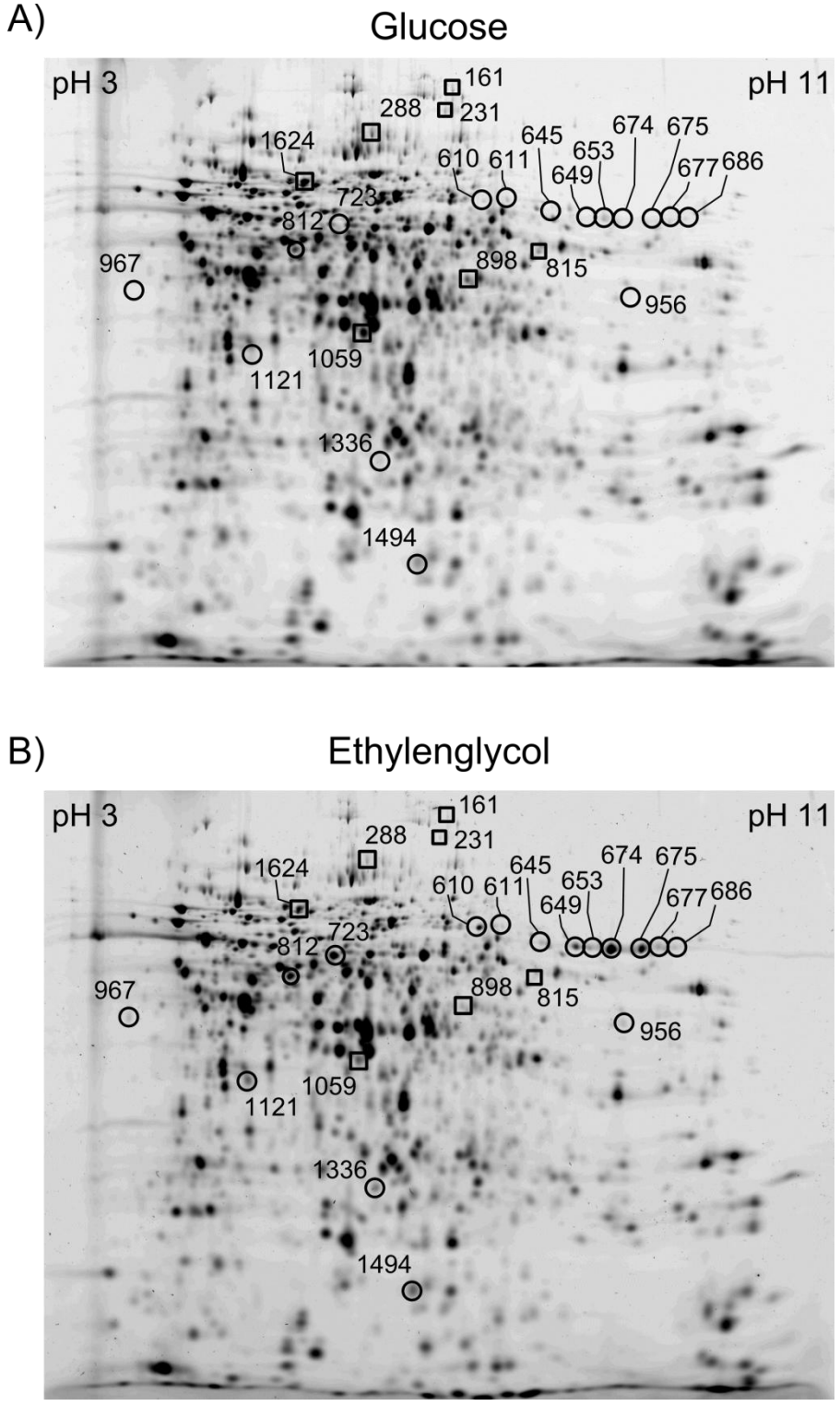
Annotierung 2D DIGE Daten (Python-Skript auf Anfrage)

Annotierung LCMS Daten (Python-Skript auf Anfrage)

Kapitel 5

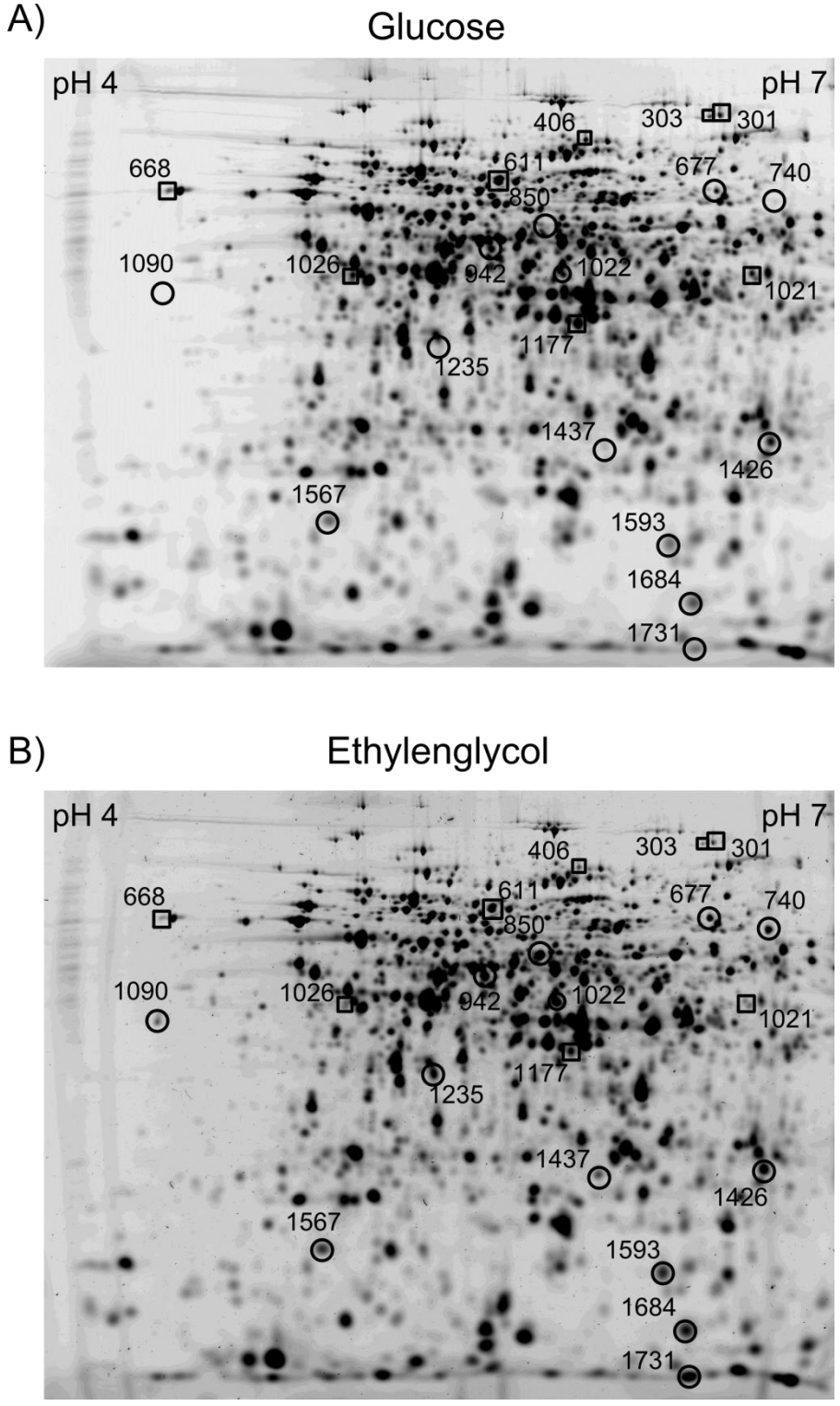
5.1 Teilprojekt EG und GXS

5.1.1 2D-DIGE-Analysen



Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 3-11). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

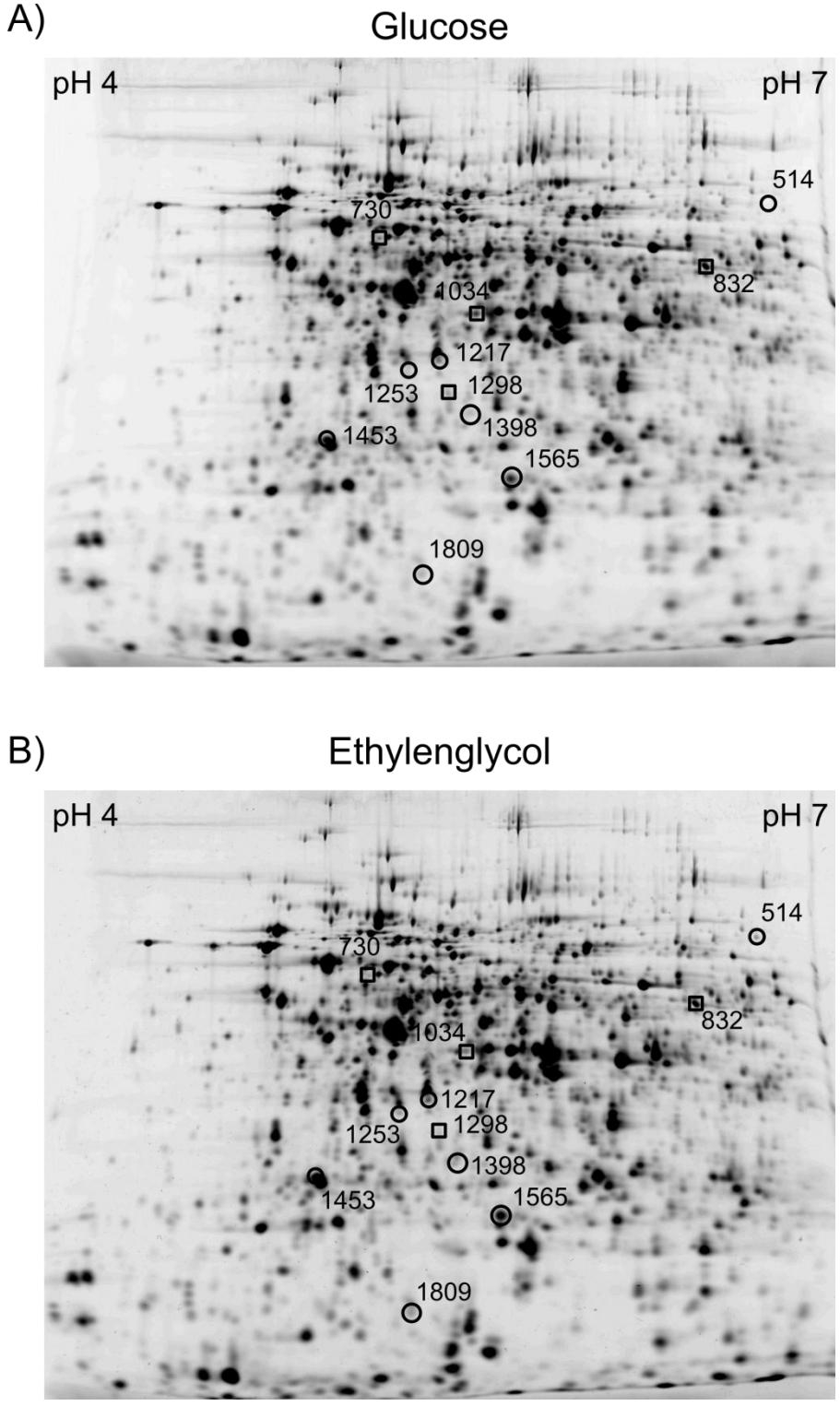
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
161	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2	2,68E-03	control	6,5	106521	22	24%	Cytoplasmic	COG0567	Energy production and conversion	
231	26988517	PP_1786		glycosyl transferase	2,3	1,51E-04	control	6,4	128499	23	20%	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
288	26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	2,1	3,78E-04	control	5,7	106948	12	15%	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
610	26989398	PP_2679		quinoprotein ethanol dehydrogenase	16	4,72E-04	EG	9,1	64883	2	5%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
610	313499247	not in database			16	4,72E-04	EG			14	22%				
645	26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	2,6	3,69E-03	EG	7,4	62241	14	25%	Cytoplasmic	COG3243	Lipid metabolism	
649	26989398	PP_2679		quinoprotein ethanol dehydrogenase	10	1,19E-03	EG	9,1	64883	16	29%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
653	26988095	PP_1361	groEL	chaperonin GroEL	7,4	7,12E-05	EG	4,7	56743	6	14%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
653	26989398	PP_2679		quinoprotein ethanol dehydrogenase	7,4	7,12E-05	EG	9,1	64883	13	22%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
674	26989398	PP_2679		quinoprotein ethanol dehydrogenase	21	1,02E-05	EG	9,1	64883	21	38%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
674	70729590	not in database			21	1,02E-05	EG			2	23%				
675	26989398	PP_2679		quinoprotein ethanol dehydrogenase	21	1,49E-04	EG	9,1	64883	19	33%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
675	26988095	PP_1361	groEL	chaperonin GroEL	21	1,49E-04	EG	4,7	56743	3	8%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
677	26989398	PP_2679		quinoprotein ethanol dehydrogenase	6,2	2,15E-03	EG	9,1	64883	2	4%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
677	26988731	PP_2006		hypothetical protein	6,2	2,15E-03	EG	5,1	63743	2	4%	Unknown			
686	26988731	PP_2006		hypothetical protein	4,4	1,16E-04	EG	5,1	63743	6	15%	Unknown			
686	26989398	PP_2679		quinoprotein ethanol dehydrogenase	4,4	1,16E-04	EG	9,1	64883	5	11%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
723	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	5,1	4,96E-03	EG	6,0	54367	3	6%	Cytoplasmic	COG1012	Energy production and conversion	
723	26989399	PP_2680		aldehyde dehydrogenase family protein	5,1	4,96E-03	EG	5,5	54903	14	41%	Cytoplasmic	COG1012	Energy production and conversion	
812	26988046	PP_1311		tryptophanyl-tRNA synthetase	2,1	1,51E-05	EG	5,4	49297	5	14%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
812	26990810	PP_4116	aceA	isocitrate lyase	2,1	1,51E-05	EG	5,3	48633	14	30%	Cytoplasmic	COG2224	Energy production and conversion	
812	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2,1	1,51E-05	EG	5,4	50393	4	11%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
815	26990915	PP_4223		diaminobutyrate--2-oxoglutarate aminotransferase	4,2	9,30E-07	control	7,0	48859	7	18%	Cytoplasmic	COG0160	Amino acid transport and metabolism	
815	26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	4,2	9,30E-07	control	7,7	53014	10	26%	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
898	26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	2,6	1,12E-05	control	6,6	42328	2	5%	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
898	148545952	not in database			2,6	1,12E-05	control			12	29%				
956	148548303	not in database			7,8	1,00E-05	EG			5	10%				
967	26989381	PP_2662		hypothetical protein	8,1	1,39E-04	EG	4,3	42858	4	14%	Outer Membrane			
1059	26990488	PP_3783		hypothetical protein	2	3,40E-04	control	5,8	34938	10	31%	Cytoplasmic			
1059	26990270	PP_3558		substrate-binding region of ABC-type glycine betaine transport system	2	3,40E-04	control	5,5	36928	5	17%	Periplasmic	COG2113	Amino acid transport and metabolism	
1121	207094127	not in database			2,9	1,61E-04	EG			2	54%				
1121	26987522	PP_0786	trxB	thioredoxin reductase	2,9	1,61E-04	EG	5,1	33841	3	18%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
1121	26989388	PP_2669		YVTN family beta-propeller repeat-containing protein	2,9	1,61E-04	EG	6,2	36051	5	20%	Unknown	COG3391	Function unknown	
1336	26989384	PP_2665	agmR	LuxR family two component transcriptional regulator	4,1	8,11E-06	EG	5,9	24536	5	23%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
1336	26987147	PP_0406		nucleotidyl transferase	4,1	8,11E-06	EG	6,0	23814	3	16%	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
1624	26987981	PP_1246		hypothetical protein	2,4	7,44E-05	control	6,0	65952	5	7%	Unknown	COG5373	Function unknown	
1624	26987510	PP_0774	pta	phosphate acetyltransferase	2,4	7,44E-05	control	5,2	74642	2	3%	Cytoplasmic Membrane	COG0280	Energy production and conversion	
1624	26988393	PP_1661		dehydrogenase subunit	2,4	7,44E-05	control	5,5	81020	2	4%	Extracellular	COG2303	Amino acid transport and metabolism	
1624	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2,4	7,44E-05	control	5,4	79899	20	29%	Cytoplasmic	COG2838	Energy production and conversion	



Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet, sind nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
301	26988517	PP_1786		glycosyl transferase	2.0	1.36E-04	control	6.4	128499	30	26%	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
303	26988517	PP_1786		glycosyl transferase	2.2	1.69E-04	control	6.4	128499	31	29%	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
406	26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	2.0	1.37E-04	control	6.0	105800	9	11%	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
406	26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	2.0	1.37E-04	control	5.7	106948	28	39%	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
611	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.1	6.38E-06	control	5.4	79899	32	49%	Cytoplasmic	COG2838	Energy production and conversion	
611	26987981	PP_1246		hypothetical protein	2.1	6.38E-06	control	6.0	65952	20	36%	Unknown	COG5373	Function unknown	
611	26987510	PP_0774	pta	phosphate acetyltransferase	2.1	6.38E-06	control	5.2	74642	19	33%	Cytoplasmic Membrane	COG0280	Energy production and conversion	
611	26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	2.1	6.38E-06	control	5.6	69049	6	11%	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
611	26990753	PP_4052	malQ	4-alpha-glucanotransferase	2.1	6.38E-06	control	5.5	76475	8	10%	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
611	26990489	PP_3784		hypothetical protein	2.1	6.38E-06	control	5.4	41070	4	13%	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
611	26991720	PP_5044		GTP-binding protein TypA	2.1	6.38E-06	control	5.3	67157	20	29%	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
611	26988393	PP_1661		dehydrogenase subunit	2.1	6.38E-06	control	5.5	81020	8	14%	Extracellular	COG2303	Amino acid transport and metabolism	
611	26991410	PP_4727	dnaK	molecular chaperone DnaK	2.1	6.38E-06	control	4.6	68800	13	23%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
668	226366	not in database		enolase	2.0	1.41E-03	control			2	7%				
668	317055545	not in database		ubiquitin	2.0	1.41E-03	control			2	9%				
668	26991067	PP_4378	fliC	flagellin FliC	2.0	1.41E-03	control	4.2	67846	11	24%	Extracellular	COG1344	Cell motility and secretion	
677	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.6	5.39E-05	EG	6.4	71796	18	33%	Cytoplasmic	COG0365	Lipid metabolism	
677	26990488	PP_3783		hypothetical protein	2.6	5.39E-05	EG	5.8	34938	2	11%	Cytoplasmic			
677	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.6	5.39E-05	EG	6.4	71796	24	49%	Cytoplasmic	COG0365	Lipid metabolism	
677	26987746	PP_1010	edd	phosphogluconate dehydratase	2.6	5.39E-05	EG	6.4	65359	2	5%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
740	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	34.0	1.22E-05		7.0	69173	17	32%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
850	148550051	not in database		S-adenosyl-L-homocysteine hydrolase	5.2	8.67E-04	EG			9	20%				
850	26989399	PP_2680		aldehyde dehydrogenase family protein	5.2	8.67E-04	EG	5.5	54903	12	36%	Cytoplasmic	COG1012	Energy production and conversion	
850	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	5.2	8.67E-04	EG	6.0	54367	10	23%	Cytoplasmic	COG1012	Energy production and conversion	
850	26988522	PP_1791		aldolase/synthase	5.2	8.67E-04	EG	5.9	58534	2	6%	Cytoplasmic	COG0119	Amino acid transport and metabolism	
850	26989661	PP_2942		response regulator	5.2	8.67E-04	EG	5.6	51291	15	34%	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
850	26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	5.2	8.67E-04	EG	5.4	55551	2	4%	Cytoplasmic	COG2204	Signal transduction mechanisms	
850	26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	5.2	8.67E-04	EG	5.6	51255	8	21%	Cytoplasmic	COG0065	Amino acid transport and metabolism	
942	26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	2.8	9.64E-08	EG	4.6	49359	5	13%	Cytoplasmic	COG0055	Energy production and conversion	
942	26987824	PP_1088	argG	argininosuccinate synthase	2.8	9.64E-08	EG	5.1	45164	14	32%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
942	26988046	PP_1311		tryptophanyl-tRNA synthetase	2.8	9.64E-08	EG	5.4	49297	7	16%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
942	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.8	9.64E-08	EG	5.2	55352	4	8%	Cytoplasmic	COG0056	Energy production and conversion	
942	26991734	PP_5058		carboxyl-terminal protease	2.8	9.64E-08	EG	5.6	46333	2	5%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
942	26988203	PP_1470	hom	homoserine dehydrogenase	2.8	9.64E-08	EG	5.1	46194	2	4%	Cytoplasmic	COG0460	Amino acid transport and metabolism	
942	26990705	PP_4000	serS	seryl-tRNA synthetase	2.8	9.64E-08	EG	5.1	46849	8	21%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
942	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.8	9.64E-08	EG	5.4	50393	12	31%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
942	26987824	PP_1088	argG	argininosuccinate synthase	2.8	9.64E-08	EG	5.1	45164	5	15%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
942	26990810	PP_4116	aceA	isocitrate lyase	2.8	9.64E-08	EG	5.3	48633	20	53%	Cytoplasmic	COG2224	Energy production and conversion	
942	26988046	PP_1311		tryptophanyl-tRNA synthetase	2.8	9.64E-08	EG	5.4	49297	5	14%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
942	317055545	not in database		ubiquitin	2.8	9.64E-08	EG			2	9%				
942	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.8	9.64E-08	EG	5.4	50393	7	19%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1021	26987193	PP_0452	tuf	elongation factor Tu	2.6	2.57E-05	control	5.0	43478	4	11%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1021	26991409	PP_4726	dnaJ	chaperone protein DnaJ	2.6	2.57E-05	control	6.7	40181	9	28%	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
1021	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	2.6	2.57E-05	control	6.7	41895	12	37%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
1021	26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	2.6	2.57E-05	control	7.5	47782	4	11%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
1021	26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	2.6	2.57E-05	control	6.6	42328	10	27%	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
1021	26990127	PP_3414		methyl-accepting chemotaxis transducer/sensory box protein	2.6	2.57E-05	control	6.8	48686	12	28%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1021	26991409	PP_4726	dnaJ	chaperone protein DnaJ	2.6	2.57E-05	control	6.7	40181	8	25%	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
1021	26990127	PP_3414		methyl-accepting chemotaxis transducer/sensory box protein	2.6	2.57E-05	control	6.8	48686	3	7%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1021	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	2.6	2.57E-05	control	6.7	41895	19	68%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
1021	26987193	PP_0452	tuf	elongation factor Tu	2.6	2.57E-05	control	5.0	43478	2	6%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1021	26989160	PP_2437		acyl-CoA dehydrogenase domain-containing protein	2.6	2.57E-05	control	6.8	45812	8	19%	Cytoplasmic	COG1960	Lipid metabolism	
1021	26987152	PP_0411		spermidine/putrescine ABC transporter ATPase	2.6	2.57E-05	control	6.6	41197	11	34%	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
1021	26989160	PP_2437		acyl-CoA dehydrogenase domain-containing protein	2.6	2.57E-05	control	6.8	45812	6	16%	Cytoplasmic	COG1960	Lipid metabolism	
1021	26987152	PP_0411		spermidine/putrescine ABC transporter ATPase	2.6	2.57E-05	control	6.6	41197	14	33%	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
1022	26988732	PP_2007		P-47-related protein	2.7	1.34E-05	EG	5.8	44707	8	29%	Unknown			
1022	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	2.7	1.34E-05	EG	5.7	45178	10	30%	Cytoplasmic	COG0001	Coenzyme metabolism	
1022	26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	2.7	1.34E-05	EG	5.7	42575	3	8%	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
1022	26988361	PP_1629	recA	recombinase A	2.7	1.34E-05	EG	5.3	37545	10	40%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1022	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.7	1.34E-05	EG	5.4	45695	2	6%	Unknown	COG0538	Energy production and conversion	
1022	26987193	PP_0452	tuf	elongation factor Tu	2.7	1.34E-05	EG	5.0	43478	5	20%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1022	313500276	not in database		Hypothetical protein, conserved	2.7	1.34E-05	EG			12	32%				
1022	26987737	PP_1001	arcA	arginine deiminase	2.7	1.34E-05	EG	5.7	46462	2	6%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1022	26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	2.7	1.34E-05	EG	5.8	40574	4	12%	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
1022	26989586	PP_2867		pyridine nucleotide-disulphide oxidoreductase family protein	2.7	1.34E-05	EG	5.6	42483	2	6%	Cytoplasmic Membrane	COG1252	Energy production and conversion	
1022	26991570	PP_4892	hflK	HflK protein	2.7	1.34E-05	EG	5.1	44762	4	15%	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
1022	26988732	PP_2007		P-47-related protein	2.7	1.34E-05	EG	5.8	44707	14	56%	Unknown			
1022	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.7	1.34E-05	EG	5.4	45695	4	12%	Unknown	COG0538	Energy production and conversion	
1022	26988361	PP_1629	recA	recombinase A	2.7	1.34E-05	EG	5.3	37545	7	27%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1022	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	2.7	1.34E-05	EG	5.7	45178	6	19%	Cytoplasmic	COG0001	Coenzyme metabolism	
1022	26988645	PP_1916	fabF	3-oxoacyl-(acyl carrier protein) synthase II	2.7	1.34E-05	EG	5.8	43152	2	4%	Cytoplasmic Membrane	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1022	26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	2.7	1.34E-05	EG	5.7	42575	3	8%	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
1022	26991570	PP_4892	hflK	HflK protein	2.7	1.34E-05	EG	5.1	44762	2	6%	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
1022	313500276	not in database		Hypothetical protein, conserved	2.7	1.34E-05	EG			4	10%				
1022	26988361	PP_1629	recA	recombinase A	2.7	1.34E-05	EG	5.3	37545	2	7%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1026	104780253	not in database		ornithine decarboxylase	2.1	1.23E-05	control			3	9%				
1026	26988076	PP_1342	ftsZ	cell division protein FtsZ	2.1	1.23E-05	control	4.7	41830	14	47%	Cytoplasmic	COG0206	Cell division and chromosome partitioning	
1026	26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	2.1	1.23E-05	control	4.7	36629	7	22%	Cytoplasmic	COG0202	Transcription	
1090	26989381	PP_2662		hypothetical protein	31.0	1.40E-03	EG	4.3	42858	6	20%	Outer Membrane			
1177	26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	2.2	5.77E-06	control	5.6	35858	4	13%	Unknown	COG2171	Amino acid transport and metabolism	
1177	26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	2.2	5.77E-06	control	6.3	36692	5	13%	Periplasmic	COG1613	Inorganic ion transport and metabolism	
1177	26991362	PP_4678	ilvC	ketol-acid reductoisomerase	2.2	5.77E-06	control	5.4	36370	4	15%	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
1177	26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	2.2	5.77E-06	control	6.3	36692	2	8%	Periplasmic	COG1613	Inorganic ion transport and metabolism	
1177	26990488	PP_3783		hypothetical protein	2.2	5.77E-06	control	5.8	34938	15	58%	Cytoplasmic			
1177	26987498	PP_0762	hprA	glycerate dehydrogenase	2.2	5.77E-06	control	6.1	34094	5	21%	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
1177	26988732	PP_2007		P-47-related protein	2.2	5.77E-06	control	5.8	44707	6	25%	Unknown			
1177	26990270	PP_3558		substrate-binding region of ABC-type glycine betaine transport system	2.2	5.77E-06	control	5.5	36928	8	32%	Periplasmic	COG2113	Amino acid transport and metabolism	
1235	26987193	PP_0452	tuf	elongation factor Tu	5.4	1.26E-03	EG	5.0	43478	2	6%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1235	26988324	PP_1592	tsf	elongation factor Ts	5.4	1.26E-03	EG	4.9	30432	6	22%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
1235	26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	5.4	1.26E-03	EG	5.6	36424	2	6%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
1235	26989631	PP_2912		hypothetical protein	5.4	1.26E-03	EG	5.0	33023	5	17%	Cytoplasmic	COG1718	Signal transduction mechanisms	Cell division and chromosome partitioning
1235	26990421	PP_3713	catA	catechol 1,2-dioxygenase	5.4	1.26E-03	EG	5.1	34249	10	33%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
1235	148545934	not in database		malate dehydrogenase	5.4	1.26E-03	EG			7	24%				
1235	26991937	PP_5261		LysR family transcriptional regulator	5.4	1.26E-03	EG	4.9	34774	2	9%	Cytoplasmic	COG0583	Transcription	
1235	26987522	PP_0786	trxB	thioredoxin reductase	5.4	1.26E-03	EG	5.1	33841	8	38%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
1235	26988892	PP_2168	tal	transaldolase B	5.4	1.26E-03	EG	5.0	33615	14	55%	Unknown	COG0176	Carbohydrate transport and metabolism	

1235	26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	5.4	1.26E-03	EG	10.9	26214	7	24%	Cytoplasmic	COG3937	Function unknown		
1235	26989388	PP_2669		YVTN family beta-propeller repeat-containing protein	5.4	1.26E-03	EG	6.2	36051	4	12%	Unknown	COG3391	Function unknown		
1235	26989388	PP_2669		YVTN family beta-propeller repeat-containing protein	5.4	1.26E-03	EG	6.2	36051	9	33%	Unknown	COG3391	Function unknown		
1235	26987522	PP_0786	trxB	thioredoxin reductase	5.4	1.26E-03	EG	5.1	33841	9	47%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones		
1235	26987193	PP_0452	tuf	elongation factor Tu	5.4	1.26E-03	EG	5.0	43478	3	9%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis		
1235	26986885	PP_0140		hypothetical protein	5.4	1.26E-03	EG	5.4	33062	2	9%	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism		
1235	26989631	PP_2912		hypothetical protein	5.4	1.26E-03	EG	5.0	33023	6	20%	Cytoplasmic	COG1718	Signal transduction mechanisms	Cell division and chromosome partitioning	
1235	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	5.4	1.26E-03	EG	4.9	31237	3	12%	Unknown	COG2025	Energy production and conversion		
1235	26990421	PP_3713	catA	catechol 1,2-dioxygenase	5.4	1.26E-03	EG	5.1	34249	6	23%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism		
1426	26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	2.0	2.37E-05	EG	6.8	29075	5	21%	Cytoplasmic	COG5424	Coenzyme metabolism		
1426	26990870	PP_4178		dienelactone hydrolase	2.0	2.37E-05	EG	7.1	26269	2	11%	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism		
1426	26988220	PP_1487		hypothetical protein	2.0	2.37E-05	EG	6.5	24063	3	12%	Cytoplasmic Membrane	COG2979	Function unknown		
1426	26988395	PP_1663		hypothetical protein	2.0	2.37E-05	EG	9.2	26313	2	8%	Periplasmic				
1426	26986845	PP_0100	cynT	carbonate dehydratase	2.0	2.37E-05	EG	6.8	26001	4	17%	Cytoplasmic	COG0288	Inorganic ion transport and metabolism		
1426	26987919	PP_1184		dienelactone hydrolase	2.0	2.37E-05	EG	6.8	28722	5	21%	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism		
1426	26987598	PP_0862		hydroxylase	2.0	2.37E-05	EG	6.7	25336	2	11%	Cytoplasmic	COG3128	Function unknown		
1426	26988220	PP_1487		hypothetical protein	2.0	2.37E-05	EG	6.5	24063	7	34%	Cytoplasmic Membrane	COG2979	Function unknown		
1426	26988220	PP_1487		hypothetical protein	2.0	2.37E-05	EG	6.5	24063	6	27%	Cytoplasmic Membrane	COG2979	Function unknown		
1426	26990144	PP_3431		ThiJ/Pfpl domain protein	2.0	2.37E-05	EG	6.5	25246	12	69%	Unknown	COG0693	General function prediction only		
1437	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	4.8	2.95E-05	EG	6.0	26030	8	36%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
1437	26987219	PP_0478	rpsD	30S ribosomal protein S4	4.8	2.95E-05	EG	10.5	23056	2	9%	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis		
1437	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	4.8	2.95E-05	EG	6.0	26030	11	51%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
1437	26987954	PP_1219	tolQ	biopolymer transport protein TolQ	4.8	2.95E-05	EG	6.3	25310	3	14%	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion		
1437	26989384	PP_2665	aqmR	LuxR family two component transcriptional regulator	4.8	2.95E-05	EG	5.9	24536	8	39%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
1437	26987147	PP_0406		nucleotidyl transferase	4.8	2.95E-05	EG	6.0	23814	2	9%	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis	
1437	26988239	PP_1507		hypothetical protein	4.8	2.95E-05	EG	6.0	23544	5	34%	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones		
1567	26988809	PP_2084	menG	ribonuclease activity regulator protein RraA	1.9	4.48E-04	EG	4.6	17646	2	14%	Cytoplasmic	COG0684	Coenzyme metabolism		
1567	26988196	PP_1463	rimM	16S rRNA-processing protein RimM	1.9	4.48E-04	EG	4.6	20064	2	11%	Cytoplasmic	COG0806	Translation, ribosomal structure and biogenesis		
1567	26989845	PP_3126		polysaccharide export protein	1.9	4.48E-04	EG	4.9	19528	7	53%	Unknown	COG1596	Cell wall	membrane	
1593	26991516	PP_4836		hypothetical protein	2.3	6.62E-05	EG	6.5	17387	3	21%	Periplasmic	COG2847	Inorganic ion transport and metabolism		
1593	26987970	PP_1235		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	2.3	6.62E-05	EG	6.3	17170	3	24%	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones		
1593	26989622	PP_2903	ppiB	peptidyl-prolyl cis-trans isomerase B	2.3	6.62E-05	EG	6.5	18200	8	65%	Cytoplasmic	COG0652	Posttranslational modification, protein turnover, chaperones		
1593	26991516	PP_4836		hypothetical protein	2.3	6.62E-05	EG	6.5	17387	4	26%	Periplasmic	COG2847	Inorganic ion transport and metabolism		
1593	26992012	PP_5336	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.3	6.62E-05	EG	6.3	16943	4	35%	Unknown	COG0041	Nucleotide transport and metabolism		
1593	26991236	PP_4552	phaJ1	MaoC domain protein dehydratase	2.3	6.62E-05	EG	6.3	17135	3	26%	Unknown	COG2030	Lipid metabolism		
1684	26991550	PP_4870		azurin	2.1	1.30E-04	EG	6.9	16028	5	35%	Periplasmic	COG3241	Energy production and conversion		
1684	26989657	PP_2938		OsmC family protein	2.1	1.30E-04	EG	6.0	25527	2	10%	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism		
1684	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.1	1.30E-04	EG	5.4	79899	14	23%	Cytoplasmic	COG2838	Energy production and conversion		
1684	26987166	PP_0425		OsmC family protein	2.1	1.30E-04	EG	6.3	15143	4	24%	Unknown	COG1765	Posttranslational modification, protein turnover, chaperones		
1684	26991550	PP_4870		azurin	2.1	1.30E-04	EG	6.9	16028	4	29%	Periplasmic	COG3241	Energy production and conversion		
1684	26989657	PP_2938		OsmC family protein	2.1	1.30E-04	EG	6.0	25527	2	11%	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism		
1684	26987166	PP_0425		OsmC family protein	2.1	1.30E-04	EG	6.3	15143	3	23%	Unknown	COG1765	Posttranslational modification, protein turnover, chaperones		
1731	104781268	not in database		carboxymuconolactone decarboxylase	5.0	3.19E-05	EG			6	57%					
1731	26991995	PP_5319		hypothetical protein	5.0	3.19E-05	EG	7.2	15525	2	24%	Periplasmic	COG4315	Function unknown		
1731	26991053	PP_4364		anti-sigma-factor antagonist	5.0	3.19E-05	EG	6.3	11458	3	21%	Unknown	COG1366	Signal transduction mechanisms		
1731	26986987	PP_0244		thioesterase superfamily protein	5.0	3.19E-05	EG	6.5	13625	2	20%	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism		
1731	104780056	not in database			5.0	3.19E-05	EG			2	19%					
1731	104781268	not in database		carboxymuconolactone decarboxylase	5.0	3.19E-05	EG			9	79%					
1731	26990222	PP_3510		hypothetical protein	5.0	3.19E-05	EG	6.2	13211	2	19%	Cytoplasmic				
1731	26987217	PP_0476	rpsM	30S ribosomal protein S13	5.0	3.19E-05	EG	11.3	13256	2	17%	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis		
1731	170722829	not in database			5.0	3.19E-05	EG			3	38%					

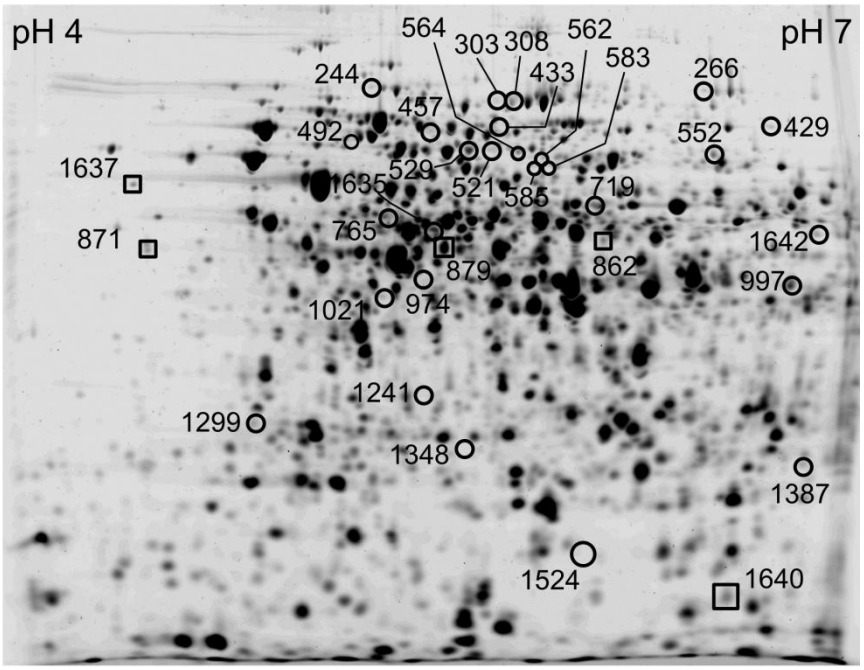


Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). Die in dieser Abbildung dargestellten Analysen wurden mit „G-Dyes“ anstelle von „Cy-Dyes“ durchgeführt. A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

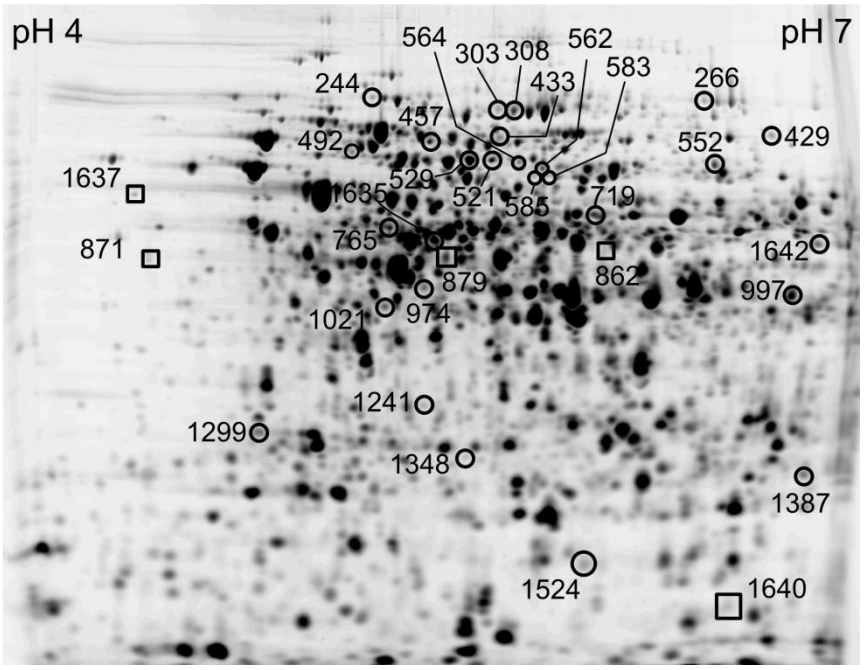
5.1.1.1 2D_DIGE_P_putida_KT2440_EG_pH_4_7_G_Dyes_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
514	26989383	PP_2664		PAS/PAC sensor hybrid histidine kinase	7,7	2,01E-02	EG	6,6	73094	9	15%	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
730	26989210	PP_2487		aldehyde dehydrogenase family protein	2,4	5,19E-06	control	5,0	54721	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
730	26989818	PP_3099		hypothetical protein	2,4	5,19E-06	control	4,9	56072	5	10%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
730	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2,4	5,19E-06	control	4,9	54767	7	13%	Cytoplasmic	COG1951	Energy production and conversion	
730	26986810	PP_0065	trkA	potassium transporter peripheral membrane component	2,4	5,19E-06	control	5,0	49812	3	6%	Cytoplasmic Membrane	COG0569	Inorganic ion transport and metabolism	
832	26990490	PP_3785		hypothetical protein	1,8	2,21E-03	control	6,5	50495	3	5%	Cytoplasmic			
1034	26990489	PP_3784		hypothetical protein	1,9	3,45E-05	control	5,4	41070	5	13%	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
1217	26987312	PP_0574		LuxR family DNA-binding response regulator	1,8	2,70E-03	EG	5,1	29040	5	20%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
1217	26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1,8	2,70E-03	EG	5,6	36424	2	6%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
1253	26987522	PP_0786	trxB	thioredoxin reductase	2,3	2,50E-04	EG	5,1	33841	5	21%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
1298	26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	2,1	7,77E-04	control	5,3	30957	3	14%	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
1298	26989708	PP_2989		short chain dehydrogenase/reductase family oxidoreductase	2,1	7,77E-04	control	5,1	28161	3	12%	Cytoplasmic	COG0300	General function prediction only	
1398	26991400	PP_4717	folP	dihydropteroate synthase	2,2	1,29E-04	EG	5,4	30274	5	19%	Cytoplasmic	COG0294	Coenzyme metabolism	
1453	26987247	PP_0508		hypothetical protein	1,9	1,96E-03	EG	5,0	20628	4	26%	Unknown			
1453	26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding protein	1,9	1,96E-03	EG	5,2	27869	5	22%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
1809	26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	2,2	2,61E-05	EG	5,3	16898	2	15%	Cytoplasmic Membrane	COG0711	Energy production and conversion	

A)



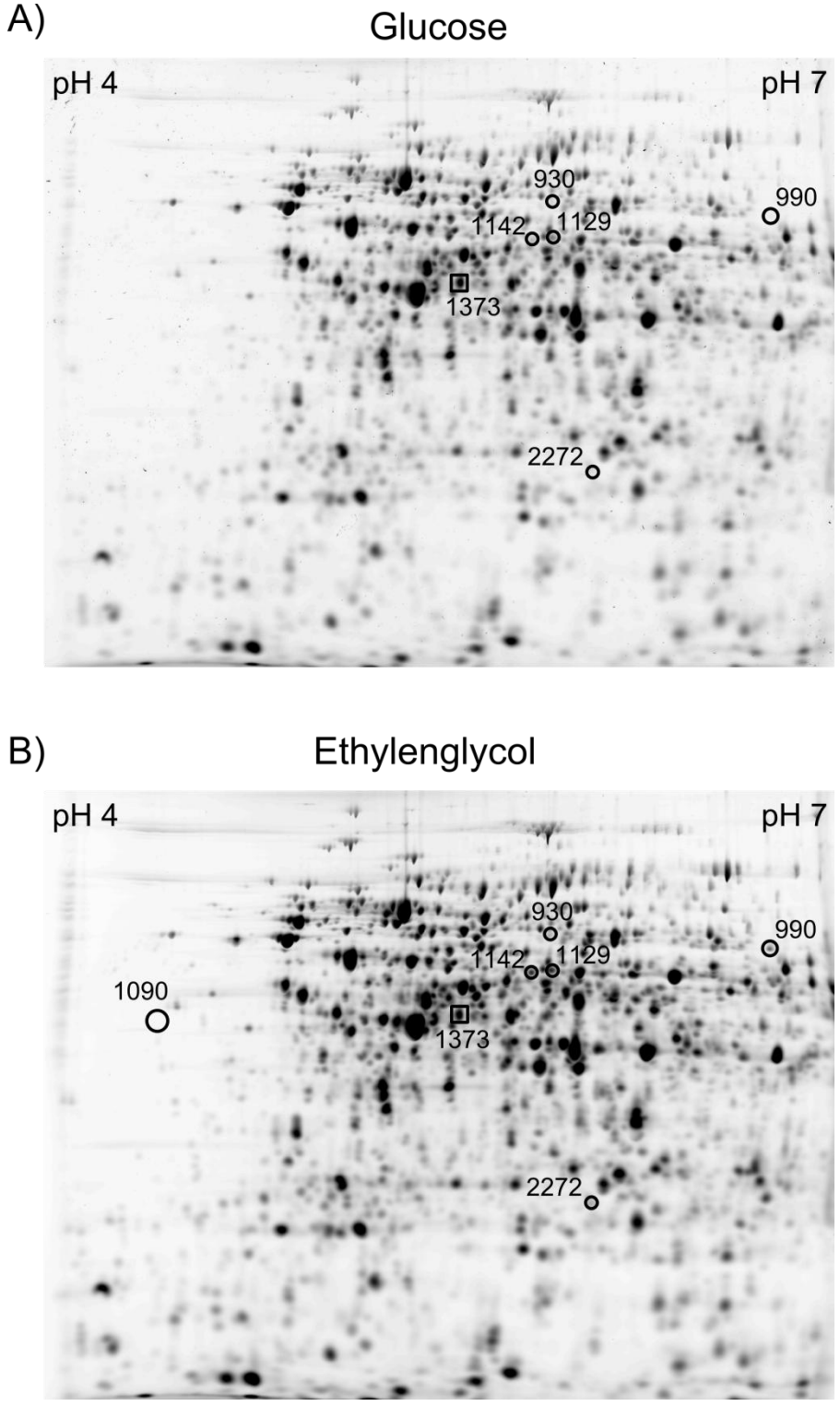
B)



Differenziell regulierte Spots zwischen mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Glyoxylsäure behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.1.1.1 2D_DIGE_P_putida_KT2440_GXS_pH_4_7_Tabelle

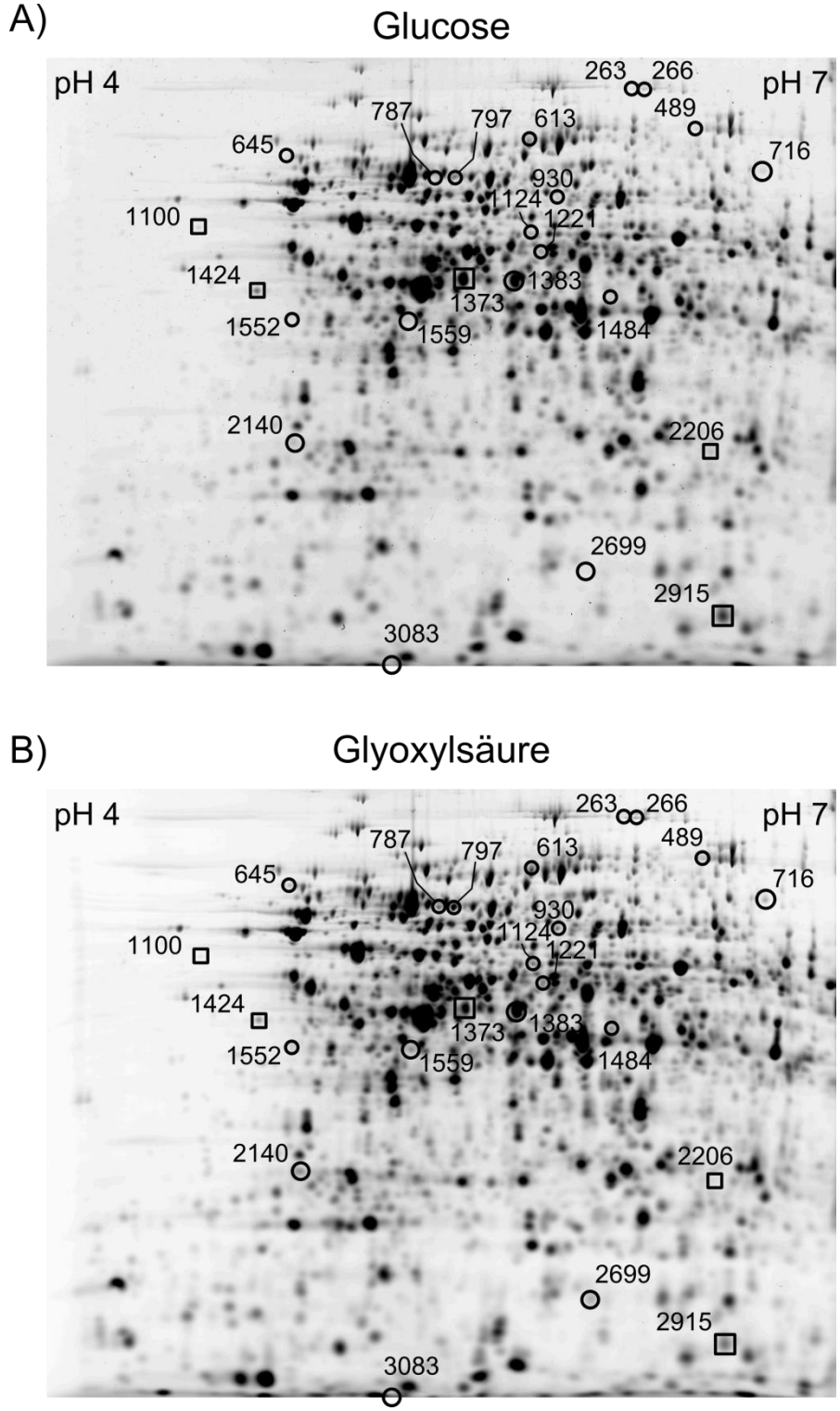
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
244	26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1,9	3,36E-04	GXS	5,0	93609	4	5%	Cytoplasmic	COG1049	Energy production and conversion	
266	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2,3	3,04E-04	GXS	6,5	106521	9	9%	Cytoplasmic	COG0567	Energy production and conversion	
303	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	2,0	5,98E-03	GXS	5,6	99332	8	8%	Cytoplasmic	COG2609	Energy production and conversion	
303	26991474	PP_4794	leuS	leucyl-tRNA synthetase	2,0	5,98E-03	GXS	5,6	96697	2	2%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
308	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1,9	2,34E-05	GXS	5,6	99332	30	31%	Cytoplasmic	COG2609	Energy production and conversion	
308	26991474	PP_4794	leuS	leucyl-tRNA synthetase	1,9	2,34E-05	GXS	5,6	96697	11	13%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
433	26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	3,5	1,06E-03	GXS	5,6	69049	5	8%	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
433	26988393	PP_1661		dehydrogenase subunit	3,5	1,06E-03	GXS	5,5	81020	4	5%	Extracellular	COG2303	Amino acid transport and metabolism	
433	26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	3,5	1,06E-03	GXS	5,9	77449	6	9%	Cytoplasmic	COG1250	Lipid metabolism	
457	26988855	PP_2131		ABC transporter ATP-binding protein	5,0	5,75E-06	GXS	5,1	71398	5	8%	Cytoplasmic	COG0488	General function prediction only	
457	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	5,0	5,75E-06	GXS	5,4	79899	11	15%	Cytoplasmic	COG2838	Energy production and conversion	
492	26988179	PP_1446		TonB-dependent receptor	2,7	2,22E-03	GXS	4,9	74207	5	8%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
492	26990871	PP_4179	htpG	heat shock protein 90	2,7	2,22E-03	GXS	5,0	71610	4	6%	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
492	26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	2,7	2,22E-03	GXS	4,8	78896	2	3%	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
521	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	5,1	1,50E-05	GXS	5,3	55654	8	21%	Cytoplasmic	COG0508	Energy production and conversion	
529	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	3,4	2,79E-04	GXS	5,3	55654	20	47%	Cytoplasmic	COG0508	Energy production and conversion	
529	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	3,4	2,79E-04	GXS	5,3	65626	3	5%	Cytoplasmic	COG5016	Energy production and conversion	
552	26991173	PP_4487	acsA	acetyl-CoA synthetase	1,8	1,24E-04	GXS	6,4	71796	8	15%	Cytoplasmic	COG0365	Lipid metabolism	
552	26991173	PP_4487	acsA	acetyl-CoA synthetase	1,8	1,24E-04	GXS	6,4	71796	11	17%	Cytoplasmic	COG0365	Lipid metabolism	
585	26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	2,0	1,19E-04	GXS	5,8	65541	2	4%	Cytoplasmic	COG1960	Lipid metabolism	
719	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1,8	5,95E-04	GXS	6,3	49912	5	10%	Cytoplasmic	COG1249	Energy production and conversion	
719	26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	1,8	5,95E-04	GXS	6,0	49353	2	5%	Cytoplasmic	COG1249	Energy production and conversion	
765	26987824	PP_1088	argG	argininosuccinate synthase	1,8	4,44E-05	GXS	5,1	45164	4	9%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
765	26991601	PP_4923		TolC family type I secretion outer membrane protein	1,8	4,44E-05	GXS	5,2	52637	8	20%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
765	26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1,8	4,44E-05	GXS	5,2	52989	3	5%	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
765	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1,8	4,44E-05	GXS	5,2	55352	16	28%	Cytoplasmic	COG0056	Energy production and conversion	
879	26991159	PP_4473		aspartate kinase	2,6	2,18E-03	control	5,0	44605	7	18%	Cytoplasmic	COG0527	Amino acid transport and metabolism	
879	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2,6	2,18E-03	control	5,4	45695	10	21%	Unknown	COG0538	Energy production and conversion	
879	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	2,6	2,18E-03	control	5,3	43264	2	4%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
974	26988458	PP_1726		ABC transporter periplasmic protein	4,6	1,13E-04	GXS	6,0	38636	3	9%	Unknown	COG1840	Inorganic ion transport and metabolism	
974	26988841	PP_2117	pdxB	erythronate-4-phosphate dehydrogenase	4,6	1,13E-04	GXS	5,1	41614	4	11%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
997	26989059	PP_2335		methylcitrate synthase	1,8	4,69E-08	GXS	6,7	41995	5	11%	Cytoplasmic	COG0372	Energy production and conversion	
997	26989059	PP_2335		methylcitrate synthase	1,8	4,69E-08	GXS	6,7	41995	6	15%	Cytoplasmic	COG0372	Energy production and conversion	
997	26988363	PP_1631		hypothetical protein	1,8	4,69E-08	GXS	6,7	42143	4	8%	Cytoplasmic	COG1611	General function prediction only	
1021	26990673	PP_3968		sensor histidine kinase	3,7	5,17E-05	GXS	5,0	40394	4	11%	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
1241	26992070	PP_5395		hypothetical protein	4,2	4,64E-04	GXS	5,6	31623	3	9%	Cytoplasmic	COG1568	General function prediction only	
1241	26990252	PP_3540	mvaB	hydroxymethylglutaryl-CoA lyase	4,2	4,64E-04	GXS	5,4	31341	3	8%	Cytoplasmic	COG0119	Amino acid transport and metabolism	
1387	26987897	PP_1162		glutathione S-transferase family protein	2,2	8,63E-06	GXS	6,8	22677	5	29%	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
1635	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2,8	8,58E-05	GXS	5,4	50393	2	4%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1635	26990810	PP_4116	aceA	isocitrate lyase	2,8	8,58E-05	GXS	5,3	48633	6	13%	Cytoplasmic	COG2224	Energy production and conversion	
1635	26990705	PP_4000	serS	seryl-tRNA synthetase	2,8	8,58E-05	GXS	5,1	46849	4	9%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
1635	26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	2,8	8,58E-05	GXS	5,1	42434	6	15%	Cytoplasmic	COG0508	Energy production and conversion	
1637	26991069	PP_4380	flgL	flagellar hook-associated protein FlgL	2,1	3,04E-03	control	4,3	54938	8	20%	Extracellular	COG1344	Cell motility and secretion	
1640	26986945	PP_0201		YbaK/prolyl-tRNA synthetase associated region	3,3	2,36E-06	control	6,8	18267	4	26%	Cytoplasmic	COG2606	Function unknown	
1642	26987334	PP_0596		beta alanine--pyruvate transaminase	2,3	2,01E-05	GXS	6,8	48529	5	12%	Cytoplasmic	COG0161	Coenzyme metabolism	



Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* GN187 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

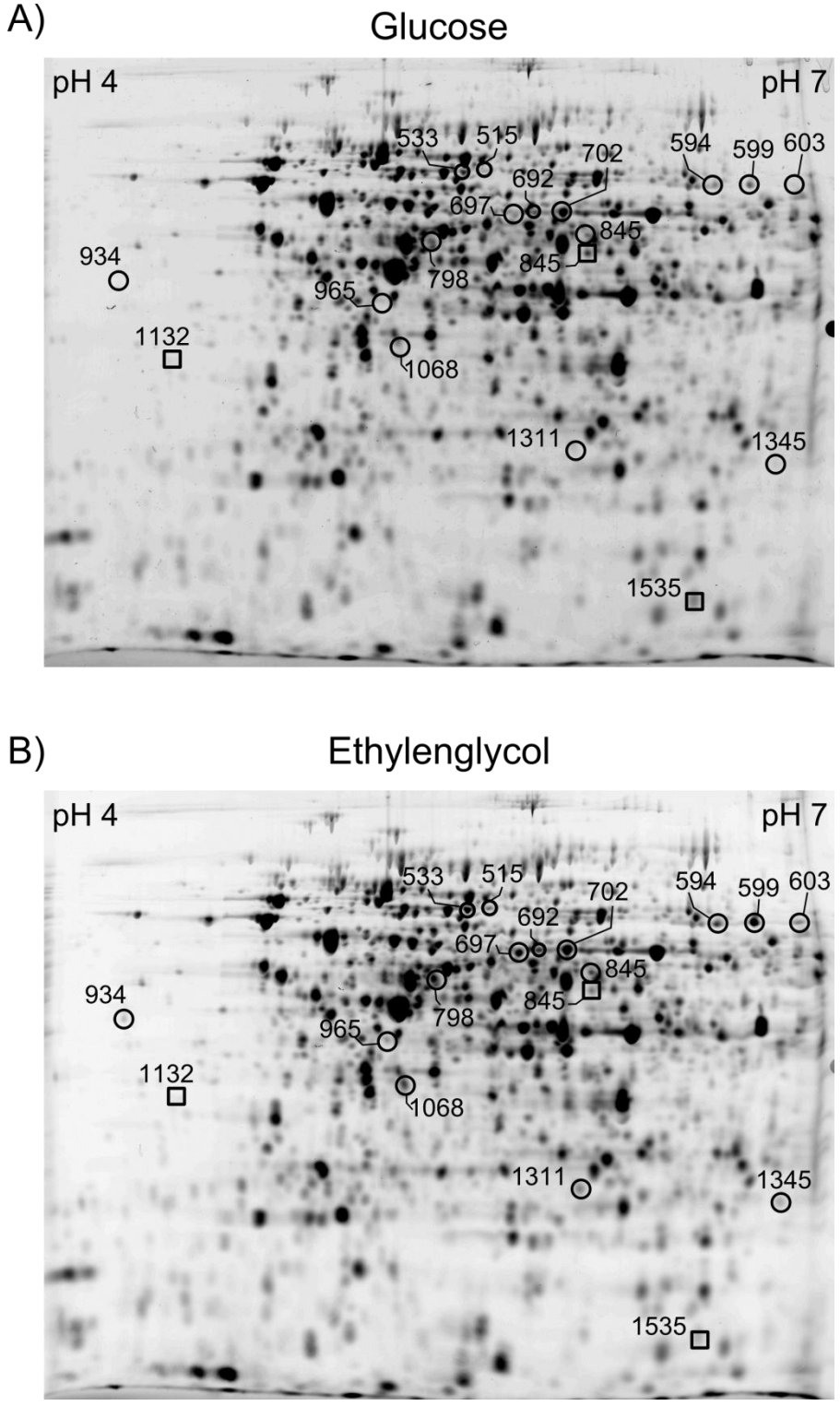
5.1.1.2 2D_DIGE_P_putida_GN187_EG_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
930	26987139	PP_0397		serine protein kinase, PrkA	1.8	7.55E-04	EG	5.8	73782	7	10%	Cytoplasmic	COG2766	Signal transduction mechanisms	
930	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.8	7.55E-04	EG	5.8	65671	5	8%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
930	26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	1.8	7.55E-04	EG	5.8	69729	2	4%	Cytoplasmic	COG4770	Lipid metabolism	
930	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.8	7.55E-04	EG	6.2	63448	3	5%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
930	26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.8	7.55E-04	EG	6.0	66312	7	15%	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
990	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	16	7.61E-04	EG	7.0	69173	11	18%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1129	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.7	8.08E-05	EG	6.0	54367	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
1129	26987283	PP_0545		aldehyde dehydrogenase family protein	1.7	8.08E-05	EG	5.9	55268	12	28%	Cytoplasmic	COG1012	Energy production and conversion	
1129	26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	1.7	8.08E-05	EG	6.0	49353	3	7%	Cytoplasmic	COG1249	Energy production and conversion	
1129	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.7	8.08E-05	EG	6.3	49912	4	9%	Cytoplasmic	COG1249	Energy production and conversion	
1129	26991765	PP_5089	argS	arginyl-tRNA synthetase	1.7	8.08E-05	EG	5.7	63668	5	8%	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
1129	26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	1.7	8.08E-05	EG	5.8	51676	2	4%	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
1129	26991954	PP_5278		aldehyde dehydrogenase family protein	1.7	8.08E-05	EG	5.5	53053	3	6%	Cytoplasmic	COG1012	Energy production and conversion	
1129	26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.7	8.08E-05	EG	5.8	62191	3	5%	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
1142	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	3.5	4.51E-05	EG	6.0	54367	3	6%	Cytoplasmic	COG1012	Energy production and conversion	
1142	26987283	PP_0545		aldehyde dehydrogenase family protein	3.5	4.51E-05	EG	5.9	55268	3	7%	Cytoplasmic	COG1012	Energy production and conversion	
1142	26989399	PP_2680		aldehyde dehydrogenase family protein	3.5	4.51E-05	EG	5.5	54903	4	17%	Cytoplasmic	COG1012	Energy production and conversion	
1142	26991954	PP_5278		aldehyde dehydrogenase family protein	3.5	4.51E-05	EG	5.5	53053	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
1373	26988847	PP_2123	moeA	molybdopterin biosynthesis MoeA protein	1.7	4.15E-03	control	5.1	43963	3	9%	Cytoplasmic	COG0303	Coenzyme metabolism	
1373	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.7	4.15E-03	control	5.2	55352	3	7%	Cytoplasmic	COG0056	Energy production and conversion	
1373	26987283	PP_0545		aldehyde dehydrogenase family protein	1.7	4.15E-03	control	5.9	55268	2	6%	Cytoplasmic	COG1012	Energy production and conversion	
1373	26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.7	4.15E-03	control	5.1	47738	5	15%	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
1373	26989061	PP_2337		hypothetical protein	1.7	4.15E-03	control	5.2	41312	4	11%	Cytoplasmic	COG2828	Function unknown	
1373	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.7	4.15E-03	control	5.4	45695	16	32%	Unknown	COG0538	Energy production and conversion	
1373	26988320	PP_1588		succinyldiaminopimelate transaminase	1.7	4.15E-03	control	5.4	43759	2	5%	Cytoplasmic	COG0436	Amino acid transport and metabolism	
1373	26988361	PP_1629	recA	recombinase A	1.7	4.15E-03	control	5.3	37545	3	10%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1373	2698719	not in database			1.7	4.15E-03	control			3	8%				
1373	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.7	4.15E-03	control	5.3	43264	2	5%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1373	26991159	PP_4473		aspartate kinase	1.7	4.15E-03	control	5.0	44605	11	28%	Cytoplasmic	COG0527	Amino acid transport and metabolism	
1373	26988095	PP_1361	groEL	chaperonin GroEL	1.7	4.15E-03	control	4.7	56743	4	8%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
2272	26988599	PP_1869		hypothetical protein	2.8	5.06E-04	EG	5.9	28590	2	8%	Unknown	COG3384	Amino acid transport and metabolism	
2272	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	2.8	5.06E-04	EG	6.0	26030	10	47%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
2272	26988239	PP_1507		hypothetical protein	2.8	5.06E-04	EG	6.0	23544	4	21%	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones	
2272	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.8	5.06E-04	EG	5.4	45695	7	17%	Unknown	COG0538	Energy production and conversion	
2272	26989384	PP_2665	agmR	LuxR family two component transcriptional regulator	2.8	5.06E-04	EG	5.9	24536	5	23%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription



Differenziell regulierte Spots zwischen mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* GN187 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Glyoxylsäure behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

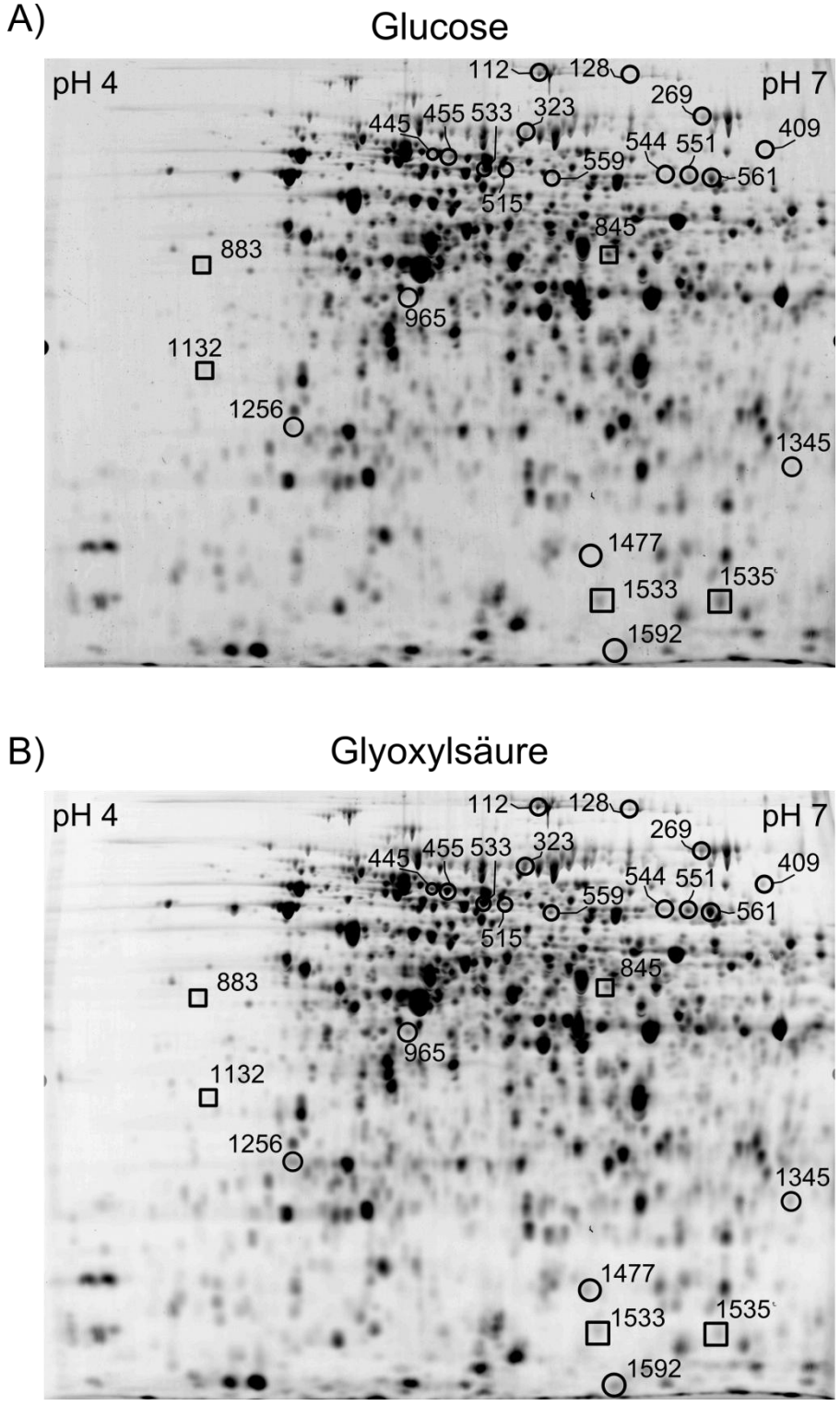
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
266	26991752	PP_5076	gltB	glutamate synthase subunit alpha	2.5	1.20E-05	GXS	6.2	161772	36	27%	Cytoplasmic	COG0069	Amino acid transport and metabolism	
266	26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	2.5	1.20E-05	GXS	6.3	142580	6	6%	Cytoplasmic	COG4230	Energy production and conversion	
263	26991752	PP_5076	gltB	glutamate synthase subunit alpha	2.9	1.15E-04	GXS	6.2	161772	18	13%	Cytoplasmic	COG0069	Amino acid transport and metabolism	
263	26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	2.9	1.15E-04	GXS	5.5	150992	3	2%	Cytoplasmic	COG0085	Transcription	
489	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.5	1.36E-04	GXS	6.5	106521	18	18%	Cytoplasmic	COG0567	Energy production and conversion	
613	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.8	3.49E-05	GXS	5.6	99332	27	26%	Cytoplasmic	COG2609	Energy production and conversion	
613	26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	1.8	3.49E-05	GXS	5.6	84730	3	4%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
613	26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.8	3.49E-05	GXS	5.6	96697	17	19%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
613	26989060	PP_2336		aconitate hydratase	1.8	3.49E-05	GXS	5.3	93961	2	2%	Cytoplasmic	COG1048	Energy production and conversion	
645	26987416	PP_0680		ATP-dependent protease	2.6	2.49E-03	GXS	4.5	89677	6	8%	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
716	26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	2.0	2.70E-05	GXS	6.8	55000	5	9%	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
716	26988451	PP_1719	prc	carboxyl-terminal protease	2.0	2.70E-05	GXS	7.1	79096	7	10%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
716	26987941	PP_1206	oprD	outer membrane porin	2.0	2.70E-05	GXS	4.6	46120	6	13%	Outer Membrane			
787	26990806	PP_4111	fusA	elongation factor G	3.1	7.19E-05	GXS	5.0	77832	4	6%	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
787	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	3.1	7.19E-05	GXS	5.4	79899	17	23%	Cytoplasmic	COG2838	Energy production and conversion	
787	26991199	PP_4514		patatin	3.1	7.19E-05	GXS	6.1	83173	3	4%	Outer Membrane	COG1752	General function prediction only	
787	26991643	PP_4965	tktA	transketolase	3.1	7.19E-05	GXS	5.0	72463	4	6%	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
787	26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	3.1	7.19E-05	GXS	5.5	89725	7	9%	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
797	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	3.2	5.82E-05	GXS	5.4	79899	25	35%	Cytoplasmic	COG2838	Energy production and conversion	
797	26988855	PP_2131		ABC transporter ATP-binding protein	3.2	5.82E-05	GXS	5.1	71398	7	12%	Cytoplasmic	COG0488	General function prediction only	
930	26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	4.0	2.15E-05	GXS	6.0	66312	6	11%	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
930	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	4.0	2.15E-05	GXS	6.2	63448	5	9%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
930	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	4.0	2.15E-05	GXS	5.8	65671	4	6%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
930	26987139	PP_0397		serine protein kinase, PrkA	4.0	2.15E-05	GXS	5.8	73782	2	3%	Cytoplasmic	COG2766	Signal transduction mechanisms	
1100	26991069	PP_4380	flgL	flagellar hook-associated protein FlgL	3.4	6.19E-05	control	4.3	54938	7	18%	Extracellular	COG1344	Cell motility and secretion	
1124	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.8	4.30E-04	GXS	6.0	54367	11	25%	Cytoplasmic	COG1012	Energy production and conversion	
1124	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.8	4.30E-04	GXS	6.3	49912	3	6%	Cytoplasmic	COG1249	Energy production and conversion	
1124	26987283	PP_0545		aldehyde dehydrogenase family protein	1.8	4.30E-04	GXS	5.9	55268	4	9%	Cytoplasmic	COG1012	Energy production and conversion	
1124	26991954	PP_5278		aldehyde dehydrogenase family protein	1.8	4.30E-04	GXS	5.5	53053	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
1124	26990290	PP_3578		phosphoglucomutase	1.8	4.30E-04	GXS	5.6	58620	4	10%	Unknown	COG0033	Carbohydrate transport and metabolism	
1124	26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.8	4.30E-04	GXS	5.3	53602	3	6%	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
1221	26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.9	1.78E-04	GXS	5.6	56483	4	8%	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
1221	26988046	PP_1311		tryptophanyl-tRNA synthetase	1.9	1.78E-04	GXS	5.4	49297	2	5%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
1221	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.9	1.78E-04	GXS	5.2	55352	3	6%	Cytoplasmic	COG0056	Energy production and conversion	
1221	26991863	PP_5187		adenylate cyclase	1.9	1.78E-04	GXS	5.6	52133	3	7%	Cytoplasmic	COG3025	Function unknown	
1221	26991090	PP_4401	bkdA1	3-methyl-2-oxobutanoate dehydrogenase	1.9	1.78E-04	GXS	6.0	45220	4	9%	Cytoplasmic	COG1071	Energy production and conversion	
1221	26987737	PP_1001	arcA	arginine deiminase	1.9	1.78E-04	GXS	5.7	46462	2	5%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1373	26989061	PP_2337		hypothetical protein	2.7	2.22E-03	control	5.2	41312	6	18%	Cytoplasmic	COG2828	Function unknown	
1373	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.7	2.22E-03	control	5.2	55352	6	13%	Cytoplasmic	COG0056	Energy production and conversion	
1373	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.7	2.22E-03	control	5.4	45695	17	36%	Unknown	COG0538	Energy production and conversion	
1373	26991159	PP_4473		aspartate kinase	2.7	2.22E-03	control	5.0	44605	8	21%	Cytoplasmic	COG0527	Amino acid transport and metabolism	
1383	26988361	PP_1629	recA	recombinase A	1.8	2.57E-04	GXS	5.3	37545	3	8%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1383	26989061	PP_2337		hypothetical protein	1.8	2.57E-04	GXS	5.2	41312	2	6%	Cytoplasmic	COG2828	Function unknown	
1383	26987515	PP_0779		methyl-accepting chemotaxis transducer/sensory box protein	1.8	2.57E-04	GXS	6.2	49856	4	9%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1383	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.8	2.57E-04	GXS	5.7	45178	3	8%	Cytoplasmic	COG0001	Coenzyme metabolism	
1383	26988462	PP_1730		aminopeptidase 2	1.8	2.57E-04	GXS	5.6	46996	4	8%	Cytoplasmic	COG1362	Amino acid transport and metabolism	
1383	26987468	PP_0732	hemA	glutamyl-tRNA reductase	1.8	2.57E-04	GXS	5.5	46305	3	7%	Cytoplasmic	COG0373	Coenzyme metabolism	
1383	26990737	PP_4034		allantoate amidohydrolase	1.8	2.57E-04	GXS	5.7	45010	2	5%	Cytoplasmic	COG0624	Amino acid transport and metabolism	
1383	26991676	PP_4999	pyrC	dihydroorotase	1.8	2.57E-04	GXS	5.4	44116	3	8%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
1383	26987351	PP_0614		allantoate amidohydrolase	1.8	2.57E-04	GXS	5.6	45279	3	7%	Cytoplasmic	COG0624	Amino acid transport and metabolism	
1383	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.8	2.57E-04	GXS	5.4	45695	18	35%	Unknown	COG0538	Energy production and conversion	
1383	26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.8	2.57E-04	GXS	5.6	56483	3	6%	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
1383	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.8	2.57E-04	GXS	5.3	43264	5	14%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1424	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.8	8.26E-03	control	5.4	45695	2	6%	Unknown	COG0538	Energy production and conversion	
1424	26987941	PP_1206	oprD	outer membrane porin	1.8	8.26E-03	control	4.6	46120	8	18%	Outer Membrane			
1484	26987578	PP_0842	iscS	cysteine desulfurase	2.4	4.84E-05	GXS	6.2	44468	4	10%	Cytoplasmic	COG1104	Amino acid transport and metabolism	
1484	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	2.4	4.84E-05	GXS	6.0	41851	7	17%	Cytoplasmic	COG0183	Lipid metabolism	
1484	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	2.4	4.84E-05	GXS	6.3	44339	6	16%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1484	26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	2.4	4.84E-05	GXS	6.1	44824	3	8%	Cytoplasmic	COG0160	Amino acid transport and metabolism	
1484	26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	2.4	4.84E-05	GXS	6.1	41239	4	10%	Cytoplasmic	COG0045	Energy production and conversion	
1552	26991616	PP_4938		glycosyl transferase	2.0	2.43E-03	GXS	9.4	41783	3	8%	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
1559	26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	2.9	1.31E-05	GXS	5.0	35225	2	6%	Cytoplasmic	COG0113	Coenzyme metabolism	
1559	26991362	PP_4678	ilvC	ketol-acid reductoisomerase	2.9	1.31E-05	GXS	5.4	36370	5	19%	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
1559	26990218	PP_3506		magnesium chelatase	2.9	1.31E-05	GXS	5.0	36032	3	8%	Cytoplasmic	COG1239	Coenzyme metabolism	
1559	26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	2.9	1.31E-05	GXS	5.2	38702	2	6%	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
1559	26991641	PP_4963	pgk	phosphoglycerate kinase	2.9	1.31E-05	GXS	4.9	40005	2	6%	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
1559	26990673	PP_3968		sensor histidine kinase	2.9	1.31E-05	GXS	5.0	40394	5	16%	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
1559	26988499	PP_1768	serC	phosphoserine aminotransferase	2.9	1.31E-05	GXS	5.1	39911	2	5%	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
2140	26991006	PP_4315		PhzF family phenazine biosynthesis protein	2.0	2.49E-05	GXS	4.5	28437	3	13%	Cytoplasmic	COG0384	General function prediction only	
2140	26989972	PP_3254		nucleosidase	2.0	2.49E-05	GXS	4.9	23368	4	19%	Unknown	COG0775	Nucleotide transport and metabolism	
2140	26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding protein	2.0	2.49E-05	GXS	5.2	27869	2	7%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
2140	26987505	PP_0769		histidine kinase	2.0	2.49E-05	GXS	4.6	25229	3	13%	Cytoplasmic	COG0642	Signal transduction mechanisms	
2140	26989214	PP_2491		ThiJ/Pfpl family protein	2.0	2.49E-05	GXS	4.6	23692	3	19%	Unknown	COG0693	General function prediction only	
2206	26987748	PP_1012	gltR-2	winged helix family two component transcriptional regulator	2.6	4.45E-06	control	6.4	27124	4	17%	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
2206	26987918	PP_1183		4'-phosphopantetheinyl transferase	2.6	4.45E-06	control	6.4	25717	3	13%	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism	



Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* GN259 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.1.1.3 2D_DIGE_P_putida_GN259_EG_pH_4_7_Tabelle

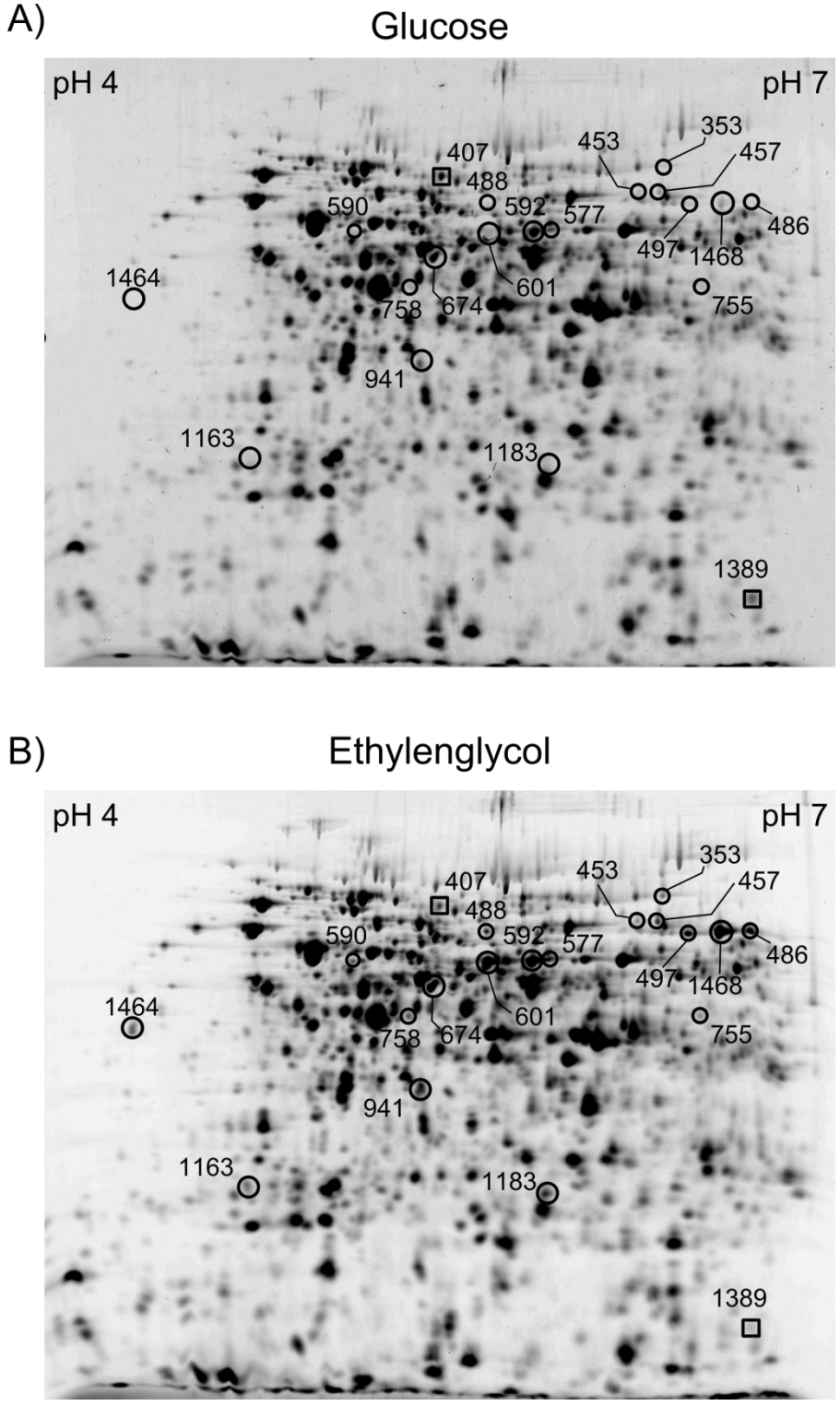
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
515	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.4	2.81E-05	EG	5.3	55654	18	44%	Cytoplasmic	COG0508	Energy production and conversion	
515	26987833	PP_1097	metG	methionyl-tRNA synthetase	2.4	2.81E-05	EG	5.5	75186	5	7%	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
515	26988164	PP_1431	lepA	GTP-binding protein LepA	2.4	2.81E-05	EG	5.5	66116	5	9%	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
515	26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	2.4	2.81E-05	EG	5.8	69729	2	3%	Cytoplasmic	COG4770	Lipid metabolism	
533	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.5	1.38E-04	EG	5.4	79899	5	8%	Cytoplasmic	COG2838	Energy production and conversion	
533	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.5	1.38E-04	EG	5.3	55654	18	39%	Cytoplasmic	COG0508	Energy production and conversion	
533	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.5	1.38E-04	EG	5.3	65626	2	3%	Cytoplasmic	COG5016	Energy production and conversion	
533	26987833	PP_1097	metG	methionyl-tRNA synthetase	2.5	1.38E-04	EG	5.5	75186	2	3%	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
594	26990840	PP_4147		peptide ABC transporter periplamic peptide-binding protein	2.7	6.06E-05	EG	7.2	69637	12	19%	Periplasmic	COG4166	Amino acid transport and metabolism	
594	26989611	PP_2892		surface antigen (D15)	2.7	6.06E-05	EG	7.0	64471	3	4%	Outer Membrane	COG0729	Cell envelope biogenesis, outer membrane	
594	26987746	PP_1010	edd	phosphogluconate dehydratase	2.7	6.06E-05	EG	6.4	65359	6	11%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
594	26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	2.7	6.06E-05	EG	6.5	67609	4	6%	Cytoplasmic	COG0649	Energy production and conversion	
594	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.7	6.06E-05	EG	7.0	69173	9	15%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
599	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	8.2	9.97E-06	EG	5.3	55654	2	3%	Cytoplasmic	COG0508	Energy production and conversion	
599	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	8.2	9.97E-06	EG	7.0	69173	22	34%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
603	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	4.1	6.62E-04	EG	7.0	69173	4	7%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
692	26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	2.0	2.22E-06	EG	6.0	49353	3	7%	Cytoplasmic	COG1249	Energy production and conversion	
692	26987283	PP_0545		aldehyde dehydrogenase family protein	2.0	2.22E-06	EG	5.9	55268	12	31%	Cytoplasmic	COG1012	Energy production and conversion	
692	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	2.0	2.22E-06	EG	6.0	54367	2	6%	Cytoplasmic	COG1012	Energy production and conversion	
692	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	2.0	2.22E-06	EG	6.3	49912	3	6%	Cytoplasmic	COG1249	Energy production and conversion	
697	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	5.5	1.04E-05	EG	6.0	54367	8	18%	Cytoplasmic	COG1012	Energy production and conversion	
697	26987283	PP_0545		aldehyde dehydrogenase family protein	5.5	1.04E-05	EG	5.9	55268	7	14%	Cytoplasmic	COG1012	Energy production and conversion	
697	26989399	PP_2680		aldehyde dehydrogenase family protein	5.5	1.04E-05	EG	5.5	54903	4	19%	Cytoplasmic	COG1012	Energy production and conversion	
702	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.8	3.30E-04	EG	6.0	54367	8	17%	Cytoplasmic	COG1012	Energy production and conversion	
702	26987283	PP_0545		aldehyde dehydrogenase family protein	1.8	3.30E-04	EG	5.9	55268	26	64%	Cytoplasmic	COG1012	Energy production and conversion	
702	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.8	3.30E-04	EG	6.3	49912	7	14%	Cytoplasmic	COG1249	Energy production and conversion	
702	26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	1.8	3.30E-04	EG	5.8	51676	4	9%	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
787	26991399	PP_4716	glmM	phosphoglucosamine mutase	2.0	2.50E-05	EG	6.0	47744	2	4%	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
787	26990721	PP_4016	purB	adenylosuccinate lyase	2.0	2.50E-05	EG	5.9	50555	2	5%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
787	313498081	not in database			2.0	2.50E-05	EG			13	38%				
787	26991090	PP_4401	bkdA1	3-methyl-2-oxobutanoate dehydrogenase	2.0	2.50E-05	EG	6.0	45220	2	4%	Cytoplasmic	COG1071	Energy production and conversion	
787	26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	2.0	2.50E-05	EG	6.2	51518	3	7%	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
798	26987824	PP_1088	argG	argininosuccinate synthase	1.9	5.44E-04	EG	5.1	45164	4	12%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
798	26991065	PP_4376	fliD	flagellar cap protein FliD	1.9	5.44E-04	EG	5.2	46522	2	5%	Extracellular	COG1345	Cell motility and secretion	
798	26988046	PP_1311		tryptophanyl-tRNA synthetase	1.9	5.44E-04	EG	5.4	49297	4	10%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
798	26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.9	5.44E-04	EG	5.1	42434	13	31%	Cytoplasmic	COG0508	Energy production and conversion	
798	26990705	PP_4000	serS	seryl-tRNA synthetase	1.9	5.44E-04	EG	5.1	46849	11	28%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
798	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.9	5.44E-04	EG	5.4	50393	2	5%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
845	26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.9	3.65E-06	glucose	6.2	44897	5	10%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
845	26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	1.9	3.65E-06	glucose	5.9	48114	9	20%	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
934	26989381	PP_2662		hypothetical protein	15.0	3.15E-05	EG	4.3	42858	2	8%	Outer Membrane			
965	260549051	not in database			2.8	1.41E-05	EG			2	7%				
965	26990673	PP_3968		sensor histidine kinase	2.8	1.41E-05	EG	5	40394	3	9%	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
1068	26988324	PP_1592	tsf	elongation factor Ts	4.0	3.82E-06	EG	4.9	30432	3	9%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
1068	26989631	PP_2912		hypothetical protein	4.0	3.82E-06	EG	5.0	33023	2	6%	Cytoplasmic	COG1718	Signal transduction mechanisms	Cell division and chromosome partitioning
1068	26987522	PP_0786	trxB	thioredoxin reductase	4.0	3.82E-06	EG	5.1	33841	7	33%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
1068	26989388	PP_2669		YVTN family beta-propeller repeat-containing protein	4.0	3.82E-06	EG	6.2	36051	3	10%	Unknown	COG3391	Function unknown	
1132	148547850	not in database			2.2	2.05E-05	glucose			2	19%				
1535	26986945	PP_0201		YbaK/prolyl-tRNA synthetase associated region	2.2	1.19E-04	EG	6.8	18267	7	44%	Cytoplasmic	COG2606	Function unknown	



Differenziell regulierte Spots zwischen mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* GN259 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Glyoxylsäure behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.1.1.3 2D_DIGE_P_putida_GN259_GXS_pH_4_7_Tabelle

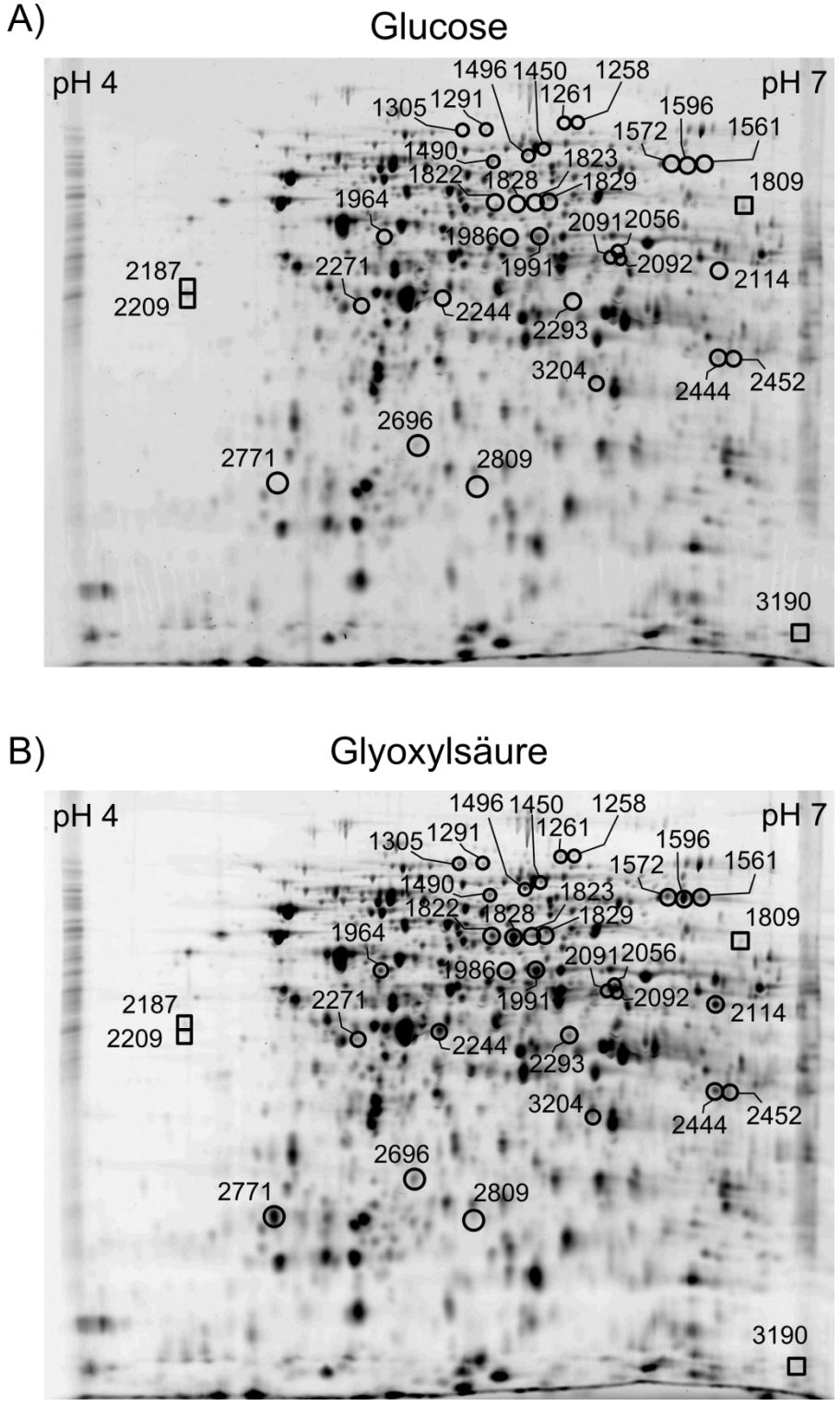
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
269	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.0	8.82E-04	GXS	6.5	106521	14	14%	Cytoplasmic	COG0567	Energy production and conversion	
323	26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.8	8.93E-03	GXS	5.6	96697	2	3%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
323	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.8	8.93E-03	GXS	5.6	99332	12	13%	Cytoplasmic	COG2609	Energy production and conversion	
409	26988451	PP_1719	prc	carboxyl-terminal protease	1.9	3.24E-04	GXS	7.1	79096	2	4%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
409	26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.9	3.24E-04	GXS	6.8	55000	3	5%	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
445	26991199	PP_4514		patatin	2.2	3.95E-02	GXS	6.1	83173	2	3%	Outer Membrane	COG1752	General function prediction only	
445	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.2	3.95E-02	GXS	5.4	79899	12	15%	Cytoplasmic	COG2838	Energy production and conversion	
455	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.4	1.29E-02	GXS	5.4	79899	20	25%	Cytoplasmic	COG2838	Energy production and conversion	
515	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.8	3.00E-02	GXS	5.3	55654	18	44%	Cytoplasmic	COG0508	Energy production and conversion	
515	26987833	PP_1097	metG	methionyl-tRNA synthetase	1.8	3.00E-02	GXS	5.5	75186	5	7%	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
515	26988164	PP_1431	lepA	GTP-binding protein LepA	1.8	3.00E-02	GXS	5.5	66116	5	9%	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
515	26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	1.8	3.00E-02	GXS	5.8	69729	2	3%	Cytoplasmic	COG4770	Lipid metabolism	
533	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.8	1.54E-02	GXS	5.3	55654	18	39%	Cytoplasmic	COG0508	Energy production and conversion	
533	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.8	1.54E-02	GXS	5.3	65626	2	3%	Cytoplasmic	COG5016	Energy production and conversion	
533	26987833	PP_1097	metG	methionyl-tRNA synthetase	1.8	1.54E-02	GXS	5.5	75186	2	3%	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
533	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.8	1.54E-02	GXS	5.4	79899	5	8%	Cytoplasmic	COG2838	Energy production and conversion	
544	26991173	PP_4487	acsA	acetyl-CoA synthetase	1.8	4.77E-03	GXS	6.4	71796	4	4%	Cytoplasmic	COG0365	Lipid metabolism	
561	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.2	6.81E-05	GXS	6.4	71796	20	39%	Cytoplasmic	COG0365	Lipid metabolism	
845	26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.0	1.24E-04	control	6.2	44897	5	10%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
845	26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	2.0	1.24E-04	control	5.9	48114	9	20%	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
965	262374212	not in database			1.9	2.89E-02	GXS			2	7%				
965	26990673	PP_3968		sensor histidine kinase	1.9	2.89E-02	GXS	5.0	40394	3	9%	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
1256	26989214	PP_2491		ThiJ/PfpI family protein	1.9	2.81E-04	GXS	4.6	23692	2	10%	Unknown	COG0693	General function prediction only	
551	148547850	not in database			1.8	8.26E-05	GXS			6	59%				
551	26987746	PP_1010	edd	phosphogluconate dehydratase	1.8	8.26E-05	GXS	6.4	65359	13	29%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
551	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.8	8.26E-05	GXS	6.2	63448	4	7%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
559	26987139	PP_0397		serine protein kinase, PrkA	3.1	3.89E-03	GXS	5.8	73782	5	7%	Cytoplasmic	COG2766	Signal transduction mechanisms	
559	26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	3.1	3.89E-03	GXS	6.0	66312	3	5%	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
559	148547850	not in database			3.1	3.89E-03	GXS			3	31%				
559	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	3.1	3.89E-03	GXS	5.8	65671	2	3%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
883	148547850	not in database			2.1	1.65E-03	control			2	29%				
883	26991077	PP_4388	flgE	flagellar hook protein FlgE	2.1	1.65E-03	control	4.3	45796	5	17%	Extracellular	COG1749	Cell motility and secretion	
1132	148547850	not in database			3.3	7.79E-04	control			2	19%				
1477	26987513	PP_0777		glutathione peroxidase	3.9	9.65E-03	GXS	5.8	17443	4	36%	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
1533	26987274	PP_0536		hypothetical protein	2.0	2.90E-05	control	6.0	18271	5	35%	Cytoplasmic			
1535	26986945	PP_0201		YbaK/prolyl-tRNA synthetase associated region	3.7	8.06E-06	control	6.8	18267	7	44%	Cytoplasmic	COG2606	Function unknown	



Differenziell regulierte Spots zwischen mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* JM37 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Ethylenglycol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.1.1.4 2D_DIGE_P_putida_JM37_EG_pH_4_7_Tabelle

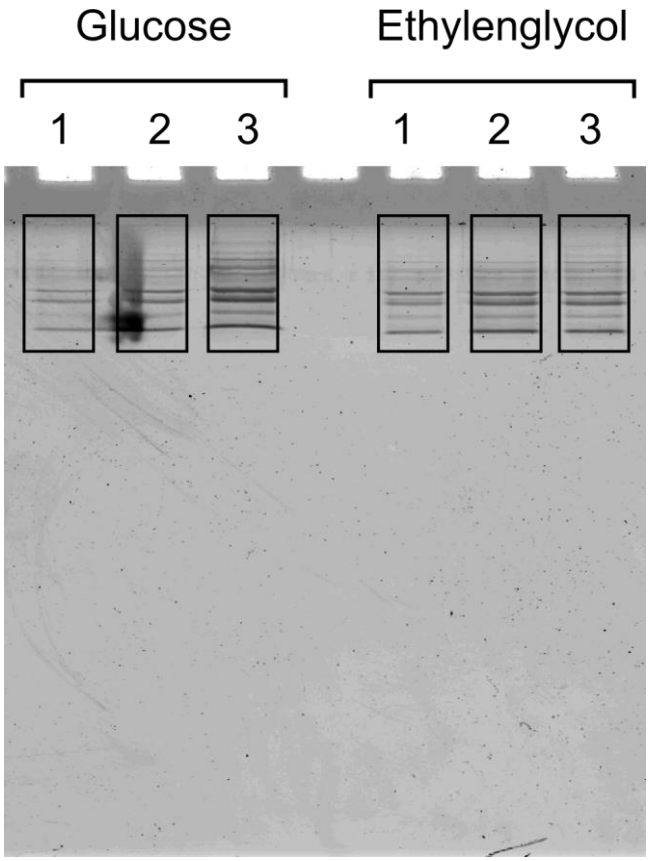
Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
353	170721483	PputW619_2302		malate synthase G	3.7	1.34E-04	EG	6.5	79656	16	21%	Cytoplasmic	COG2225	Energy production and conversion	
353	148549206	Pput_4000		carboxyl-terminal protease	3.7	1.34E-04	EG	7.1	79008	16	23%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
353	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.7	1.34E-04	EG	6.4	71796	3	6%	Cytoplasmic	COG0365	Lipid metabolism	
407	148547026	Pput_1791		4-alpha-glucanotransferase	2.0	6.12E-05	control	5.3	76445	8	10%	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
407	26987981	PP_1246		hypothetical protein	2.0	6.12E-05	control	6.0	65952	2	3%	Unknown	COG5373	Function unknown	
407	26988855	PP_2131		ABC transporter ATP-binding protein	2.0	6.12E-05	control	5.1	71398	3	5%	Cytoplasmic	COG0488	General function prediction only	
407	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.0	6.12E-05	control	5.3	55654	2	3%	Cytoplasmic	COG0508	Energy production and conversion	
407	26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	2.0	6.12E-05	control	5.6	69049	8	13%	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
407	26991720	PP_5044		GTP-binding protein TypA	2.0	6.12E-05	control	5.3	67157	9	13%	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
407	262273672	not in database			2.0	6.12E-05	control			2	3%				
407	148547056	Pput_1821		isocitrate dehydrogenase, NADP-dependent	2.0	6.12E-05	control	6.0	82873	26	39%	Cytoplasmic	COG2838	Energy production and conversion	
453	83594668	not in database			2.4	5.69E-06	EG			9	21%				
453	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.4	5.69E-06	EG	6.4	71796	6	12%	Cytoplasmic	COG0365	Lipid metabolism	
457	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.3	2.62E-05	EG	6.4	71796	19	42%	Cytoplasmic	COG0365	Lipid metabolism	
457	148547056	Pput_1821		isocitrate dehydrogenase, NADP-dependent	3.3	2.62E-05	EG	6.0	82873	4	6%	Cytoplasmic	COG2838	Energy production and conversion	
457	26991574	PP_4896	mutL	DNA mismatch repair protein	3.3	2.62E-05	EG	6.7	69745	6	9%	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
486	148550152	Pput_4950		sporulation domain-containing protein	10.0	4.45E-04	EG	6.8	55866	2	5%	Cytoplasmic	COG3267	Intracellular trafficking and secretion	
486	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	10.0	4.45E-04	EG	7.0	69173	9	14%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
486	26989797	PP_3078		ABC transporter periplasmic protein	10.0	4.45E-04	EG	7.9	72190	4	6%	Periplasmic	COG4166	Amino acid transport and metabolism	
488	146307246	not in database			9.6	4.41E-06	EG			3	4%				
488	170721493	PputW619_2312		glyoxylate carboligase	9.6	4.41E-06	EG	5.6	64347	8	15%	Cytoplasmic	COG3960	General function prediction only	
497	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.0	2.03E-05	EG	7.0	69173	8	13%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
497	26987746	PP_1010	edd	phosphogluconate dehydratase	6.0	2.03E-05	EG	6.4	65359	5	10%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
577	167034753	not in database			1.8	3.38E-05	EG			7	17%				
577	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.8	3.38E-05	EG	6.0	54367	8	19%	Cytoplasmic	COG1012	Energy production and conversion	
577	26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	1.8	3.38E-05	EG	6.0	49353	7	18%	Cytoplasmic	COG1249	Energy production and conversion	
577	26987283	PP_0545		aldehyde dehydrogenase family protein	1.8	3.38E-05	EG	5.9	55268	6	23%	Cytoplasmic	COG1012	Energy production and conversion	
577	26989399	PP_2680		aldehyde dehydrogenase family protein	1.8	3.38E-05	EG	5.5	54903	6	16%	Cytoplasmic	COG1012	Energy production and conversion	
577	26991708	PP_5032	hutH	histidine ammonia-lyase	1.8	3.38E-05	EG	5.9	53747	4	8%	Cytoplasmic	COG2986	Amino acid transport and metabolism	
577	152981056	not in database			1.8	3.38E-05	EG			2	5%				
590	167034753	not in database			2.9	7.69E-05	EG			3	6%				
590	26989818	PP_3099		hypothetical protein	2.9	7.69E-05	EG	4.9	56072	9	18%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
590	170721487	PputW619_2306		glycolate oxidase subunit GlcD	2.9	7.69E-05	EG	4.9	53720	16	26%	Cytoplasmic	COG0277	Energy production and conversion	
590	26987283	PP_0545		aldehyde dehydrogenase family protein	2.9	7.69E-05	EG	5.9	55268	2	7%	Cytoplasmic	COG1012	Energy production and conversion	
590	26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	2.9	7.69E-05	EG	4.8	86015	2	3%	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
590	26989399	PP_2680		aldehyde dehydrogenase family protein	2.9	7.69E-05	EG	5.5	54903	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
590	26987965	PP_1230		hypothetical protein	2.9	7.69E-05	EG	5.1	53328	3	5%	Cytoplasmic Membrane	COG5339	Function unknown	
590	26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	2.9	7.69E-05	EG	4.8	48526	6	14%	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
590	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2.9	7.69E-05	EG	4.9	54767	6	11%	Cytoplasmic	COG1951	Energy production and conversion	
592	26987737	PP_1001	arcA	arginine deiminase	2.0	1.31E-05	EG	5.7	46462	2	5%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
592	167034753	not in database			2.0	1.31E-05	EG			5	11%				
592	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	2.0	1.31E-05	EG	6.0	54367	9	21%	Cytoplasmic	COG1012	Energy production and conversion	
592	26987283	PP_0545		aldehyde dehydrogenase family protein	2.0	1.31E-05	EG	5.9	55268	10	32%	Cytoplasmic	COG1012	Energy production and conversion	
592	26989399	PP_2680		aldehyde dehydrogenase family protein	2.0	1.31E-05	EG	5.5	54903	7	15%	Cytoplasmic	COG1012	Energy production and conversion	
592	26991954	PP_5278		aldehyde dehydrogenase family protein	2.0	1.31E-05	EG	5.5	53053	2	6%	Cytoplasmic	COG1012	Energy production and conversion	
592	26987680	PP_0944	fumC	fumarate hydratase	2.0	1.31E-05	EG	5.9	48541	2	5%	Cytoplasmic	COG0114	Energy production and conversion	
592	108762519	not in database			2.0	1.31E-05	EG			2	5%				
601	167034753	not in database			7.9	1.19E-04	EG			2	5%				
601	26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	7.9	1.19E-04	EG	6.0	54367	9	19%	Cytoplasmic	COG1012	Energy production and conversion	
601	26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	7.9	1.19E-04	EG	5.4	55551	3	6%	Cytoplasmic	COG2204	Signal transduction mechanisms	
601	26987283	PP_0545		aldehyde dehydrogenase family protein	7.9	1.19E-04	EG	5.9	55268	3	20%	Cytoplasmic	COG1012	Energy production and conversion	
601	26989399	PP_2680		aldehyde dehydrogenase family protein	7.9	1.19E-04	EG	5.5	54903	15	38%	Cytoplasmic	COG1012	Energy production and conversion	
601	26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	7.9	1.19E-04	EG	5.8	51676	10	22%	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
601	148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	7.9	1.19E-04	EG	5.4	51447	3	7%	Cytoplasmic	COG0499	Coenzyme metabolism	
674	26987824	PP_1088	argG	argininosuccinate synthase	1.9	1.59E-06	EG	5.1	45164	5	13%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
674	26990810	PP_4116	aceA	isocitrate lyase	1.9	1.59E-06	EG	5.3	48633	19	50%	Cytoplasmic	COG2224	Energy production and conversion	
674	26991734	PP_5058		carboxyl-terminal protease	1.9	1.59E-06	EG	5.6	46333	3	7%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
674	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.9	1.59E-06	EG	5.4	50393	3	8%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
755	26991409	PP_4726	dnaJ	chaperone protein DnaJ	2.1	4.40E-05	EG	6.7	40181	11	33%	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
755	26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	2.1	4.40E-05	EG	6.6	42328	9	22%	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
755	26986828	PP_0083	trpB	tryptophan synthase subunit beta	2.1	4.40E-05	EG	6.4	44046	3	9%	Cytoplasmic	COG0133	Amino acid transport and metabolism	
755	26990810	PP_4116	aceA	isocitrate lyase	2.1	4.40E-05	EG	5.3	48633	2	5%	Cytoplasmic	COG2224	Energy production and conversion	
755	26988984	PP_2260		sugar ABC transporter ATP-binding protein	2.1	4.40E-05	EG	6.3	40769	7	21%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
755	148545952	Pput_0706		glutamate dehydrogenase	2.1	4.40E-05	EG	6.5	48551	10	29%	Unknown	COG0334	Amino acid transport and metabolism	
755	26987152	PP_0411		spermidine/putrescine ABC transporter ATPase	2.1	4.40E-05	EG	6.6	41197	6	16%	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
758	26991570	PP_4892	hflK	HflK protein	2.2	8.15E-06	EG	5.1	44762	3	10%	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
758	170721481	PputW619_2300		malate dehydrogenase	2.2	8.15E-06	EG	5.2	44227	8	21%	Cytoplasmic	COG0281	Energy production and conversion	
758	148545505	Pput_0249		outer membrane porin	2.2	8.15E-06	EG	5.4	48366	3	7%	Outer Membrane			
758	26987755	PP_1019	oprB-1	porin B	2.2	8.15E-06	EG	5.9	49646	4	8%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
758	26987181	PP_0440	tuf	elongation factor Tu	2.2	8.15E-06	EG	5.0	43495	6	15%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
758	26991645	PP_4967	metK	S-adenosylmethionine synthetase	2.2	8.15E-06	EG	5.1	42779	4	10%	Cytoplasmic	COG0192	Coenzyme metabolism	
1163	170721492	PputW619_2311		hydroxypyruvate isomerase	3.2	8.96E-07	EG	4.5	28658	7	33%	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
1163	26987078	PP_0336	msrA	methionine sulfoxide reductase A	3.2	8.96E-07	EG	4.7	24565	4	21%	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
1183	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	4.8	9.09E-04	EG	6.0	26030	3	13%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
1183	26989384	PP_2665	agmR	LuxR family two component transcriptional regulator	4.8	9.09E-04	EG	5.9	24536	5	33%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
1183	26991905	PP_5229		hypothetical protein	4.8	9.09E-04	EG	6.1	26395	2	8%	Cytoplasmic	COG3159	Function unknown	
1183	26988239	PP_1507		hypothetical protein	4.8	9.09E-04	EG	6.0	23544	2	11%	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones	
1464	26989381	PP_2662		hypothetical protein	34.0	1.43E-06	EG	4.3	42858	10	30%	Outer Membrane			
1468	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	31.0	1.36E-07	EG	7.0	69173	15	30%	Periplasmic	COG4993	Carbohydrate transport and metabolism	



Differenziell regulierte Spots zwischen mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* JM37 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit Glyoxylsäure behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
1258	148546913	Pput_1675		amino acid adenylation domain-containing protein	3.0	1.32E-02	GXS	5.9	123901	5	5%	Cytoplasmic Membrane	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
1291	148546915	Pput_1677		amino acid adenylation domain-containing protein	1.9	6.11E-03	GXS	5.4	114197	7	6%	Cytoplasmic Membrane	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
1291	148545620	Pput_0365		bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.9	6.11E-03	GXS	5.3	109445	12	12%	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
1305	148546915	Pput_1677		amino acid adenylation domain-containing protein	5.6	2.77E-04	GXS	5.4	114197	16	17%	Cytoplasmic Membrane	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
1450	26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.9	6.00E-03	GXS	7.2	154797	3	2%	Cytoplasmic	COG0086	Transcription	
1450	148547843	Pput_2627		ATPase	1.9	6.00E-03	GXS	5.7	94759	26	34%	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
1450	26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.9	6.00E-03	GXS	5.6	96697	9	11%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
1450	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.9	6.00E-03	GXS	5.6	99332	9	10%	Cytoplasmic	COG2609	Energy production and conversion	
1496	148546286	Pput_1043		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	2.7	1.42E-04	GXS	6.3	94800	27	36%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1496	26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	2.7	1.42E-04	GXS	5.6	84730	3	42%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1561	134294113	not in database			3.6	1.04E-03	GXS			2	2%				
1561	170721483	PputW619_2302		malate synthase G	3.6	1.04E-03	GXS	6.5	79656	21	30%	Cytoplasmic	COG2225	Energy production and conversion	
1561	148549206	Pput_4000		carboxyl-terminal protease	3.6	1.04E-03	GXS	7.1	79008	13	19%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
1596	170721483	PputW619_2302		malate synthase G	17.0	7.65E-06	GXS	6.5	79656	25	35%	Cytoplasmic	COG2225	Energy production and conversion	
1596	134294113	not in database			17.0	7.65E-06	GXS			2	2%				
1596	148549206	Pput_4000		carboxyl-terminal protease	17.0	7.65E-06	GXS	7.1	79008	8	12%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
1809	26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	2.1	1.93E-03	control	6.8	62781	4	6%	Cytoplasmic	COG0028		
1809	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.1	1.93E-03	control	7.0	69173	13	23%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1823	26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	5.2	2.77E-05	GXS	6.1	64654	5	9%	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
1823	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	5.2	2.77E-05	GXS	5.8	65671	2	3%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1823	170721493	PputW619_2312		glyoxylate carboligase	5.2	2.77E-05	GXS	5.6	64347	13	19%	Cytoplasmic	COG3960	General function prediction only	
1823	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	5.2	2.77E-05	GXS	5.6	99332	3	3%	Cytoplasmic	COG2609	Energy production and conversion	
1828	170721493	PputW619_2312		glyoxylate carboligase	16.0	9.50E-06	GXS	5.6	64347	17	27%	Cytoplasmic	COG3960	General function prediction only	
1829	26990742	PP_4041		glycoside hydrolase 15-related	1.8	3.19E-03	GXS	6.4	69769	2	3%	Cytoplasmic	COG3387	Carbohydrate transport and metabolism	
1829	26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.8	3.19E-03	GXS	5.8	65541	12	21%	Cytoplasmic	COG1960	Lipid metabolism	
1829	170721493	PputW619_2312		glyoxylate carboligase	1.8	3.19E-03	GXS	5.6	64347	5	8%	Cytoplasmic	COG3960	General function prediction only	
1986	148549733	Pput_4531		methylmalonate-semialdehyde dehydrogenase	1.9	3.02E-04	GXS	6.1	54376	3	7%	Cytoplasmic	COG1012	Energy production and conversion	
1991	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	2.4	2.28E-05	GXS	6.3	49912	3	7%	Cytoplasmic	COG1249	Energy production and conversion	
1991	148549733	Pput_4531		methylmalonate-semialdehyde dehydrogenase	2.4	2.28E-05	GXS	6.1	54376	20	43%	Cytoplasmic	COG1012	Energy production and conversion	
1991	26987283	PP_0545		aldehyde dehydrogenase family protein	2.4	2.28E-05	GXS	5.9	55268	12	26%	Cytoplasmic	COG1012	Energy production and conversion	
1991	26991954	PP_5278		aldehyde dehydrogenase family protein	2.4	2.28E-05	GXS	5.5	53053	6	13%	Cytoplasmic	COG1012	Energy production and conversion	
2056	26989908	PP_3189	codA	N-isopropylammelide isopropylaminohydrolase	5.3	8.45E-05	GXS	6.1	45821	2	5%	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
2056	26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	5.3	8.45E-05	GXS	5.7	49982	9	20%	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
2056	26988204	PP_1471	thrC	threonine synthase	5.3	8.45E-05	GXS	6.2	51645	2	4%	Cytoplasmic	COG0498	Amino acid transport and metabolism	
2056	26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	5.3	8.45E-05	GXS	5.9	53498	4	9%	Cytoplasmic	COG1012	Energy production and conversion	
2056	170721490	PputW619_2309		hydroxypyruvate reductase	5.3	8.45E-05	GXS	6.2	44600	10	26%	Cytoplasmic	COG2379	Carbohydrate transport and metabolism	
2056	148549784	Pput_4582	glmM	phosphoglucosamine mutase	5.3	8.45E-05	GXS	6.0	47774	8	16%	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
2091	170721489	PputW619_2308		pyruvate kinase	2.8	2.89E-06	GXS	6.0	51590	7	14%	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
2091	26987737	PP_1001	arcA	arginine deiminase	2.8	2.89E-06	GXS	5.7	46462	5	13%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
2091	26987770	PP_1034	cumA	multicopper oxidase	2.8	2.89E-06	GXS	6.4	52374	2	5%	Unknown	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
2091	148549784	Pput_4582	glmM	phosphoglucosamine mutase	2.8	2.89E-06	GXS	6.0	47774	3	6%	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
2091	148547037	Pput_1802		phenylhydantoinase	2.8	2.89E-06	GXS	6.1	54425	2	4%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
2091	26988163	PP_1430	algY	protease Do	2.8	2.89E-06	GXS	6.6	52617	4	7%	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
2091	26991090	PP_4401	bkdA1	3-methyl-2-oxobutanoate dehydrogenase	2.8	2.89E-06	GXS	6.0	45220	4	9%	Cytoplasmic	COG1071	Energy production and conversion	
2092	170721489	PputW619_2308		pyruvate kinase	1.8	2.58E-04	GXS	6.0	51590	4	8%	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
2092	148547037	Pput_1802		phenylhydantoinase	1.8	2.58E-04	GXS	6.1	54425	2	4%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
2092	26988163	PP_1430	algY	protease Do	1.8	2.58E-04	GXS	6.6	52617	4	7%	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
2092	26990721	PP_4016	purB	adenylosuccinate lyase	1.8	2.58E-04	GXS	5.9	50555	4	6%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
2092	26991090	PP_4401	bkdA1	3-methyl-2-oxobutanoate dehydrogenase	1.8	2.58E-04	GXS	6.0	45220	3	6%	Cytoplasmic	COG1071	Energy production and conversion	
2092	26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.8	2.58E-04	GXS	6.2	51518	4	9%	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
2092	26987737	PP_1001	arcA	arginine deiminase	1.8	2.58E-04	GXS	5.7	46462	6	16%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
2092	170721490	PputW619_2309		hydroxypyruvate reductase	1.8	2.58E-04	GXS	6.2	44600	5	11%	Cytoplasmic	COG2379	Carbohydrate transport and metabolism	
2092	148549784	Pput_4582	glmM	phosphoglucosamine mutase	1.8	2.58E-04	GXS	6.0	47774	13	24%	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
2114	148546878	Pput_1640		diaminobutyrate--2-oxoglutarate aminotransferase	16.0	5.81E-05	GXS	6.8	50052	7	15%	Cytoplasmic	COG0160	Amino acid transport and metabolism	
2209	26987181	PP_0440	tuf	elongation factor Tu	1.8	1.52E-03	control	5.0	43495	2	5%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
2209	26991077	PP_4388	flgE	flagellar hook protein FlgE	1.8	1.52E-03	control	4.3	45796	2	5%	Extracellular	COG1749	Cell motility and secretion	
2244	26987181	PP_0440	tuf	elongation factor Tu	6.8	8.11E-06	GXS	5.0	43495	10	26%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
2244	170721481	PputW619_2300		malate dehydrogenase	6.8	8.11E-06	GXS	5.2	44227	9	23%	Cytoplasmic	COG0281	Energy production and conversion	
2244	26987755	PP_1019	oprB-1	porin B	6.8	8.11E-06	GXS	5.9	49646	2	4%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
2244	26991645	PP_4967	metK	S-adenosylmethionine synthetase	6.8	8.11E-06	GXS	5.1	42779	5	13%	Cytoplasmic	COG0192	Coenzyme metabolism	
2271	26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.8	1.92E-04	GXS	4.7	36629	10	30%	Cytoplasmic	COG0202	Transcription	
2271	313498817	not in database			1.8	1.92E-04	GXS			5	17%				
2271	26987455	PP_0719		GTP-dependent nucleic acid-binding protein EngD	1.8	1.92E-04	GXS	4.7	39962	2	8%	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
2271	313501204	not in database			1.8	1.92E-04	GXS			11	28%				
2271	26988076	PP_1342	ftsZ	cell division protein FtsZ	1.8	1.92E-04	GXS	4.7	41830	3	8%	Cytoplasmic	COG0206	Cell division and chromosome partitioning	
2293	148546914	Pput_1676		amino acid adenylation domain-containing protein	3.1	1.73E-04	GXS	5.9	379854	8	2%	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
2444	148550278	Pput_5078		sulfate ABC transporter periplasmic sulfate-binding protein	2.0	1.12E-04	GXS	7.8	36675	5	15%	Periplasmic	COG1613	Inorganic ion transport and metabolism	
2444	26988049	PP_1314		aldo/keto reductase family oxidoreductase	2.0	1.12E-04	GXS	6.5	38777	5	12%	Cytoplasmic	COG0667	Energy production and conversion	
2444	26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	2.0	1.12E-04	GXS	7.2	36863	5	15%	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
2452	148550278	Pput_5078		sulfate ABC transporter periplasmic sulfate-binding protein	2.3	6.86E-05	GXS	7.8	36675	6	13%	Periplasmic	COG1613	Inorganic ion transport and metabolism	
2452	26988049	PP_1314		aldo/keto reductase family oxidoreductase	2.3	6.86E-05	GXS	6.5	38777	2	6%	Cytoplasmic	COG0667	Energy production and conversion	
2452	313499736	not in database			2.3	6.86E-05	GXS			2	4%				
2452	26988101	PP_1367	purU	formyltetrahydrofolate deformylase	2.3	6.86E-05	GXS	6.6	32376	7	23%	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
2452	26991441	PP_4760		alcohol dehydrogenase, zinc-containing	2.3	6.86E-05	GXS	6.2	35615	4	14%	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
2771	26987961	PP_1226	exsB	exsB protein	12.0	9.23E-05	GXS	4.7	23961	2	8%	Cytoplasmic	COG0603	General function prediction only	
2771	170721492	PputW619_2311		hydroxypyruvate isomerase	12.0	9.23E-05	GXS	4.5	28658	7	25%	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
2771	26987078	PP_0336	msrA	methionine sulfoxide reductase A	12.0	9.23E-05	GXS	4.7	24565	4	20%	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
2809	26988941	PP_2217	fadB1x	enoyl-CoA hydratase/isomerase	2.3	1.97E-03	GXS	5.2	27668	5	20%	Cytoplasmic	COG1024	Lipid metabolism	
2809	148548979	Pput_3773	leuD	isopropylmalate isomerase small subunit	3.6	2.09E-04	GXS	5.3	24286	7	36%	Cytoplasmic	COG0066	Amino acid transport and metabolism	
2696	26988632	PP_1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.9	3.37E-05	GXS	5.2	27809	2	6%	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
2696	26986819	PP_0074	aroE	shikimate 5-dehydrogenase	1.9	3.37E-05	GXS	5.0	29289	3	11%	Cytoplasmic	COG0169	Amino acid transport and metabolism	
2696	26988370	PP_1638	fpr	oxidoreductase FAD/NAD(P)-binding domain protein	1.9	3.37E-05	GXS	5.1	29710	8	35%	Cytoplasmic	COG1018	Energy production and conversion	
3204	148549732	Pput_4530		3-hydroxyisobutyrate dehydrogenase	1.8	1.80E-03	GXS	6.1	30308	10	56%	Cytoplasmic	COG2084	Lipid metabolism	
3204	26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.8	1.80E-03	GXS	6.0	35135	8	29%	Cytoplasmic	COG0825	Lipid metabolism	

5.1.2 Membranproteom-Analyse



1D-SDS-PAGE der Membranfraktion von mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

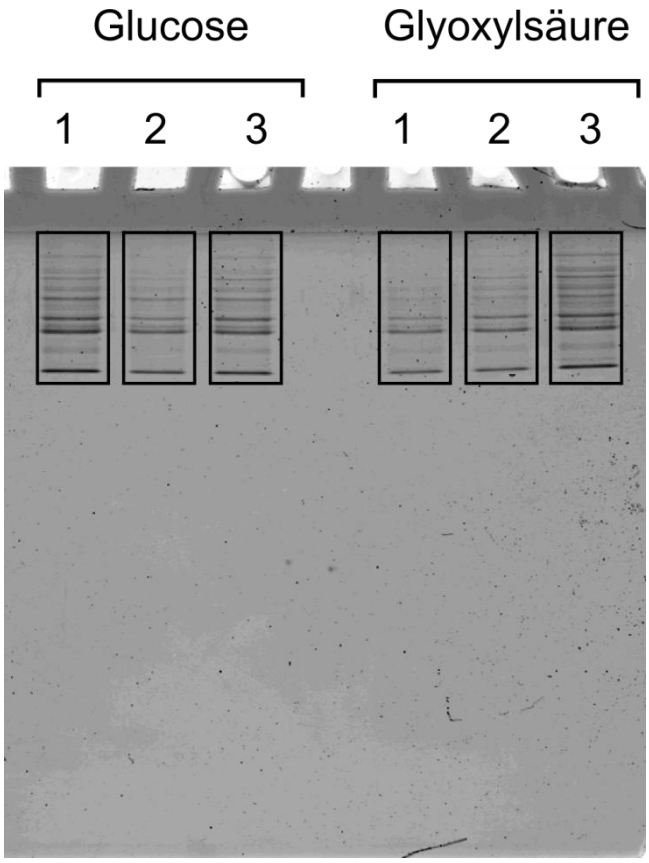
gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.1	6.90E-01	control	9.1	61919	12	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.1	8.47E-01	EG	4.9	40718	3	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.2	9.29E-01	control	8.1	34224	2	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1.2	9.01E-01	control	5.0	28482	4	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986856	PP_0111		electron transport protein SCO1/SenC	1.1	9.33E-01	control	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.2	4.99E-01	EG	7.4	25597	5	Unknown			
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.1	7.44E-01	control	9.6	29387	2	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.4	3.03E-01	EG	7.3	50185	7	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.1	7.07E-01	EG	6.3	71284	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.4	6.79E-02	EG	7.8	51116	9	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.4	1.94E-01	EG	7.7	78583	12	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986924	PP_0180		cytochrome c family protein	1.0	9.66E-01	control	4.9	68013	6	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	1.0	5.73E-01	control	5.4	52061	2	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	1.3	1.63E-01	EG	6.5	27422	3	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
26986933	PP_0189	hemY	HemY domain protein	1.1	8.21E-02	EG	9.6	46030	14	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.4	3.11E-01	EG	5.2	51549	8	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.1	7.32E-01	control	6.1	44824	4	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.0	9.61E-01	control	5.4	48317	25	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.3	7.79E-01	control	5.2	15616	11	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.1	4.20E-01	EG	6.1	47787	11	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.0	6.83E-01	EG	6.0	80277	9	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.0	8.72E-01	control	5.3	55654	9	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.1	7.68E-01	EG	5.6	99332	20	Cytoplasmic	COG2609	Energy production and conversion	
26987098	PP_0356	glcB	malate synthase G	1.7	9.37E-01	control	5.8	78346	2	Cytoplasmic	COG2225	Energy production and conversion	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	2.0	1.40E-01	EG	5.8	65541	2	Cytoplasmic	COG1960	Lipid metabolism	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	7.2	4.69E-02	EG	6.8	29075	2	Cytoplasmic	COG5424	Coenzyme metabolism	
26987128	PP_0386		sensory box protein	1.7	2.80E-01	EG	5.6	139392	3	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.0	7.65E-01	EG	4.6	69396	4	Cytoplasmic	COG0568	Transcription	
26987138	PP_0396		hypothetical protein	3.0	5.15E-01	control	7.0	50488	4	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.1	5.69E-01	control	5.8	73782	19	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987159	PP_0418		GDSL family lipase	1.1	8.17E-01	control	4.4	67175	6	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987181	PP_0440	tuf	elongation factor Tu	1.0	8.15E-01	control	5.0	43495	2	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	1.0	9.89E-01	control	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.4	4.54E-01	EG	10.1	24251	5	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.1	6.24E-01	control	10.2	17686	9	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.2	2.61E-01	EG	5.5	150992	33	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.1	4.98E-01	EG	7.2	154797	32	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.2	7.13E-01	EG	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.0	9.69E-01	EG	10.8	17578	10	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.1	4.85E-01	control	4.9	78817	31	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.1	6.91E-01	control	5.0	43478	27	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	2.1	1.32E-01	EG	10.5	11753	4	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.1	6.33E-01	EG	10.3	21811	5	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.3	3.63E-01	EG	10.7	10900	7	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.2	6.26E-01	control	11.7	29669	6	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.8	3.71E-01	control	11.9	15373	2	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.5	1.96E-01	EG	11.6	13410	7	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.3	2.80E-01	EG	10.3	20329	13	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.8	2.15E-01	EG	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.9	2.16E-01	EG	10.4	19143	5	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.9	2.18E-03	EG	10.9	12628	3	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.0	8.25E-01	EG	10.6	17666	10	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.9	1.33E-01	EG	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.5	3.04E-01	EG	10.4	47853	3	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.8	2.41E-01	EG	11.3	13256	4	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.1	5.37E-01	EG	11.5	13660	2	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.2	5.21E-01	EG	10.5	23056	10	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.3	6.30E-01	control	4.7	36629	7	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	2.1	7.56E-01	control	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987243	PP_0504	oprG	OmpW family protein	1.9	3.84E-02	EG	4.8	24196	7	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	1.1	5.45E-01	EG	9.7	45834	8	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	1.5	2.96E-01	control	7.2	25648	3	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.4	1.93E-02	EG	5.9	55268	19	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.4	2.68E-01	EG	6.5	49088	3	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	1.2	2.71E-01	EG	6.6	40223	3	Unknown	COG5345	Function unknown	
26987308	PP_0570		alpha-2-macroglobulin domain protein	1.6	9.87E-01	control	5.2	178472	5	Unknown	COG2373	General function prediction only	
26987314	PP_0576		lipoprotein	1.6	1.88E-01	EG	9.5	21449	4	Unknown			
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.6	1.70E-01	EG	5.0	69953	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987336	PP_0599		hypothetical protein	1.7	8.69E-01	control	9.6	83247	4	Unknown	COG3008	General function prediction only	
26987359	PP_0622		competence lipoprotein ComL	1.1	4.88E-01	EG	4.8	38410	3	Unknown	COG4105	General function prediction only	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.1	8.12E-01	control	6.2	44897	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.8	1.07E-01	EG	5.3	61860	2	Cytoplasmic	COG0488	General function prediction only	
26987443	PP_0707		MscS mechanosensitive ion channel	1.9	1.12E-01	EG	9.9	92124	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	1.2	5.30E-01	EG	5.3	23026	5	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	1.4	3.17E-01	EG	10.5	31284	3	Cytoplasmic	COG2326	Function unknown	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	2.0	2.16E-01	EG	6.4	23242	2	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.2	4.77E-01	control	5.9	34192	2	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987478	PP_0742		hypothetical protein	6.3	2.58E-02	control	6.2	36114	2	Unknown	COG3380	General function prediction only	
26987479	PP_0743		NAD-dependent epimerase/dehydratase	1.0	5.82E-01	EG	9.7	33119	1	Cytoplasmic Membrane	COG1090	General function prediction only	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.2	3.13E-01	EG	8.4	54282	2	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.2	8.36E-01	control	9.5	20483	9	Unknown			
26987495	PP_0759		hypothetical protein	3.8	2.54E-01	control	7.0	29743	4	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.0	9.72E-01	control	5.5	62125	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.2	7.23E-01	control	5.0	67937	25	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.2	7.76E-01	control	9.6	50572	9	Unknown			
26987509	PP_0773		OmpA/MotB domain protein	1.1	5.14E-01	EG	9.5	24753	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding protein	1.1	7.16E-01	control	9.2	79558	2	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.3	5.00E-02	control	6.7	34557	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	1.7	3.59E-01	EG	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.5	2.14E-01	EG	9.6	66913	15	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.2	4.23E-01	EG	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.1	9.89E-01	control	6.6	29753	4	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.0	9.29E-01	control	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP_0856		hypothetical protein	2.0	8.89E-01	control	4.7	40737	6	Outer Membrane	COG1520	Function unknown	
26987617	PP_0881	dppB	alkaline phosphatase	1.1	8.77E-01	EG	8.4	36980	4	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987619	PP_0883		outer membrane porin	1.3	2.79E-01	EG	6.6	50256	9	Outer Membrane			
26987623	PP_0887		integral membrane sensor signal transduction histidine kinase	2.6	4.90E-01	control	6.1	49523	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987643	PP_0907		RND efflux membrane fusion protein-related protein	1.1	5.88E-01	EG	9.7	43537	4	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26987645	PP_0909		hypothetical protein	1.3	2.40E-01	EG	6.4	38380	9	Unknown	COG3489	General function prediction only	

26987649	PP_0913		hypothetical protein	1.2	3.25E-01	EG	4.4	47019	16	Outer Membrane	COG3487	Inorganic ion transport and metabolism
26987650	PP_0914		GGDEF domain-containing protein	1.7	2.15E-01	EG	5.8	78578	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.1	6.84E-01	EG	6.2	51518	3	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis
26987680	PP_0944	fumC	fumarate hydratase	2.5	1.10E-01	control	5.9	48541	11	Cytoplasmic	COG0114	Energy production and conversion
26987695	PP_0959	ttg2B	hypothetical protein	2.0	2.03E-01	EG	8.2	28489	2	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.3	5.14E-01	control	8.4	22938	3	Cytoplasmic	COG0040	Amino acid transport and metabolism
26987713	PP_0977	valS	valyl-tRNA synthetase	2.0	5.49E-02	EG	5.1	107495	6	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis
26987716	PP_0980	pepA	leucyl aminopeptidase	1.8	1.58E-01	EG	7.4	52433	6	Cytoplasmic	COG0260	Amino acid transport and metabolism
26987735	PP_0999	arcC	carbamate kinase	1.1	7.91E-01	EG	5.5	33423	4	Cytoplasmic	COG0549	Amino acid transport and metabolism
26987736	PP_1000	argI	ornithine carbamoyltransferase	1.1	7.26E-01	EG	6.3	37911	14	Cytoplasmic	COG0078	Amino acid transport and metabolism
26987737	PP_1001	arcA	arginine deiminase	1.2	7.04E-01	control	5.7	46462	13	Cytoplasmic	COG2235	Amino acid transport and metabolism
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.1	4.02E-01	EG	9.1	51061	3	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	3.3	3.67E-02	control	7.0	36057	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism
26987746	PP_1010	edd	phosphogluconate dehydratase	1.5	1.38E-01	control	6.4	65359	4	Cytoplasmic	COG0129	Amino acid transport and metabolism Carbohydrate transport and metabolism
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.5	2.23E-01	EG	6.2	45449	5	Periplasmic	COG1653	Carbohydrate transport and metabolism
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.1	7.46E-01	EG	10.1	33781	5	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.5	2.48E-01	EG	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.3	3.47E-01	EG	6.7	41895	2	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism
26987755	PP_1019	oprB-1	porin B	1.1	5.54E-01	control	5.9	49646	32	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.3	2.37E-01	control	6.8	55000	6	Cytoplasmic	COG0364	Carbohydrate transport and metabolism
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.7	1.93E-01	control	6.7	25476	8	Unknown	COG0363	Carbohydrate transport and metabolism
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.2	7.97E-01	control	5.4	25004	7	Cytoplasmic	COG0800	Carbohydrate transport and metabolism
26987761	PP_1025	leuA	2-isopropylmalate synthase	2.4	1.78E-01	control	5.1	61712	2	Cytoplasmic	COG0119	Amino acid transport and metabolism
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	2.6	2.55E-01	EG	7.0	51765	4	Cytoplasmic	COG0516	Nucleotide transport and metabolism
26987768	PP_1032	guaA	GMP synthase	1.6	2.09E-01	EG	5.2	58204	4	Cytoplasmic	COG0519	Nucleotide transport and metabolism
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.3	3.21E-01	EG	4.7	140818	7	Cytoplasmic	COG0046	Nucleotide transport and metabolism
26987794	PP_1058		hypothetical protein	1.0	9.36E-01	control	9.5	117041	8	Unknown	COG0744	Cell envelope biogenesis, outer membrane
26987805	PP_1069		polar amino acid ABC transporter inner membrane subunit	1.2	3.20E-01	EG	9.4	24744	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.6	2.20E-01	control	8.2	27464	5	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.4	9.42E-01	control	8.9	33428	2	Periplasmic	COG0834	Amino acid transport and metabolism Signal transduction mechanisms
26987818	PP_1082	bfr	bacterioferritin	1.3	3.86E-01	EG	4.4	17971	2	Cytoplasmic	COG2193	Inorganic ion transport and metabolism
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.6	2.13E-01	EG	4.9	21730	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
26987844	PP_1108		acylase	1.0	8.09E-01	EG	8.7	88728	17	Periplasmic	COG2366	General function prediction only
26987857	PP_1121		OmpA/MotB domain protein	1.1	5.82E-01	control	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987858	PP_1122		OmpA/MotB domain protein	1.5	1.54E-01	EG	4.7	27345	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987867	PP_1131		17 kDa surface antigen	1.1	4.57E-01	control	9.3	15682	7	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane
26987890	PP_1154		sensory box protein	1.1	7.90E-01	control	5.7	95980	4	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26987923	PP_1188	dctA	C4-dicarboxylate transporter DctA	1.9	1.47E-02	EG	8.8	46298	2	Cytoplasmic Membrane	COG1301	Energy production and conversion
26987936	PP_1201		virulence factor family protein	1.8	1.71E-01	EG	5.0	46885	3	Unknown	COG3946	Intracellular trafficking and secretion
26987937	PP_1202		hypothetical protein	2.0	2.82E-02	EG	9.7	95622	2	Cytoplasmic Membrane	COG2898	Function unknown
26987941	PP_1206	oprD	outer membrane porin	1.3	3.45E-01	control	4.6	46120	23	Outer Membrane		
26987945	PP_1210		DNA-binding stress protein	1.5	5.71E-01	control	5.0	17861	2	Cytoplasmic	COG0783	Inorganic ion transport and metabolism
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.0	8.95E-01	EG	5.1	66568	10	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.2	4.29E-01	EG	6.3	25310	3	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion
26987957	PP_1222	tolB	translocation protein TolB	1.4	3.76E-01	EG	9.8	47431	2	Unknown	COG0823	Intracellular trafficking and secretion
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.5	3.43E-01	control	4.9	17833	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987973	PP_1238		lipoprotein	1.2	4.82E-01	EG	4.8	40784	6	Unknown	COG3317	Cell envelope biogenesis, outer membrane
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.6	2.11E-01	EG	5.1	26916	2	Cytoplasmic	COG0152	Nucleotide transport and metabolism
26987980	PP_1245		hypothetical protein	1.9	2.38E-02	EG	9.4	31144	3	Unknown		
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.1	9.48E-01	control	5.6	36424	3	Periplasmic	COG0834	Amino acid transport and metabolism Signal transduction mechanisms
26988044	PP_1309		hypothetical protein	2.0	8.69E-01	control	6.3	16018	2	Unknown	COG3105	Function unknown
26988050	PP_1315	rplM	50S ribosomal protein L13	1.4	9.61E-01	control	10.3	15862	3	Unknown	COG0102	Translation, ribosomal structure and biogenesis
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.4	3.73E-01	EG	11.7	14592	3	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis
26988052	PP_1317	petA	ubiquinol-cytochrome c reductase, iron-sulfur subunit	1.5	2.73E-01	EG	7.5	20855	2	Cytoplasmic Membrane	COG0723	Energy production and conversion
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.3	4.84E-02	EG	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.1	6.07E-01	EG	7.1	29032	8	Unknown	COG2857	Energy production and conversion
26988057	PP_1322		transport-associated protein	1.2	8.20E-01	EG	9.8	20680	3	Periplasmic	COG2823	General function prediction only
26988060	PP_1325		LppC family lipoprotein	1.2	5.43E-01	EG	7.5	64637	16	Cytoplasmic Membrane	COG3107	General function prediction only
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.3	1.51E-01	EG	5.3	53602	2	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane
26988075	PP_1341	ftsA	cell division protein FtsA	1.0	7.39E-01	EG	4.9	47444	2	Cytoplasmic	COG0849	Cell division and chromosome partitioning
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.0	8.69E-01	control	5	42236	2	Cytoplasmic	COG1364	Amino acid transport and metabolism
26988095	PP_1361	groEL	chaperonin GroEL	1.5	2.86E-01	control	4.7	56743	30	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones
26988096	PP_1362	pykA	pyruvate kinase	1.0	8.04E-01	EG	6.7	52057	4	Cytoplasmic	COG0469	Carbohydrate transport and metabolism
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.2	4.66E-01	EG	4.8	67652	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	1.1	8.02E-01	control	9.6	52425	2	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism
26988117	PP_1383		BenF-like porin	1.5	1.84E-01	EG	6.8	46022	7	Outer Membrane		
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.1	4.01E-01	EG	5.1	52864	19	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.2	2.55E-01	EG	5.3	112835	5	Cytoplasmic Membrane	COG0841	Defense mechanisms
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	1.1	8.94E-01	control	6	41250	3	Unknown	COG0845	Cell envelope biogenesis, outer membrane
26988152	PP_1419		outer membrane porin	1.2	3.60E-01	EG	4.9	46644	2	Outer Membrane		
26988165	PP_1432	lepB	signal peptidase I	1.3	3.79E-01	EG	9.2	32060	2	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion
26988176	PP_1443	lon-1	ATP-dependent protease La	1.5	3.76E-01	EG	6.4	89794	2	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.0	9.63E-01	control	6.0	86581	22	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism
26988179	PP_1446		TonB-dependent receptor	1.2	4.53E-01	EG	4.9	74207	23	Outer Membrane	COG1629	Inorganic ion transport and metabolism
26988198	PP_1465	rplS	50S ribosomal protein L19	1.1	9.14E-01	control	11.0	13012	6	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis
26988204	PP_1471	thrC	threonine synthase	1.6	5.89E-03	EG	6.2	51645	4	Cytoplasmic	COG0498	Amino acid transport and metabolism
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.2	7.73E-01	control	5.8	40626	4	Cytoplasmic	COG1902	Energy production and conversion
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.0	6.68E-01	EG	5.7	50918	2	Unknown	COG1012	Energy production and conversion
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.1	4.65E-01	EG	4.7	58605	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion Signal transduction mechanisms
26988258	PP_1526		beta-(1-3)-glucosyl transferase	1.5	3.10E-01	EG	8.1	97324	2	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	9.97E-01	control	9.3	27023	16	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis
26988331	PP_1599		surface antigen family outer membrane protein	2.0	5.56E-01	control	4.7	86513	13	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane
26988342	PP_1610	pyrG	CTP synthetase	2.3	3.04E-02	EG	5.8	59474	4	Cytoplasmic	COG0504	Nucleotide transport and metabolism
26988344	PP_1612	eno	phosphopyruvate hydratase	1.4	9.64E-01	EG	4.7	45490	2	Cytoplasmic	COG0148	Carbohydrate transport and metabolism
26988354	PP_1622	nlpD	peptidase M23B	1.5	9.52E-02	EG	11.0	27506	9	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	1.7	1.51E-02	EG	4.8	16590	2	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones Energy production and conversion
26988391	PP_1659		hypothetical protein	1.4	4.48E-01	EG	5.9	48336	4	Periplasmic		
26988393	PP_1661		dehydrogenase subunit	1.1	5.90E-01	EG	5.5	81020	9	Extracellular	COG2303	Amino acid transport and metabolism
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.0	8.78E-01	control	5.4	45693	12	Outer Membrane	COG2067	Lipid metabolism
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.6	2.67E-01	EG	4.8	26520	4	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones
26988474	PP_1743	actP	acetate permease	17.5	4.02E-03	EG	9.6	58972	5	Cytoplasmic Membrane	COG4147	General function prediction only
26988483	PP_1752		hypothetical protein	1.3	4.13E-01	EG	8.2	57637	6	Cytoplasmic	COG2326	Function unknown
26988492	PP_1761		sensory box protein/GGDEF family protein	1.3	3.59E-01	EG	6.8	108193	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms
26988498	PP_1767	gyrA	DNA gyrase subunit A	2.5	1.78E-01	EG	4.7	102037	2	Cytoplasmic	COG0188	DNA replication, recombination, and repair
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.0	8.77E-01	EG	6.4	40124	4	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane
26988538	PP_1808	pgi	glucose-6-phosphate isomerase	1.2	5.67E-01	EG	6.8	61383	3	Cytoplasmic	COG0166	Carbohydrate transport and metabolism
26988546	PP_1816		alcohol dehydrogenase, zinc-containing	3.6	3.18E-01	EG	7.4	35802	2	Cytoplasmic	COG2130	General function prediction only
26988568	PP_1838		hypothetical protein	1.8	1.99E-01	EG	6.8	76615	9	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.1	5.97E-01	EG	6.9	89194	23	Cytoplasmic Membrane	COG1960	Lipid metabolism
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.0	9.87E-01	EG	4.7	120904	6	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis

26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.5	2.44E-01	EG	6.4	36497	2	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.3	4.21E-01	EG	4.7	32614	2	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.3	2.60E-01	EG	6.0	25470	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988696	PP_1970		lipoprotein	2.0	1.99E-01	EG	4.9	22337	4	Unknown			
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.1	2.74E-01	control	5.9	43290	10	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.5	3.54E-01	EG	5.6	56483	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.3	5.80E-01	control	5.3	40672	4	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.3	4.24E-01	control	3.9	96918	20	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.6	2.58E-01	EG	7.8	32510	2	Cytoplasmic	COG0777	Lipid metabolism	
26988731	PP_2006		hypothetical protein	1.0	8.88E-01	control	5.1	63743	40	Unknown			
26988732	PP_2007		P-47-related protein	8.6	2.09E-01	control	5.8	44707	11	Unknown			
26988742	PP_2017	pepN	aminopeptidase N	1.4	3.25E-01	EG	4.8	99573	3	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988744	PP_2019		hypothetical protein	1.0	8.78E-01	control	6.6	87732	4	Cytoplasmic Membrane	COG1033	General function prediction only	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.3	3.77E-01	EG	5.8	187043	16	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.1	4.18E-01	EG	4.8	86015	10	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.0	9.71E-01	control	5.8	29111	4	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.2	9.88E-02	EG	4.5	37012	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988836	PP_2112	acnA	aconitate hydratase	1.7	6.12E-02	EG	5.7	99147	5	Cytoplasmic	COG1048	Energy production and conversion	
26988854	PP_2130		soluble lytic transglycosylase	1.1	5.90E-01	EG	9.9	75337	7	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.0	9.54E-01	control	7.7	53014	8	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.1	6.88E-01	control	5.3	26061	9	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.1	6.08E-01	EG	5.1	68646	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989026	PP_2302	lon-2	ATP-dependent protease La	1.1	5.39E-01	EG	5.9	88722	5	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.1	4.51E-01	control	4.8	68580	2	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.4	5.33E-01	EG	9.3	9997	3	Unknown			
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	1.1	2.91E-01	control	5.3	52127	10	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.5	1.86E-01	EG	8.5	8801	5	Outer Membrane			
26989051	PP_2327	cysB	transcriptional regulator CysB	1.1	5.84E-01	EG	6.7	35955	3	Cytoplasmic	COG0583	Transcription	
26989055	PP_2331		hypothetical protein	1.1	6.18E-01	EG	7.9	57064	3	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	8.12E-01	control	5.0	93609	6	Cytoplasmic	COG1049	Energy production and conversion	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.8	1.66E-01	EG	5.8	62191	2	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989142	PP_2419		hypothetical protein	1.4	3.38E-02	EG	10.2	47269	2	Cytoplasmic Membrane	COG3503	Function unknown	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.8	9.48E-02	EG	5.8	72697	3	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.1	7.89E-01	control	12.1	13280	2	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989289	PP_2569		major facilitator transporter	1.2	7.64E-02	EG	9.0	60538	9	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989297	PP_2578		hypothetical protein	1.3	9.27E-01	control	9.5	19010	2	Unknown	COG3009	Function unknown	
26989381	PP_2662		hypothetical protein	17.0	4.03E-03	EG	4.3	42858	9	Outer Membrane			
26989399	PP_2680		aldehyde dehydrogenase family protein	94.8	1.57E-05	EG	5.5	54903	11	Cytoplasmic	COG1012	Energy production and conversion	
26989572	PP_2853		hypothetical protein	1.2	9.66E-01	control	4.5	46020	9	Unknown			
26989620	PP_2901		penicillin amidase family protein	2.5	3.16E-01	EG	8	83333	2	Periplasmic	COG2366	General function prediction only	
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	5.7	1.92E-01	EG	6.1	64654	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989663	PP_2944		sensor histidine kinase	1.7	2.27E-01	EG	6.1	67470	4	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989666	PP_2947		transcriptional regulator MvaT, P16 subunit	2.0	2.57E-01	EG	9.7	14096	2	Cytoplasmic			
26989808	PP_3089		hypothetical protein	1.3	3.95E-01	control	5.3	19453	3	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	1.4	1.32E-01	EG	6.8	138655	12	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	2.5	1.09E-02	EG	5.7	26868	3	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989818	PP_3099		hypothetical protein	1.2	4.89E-01	EG	4.9	56072	30	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989819	PP_3100		hypothetical protein	1.5	3.56E-01	EG	7.7	21741	4	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.5	3.18E-03	EG	9.0	57141	19	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989853	PP_3134		transferase hexapeptide repeat containing protein	1.2	7.16E-01	control	9.9	25699	4	Cytoplasmic	COG0110	General function prediction only	
26989854	PP_3135		glycosyl transferase	1.4	1.53E-01	EG	8.6	35887	6	Cytoplasmic	COG1216	General function prediction only	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.2	2.02E-01	EG	9.4	43092	4	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989860	PP_3141		WecB/TagA/CpsF family glycosyl transferase	1.1	6.34E-01	EG	10.2	27576	3	Unknown	COG1922	Cell envelope biogenesis, outer membrane	
26989861	PP_3142		sugar transferase	1.9	2.25E-01	EG	9.1	53464	2	Cytoplasmic Membrane	COG2148	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	1.3	4.27E-01	control	9.7	29885	11	Unknown			
26989887	PP_3168	benF	benzoate-specific porin	1.1	6.87E-01	control	5.6	45611	2	Outer Membrane			
26990039	PP_3321		hypothetical protein	1.9	2.72E-01	EG	6.1	19365	2	Unknown	COG4875	Function unknown	
26990043	PP_3325		outer membrane ferric siderophore receptor	1.1	5.57E-01	EG	4.8	76226	29	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990047	PP_3330		TonB-dependent siderophore receptor	1.3	2.77E-01	EG	5.8	80740	16	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	1.3	4.39E-01	EG	4.8	77137	12	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	1.4	3.56E-01	control	8.9	47532	11	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990134	PP_3421		sensor histidine kinase	1.8	2.12E-01	EG	7.4	53788	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.9	8.84E-01	control	6.2	59980	2	Cytoplasmic	COG1012	Energy production and conversion	
26990161	PP_3448	nfrB	bacteriophage N4 adsorption protein B	1.3	3.95E-01	EG	7.4	82370	3	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.5	3.66E-01	EG	7.2	36863	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	1.3	2.84E-01	EG	6.9	85338	11	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	1.1	6.78E-01	EG	5.2	53952	11	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990296	PP_3585		efflux transporter RND family, MFP subunit	1.2	4.66E-01	EG	9.4	46468	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990323	PP_3612		TonB-dependent siderophore receptor	1.5	3.16E-01	EG	5.2	85491	2	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990379	PP_3668		catalase/peroxidase HPI	1.7	2.08E-03	control	5.8	82061	15	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990459	PP_3754		beta-ketothiolase	1.6	2.83E-01	control	6.9	40988	4	Cytoplasmic	COG0183	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.7	5.50E-02	EG	4.9	129450	14	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990470	PP_3765		transcriptional regulator MvaT, P16 subunit	2.3	5.17E-02	EG	10.7	13559	2	Cytoplasmic			
26990480	PP_3775		sarcosine oxidase	1.5	4.12E-03	control	6.4	41164	10	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	2.4	5.06E-02	control	6.2	27714	6	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990489	PP_3784		hypothetical protein	10.4	1.03E-01	control	5.4	41070	2	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	2.2	6.39E-02	EG	5.3	30957	4	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990662	PP_3957		choline/carnitine/betaine transporter family protein	1.7	2.44E-01	EG	7.6	72789	3	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane	
26990695	PP_3990		hypothetical protein	1.8	3.73E-01	control	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.4	5.40E-01	control	5.4	45695	3	Unknown	COG0538	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.7	3.38E-01	EG	5.9	50555	3	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.3	2.24E-01	EG	7.9	53519	4	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990806	PP_4111	fusA	elongation factor G	1.0	6.53E-01	EG	5.0	77832	5	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990809	PP_4115		NoIW domain protein	1.7	7.44E-01	control	6.7	29306	3	Unknown			
26990810	PP_4116	aceA	isocitrate lyase	5.7	3.13E-02	EG	5.3	48633	4	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.5	4.09E-01	EG	6.5	67609	3	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	2.0	2.02E-01	EG	5.9	97582	7	Unknown	COG1034	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.2	2.03E-01	control	8.7	20354	2	Cytoplasmic	COG0431	General function prediction only	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.3	8.81E-02	control	5.3	43264	4	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990870	PP_4178		dienelactone hydrolase	1.6	6.80E-01	control	7.1	26269	2	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26990871	PP_4179	htpG	heat shock protein 90	1.2	8.13E-01	control	5	71610	5	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.7	1.67E-01	EG	6.2	30111	8	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.0	8.83E-01	control	6.1	41239	17	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.2	5.13E-01	EG	6.3	49912	10	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.5	4.83E-03	control	5.1	42434	9	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.2	4.08E-01	EG	6.5	106521	10	Cytoplasmic	COG0567	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.1	9.98E-01	control	6.2	63448	4	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.1	9.18E-01	control	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.6	1.99E-01	control	7.0	47622	5	Cytoplasmic	COG0372	Energy production and conversion	
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.7	5.87E-01	EG	4.9	31237	2	Unknown	COG2025	Energy production and conversion	

26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.2	4.84E-01	EG	9.7	26361	4	Unknown	COG2086	Energy production and conversion							
26990903	PP_4211		RND efflux transporter	1.1	2.43E-01	control	8.2	51199	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane						Intracellular trafficking and secretion	
26990905	PP_4213		dipeptidase	1.4	4.86E-01	EG	5.0	50104	3	Unknown	COG2355	Amino acid transport and metabolism							
26990906	PP_4214		aminotransferase, class V	1.3	5.45E-01	EG	7.6	47747	3	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones							
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.3	1.31E-01	EG	5.5	89725	48	Outer Membrane	COG4773	Inorganic ion transport and metabolism							
26990942	PP_4251	ccoO-1	cbb3-type cytochrome c oxidase subunit II	1.1	7.10E-01	EG	8.6	22745	3	Unknown	COG2993	Energy production and conversion							
26990944	PP_4253	ccoP-1	cytochrome c oxidase, cbb3-type, subunit III	2.0	2.23E-02	EG	5.3	33915	2	Unknown	COG2010	Energy production and conversion							
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	1.0	6.72E-01	EG	9.6	53567	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones							
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.2	4.89E-01	EG	5.2	35613	7	Unknown	COG2010	Energy production and conversion							
26990966	PP_4275	zipA	cell division protein ZipA	1.5	1.31E-01	EG	6.0	35312	10	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning							
26991006	PP_4315		PhzF family phenazine biosynthesis protein	1.4	2.31E-01	control	4.5	28437	4	Cytoplasmic	COG0384	General function prediction only							
26991072	PP_4383	flgI	flagellar basal body P-ring protein	1.2	6.64E-01	EG	8.5	38182	8	Periplasmic	COG1706	Cell motility and secretion							
26991073	PP_4384	flgH	flagellar basal body L-ring protein	1.2	6.80E-01	EG	6.8	24302	4	Outer Membrane	COG2063	Cell motility and secretion							
26991134	PP_4448		hypothetical protein	1.4	2.56E-01	EG	6	66331	6	Cytoplasmic	COG0433	Replication, recombination, and repair							
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.1	8.05E-01	EG	5.1	94711	3	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis							
26991161	PP_4475	astE	succinylglutamate desuccinylase	1.0	5.19E-01	control	6.2	37580	2	Cytoplasmic	COG2988	Amino acid transport and metabolism							
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.1	9.88E-01	control	6.5	43490	6	Cytoplasmic	COG4992	Amino acid transport and metabolism							
26991173	PP_4487	acsA	acetyl-CoA synthetase	30.3	1.55E-03	EG	6.4	71796	5	Cytoplasmic	COG0365	Lipid metabolism							
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.3	2.21E-01	control	5.4	50393	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane						Intracellular trafficking and secretion	
26991206	PP_4521		aerotaxis receptor	1.1	5.38E-01	EG	6.4	56605	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion						Signal transduction mechanisms	
26991226	PP_4542		ABC transporter ATP-binding protein/permease	1.6	1.37E-01	EG	7.6	67748	3	Cytoplasmic Membrane	COG1132	Defense mechanisms							
26991325	PP_4641	cstA	carbon starvation protein CstA	1.1	1.92E-01	control	9.0	73763	10	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms							
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.7	2.64E-01	EG	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane							
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	1.0	6.06E-01	EG	9.1	53016	3	Cytoplasmic Membrane	COG1271	Energy production and conversion							
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.0	7.55E-01	EG	4.8	68764	3	Unknown	COG0840	Cell motility and secretion						Signal transduction mechanisms	
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	1.3	3.09E-01	EG	6.1	30321	2	Cytoplasmic	COG2084	Lipid metabolism							
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	8.93E-01	control	5.4	36370	4	Cytoplasmic	COG0059	Amino acid transport and metabolism						Coenzyme metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	3.2	1.28E-01	EG	6.8	62781	2	Cytoplasmic	COG0028	Amino acid transport and metabolism						Coenzyme metabolism	
26991388	PP_4704		hypothetical protein	1.6	1.84E-01	EG	5.6	107252	5	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane							
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.3	1.67E-01	EG	4.9	75010	9	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis							
26991395	PP_4712	infB	translation initiation factor IF-2	1.3	3.40E-01	EG	6.8	91460	10	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis							
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.2	1.28E-01	EG	5.4	69722	15	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones							
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.0	9.00E-01	control	4.6	68800	3	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones							
26991414	PP_4731	omlA	SmpA/OmlA domain protein	1.5	3.56E-01	control	4.4	19586	2	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane							
26991475	PP_4795		rare lipoprotein B	1.1	6.13E-01	EG	6.1	22414	6	Unknown	COG2980	Cell envelope biogenesis, outer membrane							
26991478	PP_4798		lytic murein transglycosylase	1.2	8.23E-01	control	7.7	48000	3	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane							
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.6	3.33E-01	EG	6.6	42288	4	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane							
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	1.7	3.32E-01	control	5.0	31015	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones							
26991518	PP_4838	oprC	TonB-dependent copper receptor	1.0	5.54E-01	control	6.2	74540	53	Outer Membrane	COG1629	Inorganic ion transport and metabolism							
26991519	PP_4839		hypothetical protein	2.7	1.27E-01	EG	9.6	50581	4	Cytoplasmic Membrane	COG3182	Function unknown							
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	1.3	7.89E-01	EG	6.6	32427	2	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism							
26991554	PP_4874	rplI	50S ribosomal protein L9	2.0	1.58E-01	EG	5.3	15466	2	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis							
26991556	PP_4876	rpsR	30S ribosomal protein S18	2.0	9.84E-01	control	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis							
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.6	2.67E-01	EG	6.1	71958	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion						Signal transduction mechanisms	
26991567	PP_4889	purA	adenylosuccinate synthetase	1.2	3.76E-01	control	5.6	46833	2	Cytoplasmic	COG0104	Nucleotide transport and metabolism							
26991569	PP_4891	hflC	HflC protein	1.3	7.75E-02	EG	9.8	33001	16	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones							
26991570	PP_4892	hflK	HflK protein	1.4	1.51E-01	EG	5.1	44762	8	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones							
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.2	4.53E-01	EG	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism							
26991588	PP_4910		hypothetical protein	1.2	4.01E-01	EG	4.7	53632	4	Cytoplasmic	COG3726	General function prediction only							
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.0	7.83E-01	EG	5.2	52637	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane						Intracellular trafficking and secretion	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.3	2.59E-02	control	7.6	66279	5	Cytoplasmic Membrane	COG1132	Defense mechanisms							
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	4.9	9.59E-02	EG	6.3	142580	2	Cytoplasmic	COG4230	Energy production and conversion							
26991643	PP_4965	tktA	transketolase	1.1	5.82E-01	control	5.0	72463	8	Cytoplasmic	COG0021	Carbohydrate transport and metabolism							
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.2	4.62E-01	control	5.1	42779	11	Cytoplasmic	COG0192	Coenzyme metabolism							
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.7	3.49E-01	EG	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones							
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	1.1	9.15E-01	control	7.4	62241	3	Cytoplasmic	COG3243	Lipid metabolism							
26991682	PP_5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	1.3	6.27E-01	EG	9.6	62722	3	Cytoplasmic	COG3243	Lipid metabolism							
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.8	2.53E-01	EG	10.9	26214	10	Cytoplasmic	COG3937	Function unknown							
26991685	PP_5008		poly(hydroxyalkanoate) granule-associated protein	1.5	2.65E-01	EG	9.7	15550	10	Cytoplasmic									
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.4	1.35E-01	EG	4.9	69017	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion						Signal transduction mechanisms	
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.2	3.29E-01	EG	8.3	95875	7	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane							
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.5	3.51E-01	EG	6.4	92004	4	Cytoplasmic	COG0058	Carbohydrate transport and metabolism							
26991720	PP_5044		GTP-binding protein TypA	1.0	7.79E-01	EG	5.3	67157	3	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms							
26991722	PP_5046	glnA	glutamine synthetase, type I	1.1	7.94E-01	control	5.1	51740	11	Cytoplasmic	COG0174	Amino acid transport and metabolism							
26991743	PP_5067		potassium efflux protein KefA	2.8	4.88E-01	control	8.9	122371	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane							
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.4	3.85E-01	EG	6.2	161772	7	Cytoplasmic	COG0069	Amino acid transport and metabolism							
26991753	PP_5077		sporulation domain protein	1.6	3.17E-01	EG	7.1	55434	2	Unknown	COG3267	Intracellular trafficking and secretion							
26991761	PP_5085	maeB	malic enzyme	1.0	7.84E-01	control	4.9	45127	4	Cytoplasmic	COG0281	Energy production and conversion							
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.1	5.64E-01	EG	5.7	63668	3	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis							
26991766	PP_5090		sporulation domain protein	1.0	7.81E-01	control	10.6	24964	3	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning							
26991785	PP_5109	ftsX	hypothetical protein	1.3	6.83E-02	control	6.5	36984	2	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning							
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.4	4.06E-02	EG	5.8	65671	4	Cytoplasmic	COG0129	Amino acid transport and metabolism						Carbohydrate transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.2	2.88E-01	control	6.3	44339	5	Cytoplasmic	COG0111	Amino acid transport and metabolism							
26991849	PP_5173		acriflavin resistance protein	1.4	1.52E-01	EG	5.4	112277	11	Cytoplasmic Membrane	COG0841	Defense mechanisms							
26991850	PP_5174		RND efflux transporter	1.3	6.45E-01	control	5.5	38032	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane							
26991851	PP_5175		efflux transporter RND family, MFP subunit	1.2	9.12E-01	control	6.5	38304	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane							
26991868	PP_5192	gcvP-2	glycine dehydrogenase	3.2	2.09E-01	EG	6.3	104037	2	Cytoplasmic	COG1003	Amino acid transport and metabolism							
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.9	3.47E-01	EG	12.3	8922	3	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis							
26991980	PP_5304		lipoprotein	1.7	3.22E-01	EG	5.1	26284	2	Unknown									
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.0	7.51E-01	control	5.3	65626	4	Cytoplasmic	COG5016	Energy production and conversion							
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.1	3.03E-01	EG	6.5	51942	6	Cytoplasmic	COG0439	Lipid metabolism							
26992029	PP_5353		hypothetical protein	1.9	2.07E-01	EG	7.2	30672	3	Cytoplasmic Membrane	COG4395	Function unknown							
26992055	PP_5379	copB	copper resistance B precursor	2.1	1.97E-01	EG	5	40230	2	Outer Membrane	COG3667	Inorganic ion transport and metabolism							
26992070	PP_5395		hypothetical protein	1.6	3.50E-01	EG	5.6	31623	4	Cytoplasmic	COG1568	General function prediction only							
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.0	8.89E-01	control	4.6	49359	15	Cytoplasmic	COG0055	Energy production and conversion							
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.4	2.07E-01	EG	9.2	31464	9	Cytoplasmic	COG0224	Energy production and conversion							
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.0	9.34E-01	control	5.2	55352	19	Cytoplasmic	COG0056	Energy production and conversion							
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.3	2.13E-01	control	5.3	16898	9	Cytoplasmic Membrane	COG0711	Energy production and conversion							
313496770				1.1	6.16E-01	control			19										
24986476				1.4	4.68E-02	EG			13										
148550051				1.1	4.72E-01	control			13										
313498866				1.1	6.85E-01	control			12										
24983268				1.1	4.85E-01	EG			11										
24981839				1.4	3.72E-01	EG			9										
24981833				1.1	6.05E-01	EG			7										
24982353				1.1	7.34E-01	EG			5										
313498081				1.5	1.83E-01	EG			5										
24982083				1.5	8.46E-02	EG			4										
148545524				1.2	5.52E-01	EG			4										
15599454				1.1	9.39E-01	control			3										

269200090	1.7	2.59E-03	control	3
313500100	1.1	6.81E-01	control	3
148546787	4.8	7.05E-02	EG	2
148548654	1.1	8.29E-01	EG	2



1D-SDS-PAGE der Membranfraktion von mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.1.2.1 Membranfraktion_P_putida_KT2440_GXS_Tabelle

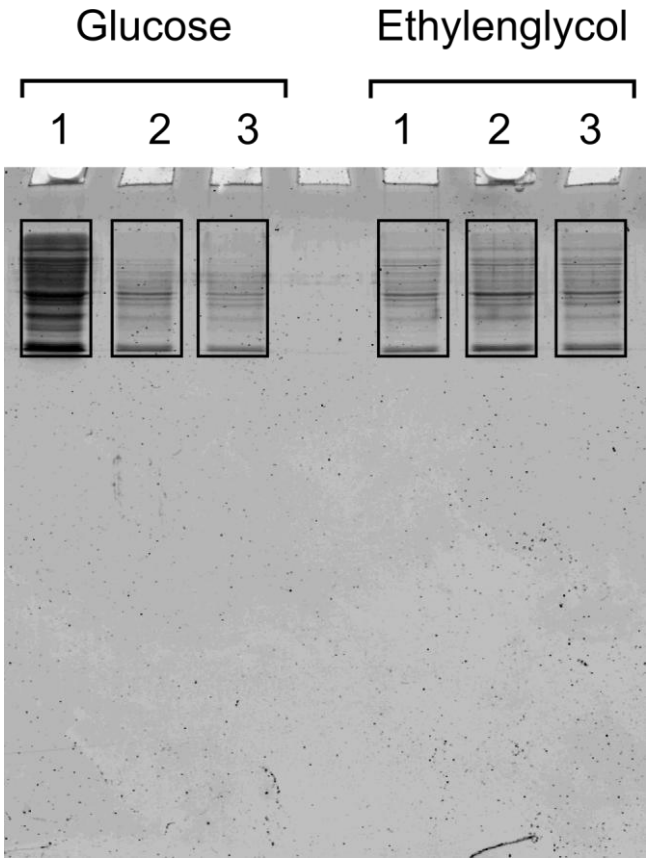
gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.3	3.17E-01	control	9.1	61919	13	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986771	PP_0026		CDF family cobalt/cadmium/zinc transporter	1.0	5.56E-01	GXS	5.5	32393	2	Cytoplasmic Membrane	COG1230	Inorganic ion transport and metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.5	1.38E-01	control	4.9	75112	5	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.3	7.00E-01	GXS	6.8	42059	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.2	6.68E-01	control	8.2	22960	3	Cytoplasmic Membrane	COG1999	General function prediction only	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	2.0	8.03E-01	control	7.3	50185	4	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.7	2.38E-01	GXS	6.3	71284	11	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.1	6.46E-01	GXS	7.8	51116	8	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.1	8.45E-01	control	7.7	78583	15	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986924	PP_0180		cytochrome c family protein	1.5	3.54E-01	control	4.9	68013	7	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	1.1	7.50E-01	control	5.4	52061	3	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.2	5.58E-01	control	9.6	46030	16	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986943	PP_0199		hypothetical protein	2.1	2.82E-01	control	6.8	27782	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.4	3.29E-01	control	5.2	51549	9	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.4	2.95E-01	control	6.1	44824	7	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.3	5.59E-01	GXS	5.4	48317	25	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.1	9.33E-01	GXS	5.2	15616	13	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.0	8.58E-01	control	6.1	47787	8	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.3	2.54E-01	control	6.0	80277	13	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.2	4.73E-01	control	5.3	55654	10	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.4	6.07E-01	GXS	5.6	99332	48	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	2.7	1.50E-02	control	5.3	109432	2	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	6.93E-01	control	5.8	65541	9	Cytoplasmic	COG1960	Lipid metabolism	
26987128	PP_0386		sensory box protein	1.3	3.98E-01	control	5.6	139392	5	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	4.2	2.66E-01	GXS	4.6	69396	5	Cytoplasmic	COG0568	Transcription	
26987138	PP_0396		hypothetical protein	1.6	2.68E-01	control	7.0	50488	7	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.1	7.67E-01	GXS	5.8	73782	28	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987159	PP_0418		GDSL family lipase	1.5	2.71E-01	control	4.4	67175	2	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987184	PP_0443	rplK	50S ribosomal protein L11	1.7	5.83E-01	GXS	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	2.3	1.16E-01	control	10.1	24251	3	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	2.1	3.31E-01	control	10.2	17686	11	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	1.2	6.62E-01	control	4.4	12599	2	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.0	7.66E-01	GXS	5.5	150992	53	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.7	8.69E-01	GXS	7.2	154797	42	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	2.1	6.98E-01	GXS	11.7	13727	2	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	2.2	7.05E-01	control	10.8	17578	9	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.6	9.02E-01	GXS	4.9	78817	39	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.3	2.93E-01	control	5.0	43478	35	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.2	7.01E-01	GXS	10.3	21811	7	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	4.8	7.40E-01	GXS	11.7	29669	9	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.6	9.26E-01	GXS	11.9	15373	3	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.5	5.63E-01	control	11.6	13410	10	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.0	7.89E-01	GXS	10.3	20329	9	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.4	7.62E-01	control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	2.2	2.24E-01	control	10.2	13975	3	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.5	3.20E-01	GXS	10.9	12628	4	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.6	5.98E-01	GXS	10.6	17666	9	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.1	9.54E-01	control	11.5	15189	4	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.2	4.86E-01	GXS	10.4	47853	7	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.3	7.37E-01	control	11.3	13256	5	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	2.0	4.93E-01	control	11.5	13660	4	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.4	8.79E-01	GXS	10.5	23056	10	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.4	5.42E-01	control	4.7	36629	4	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	2.0	1.33E-01	control	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.1	4.44E-01	control	4.6	17972	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	2.7	1.44E-01	GXS	4.8	24196	2	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	1.7	1.06E-01	control	9.7	45834	9	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	1.2	4.98E-01	control	7.2	25648	3	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987255	PP_0517	ribH	6,7-dimethyl-8-ribityllumazine synthase	1.3	4.95E-01	GXS	5.2	16420	2	Cytoplasmic	COG0054	Coenzyme metabolism	
26987282	PP_0544		ethanolamine transproter	1.0	5.21E-01	GXS	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.3	3.81E-01	control	5.9	55268	13	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.2	6.99E-01	control	6.5	49088	6	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	2.2	3.56E-01	GXS	6.6	40223	4	Unknown	COG5345	Function unknown	
26987308	PP_0570		alpha-2-macroglobulin domain protein	1.3	4.68E-01	control	5.2	178472	4	Unknown	COG2373	General function prediction only	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.1	9.70E-01	control	5.0	69953	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	4.2	7.16E-02	control	6.6	83475	2	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	3.0	2.22E-01	control	6.0	105800	3	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	6.5	3.58E-01	GXS	5.2	94861	3	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.0	2.48E-01	GXS	6.2	44897	5	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.7	2.01E-01	control	5.3	61860	6	Cytoplasmic	COG0488	General function prediction only	
26987416	PP_0680		ATP-dependent protease	4.2	1.24E-01	control	4.5	89677	2	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987443	PP_0707		MscS mechanosensitive ion channel	1.4	1.86E-01	GXS	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987448	PP_0712		hypothetical protein	1.0	9.05E-01	control	10.5	31284	3	Cytoplasmic	COG2326	Function unknown	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.2	5.92E-01	control	8.4	54282	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.2	6.25E-01	GXS	9.5	20483	7	Unknown			
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.3	5.69E-01	control	5.5	62125	9	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.3	9.04E-01	GXS	5.0	67937	20	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.1	7.34E-01	control	9.6	50572	6	Unknown			
26987531	PP_0795	fruA	PTS system, fructose subfamily, IIC subunit	1.4	8.86E-01	control	8.7	59235	3	Cytoplasmic Membrane	COG1299	Carbohydrate transport and metabolism	
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding protein	2.4	2.54E-01	control	9.2	79558	3	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.8	4.02E-01	control	6.7	34557	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.2	5.14E-01	control	9.6	66913	15	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.8	3.08E-01	control	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.1	9.36E-01	GXS	6.6	29753	4	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987619	PP_0883		outer membrane porin	1.1	8.92E-01	control	6.6	50256	11	Outer Membrane			
26987642	PP_0906		multidrug efflux protein	2.3	2.80E-01	control	4.8	110352	6	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26987645	PP_0909		hypothetical protein	2.1	1.37E-01	control	6.4	38380	9	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	2.4	4.67E-01	GXS	4.4	47019	15	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.1	6.96E-01	control	5.8	78578	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.0	7.61E-01	GXS	6.2	51518	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	

26987680	PP_0944	fumC	fumarate hydratase	1.8	1.14E-01	control	5.9	48541	15	Cytoplasmic	COG0114	Energy production and conversion	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.0	7.31E-01	GXS	5.1	107495	10	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.8	1.90E-01	control	7.4	52433	11	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.0	6.67E-01	control	9.7	41323	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987735	PP_0999	arcC	carbamate kinase	1.4	6.57E-01	control	5.5	33423	3	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	1.5	2.78E-01	control	6.3	37911	10	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	1.4	5.04E-02	control	5.7	46462	20	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.2	6.92E-01	control	9.1	51061	4	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.7	1.91E-01	GXS	7.0	36057	5	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.3	5.42E-01	control	6.4	65359	6	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.6	2.05E-01	GXS	6.2	45449	5	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.0	9.43E-01	GXS	10.1	33781	5	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	2.1	2.28E-01	control	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.4	5.65E-01	GXS	6.7	41895	2	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.8	3.36E-01	GXS	5.9	49646	22	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.5	2.53E-01	control	6.8	55000	11	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.2	3.79E-01	GXS	6.7	25476	7	Unknown	COG0363	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	3.0	4.83E-02	control	5.1	61712	3	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.7	4.24E-02	control	5.2	58204	7	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.9	2.05E-02	control	4.7	140818	27	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987794	PP_1058		hypothetical protein	1.4	3.02E-01	control	9.5	117041	9	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	2.0	3.19E-01	control	8.2	27464	6	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	3.7	2.36E-01	control	8.9	33428	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987818	PP_1082	bfr	bacterioferritin	1.9	2.04E-01	control	4.4	17971	7	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.6	1.66E-01	control	4.9	21730	6	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987844	PP_1108		acylase	1.1	9.01E-01	GXS	8.7	88728	7	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.1	8.37E-01	control	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.7	3.74E-01	GXS	4.7	27345	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.5	1.11E-01	GXS	9.3	15682	8	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	1.4	6.15E-01	control	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.8	7.44E-01	control	4.8	105994	2	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987890	PP_1154		sensory box protein	1.2	4.61E-01	control	5.7	95980	11	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987893	PP_1157		acetolactate synthase	2.4	2.31E-01	control	6.1	60059	4	Cytoplasmic	COG0028	Coenzyme metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.0	8.50E-01	GXS	5.7	106948	9	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987936	PP_1201		virulence factor family protein	2.0	1.56E-01	control	5.0	46885	3	Unknown	COG3946	Intracellular trafficking and secretion	
26987937	PP_1202		hypothetical protein	1.3	4.55E-01	control	9.7	95622	2	Cytoplasmic Membrane	COG2898	Function unknown	
26987941	PP_1206	oprD	outer membrane porin	1.2	4.17E-01	control	4.6	46120	20	Outer Membrane			
26987945	PP_1210		DNA-binding stress protein	1.5	4.98E-01	control	5.0	17861	3	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.6	9.72E-02	control	5.1	66568	9	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987957	PP_1222	tolB	translocation protein TolB	2.3	4.19E-01	GXS	9.8	47431	4	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.1	4.15E-01	control	4.9	17833	12	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988009	PP_1274		short chain dehydrogenase	1.9	2.67E-01	control	10.2	28618	2	Cytoplasmic	COG0300	General function prediction only	
26988026	PP_1291		PhoH family protein	1.1	5.05E-01	GXS	5.7	51856	2	Cytoplasmic	COG1875	General function prediction only	
26988044	PP_1309		hypothetical protein	1.3	6.10E-01	control	6.3	16018	3	Unknown	COG3105	Function unknown	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.8	5.14E-01	control	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.8	3.01E-01	control	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.2	8.60E-01	GXS	7.1	29032	4	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	2.2	2.22E-01	control	7.5	64637	7	Cytoplasmic Membrane	COG3107	General function prediction only	
26988068	PP_1334	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	1.7	8.11E-01	control	10.0	39307	2	Cytoplasmic Membrane	COG0472	Cell envelope biogenesis, outer membrane	
26988095	PP_1361	groEL	chaperonin GroEL	1.2	4.77E-01	control	4.7	56743	12	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	5.3	6.17E-01	GXS	6.7	52057	5	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.8	3.61E-02	control	4.8	67652	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988106	PP_1372		hypothetical protein	1.6	3.26E-01	GXS	6.5	52321	2	Unknown	COG0433	Replication, recombination, and repair	
26988116	PP_1382		hypothetical protein	2.0	9.53E-01	control	9.1	18936	2	Cytoplasmic Membrane	COG4539	Function unknown	
26988117	PP_1383		BenF-like porin	1.3	5.00E-01	control	6.8	46022	4	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.0	7.34E-01	control	5.1	52864	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.2	5.48E-01	control	5.3	112835	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988152	PP_1419		outer membrane porin	1.0	7.68E-01	GXS	4.9	46644	3	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	1.3	4.57E-01	control	9.2	32060	7	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988176	PP_1443	lon-1	ATP-dependent protease La	1.4	3.53E-01	GXS	6.4	89794	2	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.3	2.25E-02	control	6.0	86581	30	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988179	PP_1446		TonB-dependent receptor	1.9	3.17E-01	GXS	4.9	74207	9	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	1.1	8.12E-01	control	9	45563	2	Cytoplasmic Membrane			
26988198	PP_1465	rplS	50S ribosomal protein L19	1.5	4.26E-01	GXS	11.0	13012	4	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	1.0	7.43E-01	control	6.2	51645	10	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.9	6.37E-02	control	5.7	50918	3	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.8	2.93E-01	control	4.7	58605	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.1	7.40E-01	control	6.6	96963	5	Cytoplasmic	COG2352	Energy production and conversion	
26988258	PP_1526		beta-(1-3)-glucosyl transferase	1.7	3.72E-01	control	8.1	97324	4	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	5.20E-01	control	9.3	27023	15	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.8	3.30E-01	GXS	4.7	86513	2	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988342	PP_1610	pyrG	CTP synthetase	1.9	5.75E-02	control	5.8	59474	7	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	2.1	2.60E-01	control	4.7	45490	4	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	1.2	4.89E-01	control	4.8	16590	2	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26988393	PP_1661		dehydrogenase subunit	1.9	2.45E-01	control	5.5	81020	5	Extracellular	COG2303	Amino acid transport and metabolism	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.7	4.33E-02	GXS	5.4	45693	3	Outer Membrane	COG2067	Lipid metabolism	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.1	8.83E-01	control	4.8	26520	3	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988474	PP_1743	actP	acetate permease	4.2	2.54E-03	GXS	9.6	58972	6	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	1.8	7.38E-01	GXS	8.2	57637	2	Cytoplasmic	COG2326	Function unknown	
26988486	PP_1755	fumC-2	fumarate hydratase	1.5	2.82E-01	control	6.4	49131	8	Cytoplasmic	COG0114	Energy production and conversion	
26988492	PP_1761		sensory box protein/GGDEF family protein	1.2	4.06E-01	GXS	6.8	108193	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.2	5.51E-01	control	4.7	102037	3	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	1.6	3.29E-01	control	6.4	79133	2	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1.2	4.93E-01	control	5.2	52989	2	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP_1780		mannosyltransferase	1.7	6.00E-01	GXS	5.8	180042	4	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	1.3	5.17E-01	control	6.4	128499	5	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.1	6.12E-01	control	6.4	40124	6	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988538	PP_1808	pgi	glucose-6-phosphate isomerase	1.7	3.94E-01	control	6.8	61383	5	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26988568	PP_1838		hypothetical protein	1.3	4.25E-01	control	6.8	76615	8	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988601	PP_1871	htpX	heat shock protein HtpX	1.2	9.61E-01	GXS	7.2	32199	2	Cytoplasmic Membrane	COG0501	Posttranslational modification, protein turnover, chaperones	
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.4	2.50E-01	control	6.9	89194	25	Cytoplasmic Membrane	COG1960	Lipid metabolism	

26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.6	4.73E-01	control	4.7	120904	2	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.1	8.19E-01	control	6.0	25470	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988686	PP_1959		hypothetical protein	2.0	1.41E-01	GXS	6.4	43578	2	Unknown			
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.1	9.61E-01	GXS	5.9	43290	11	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	2.3	7.69E-02	control	5.6	56483	7	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.7	9.63E-01	GXS	4.8	38824	2	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.1	7.76E-01	control	5.3	40672	3	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.2	6.16E-01	control	3.9	96918	25	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.3	5.83E-01	control	7.8	32510	3	Cytoplasmic	COG0777	Lipid metabolism	
26988723	PP_1998		sporulation domain protein	1.2	3.42E-01	GXS	10.1	22947	2	Cytoplasmic Membrane	COG3147	Function unknown	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.5	8.69E-01	GXS	6.5	55400	5	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988731	PP_2006		hypothetical protein	2.0	5.86E-02	control	5.1	63743	44	Unknown			
26988732	PP_2007		P-47-related protein	2.1	7.72E-03	control	5.8	44707	11	Unknown			
26988742	PP_2017	pepN	aminopeptidase N	1.4	9.88E-01	GXS	4.8	99573	6	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988744	PP_2019		hypothetical protein	1.2	7.83E-01	control	6.6	87732	3	Cytoplasmic Membrane	COG1033	General function prediction only	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.5	8.67E-03	control	5.8	187043	35	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.5	1.67E-01	control	4.8	86015	10	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.0	8.91E-01	GXS	5.8	29111	4	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.3	6.56E-01	control	4.5	37012	32	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988830	PP_2105		hypothetical protein	1.0	9.75E-01	control	4.9	11370	3	Unknown	COG4575	Function unknown	
26988836	PP_2112	acnA	aconitate hydratase	2.2	3.84E-02	control	5.7	99147	6	Cytoplasmic	COG1048	Energy production and conversion	
26988854	PP_2130		soluble lytic transglycosylase	1.1	6.39E-01	control	9.9	75337	6	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.9	8.97E-02	control	5.9	77449	2	Cytoplasmic	COG1250	Lipid metabolism	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.0	8.77E-01	control	7.7	53014	13	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	3.9	8.70E-01	GXS	5.3	26061	3	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988911	PP_2187		universal stress protein	3.7	1.91E-01	control	6.3	31384	2	Cytoplasmic	COG0589	Signal transduction mechanisms	
26988913	PP_2189		hypothetical protein	3.5	3.93E-02	control	4.9	15175	2	Unknown	COG4575	Function unknown	
26988964	PP_2240		ABC transporter	1.3	6.04E-01	control	9.6	70269	4	Cytoplasmic Membrane	COG4178	General function prediction only	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.1	9.43E-01	control	5.1	68646	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989026	PP_2302	lon-2	ATP-dependent protease La	1.0	8.92E-01	GXS	5.9	88722	4	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.5	2.53E-01	GXS	9.3	9997	3	Unknown			
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.1	9.80E-01	GXS	8.5	8801	4	Outer Membrane			
26989051	PP_2327	cysB	transcriptional regulator CysB	1.6	3.54E-01	control	6.7	35955	4	Cytoplasmic	COG0583	Transcription	
26989055	PP_2331		hypothetical protein	1.2	3.29E-01	GXS	7.9	57064	6	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.0	7.80E-01	GXS	5.0	93609	10	Cytoplasmic	COG1049	Energy production and conversion	
26989145	PP_2422		alkylhydroperoxidase-like protein	1.1	9.93E-01	GXS	7.4	12135	2	Unknown	COG0599	Function unknown	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	2.1	5.57E-01	GXS	5.8	72697	10	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.5	5.23E-01	control	12.1	13280	2	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989283	PP_2563		antibiotic biosynthesis protein	3.4	4.95E-01	control	7.1	100863	3	Cytoplasmic Membrane	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26989289	PP_2569		major facilitator transporter	1.6	5.75E-02	control	9.0	60538	8	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989572	PP_2853		hypothetical protein	3.3	2.57E-01	GXS	4.5	46020	4	Unknown			
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.9	1.28E-01	control	6.1	64654	3	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989663	PP_2944		sensor histidine kinase	1.6	4.22E-02	GXS	6.1	67470	6	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989808	PP_3089		hypothetical protein	1.1	9.59E-01	GXS	5.3	19453	3	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	1.6	2.73E-01	control	6.8	138655	14	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	2.5	1.42E-01	control	5.7	26868	4	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989818	PP_3099		hypothetical protein	5.2	1.84E-03	control	4.9	56072	25	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989819	PP_3100		hypothetical protein	13.6	1.61E-02	control	7.7	21741	3	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.4	3.12E-01	control	9.0	57141	16	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989853	PP_3134		transferase hexapeptide repeat containing protein	5.5	8.39E-02	control	9.9	25699	2	Cytoplasmic	COG0110	General function prediction only	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.2	6.87E-01	control	9.4	43092	4	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989861	PP_3142		sugar transferase	3.5	1.26E-01	control	9.1	53464	2	Cytoplasmic Membrane	COG2148	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	2.0	3.11E-01	GXS	9.7	29885	10	Unknown			
26990043	PP_3325		outer membrane ferric siderophore receptor	1.7	3.59E-01	GXS	4.8	76226	11	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990092	PP_3377		major facilitator transporter	2.9	2.14E-01	control	9.6	47449	2	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	1.3	2.28E-01	control	8.9	47532	11	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990134	PP_3421		sensor histidine kinase	1.2	6.35E-01	GXS	7.4	53788	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.6	2.06E-02	control	6.2	59980	5	Cytoplasmic	COG1012	Energy production and conversion	
26990161	PP_3448	nfrB	bacteriophage N4 adsorption protein B	1.8	3.02E-01	control	7.4	82370	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	2.0	1.31E-01	control	6.9	85338	17	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	1.4	2.94E-01	control	5.2	53952	5	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990296	PP_3585		efflux transporter RND family, MFP subunit	1.1	7.64E-01	GXS	9.4	46468	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990373	PP_3662		decarboxylase family protein	2.9	2.15E-01	control	6.7	50729	3	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	1.5	6.36E-01	GXS	5.8	82061	16	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990399	PP_3691		DNA helicase-related protein	3.8	2.09E-01	control	5.0	245278	5	Unknown	COG1112	DNA replication, recombination, and repair	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.4	3.70E-01	control	4.9	129450	24	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	1.1	5.88E-01	control	6.4	41164	9	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	1.2	5.51E-01	control	6.2	27714	5	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	2.8	1.65E-01	control	5.3	30957	3	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990662	PP_3957		choline/carnitine/betaine transporter family protein	1.2	4.31E-01	GXS	7.6	72789	5	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane	
26990693	PP_3988		hypothetical protein	4.7	3.81E-01	GXS	6.3	76259	3	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	1.2	9.97E-01	GXS	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.2	5.67E-01	GXS	5.4	45695	5	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.4	4.74E-01	control	5.4	79899	3	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	3.3	6.64E-01	control	5.9	50555	4	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.2	6.78E-01	GXS	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990744	PP_4043	gnd	6-phosphogluconate dehydrogenase	1.2	8.01E-01	GXS	6.4	35366	2	Cytoplasmic	COG1023	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	1.2	4.78E-01	GXS	6.6	103167	4	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	1.6	4.84E-01	control	5.1	81044	3	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990759	PP_4058	glgB	glycogen branching enzyme	3.7	5.47E-02	control	5.9	82877	2	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990806	PP_4111	fusA	elongation factor G	3.8	9.69E-03	control	5.0	77832	2	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990809	PP_4115		NolW domain protein	1.3	8.80E-01	GXS	6.7	29306	2	Unknown			
26990810	PP_4116	aceA	isocitrate lyase	1.3	7.14E-01	control	5.3	48633	4	Cytoplasmic	COG2224	Energy production and conversion	
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	1.4	3.42E-01	control	10.4	15085	2	Cytoplasmic Membrane	COG0838	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.4	3.59E-01	control	6.5	67609	2	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	2.1	3.75E-01	GXS	5.9	97582	3	Unknown	COG1034	Energy production and conversion	
26990865	PP_4173		integral membrane sensor hybrid histidine kinase	1.9	2.72E-01	control	5.4	70995	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.1	7.72E-01	GXS	5.3	43264	2	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.5	2.63E-01	control	6.2	30111	10	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.2	2.48E-01	control	6.1	41239	19	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.5	3.83E-01	control	6.3	49912	5	Cytoplasmic	COG1249	Energy production and conversion	

26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.1	8.95E-01	GXS	5.1	42434	8	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.4	7.07E-01	GXS	6.5	106521	26	Cytoplasmic	COG0567	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	7.86E-01	GXS	6.2	63448	11	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	5.0	5.30E-02	GXS	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.0	8.07E-01	GXS	10.3	13813	3	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.3	8.28E-01	GXS	7.0	47622	7	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.5	5.50E-01	control	9.7	26361	5	Unknown	COG2086	Energy production and conversion	
26990903	PP_4211		RND efflux transporter	1.3	1.13E-01	GXS	8.2	51199	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990905	PP_4213		dipeptidase	1.2	5.28E-01	GXS	5.0	50104	4	Unknown	COG2355	Amino acid transport and metabolism	
26990906	PP_4214		aminotransferase, class V	1.2	4.37E-01	control	7.6	47747	5	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
26990908	PP_4216	pvdE	cyclic peptide transporter	1.7	1.53E-01	GXS	7.4	61169	5	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.6	2.68E-01	GXS	5.5	89725	41	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.8	3.28E-01	control	5.2	35613	6	Unknown	COG2010	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	1.3	3.52E-01	control	6.0	35312	11	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26990980	PP_4289		hypothetical protein	1.0	9.82E-01	control	8.4	48415	2	Cytoplasmic Membrane	COG3748	Function unknown	
26991021	PP_4331		hypothetical protein	1.3	3.99E-01	GXS	5.2	14696	2	Unknown			
26991032	PP_4342	fleN	flagellar number regulator FleN	19.1	3.79E-01	GXS	8.0	29670	2	Cytoplasmic Membrane	COG0455	Cell motility	
26991058	PP_4369	fliF	flagellar MS-ring protein	1.2	6.28E-01	control	4.5	63090	3	Cytoplasmic Membrane	COG1766	Cell motility and secretion	
26991087	PP_4398		major facilitator family transporter	2.4	2.24E-01	GXS	7.8	47583	2	Cytoplasmic Membrane			
26991134	PP_4448		hypothetical protein	1.3	6.88E-01	GXS	6	66331	8	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.5	3.12E-01	control	5.1	94711	5	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.7	4.55E-02	control	6.5	43490	4	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	2.2	4.41E-02	GXS	6.4	71796	2	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.5	8.05E-02	GXS	5.4	50393	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	1.0	7.77E-01	control	6.4	56605	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991226	PP_4542		ABC transporter ATP-binding protein/permease	1.6	3.80E-01	control	7.6	67748	3	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.8	2.86E-01	control	7.7	61812	4	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991325	PP_4641	cstA	carbon starvation protein CstA	1.2	4.02E-01	control	9.0	73763	12	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	2.8	2.27E-02	GXS	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	2.1	2.70E-01	GXS	9.1	53016	2	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.3	4.73E-01	GXS	4.8	68764	6	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.2	5.54E-01	GXS	5.4	36370	7	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991388	PP_4704		hypothetical protein	1.9	1.87E-01	control	5.6	107252	9	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.5	1.45E-01	control	4.9	75010	11	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.2	7.93E-01	control	6.8	91460	9	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.6	2.38E-01	control	5.4	69722	17	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.7	2.39E-01	control	4.6	68800	6	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	3.2	6.28E-02	GXS	6.2	35615	1	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26991474	PP_4794	leuS	leucyl-tRNA synthetase	2.4	7.57E-01	GXS	5.6	96697	8	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	1.7	4.77E-01	GXS	6.1	22414	2	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.9	8.42E-02	control	6.5	57695	4	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991504	PP_4824		integral membrane sensor hybrid histidine kinase	2.1	8.31E-02	GXS	6.6	101587	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	1.2	4.92E-01	control	5.0	31015	4	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991518	PP_4838	oprC	TonB-dependent copper receptor	1.3	3.28E-01	GXS	6.2	74540	35	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	2.9	6.59E-01	control	6.2	40270	2	Periplasmic	COG0683	Amino acid transport and metabolism	
26991556	PP_4876	rpsR	30S ribosomal protein S18	2.3	4.65E-01	GXS	11.3	8927	2	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.2	8.37E-01	GXS	7.9	96688	5	Cytoplasmic	COG0557	Transcription	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	2.2	8.55E-02	control	6.1	71958	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	2.6	1.76E-01	control	5.6	46833	3	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.4	2.54E-01	GXS	9.8	33001	17	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.2	5.95E-01	GXS	5.1	44762	8	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991588	PP_4910		hypothetical protein	1.2	4.73E-01	control	4.7	53632	10	Cytoplasmic	COG3726	General function prediction only	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.2	7.53E-01	control	5.2	52637	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.8	3.00E-01	control	7.6	66279	5	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991622	PP_4944		carbamoyltransferase	1.9	1.96E-01	control	7.2	65646	3	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	1.3	4.44E-01	GXS	6.3	142580	2	Cytoplasmic	COG4230	Energy production and conversion	
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.3	4.96E-01	control	5.6	38453	3	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991643	PP_4965	tktA	transketolase	1.1	8.12E-01	control	5.0	72463	14	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.3	3.73E-02	control	5.1	42779	11	Cytoplasmic	COG0192	Coenzyme metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.1	9.10E-01	control	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	1.7	1.29E-01	control	7.4	62241	3	Cytoplasmic	COG3243	Lipid metabolism	
26991682	PP_5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	1.0	9.54E-01	GXS	9.6	62722	8	Cytoplasmic	COG3243	Lipid metabolism	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	6.5	4.24E-01	GXS	10.9	26214	4	Cytoplasmic	COG3937	Function unknown	
26991685	PP_5008		poly(hydroxyalkanoate) granule-associated protein	1.5	8.67E-01	control	9.7	15550	9	Cytoplasmic			
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.2	4.48E-01	control	4.9	69017	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.2	8.83E-01	control	8.3	95875	3	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.5	1.78E-01	control	6.4	92004	13	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.2	5.59E-01	GXS	5.3	67157	2	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.0	7.60E-01	control	5.1	51740	13	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991731	PP_5055		rhodanese domain-containing protein	1.6	4.41E-01	control	9.9	14839	4	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991743	PP_5067		potassium efflux protein KefA	2.9	1.75E-01	control	8.9	122371	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.6	7.68E-01	control	6.2	161772	5	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	3.6	1.72E-02	control	4.9	45127	10	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.2	4.98E-01	GXS	5.7	63668	7	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991785	PP_5109	ftsX	hypothetical protein	1.4	9.71E-01	GXS	6.5	36984	4	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991786	PP_5110	ftsE	cell division ATP-binding protein FtsE	1.1	6.13E-01	control	11.0	24830	2	Cytoplasmic Membrane	COG2884	Cell division and chromosome partitioning	
26991794	PP_5118		rhodanese domain protein	1.6	3.62E-01	control	5.6	30750	2	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.5	1.87E-01	control	5.8	65671	7	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.0	5.46E-01	control	6.3	44339	3	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	1.6	3.56E-01	control	5.4	112277	13	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991851	PP_5175		efflux transporter RND family, MFP subunit	2.0	7.55E-01	control	6.5	38304	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.0	8.00E-01	GXS	6.3	104037	4	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991893	PP_5217	ppk	polyphosphate kinase	1.4	3.56E-01	GXS	7.8	81732	4	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28	5.3	5.73E-01	GXS	12.3	8922	2	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991983	PP_5307	exbD	biopolymer transport protein ExbD	1.1	8.97E-01	GXS	4.5	15269	2	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.2	9.97E-01	GXS	5.3	65626	13	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.5	3.57E-01	control	6.5	51942	9	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.1	6.28E-01	GXS	7.2	30672	4	Cytoplasmic Membrane	COG4395	Function unknown	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	6.37E-01	GXS	4.6	49359	5	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.1	6.76E-01	GXS	9.2	31464	10	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.1	8.38E-01	GXS	5.2	55352	17	Cytoplasmic	COG0056	Energy production and conversion	

26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	2.0	2.03E-01	GXS	5.3	16898	6	Cytoplasmic Membrane	COG0711	Energy production and conversion
24986476				1.3	4.56E-02	control			21			
24983268				1.4	1.14E-01	control			13			
148550051				1.1	3.78E-01	control			9			
313498866				1.2	5.45E-01	control			8			
313496770				1.2	5.48E-01	control			8			
24981833				1.1	4.66E-01	control			7			
148545524				2.2	4.79E-02	control			6			
148546305				1.1	4.21E-01	control			5			
24982083				1.4	5.09E-01	control			4			
15599454				1.2	8.12E-01	control			4			
24981839				1.6	9.88E-01	GXS			4			
269200090				1.2	8.47E-01	GXS			3			
128169				2.1	6.78E-01	GXS			2			



1D-SDS-PAGE der Membranfraktion von mit Ethylenglycol behandelten und unbehandelten Zellen von *P. putida* GN259. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.1.2.2 Membranfraktion_P_putida_GN259_EG_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.3	4.74E-01	control	9.1	61919	16	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.5	9.65E-01	control	4.9	40718	10	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.1	6.00E-01	EG	5.8	90030	3	Unknown	COG0187	DNA replication, recombination, and repair	
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.5	8.52E-01	control	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.4	7.97E-02	control	4.9	75112	11	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.2	4.73E-01	EG	4.8	36024	2	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.9	2.07E-01	EG	8.1	34224	6	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1.6	3.00E-01	EG	5.0	28482	2	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.2	7.46E-01	EG	6.4	44046	2	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986841	PP_0096	prlC	oligopeptidase A	1.5	1.15E-01	EG	5.0	75721	4	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.3	6.22E-01	control	6.8	42059	2	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.5	4.47E-01	control	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.6	2.15E-01	EG	7.4	25597	2	Unknown			
26986890	PP_0145		sodium-dependent inorganic phosphate (Pi) transporter	2.8	7.29E-01	control	9.8	59817	2	Cytoplasmic Membrane	COG1283	Inorganic ion transport and metabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.1	5.31E-01	control	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.5	2.49E-01	control	6.3	71284	6	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	2.1	8.06E-01	control	7.8	51116	2	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.5	5.16E-01	control	7.7	78583	8	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986924	PP_0180		cytochrome c family protein	1.1	6.60E-01	control	4.9	68013	9	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	1.1	6.42E-01	EG	5.4	52061	6	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.4	2.75E-01	control	9.6	46030	9	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	106.5	1.76E-01	control	11.3	32300	6	Cytoplasmic			
26986943	PP_0199		hypothetical protein	2.3	4.84E-01	control	6.8	27782	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.2	4.50E-01	EG	5.2	51549	8	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.4	1.26E-01	EG	6.1	44824	7	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986969	PP_0226		polar amino acid ABC transporter inner membrane subunit	2.4	2.21E-01	control	9.1	24515	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.4	4.44E-01	EG	5.4	48317	28	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.1	6.70E-01	control	5.2	15616	9	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.1	5.51E-01	EG	6.1	47787	3	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.3	9.40E-01	control	6.0	80277	10	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	1.0	6.25E-01	EG	4.7	24565	2	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.0	7.14E-01	EG	5.3	55654	15	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.0	8.20E-01	EG	5.6	99332	55	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	2.3	3.53E-01	control	5.3	109432	6	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987095	PP_0353		DNA polymerase III, epsilon subunit	1.2	7.36E-01	control	6.9	26369	2	Cytoplasmic	COG2176	DNA replication, recombination, and repair	
26987096	PP_0354		CBS domain-containing protein	1.2	9.07E-01	control	7.4	72323	10	Cytoplasmic	COG2905	Signal transduction mechanisms	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	6.59E-01	control	5.8	65541	6	Cytoplasmic	COG1960	Lipid metabolism	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	5.7	4.79E-03	EG	6.8	29075	4	Cytoplasmic	COG5424	Coenzyme metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.5	5.72E-01	control	4.6	69396	16	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	10.3	5.82E-01	control	11.4	8370	4	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987137	PP_0395		SpoVR family protein	1.0	9.14E-01	control	5.4	61330	3	Cytoplasmic	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	1.0	9.55E-01	EG	7.0	50488	8	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.9	7.86E-02	control	5.8	73782	32	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.2	9.17E-01	control	6.8	36277	9	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987181	PP_0440	tuf	elongation factor Tu	1.4	1.66E-01	EG	5.0	43495	2	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	1.4	3.89E-01	control	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.5	3.47E-01	control	10.1	24251	6	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.1	5.59E-01	EG	10.2	17686	13	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	1.2	6.43E-01	EG	4.4	12599	3	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.4	3.75E-01	control	5.5	150992	76	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.7	2.94E-01	control	7.2	154797	64	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	5.2	5.03E-01	control	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	2.4	8.50E-01	control	10.8	17578	10	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.3	1.88E-01	control	4.9	78817	44	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.4	3.09E-01	EG	5.0	43478	32	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	1.7	1.00E-01	control	10.5	11753	3	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.1	4.61E-01	control	10.3	21811	7	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	3.3	1.63E-01	control	10.7	10900	4	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	15.2	2.87E-01	control	11.7	29669	13	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987199	PP_0458	rpsS	30S ribosomal protein S19	21.7	3.54E-01	control	11.3	10348	4	Cytoplasmic	COG0185	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	11.5	1.33E-01	control	11.9	15373	6	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987204	PP_0463	rpsQ	30S ribosomal protein S17	2.8	5.97E-01	control	10.5	10058	2	Cytoplasmic	COG0186	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	2.1	4.19E-01	control	11.6	13410	11	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987206	PP_0465	rplX	50S ribosomal protein L24	24.2	3.42E-01	control	10.8	11329	4	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.8	9.87E-02	control	10.3	20329	16	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	2.8	3.36E-01	control	12.3	11403	2	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.0	7.91E-01	control	10.2	13975	6	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	2.9	2.80E-01	control	10.4	19143	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.5	3.56E-01	control	10.9	12628	6	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.9	3.90E-01	control	10.6	17666	10	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	3.7	3.45E-01	control	11.5	15189	8	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.4	3.87E-01	control	10.4	47853	8	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	3.8	5.14E-01	control	11.3	13256	8	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	13.0	3.73E-01	control	11.5	13660	5	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	2.2	2.15E-01	control	10.5	23056	12	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.7	3.05E-01	EG	4.7	36629	6	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	7.6	4.45E-01	control	11.3	14363	8	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	4.8	4.06E-02	EG	4.6	17972	2	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.6	1.74E-01	EG	4.8	24196	2	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	1.1	8.08E-01	control	9.7	45834	12	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	1.7	9.66E-01	control	7.2	25648	6	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987247	PP_0508		hypothetical protein	4.4	4.40E-01	EG	5.0	20628	2	Unknown			
26987255	PP_0517	ribH	6,7-dimethyl-8-ribityllumazine synthase	1.1	5.88E-01	EG	5.2	16420	5	Cytoplasmic	COG0054	Coenzyme metabolism	
26987271	PP_0533	pfeS	sensor protein PfeS	1.0	6.98E-01	EG	6.2	49992	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987282	PP_0544		ethanolamine transproter	4.0	1.93E-02	EG	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.2	4.67E-02	EG	5.9	55268	19	Cytoplasmic	COG1012	Energy production and conversion	

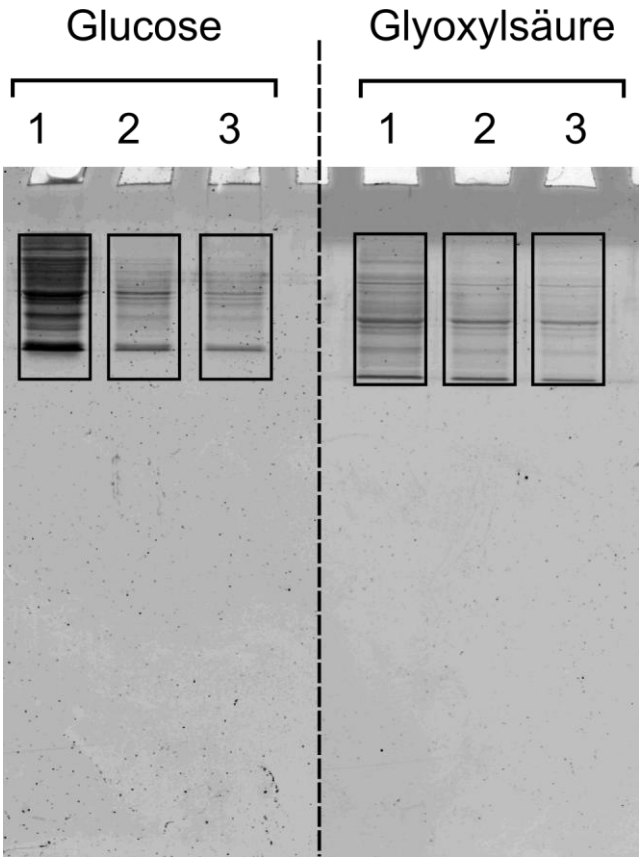
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	2.1	5.69E-02	EG	6.5	49088	5	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	1.3	5.73E-01	EG	6.6	40223	4	Unknown	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	2.1	5.42E-01	control	5.3	71043	4	Unknown	COG1166	Amino acid transport and metabolism	
26987314	PP_0576		lipoprotein	1.3	3.11E-01	EG	9.5	21449	2	Unknown			
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.5	4.70E-01	control	5.0	69953	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987334	PP_0596		beta alanine--pyruvate transaminase	1.4	2.51E-01	EG	6.8	48529	5	Cytoplasmic	COG0161	Coenzyme metabolism	
26987336	PP_0599		hypothetical protein	1.8	6.15E-01	control	9.6	83247	7	Unknown	COG3008	General function prediction only	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.2	4.47E-01	EG	6.0	105800	7	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP_0622		competence lipoprotein ComL	1.8	9.45E-01	control	4.8	38410	2	Unknown	COG4105	General function prediction only	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.0	7.66E-01	control	5.2	94861	5	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987362	PP_0626	ndh	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1.6	3.36E-01	EG	9.0	47080	7	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26987376	PP_0640		hypothetical protein	1.7	6.83E-01	control	6.6	44093	4	Cytoplasmic Membrane			
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.6	2.07E-01	EG	6.2	44897	3	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.4	7.71E-01	control	5.3	61860	10	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	20.2	2.29E-04	control	6.5	48871	2	Unknown	COG0334	Amino acid transport and metabolism	
26987425	PP_0689	rpmA	50S ribosomal protein L27	10.6	3.90E-01	control	11	9341	3	Cytoplasmic	COG0211	Translation, ribosomal structure and biogenesis	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.1	7.42E-01	EG	7.8	39661	7	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	1.1	8.21E-01	control	9.9	92124	3	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	1.0	9.51E-01	control	5.3	23026	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987450	PP_0714		permease	1.5	4.65E-01	control	9.6	38213	2	Cytoplasmic Membrane	COG0628	General function prediction only	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.3	4.88E-01	EG	6.4	23242	4	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.0	8.09E-01	control	5.9	34192	5	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987479	PP_0743		NAD-dependent epimerase/dehydratase	1.8	1.40E-01	EG	9.7	33119	2	Cytoplasmic Membrane	COG1090	General function prediction only	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.1	5.57E-01	EG	8.4	54282	14	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.1	6.76E-01	EG	9.5	20483	9	Unknown			
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.1	6.63E-01	EG	5.5	62125	10	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.0	7.88E-01	EG	5.0	67937	17	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.1	8.85E-01	control	9.6	50572	2	Unknown			
26987509	PP_0773		OmpA/MotB domain protein	1.3	9.61E-01	control	9.5	24753	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987531	PP_0795	fruA	PTS system, fructose subfamily, IIC subunit	1.7	1.45E-01	control	8.7	59235	3	Cytoplasmic Membrane	COG1299	Carbohydrate transport and metabolism	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.5	3.10E-01	control	6.7	34557	12	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	2.0	1.81E-02	control	9.6	11902	3	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.2	5.29E-01	control	9.6	66913	18	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.1	5.31E-01	control	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.2	8.71E-01	control	6.6	29753	4	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.1	7.16E-01	EG	5.3	15044	2	Extracellular	COG0105	Nucleotide transport and metabolism	
26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.5	3.29E-01	EG	5.1	47738	3	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
26987593	PP_0857	engA	GTP-binding protein EngA	16.9	8.78E-01	control	9.2	54154	2	Cytoplasmic Membrane	COG1160	General function prediction only	
26987596	PP_0860		flavodoxin/nitric oxide synthase	1.9	2.77E-01	control	7.6	93734	4	Cytoplasmic Membrane	COG0369	Inorganic ion transport and metabolism	
26987597	PP_0861		TonB-dependent siderophore receptor	2.1	5.94E-02	EG	4.8	84022	21	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26987619	PP_0883		outer membrane porin	1.1	7.61E-01	EG	6.6	50256	8	Outer Membrane			
26987645	PP_0909		hypothetical protein	2.1	3.35E-01	control	6.4	38380	14	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	2.2	5.15E-01	control	4.4	47019	21	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.8	5.39E-01	control	5.8	78578	7	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987661	PP_0925		hypothetical protein	1.6	7.91E-01	control	5.8	31410	2	Unknown			
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.6	4.54E-02	EG	6.2	51518	3	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987680	PP_0944	fumC	fumarate hydratase	1.4	4.00E-01	EG	5.9	48541	23	Cytoplasmic	COG0114	Energy production and conversion	
26987696	PP_0960	ttg2C	hypothetical protein	1.7	9.44E-02	control	4.6	16953	5	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	2.7	1.32E-01	EG	5.2	44973	2	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.7	7.67E-01	control	8.4	22938	5	Cytoplasmic	COG0040	Amino acid transport and metabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.4	2.42E-01	control	5.1	107495	25	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.2	4.46E-01	control	7.4	52433	10	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.4	7.61E-01	control	9.7	41323	4	Cytoplasmic Membrane	COG0795	General function prediction only	
26987721	PP_0985		cold-shock domain-contain protein	1.1	9.27E-01	EG	10.6	18586	2	Cytoplasmic	COG1278	Transcription	
26987737	PP_1001	arcA	arginine deiminase	1.0	8.95E-01	EG	5.7	46462	2	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	3.0	5.01E-03	EG	5.6	84730	19	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	2.4	6.91E-01	control	7.0	36057	12	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.1	5.26E-01	control	6.4	65359	9	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	1.0	7.46E-01	EG	6.5	33904	2	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	4.8	6.21E-01	control	7.3	54020	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	2.0	2.25E-01	EG	6.2	45449	10	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.4	1.25E-01	control	10.1	33781	6	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.6	2.20E-02	control	9.9	30428	3	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.1	6.90E-01	EG	6.7	41895	7	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.0	8.11E-01	EG	5.9	49646	26	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.0	7.76E-01	EG	6.8	55000	15	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.2	5.60E-01	EG	6.7	25476	11	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.2	5.57E-01	EG	5.4	25004	4	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.4	2.25E-02	EG	5.1	61712	6	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.4	4.34E-01	EG	7.0	51765	9	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.0	9.82E-01	EG	5.2	58204	20	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.3	3.82E-01	control	4.7	140818	43	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987794	PP_1058		hypothetical protein	1.8	4.05E-01	control	9.5	117041	12	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.4	6.15E-01	control	8.2	27464	8	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	2.1	9.96E-02	EG	8.9	33428	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987815	PP_1079	argF	ornithine carbamoyltransferase	1.0	6.44E-01	control	5.7	34433	3	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	5.4	1.72E-02	EG	4.4	17971	5	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.1	5.86E-01	EG	4.9	21730	8	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	2.1	6.01E-02	EG	5.1	45164	4	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987844	PP_1108		acylase	1.0	6.91E-01	control	8.7	88728	16	Periplasmic	COG2366	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	1.2	7.03E-01	control	7.6	32597	7	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	1.4	4.63E-01	EG	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.2	5.16E-01	EG	9.3	15682	6	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	2.8	8.03E-02	control	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	3.4	1.19E-01	EG	6.4	39402	3	Periplasmic	COG0683	Amino acid transport and metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.4	6.31E-01	control	4.8	105994	2	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987888	PP_1152		secretion protein HlyD family protein	1.7	1.15E-01	control	6.4	32353	2	Cytoplasmic Membrane	COG1566	Defense mechanisms	

26987893	PP_1157		acetolactate synthase	1.1	9.08E-01	control	6.1	60059	8	Cytoplasmic	COG0028	Coenzyme metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.4	1.08E-01	control	5.7	106948	32	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987936	PP_1201		virulence factor family protein	1.2	9.03E-01	control	5.0	46885	3	Unknown	COG3946	Intracellular trafficking and secretion	
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.6	1.10E-01	EG	5.0	63623	3	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.5	2.79E-01	EG	4.6	46120	17	Outer Membrane			
26987945	PP_1210		DNA-binding stress protein	1.6	1.74E-01	EG	5.0	17861	4	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.3	2.84E-01	control	5.1	66568	16	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.1	8.28E-01	control	6.3	25310	6	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.7	1.81E-01	EG	9.8	47431	9	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.1	8.69E-01	control	4.9	17833	11	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	1.2	4.48E-01	control	4.8	40784	2	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.3	3.93E-01	EG	5.1	26916	3	Cytoplasmic	COG0152	Nucleotide transport and metabolism	
26988026	PP_1291		PhoH family protein	1.1	6.67E-01	EG	5.7	51856	3	Cytoplasmic	COG1875	General function prediction only	
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.7	9.34E-02	EG	5.6	36424	6	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988033	PP_1298	aapQ	polar amino acid ABC transporter inner membrane subunit	1.4	4.52E-01	control	10.2	43229	3	Cytoplasmic Membrane	COG4597	Amino acid transport and metabolism	
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.2	4.36E-01	EG	5.6	69049	3	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988044	PP_1309		hypothetical protein	1.3	5.89E-01	control	6.3	16018	8	Unknown	COG3105	Function unknown	
26988050	PP_1315	rplM	50S ribosomal protein L13	3.1	4.80E-01	control	10.3	15862	4	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	3.6	5.48E-01	control	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	2.2	1.35E-01	control	7.1	29032	7	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.0	6.11E-01	EG	7.5	64637	8	Cytoplasmic Membrane	COG3107	General function prediction only	
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	1.2	7.24E-01	EG	9.9	38127	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	1.3	3.53E-01	EG	4.9	47444	2	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.7	2.50E-01	EG	5	42236	2	Cytoplasmic	COG1364	Amino acid transport and metabolism	
26988094	PP_1360	groES	co-chaperonin GroES	1.3	5.48E-01	EG	5.2	10224	2	Cytoplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
26988095	PP_1361	groEL	chaperonin GroEL	1.4	4.36E-01	EG	4.7	56743	18	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	1.3	5.97E-01	control	6.7	52057	13	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.1	9.92E-01	control	4.8	67652	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988106	PP_1372		hypothetical protein	1.2	5.09E-01	EG	6.5	52321	3	Unknown	COG0433	Replication, recombination, and repair	
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.1	6.53E-01	EG	5.1	52864	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.4	1.72E-01	control	5.3	112835	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	3.0	5.76E-01	control	6	41250	3	Unknown	COG0845	Cell envelope biogenesis, outer membrane	
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	1.8	6.93E-01	control	4.9	31783	2	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26988152	PP_1419		outer membrane porin	1.3	3.96E-01	EG	4.9	46644	7	Outer Membrane			
26988164	PP_1431	lepA	GTP-binding protein LepA	1.9	9.55E-01	control	5.5	66116	6	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.4	3.48E-01	control	9.2	32060	6	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988176	PP_1443	lon-1	ATP-dependent protease La	1.9	3.74E-01	control	6.4	89794	4	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.1	6.30E-01	control	6.0	86581	15	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988179	PP_1446		TonB-dependent receptor	3.1	4.12E-02	EG	4.9	74207	5	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.1	7.56E-01	EG	5.7	42575	5	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988192	PP_1459		CBS domain-containing protein	1.5	8.58E-01	control	4.7	44174	2	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism	
26988198	PP_1465	rplS	50S ribosomal protein L19	5.7	3.25E-01	control	11.0	13012	7	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988203	PP_1470	hom	homoserine dehydrogenase	1.9	1.67E-01	EG	5.1	46194	2	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.5	2.26E-01	EG	6.2	51645	10	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.1	8.95E-01	control	5.8	40626	3	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.6	4.11E-01	EG	5.7	50918	6	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.2	8.20E-01	control	4.7	58605	16	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988228	PP_1496	lysS	lysyl-tRNA synthetase	1.4	4.29E-01	EG	5.0	57137	4	Cytoplasmic	COG1190	Translation, ribosomal structure and biogenesis	
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.3	9.29E-01	control	6.6	96963	2	Cytoplasmic	COG2352	Energy production and conversion	
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.9	9.58E-01	control	5.6	35858	6	Unknown	COG2171	Amino acid transport and metabolism	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	7.76E-01	EG	9.3	27023	16	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.4	6.40E-01	EG	4.9	30432	6	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.3	7.10E-01	control	4.7	86513	6	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988342	PP_1610	pyrG	CTP synthetase	1.5	1.21E-01	EG	5.8	59474	6	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	2.5	9.07E-02	EG	4.7	45490	7	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.3	8.97E-01	control	11.0	27506	4	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988361	PP_1629	recA	recombinase A	1.0	6.30E-01	EG	5.3	37545	2	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988367	PP_1635		LuxR family two component transcriptional regulator	1.2	4.65E-01	EG	4.8	23481	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	1.4	6.38E-01	control	4.8	16590	3	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26988388	PP_1656	relA	(p)ppGpp synthetase I, SpoT/RelA	5.2	6.29E-02	control	7.9	83609	2	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.1	5.48E-01	EG	5.4	45693	6	Outer Membrane	COG2067	Lipid metabolism	
26988427	PP_1695		integral membrane sensor hybrid histidine kinase	1.6	3.40E-01	control	8.8	127309	8	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism	General function prediction only
26988434	PP_1702	rdgC	recombination associated protein	1.3	5.63E-01	EG	4.6	34283	2	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	2.2	8.85E-01	control	4.8	26520	5	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988474	PP_1743	actP	acetate permease	1.9	5.09E-02	EG	9.6	58972	5	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	7.8	7.15E-01	control	8.2	57637	3	Cytoplasmic	COG2326	Function unknown	
26988498	PP_1767	gyrA	DNA gyrase subunit A	2.5	5.16E-01	control	4.7	102037	14	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	1.0	9.76E-01	EG	6.4	79133	3	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1.4	4.89E-01	EG	5.2	52989	3	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP_1780		mannosyltransferase	1.1	5.64E-01	control	5.8	180042	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988515	PP_1784	rmlD	dTDP-4-dehydrorhamnose reductase	1.4	9.45E-01	control	6.7	32131	2	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.3	4.23E-01	EG	6.4	40124	12	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988568	PP_1838		hypothetical protein	1.3	3.03E-01	control	6.8	76615	5	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988588	PP_1858	efp	elongation factor P	2.0	1.98E-01	EG	4.5	21303	2	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	3.4	5.66E-01	control	9.2	60924	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988602	PP_1872		aminotransferase AlaT	1.3	4.27E-01	EG	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988606	PP_1876		hypothetical protein	1.1	8.04E-01	control	8.8	38962	3	Cytoplasmic	COG2607	General function prediction only	
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.6	4.57E-01	control	6.9	89194	13	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.8	6.39E-01	control	4.7	120904	24	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.4	4.78E-01	control	6.4	36497	4	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.0	6.81E-01	EG	6.0	25470	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.0	6.50E-01	EG	5.9	43290	25	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.0	9.22E-01	EG	5.6	56483	9	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.2	9.16E-01	control	4.8	38824	5	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.4	9.35E-01	control	5.3	40672	11	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.3	6.91E-01	control	3.9	96918	16	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.1	5.68E-01	EG	7.8	32510	7	Cytoplasmic	COG0777	Lipid metabolism	

26988725	PP_2000	purF	amidophosphoribosyltransferase	1.9	1.49E-01	control	6.5	55400	12	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	1.2	4.79E-01	EG	5.4	43284	3	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26988742	PP_2017	pepN	aminopeptidase N	1.0	8.83E-01	control	4.8	99573	8	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.2	3.86E-01	control	5.8	187043	49	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.0	7.95E-01	EG	4.8	86015	18	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.2	5.21E-01	control	5.8	29111	5	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.1	6.99E-01	EG	4.5	37012	34	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	1.3	9.33E-01	control	8.2	35545	2	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism	
26988836	PP_2112	acnA	aconitate hydratase	1.4	9.68E-01	control	5.7	99147	5	Cytoplasmic	COG1048	Energy production and conversion	
26988854	PP_2130		soluble lytic transglycosylase	1.1	4.99E-01	EG	9.9	75337	11	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.1	9.34E-01	EG	5.9	77449	2	Cytoplasmic	COG1250	Lipid metabolism	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.2	3.29E-02	control	7.7	53014	24	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	1.1	5.31E-01	control	7.7	50905	11	Cytoplasmic	COG1249	Energy production and conversion	
26988887	PP_2163	vacJ	VacJ family lipoprotein	5.7	5.33E-01	control	5.3	26061	5	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988964	PP_2240		ABC transporter	1.6	5.05E-01	control	9.6	70269	2	Cytoplasmic Membrane	COG4178	General function prediction only	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.2	9.97E-01	control	5.1	68646	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989023	PP_2299	tig	trigger factor	2.1	2.77E-01	EG	4.5	49190	6	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
26989024	PP_2300	clpP	ATP-dependent Clp protease proteolytic subunit	1.1	6.36E-01	EG	5.6	23515	2	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26989026	PP_2302	lon-2	ATP-dependent protease La	2.5	4.38E-01	control	5.9	88722	14	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.2	7.25E-01	control	4.8	68580	3	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.4	8.17E-01	control	9.3	9997	2	Unknown			
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	1.0	9.18E-01	EG	5.3	52127	3	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.1	7.84E-01	control	8.5	8801	4	Outer Membrane			
26989051	PP_2327	cysB	transcriptional regulator CysB	1.7	2.49E-01	EG	6.7	35955	4	Cytoplasmic	COG0583	Transcription	
26989055	PP_2331		hypothetical protein	1.2	4.52E-01	control	7.9	57064	8	Cytoplasmic Membrane			
26989059	PP_2335		methylcitrate synthase	1.5	1.01E-01	EG	6.7	41995	17	Cytoplasmic	COG0372	Energy production and conversion	
26989060	PP_2336		aconitate hydratase	1.2	2.91E-01	EG	5.3	93961	33	Cytoplasmic	COG1048	Energy production and conversion	
26989061	PP_2337		hypothetical protein	1.5	3.28E-01	EG	5.2	41312	12	Cytoplasmic	COG2828	Function unknown	
26989062	PP_2338	prpD	2-methylcitrate dehydratase	1.3	8.27E-02	EG	7.1	54860	6	Cytoplasmic	COG2079	General function prediction only	
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.0	7.19E-01	EG	5.0	93609	20	Cytoplasmic	COG1049	Energy production and conversion	
26989075	PP_2351		acetyl-CoA synthetase	2.1	8.95E-01	control	6.1	68868	4	Cytoplasmic	COG0365	Lipid metabolism	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.6	9.23E-01	control	5.8	62191	3	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989103	PP_2379		electron transport protein SCO1/SenC	1.6	4.79E-01	control	8.5	24629	2	Unknown	COG1999	General function prediction only	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.4	3.28E-01	control	5.8	72697	11	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP_2466	infC	translation initiation factor IF-3	1.9	9.16E-01	control	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	13.8	2.75E-01	control	12.1	13280	3	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989289	PP_2569		major facilitator transporter	1.6	2.09E-01	control	9.0	60538	5	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989381	PP_2662		hypothetical protein	73.6	1.37E-05	EG	4.3	42858	4	Outer Membrane			
26989398	PP_2679		quinoprotein ethanol dehydrogenase	74.4	1.15E-05	EG	9.1	64883	5	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	36.1	3.34E-03	EG	5.5	54903	5	Cytoplasmic	COG1012	Energy production and conversion	
26989572	PP_2853		hypothetical protein	5.1	3.06E-04	EG	4.5	46020	2	Unknown			
26989620	PP_2901		penicillin amidase family protein	1.7	1.58E-01	EG	8	83333	7	Periplasmic	COG2366	General function prediction only	
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase	1.7	2.19E-01	EG	8.0	59671	2	Unknown	COG0579	General function prediction only	
26989647	PP_2928		saccharopine dehydrogenase	1.4	5.85E-01	control	5.0	45363	3	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.0	7.51E-01	control	9.0	57141	7	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989854	PP_3135		glycosyl transferase	1.3	2.67E-01	control	8.6	35887	4	Cytoplasmic	COG1216	General function prediction only	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.3	5.53E-01	EG	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	1.1	6.37E-01	EG	9.7	29885	7	Unknown			
26989874	PP_3155		outer membrane ferric siderophore receptor	5.3	1.43E-02	EG	4.9	78211	12	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990039	PP_3321		hypothetical protein	1.5	3.05E-01	EG	6.1	19365	3	Unknown	COG4875	Function unknown	
26990043	PP_3325		outer membrane ferric siderophore receptor	1.6	8.31E-02	EG	4.8	76226	22	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990047	PP_3330		TonB-dependent siderophore receptor	2.1	2.90E-04	EG	5.8	80740	15	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	6.8	1.96E-02	EG	4.8	77137	3	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990092	PP_3377		major facilitator transporter	1.9	1.87E-01	control	9.6	47449	2	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990128	PP_3415		LacI family transcription regulator	1.2	8.13E-01	control	7.6	36204	4	Unknown	COG1609	Transcription	
26990130	PP_3417	gntP	gluconate transporter	1.0	8.68E-01	EG	8.9	47532	11	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.2	5.96E-01	control	6.2	59980	12	Cytoplasmic	COG1012	Energy production and conversion	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.6	2.04E-01	EG	7.2	36863	5	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	1.3	3.32E-01	control	6.9	85338	10	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	1.6	2.14E-02	EG	5.2	53952	11	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990296	PP_3585		efflux transporter RND family, MFP subunit	1.2	9.28E-01	control	9.4	46468	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990298	PP_3587	tpx	redoxin domain protein	1.6	3.69E-01	EG	4.7	17409	2	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.0	9.60E-01	control	5.9	43631	6	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990323	PP_3612		TonB-dependent siderophore receptor	2.7	7.88E-02	EG	5.2	85491	13	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990373	PP_3662		decarboxylase family protein	1.8	1.26E-01	EG	6.7	50729	4	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	1.2	4.82E-01	EG	5.8	82061	10	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990454	PP_3748	glcG	hypothetical protein	24.5	1.59E-03	EG	5.9	13717	2	Unknown	COG3193	General function prediction only	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.1	8.06E-01	control	4.9	129450	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990505	PP_3800		hypothetical protein	1.0	8.92E-01	control	4.6	20400	3	Unknown			
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.8	2.90E-01	EG	5.3	30957	3	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990627	PP_3922		periplasmic protease	1.8	7.80E-01	control	9.8	37502	4	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990662	PP_3957		choline/carnitine/betaine transporter family protein	1.6	7.92E-01	control	7.6	72789	4	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	8.9	3.96E-01	control	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.3	4.09E-01	EG	5.4	45695	10	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.0	1.99E-02	control	5.4	79899	33	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.2	5.61E-01	EG	5.9	50555	13	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.1	8.12E-01	EG	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990759	PP_4058	glgB	glycogen branching enzyme	1.1	6.97E-01	EG	5.9	82877	2	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990806	PP_4111	fusA	elongation factor G	1.3	3.56E-01	EG	5.0	77832	6	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	1.9	2.40E-01	control	10.4	15085	2	Cytoplasmic Membrane	COG0838	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.4	1.44E-01	EG	6.5	67609	3	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.6	8.79E-01	control	5.9	97582	7	Unknown	COG1034	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.1	9.86E-01	control	8.7	20354	2	Cytoplasmic	COG0431	General function prediction only	
26990841	PP_4148		binding-protein-dependent transport systems inner membrane component	1.1	6.64E-01	EG	6.7	39243	2	Cytoplasmic Membrane	COG4174	General function prediction only	
26990860	PP_4168		hypothetical protein	95.7	7.80E-03	control	5.6	12851	2	Cytoplasmic Membrane			
26990866	PP_4174	fabA	3-hydroxydecanoyl-(acyl carrier protein) dehydratase	1.3	4.47E-01	EG	6.5	18791	2	Cytoplasmic	COG0764	Lipid metabolism	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.2	3.91E-01	EG	5.3	43264	3	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism

26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.2	5.46E-01	EG	6.2	30111	16	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.3	3.44E-01	EG	6.1	41239	21	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.1	6.14E-01	EG	6.3	49912	15	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.3	4.42E-01	EG	5.1	42434	15	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.3	3.31E-01	control	6.5	106521	40	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.3	9.17E-01	EG	7.5	26000	2	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	6.90E-01	control	6.2	63448	12	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.4	2.09E-01	control	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.7	1.62E-01	control	10.3	13813	3	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.5	2.67E-01	EG	7.0	47622	20	Cytoplasmic	COG0372	Energy production and conversion	
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.1	5.78E-01	EG	4.9	31237	7	Unknown	COG2025	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.2	6.31E-01	EG	9.7	26361	10	Unknown	COG2086	Energy production and conversion	
26990903	PP_4211		RND efflux transporter	1.3	5.16E-01	EG	8.2	51199	19	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990904	PP_4212		hypothetical protein	1.0	8.25E-01	EG	7.1	62081	3	Cytoplasmic			
26990905	PP_4213		dipeptidase	1.2	5.31E-01	EG	5.0	50104	14	Unknown	COG2355	Amino acid transport and metabolism	
26990906	PP_4214		aminotransferase, class V	1.4	3.46E-01	EG	7.6	47747	11	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
26990908	PP_4216	pvdE	cyclic peptide transporter	1.1	6.22E-01	EG	7.4	61169	13	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	2.6	3.17E-03	EG	5.5	89725	47	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990912	PP_4220		non-ribosomal peptide synthetase	1.4	2.96E-01	control	5.2	287552	15	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.1	9.46E-01	EG	5.2	35613	5	Unknown	COG2010	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	1.6	2.84E-01	control	6.0	35312	12	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26990980	PP_4289		hypothetical protein	1.1	9.52E-01	control	8.4	48415	3	Cytoplasmic Membrane	COG3748	Function unknown	
26991006	PP_4315		PhzF family phenazine biosynthesis protein	1.1	6.40E-01	EG	4.5	28437	6	Cytoplasmic	COG0384	General function prediction only	
26991007	PP_4316		2-hydroxyacid dehydrogenase	1.2	8.41E-01	control	6.3	32995	4	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26991021	PP_4331		hypothetical protein	1.6	3.52E-01	control	5.2	14696	2	Unknown			
26991026	PP_4336	motC	flagellar motor protein	1.1	9.73E-01	control	4.9	25930	2	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991034	PP_4344	flhA	flagellar biosynthesis protein FlhA	1.1	9.19E-01	control	6.9	76003	2	Cytoplasmic Membrane	COG1298	Cell motility and secretion	Intracellular trafficking and secretion
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	1.4	8.45E-01	control	10.1	17847	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
26991134	PP_4448		hypothetical protein	2.2	8.34E-01	control	6	66331	2	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991159	PP_4473		aspartate kinase	1.3	4.56E-01	EG	5.0	44605	11	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.3	6.46E-01	control	5.1	94711	10	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.7	6.58E-01	control	5.4	51330	2	Cytoplasmic	COG1012	Energy production and conversion	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.7	2.00E-01	EG	6.5	43490	8	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	1.3	2.44E-01	EG	6.4	71796	16	Cytoplasmic	COG0365	Lipid metabolism	
26991206	PP_4521		aerotaxis receptor	1.4	1.09E-01	control	6.4	56605	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	4.0	4.82E-01	control	10.3	48478	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.1	5.70E-01	EG	5.7	42326	3	Cytoplasmic	COG0332	acyl-carrier-protein	
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	3.1	5.61E-01	control	8.3	146950	4	Cytoplasmic	COG1643	DNA replication, recombination, and repair	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.0	9.01E-01	control	7.7	61812	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991255	PP_4571	cysK	cysteine synthase A	1.6	2.32E-01	EG	5.5	34357	7	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991325	PP_4641	cstA	carbon starvation protein CstA	1.4	1.95E-01	control	9.0	73763	11	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.3	4.88E-01	control	4.8	14730	3	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991330	PP_4646		oxidoreductase FAD/NAD(P)-binding domain protein	1.6	3.36E-01	EG	5.2	28960	2	Cytoplasmic	COG1018	Energy production and conversion	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	1.3	3.30E-01	EG	9.1	53016	2	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.7	2.61E-01	control	4.8	68764	3	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	3.0	7.33E-01	control	6.1	30321	4	Cytoplasmic	COG2084	Lipid metabolism	
26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.1	6.69E-01	EG	6.0	54367	8	Cytoplasmic	COG1012	Energy production and conversion	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.4	4.58E-01	EG	5.4	36370	11	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	1.8	5.67E-01	control	6.3	17784	2	Cytoplasmic	COG0440	Amino acid transport and metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.7	6.86E-01	control	6.8	62781	4	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991381	PP_4697	pcnB	poly(A) polymerase	5.7	3.70E-01	control	9.6	52721	3	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.2	6.87E-01	EG	6.8	61455	7	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	2.8	3.64E-01	control	6.5	71251	3	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	1.7	8.08E-01	control	5.6	107252	2	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.3	1.41E-01	EG	4.9	75010	23	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.9	8.32E-01	control	6.8	91460	16	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP_4713	nusA	transcription elongation factor NusA	1.4	3.59E-01	EG	4.3	54673	2	Cytoplasmic	COG0195	Transcription	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.3	4.35E-01	control	5.4	69722	16	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	2.0	2.15E-01	EG	4.6	68800	7	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	1.1	5.85E-01	EG	6.2	35615	3	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26991447	PP_4766		DEAD-box ATP dependent DNA helicase	5.8	7.28E-01	control	10.4	48823	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.8	2.20E-02	EG	5.7	45178	3	Cytoplasmic	COG0001	Coenzyme metabolism	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.9	3.56E-01	control	5.6	96697	14	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	1.5	1.04E-01	EG	6.1	22414	6	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.3	4.19E-01	EG	6.6	42288	11	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.1	6.88E-01	EG	6.5	57695	4	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991518	PP_4838	oprC	TonB-dependent copper receptor	1.6	3.01E-02	EG	6.2	74540	28	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991519	PP_4839		hypothetical protein	1.1	7.16E-01	control	9.6	50581	2	Cytoplasmic Membrane	COG3182	Function unknown	
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	1.2	5.26E-01	EG	6.3	27400	4	Cytoplasmic	COG4221	General function prediction only	
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	1.4	9.33E-01	control	6.6	32427	3	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	3.3	1.93E-01	EG	6.2	40270	3	Periplasmic	COG0683	Amino acid transport and metabolism	
26991554	PP_4874	rplI	50S ribosomal protein L9	1.3	6.26E-01	EG	5.3	15466	2	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis	
26991556	PP_4876	rpsR	30S ribosomal protein S18	3.1	5.50E-01	control	11.3	8927	2	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.8	4.27E-01	control	7.9	96688	9	Cytoplasmic	COG0557	Transcription	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.0	8.92E-01	control	6.1	71958	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.2	5.31E-01	EG	5.6	46833	7	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.4	5.15E-01	control	9.8	33001	13	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.3	6.45E-01	control	5.1	44762	8	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991572	PP_4894	hfq	RNA-binding protein Hfq	4.8	3.50E-01	control	9.0	9462	3	Cytoplasmic	COG1923	General function prediction only	
26991583	PP_4905		flagellar motor protein MotA	2.0	4.64E-02	control	6.2	30312	3	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991587	PP_4909	serB	phosphoserine phosphatase SerB	1.1	6.10E-01	control	5.1	45033	2	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991588	PP_4910		hypothetical protein	1.1	7.20E-01	control	4.7	53632	10	Cytoplasmic	COG3726	General function prediction only	
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	3.3	5.58E-01	control	6.2	83181	8	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26991593	PP_4915	parE	DNA topoisomerase IV subunit B	2.9	3.54E-01	control	6.2	69556	3	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.1	6.46E-01	control	7.6	66279	5	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991622	PP_4944		carbamoyltransferase	2.2	2.84E-01	control	7.2	65646	6	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydroger	1.3	9.59E-01	control	6.3	142580	7	Cytoplasmic	COG4230	Energy production and conversion	

26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase		1.7	2.00E-01	EG	5.6	38453	2	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991643	PP_4965	tktA	transketolase		1.1	5.96E-01	EG	5.0	72463	14	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase		1.4	2.43E-01	EG	5.1	42779	6	Cytoplasmic	COG0192	Coenzyme metabolism	
26991653	PP_4975		thioesterase superfamily protein		1.1	8.71E-01	control	7.5	14902	7	Cytoplasmic	COG1607	Lipid metabolism	
26991657	PP_4980		DEAD-box ATP dependent DNA helicase		4.2	4.05E-01	control	10.7	68073	10	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991676	PP_4999	pyrC	dihydroorotase		1.8	2.62E-01	EG	5.4	44116	2	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU		1.2	6.15E-01	EG	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein		12.2	4.77E-01	control	10.9	26214	7	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer		1.5	1.48E-01	control	4.9	69017	16	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991700	PP_5024		amino acid ABC transporter periplasmic amino acid-binding protein		2.4	9.27E-01	EG	8.6	29848	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH		1.4	2.46E-01	control	8.3	95875	5	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase		1.0	9.20E-01	control	6.4	92004	11	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA		2.2	3.11E-01	control	5.3	67157	4	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I		1.4	7.75E-02	EG	5.1	51740	12	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991729	PP_5053	secB	preprotein translocase subunit SecB		1.5	3.80E-01	EG	4.2	17754	5	Cytoplasmic	COG1952	Intracellular trafficking and secretion	
26991731	PP_5055		rhodanese domain-containing protein		4.0	3.92E-01	control	9.9	14839	2	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991743	PP_5067		potassium efflux protein KefA		1.0	9.58E-01	control	8.9	122371	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26991752	PP_5076	gltB	glutamate synthase subunit alpha		2.0	6.21E-02	control	6.2	161772	17	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP_5077		sporulation domain protein		1.3	7.41E-01	control	7.1	55434	2	Unknown	COG3267	Intracellular trafficking and secretion	
26991760	PP_5084		penicillin-binding protein, 1A family		1.3	4.68E-01	control	7.2	89193	4	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP_5085	maeB	malic enzyme		1.7	1.80E-01	EG	4.9	45127	8	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase		1.3	2.49E-01	EG	5.7	63668	9	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991766	PP_5090		sporulation domain protein		2.3	4.48E-01	control	10.6	24964	4	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein		2.7	1.89E-02	control	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein		1.6	1.08E-01	control	6.5	36984	5	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991794	PP_5118		rhodanese domain protein		1.6	2.74E-01	EG	5.6	30750	4	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase		1.6	4.69E-01	control	5.8	65671	8	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991821	PP_5145	ptsP	PTSINtr with GAF domain, PtsP		1.0	8.92E-01	control	5.3	83337	4	Cytoplasmic	COG3605	Signal transduction mechanisms	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase		1.0	7.88E-01	EG	6.3	44339	6	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991846	PP_5170	cysT	sulfate ABC transporter inner membrane subunit CysT		1.5	4.66E-01	control	9.6	29454	2	Cytoplasmic Membrane	COG0555	Posttranslational modification, protein turnover, chaperones	
26991849	PP_5173		acriflavin resistance protein		1.8	2.02E-01	control	5.4	112277	4	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991854	PP_5178	potH	binding-protein-dependent transport systems inner membrane component		1.1	6.96E-01	control	7.4	34422	2	Cytoplasmic Membrane	COG1176	Amino acid transport and metabolism	
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein		1.6	5.20E-01	EG	6.4	40068	2	Periplasmic	COG0687	Amino acid transport and metabolism	
26991859	PP_5183		glutamine synthetase		1.8	1.04E-01	EG	4.8	50877	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991861	PP_5185	argA	N-acetylglutamate synthase		1.1	8.78E-01	control	5.9	47440	4	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991868	PP_5192	gcvP-2	glycine dehydrogenase		1.4	5.10E-01	control	6.3	104037	4	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991892	PP_5216	ppx	Ppx/GppA phosphatase		1.1	4.71E-01	EG	6.9	55958	2	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991893	PP_5217	ppk	polyphosphate kinase		1.3	6.58E-01	control	7.8	81732	9	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28		2.6	5.90E-01	control	12.3	8922	5	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA		2.3	7.23E-01	control	9.2	78603	6	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991982	PP_5306	exbB	ferric siderophore transport system protein ExbB		1.6	5.11E-01	control	9.5	33260	3	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26991983	PP_5307	exbD	biopolymer transport protein ExbD		1.6	5.93E-02	control	4.5	15269	4	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26991984	PP_5308	tonB	TonB family protein		1.2	1.50E-01	control	10.5	26022	5	Outer Membrane	COG0810	Cell envelope biogenesis, outer membrane	
26991989	PP_5313	hupA	histone family protein DNA-binding protein	Infinity		3.73E-01	control	11.0	10551	3	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B		1.6	1.09E-01	EG	5.3	65626	17	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A		1.3	9.96E-02	EG	6.5	51942	10	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein		1.4	3.52E-01	control	7.2	30672	5	Cytoplasmic Membrane	COG4395	Function unknown	
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase		1.0	9.23E-01	control	5.9	48114	2	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta		1.5	4.08E-01	EG	4.6	49359	17	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma		1.4	4.17E-01	EG	9.2	31464	8	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha		1.4	2.42E-01	EG	5.2	55352	23	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B		1.3	6.34E-01	control	5.3	16898	7	Cytoplasmic Membrane	COG0711	Energy production and conversion	
24986476					1.4	6.31E-01	control			35				
148550051					1.0	9.95E-01	control			15				
148549148					1.4	2.99E-01	EG			13				
313497930					2.0	2.76E-01	control			11				
24981839					2.0	3.64E-01	control			11				
313498866					1.1	4.65E-01	EG			9				
24981833					1.3	6.95E-01	control			8				
15599454					5.1	7.69E-01	control			6				
313496770					1.4	3.32E-01	EG			6				
24982083					1.4	4.19E-01	control			4				
313497915					1.1	4.67E-01	control			4				
128169					1.5	8.03E-01	control			4				
148548303					123.1	7.93E-05	EG			3				
24982804					1.1	6.87E-01	EG			3				
24982932					3.3	1.65E-01	control			2				
24982353					1.4	3.68E-01	EG			2				
148545524					1.7	1.17E-02	EG			2				
148547408					1.6	6.66E-01	control			2				
24986535					2.0	7.31E-02	EG			2				
313500100					3.0	9.09E-01	control			2				



1D-SDS-PAGE der Membranfraktion von mit Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* GN259. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut. Die beiden Zustände wurden auf separaten Gelen aufgetrennt (gestrichelte Linie).

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.3	7.69E-01	GXS	9.1	61919	16	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.2	5.09E-01	GXS	4.9	40718	9	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	2.0	6.92E-01	GXS	5.8	90030	4	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.7	5.25E-01	GXS	6.1	31236	2	Cytoplasmic			
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.2	4.27E-01	GXS	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	2.1	1.69E-02	GXS	4.9	75112	10	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	2.3	1.29E-01	GXS	4.8	36024	2	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	2.5	1.21E-01	GXS	8.1	34224	2	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.2	5.89E-01	GXS	6.4	44046	3	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986841	PP_0096	prlC	oligopeptidase A	6.7	1.03E-03	GXS	5.0	75721	4	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	2.5	8.55E-02	GXS	6.8	26001	2	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.2	8.70E-01	GXS	6.8	42059	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.1	8.74E-01	control	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	6.9	7.48E-03	GXS	7.4	25597	3	Unknown			
26986890	PP_0145		sodium-dependent inorganic phosphate (Pi) transporter	1.6	9.69E-01	control	9.8	59817	2	Cytoplasmic Membrane	COG1283	Inorganic ion transport and metabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.6	3.36E-01	control	7.3	50185	4	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.4	4.68E-01	GXS	6.3	71284	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	2.0	1.80E-01	GXS	7.8	51116	3	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.6	1.71E-01	GXS	7.7	78583	11	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986924	PP_0180		cytochrome c family protein	1.9	8.14E-02	GXS	4.9	68013	10	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	2.2	8.44E-02	GXS	5.4	52061	7	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	2.3	4.67E-02	GXS	9.6	46030	10	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	2.6	1.54E-01	GXS	11.3	32300	7	Cytoplasmic			
26986943	PP_0199		hypothetical protein	2.3	7.78E-01	control	6.8	27782	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.1	9.26E-01	GXS	5.2	51549	7	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.2	5.93E-01	GXS	6.1	44824	4	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	5.5	1.63E-02	GXS	5.4	48317	28	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	2.3	7.09E-01	control	5.2	15616	9	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.8	1.23E-01	GXS	6.1	47787	4	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.8	1.77E-01	GXS	6.0	80277	15	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	3.4	5.12E-02	GXS	4.7	24565	2	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.9	2.15E-01	GXS	5.3	55654	16	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	2.0	3.66E-02	GXS	5.6	99332	58	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.1	7.76E-01	GXS	5.3	109432	9	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987095	PP_0353		DNA polymerase III, epsilon subunit	1.1	8.07E-01	control	6.9	26369	3	Cytoplasmic	COG2176	DNA replication, recombination, and repair	
26987096	PP_0354		CBS domain-containing protein	1.2	5.71E-01	GXS	7.4	72323	9	Cytoplasmic	COG2905	Signal transduction mechanisms	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.4	3.94E-01	control	5.8	65541	6	Cytoplasmic	COG1960	Lipid metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.7	2.47E-01	GXS	4.6	69396	19	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	2.6	9.77E-01	control	11.4	8370	4	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987137	PP_0395		SpoVR family protein	1.1	8.68E-01	GXS	5.4	61330	2	Cytoplasmic	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	1.7	2.86E-01	GXS	7.0	50488	8	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.2	4.32E-01	control	5.8	73782	33	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.6	3.74E-01	GXS	6.8	36277	7	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987180	PP_0439		hypothetical protein	1.3	4.40E-01	control	7.5	17667	2	Unknown			
26987184	PP_0443	rplK	50S ribosomal protein L11	1.0	9.53E-01	control	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.5	3.13E-01	GXS	10.1	24251	6	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.7	4.18E-01	GXS	10.2	17686	10	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	1.9	2.20E-01	GXS	4.4	12599	3	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.2	4.72E-01	GXS	5.5	150992	79	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.8	1.06E-01	GXS	7.2	154797	68	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.7	2.19E-01	GXS	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	3.4	1.03E-01	GXS	10.8	17578	9	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.0	9.24E-01	control	4.9	78817	47	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.6	1.56E-01	GXS	5.0	43478	32	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	1.4	2.26E-01	GXS	10.5	11753	3	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	2.4	1.01E-02	GXS	10.3	21811	7	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.2	8.36E-01	control	10.7	10900	4	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.3	5.09E-01	GXS	11.7	29669	13	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987199	PP_0458	rpsS	30S ribosomal protein S19	1.3	4.15E-01	control	11.3	10348	4	Cytoplasmic	COG0185	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.2	4.18E-01	GXS	11.9	15373	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987204	PP_0463	rpsQ	30S ribosomal protein S17	4.8	1.79E-01	control	10.5	10058	2	Cytoplasmic	COG0186	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.4	2.88E-01	GXS	11.6	13410	11	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987206	PP_0465	rplX	50S ribosomal protein L24	15.1	4.46E-01	control	10.8	11329	4	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.5	1.00E-01	GXS	10.3	20329	15	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	3.0	6.87E-02	GXS	12.3	11403	2	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.2	4.24E-01	GXS	10.2	13975	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	6.4	8.47E-02	control	10.4	19143	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.1	5.81E-01	GXS	10.9	12628	6	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.5	2.65E-01	GXS	10.6	17666	10	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	2.6	1.09E-01	GXS	11.5	15189	8	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	2.1	5.58E-02	control	10.4	47853	8	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.7	2.26E-01	GXS	11.3	13256	9	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.0	3.27E-01	GXS	11.5	13660	5	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.1	9.66E-01	control	10.5	23056	10	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	3.0	4.41E-01	control	4.7	36629	6	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.5	2.40E-01	GXS	11.3	14363	8	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	68.7	2.64E-04	GXS	4.6	17972	5	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.9	3.72E-01	GXS	4.8	24196	2	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	1.0	7.85E-01	GXS	9.7	45834	13	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	2.0	6.87E-01	control	7.2	25648	5	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987255	PP_0517	ribH	6,7-dimethyl-8-ribityllumazine synthase	1.6	7.22E-01	control	5.2	16420	4	Cytoplasmic	COG0054	Coenzyme metabolism	
26987271	PP_0533	pfeS	sensor protein PfeS	3.2	4.57E-02	GXS	6.2	49992	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.2	1.51E-01	control	5.9	55268	14	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	8.1	1.83E-01	control	6.5	49088	5	Cytoplasmic	COG0439	Lipid metabolism	
26987298	PP_0560	aroQ-1	3-dehydroquinate dehydratase	3.9	3.49E-01	control	6.9	16491	2	Cytoplasmic	COG0757	Amino acid transport and metabolism	
26987299	PP_0561	dipZ	thiol:disulfide interchange protein precursor	1.1	6.83E-01	control	8.1	62470	2	Cytoplasmic Membrane	COG4232	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26987302	PP_0564		hypothetical protein	1.2	5.54E-01	control	6.6	40223	6	Unknown	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	1.4	3.53E-01	GXS	5.3	71043	4	Unknown	COG1166	Amino acid transport and metabolism	
26987314	PP_0576		lipoprotein	6.3	1.01E-03	GXS	9.5	21449	3	Unknown			
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.4	3.49E-01	control	5.0	69953	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987334	PP_0596		beta alanine--pyruvate transaminase	3.2	3.29E-03	GXS	6.8	48529	4	Cytoplasmic	COG0161	Coenzyme metabolism	
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	3.3	6.47E-01	control	5.9	53498	2	Cytoplasmic	COG1012	Energy production and conversion	
26987336	PP_0599		hypothetical protein	1.1	8.23E-01	GXS	9.6	83247	7	Unknown	COG3008	General function prediction only	
26987339	PP_0602	ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	6.3	1.82E-02	GXS	9.7	34827	2	Cytoplasmic	COG0196	Coenzyme metabolism	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.1	8.27E-01	GXS	6.0	105800	8	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP_0622		competence lipoprotein ComL	5.7	4.70E-02	GXS	4.8	38410	4	Unknown	COG4105	General function prediction only	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.2	7.43E-01	GXS	5.2	94861	5	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987362	PP_0626	ndh	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	3.3	4.01E-02	GXS	9.0	47080	8	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26987376	PP_0640		hypothetical protein	4.2	2.44E-01	GXS	6.6	44093	3	Cytoplasmic Membrane			
26987410	PP_0674		ABC transporter ATP-binding protein	1.6	4.09E-01	GXS	5.3	61860	9	Cytoplasmic	COG0488	General function prediction only	
26987425	PP_0689	rpmA	50S ribosomal protein L27	24.0	1.89E-01	control	11	9341	2	Cytoplasmic	COG0211	Translation, ribosomal structure and biogenesis	

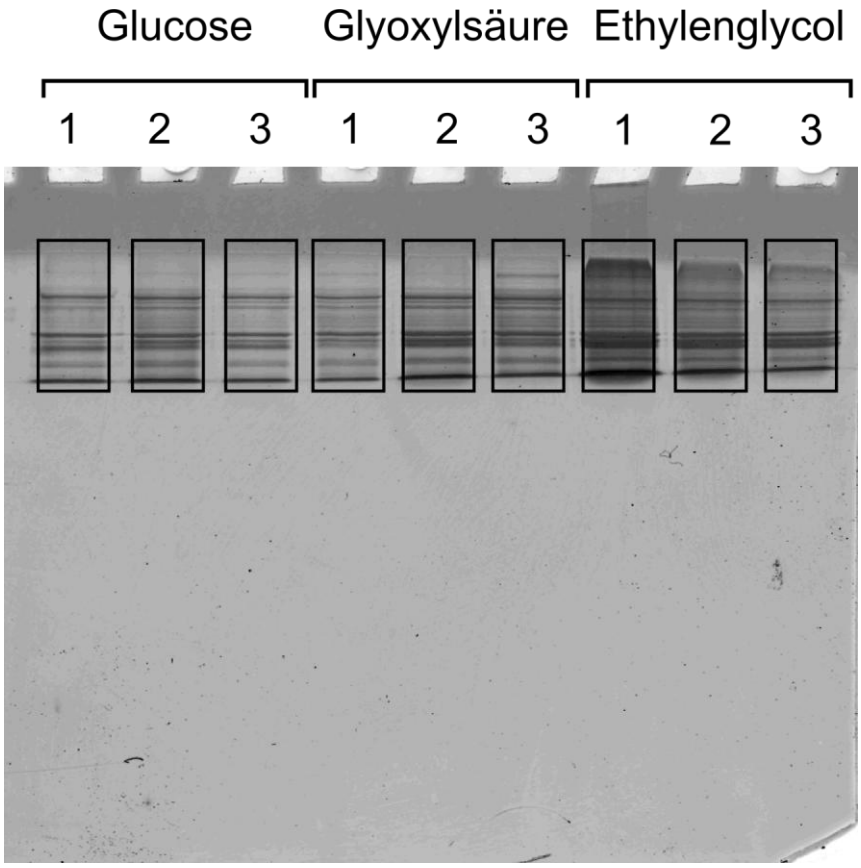
26987427	PP_0691	proB	gamma-glutamyl kinase	1.8	1.72E-01	GXS	7.8	39661	7	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	2.3	1.73E-01	GXS	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987448	PP_0712		hypothetical protein	1.3	2.84E-01	GXS	10.5	31284	2	Cytoplasmic	COG2326	Function unknown	
26987450	PP_0714		permease	4.0	1.21E-01	control	9.6	38213	2	Cytoplasmic Membrane	COG0628	General function prediction only	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.1	7.08E-01	control	5.9	34192	4	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987478	PP_0742		hypothetical protein	2.2	3.58E-01	control	6.2	36114	2	Unknown	COG3380	General function prediction only	
26987479	PP_0743		NAD-dependent epimerase/dehydratase	1.6	1.93E-01	GXS	9.7	33119	2	Cytoplasmic Membrane	COG1090	General function prediction only	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	4.7	1.60E-02	GXS	8.4	54282	14	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	4.5	2.29E-02	GXS	9.5	20483	11	Unknown			
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	2.5	4.10E-01	GXS	5.5	62125	9	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	2.2	8.27E-02	GXS	5.0	67937	15	Outer Membrane			
26987502	PP_0766		hypothetical protein	2.3	8.58E-02	GXS	9.6	50572	4	Unknown			
26987509	PP_0773		OmpA/MotB domain protein	2.0	6.63E-02	GXS	9.5	24753	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987531	PP_0795	fruA	PTS system, fructose subfamily, IIC subunit	1.6	5.08E-01	control	8.7	59235	4	Cytoplasmic Membrane	COG1299	Carbohydrate transport and metabolism	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.6	7.08E-02	GXS	6.7	34557	14	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	11.8	5.57E-03	GXS	7.8	74391	7	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	4.0	5.59E-02	control	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.6	1.75E-01	GXS	9.6	66913	15	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	3.3	2.14E-02	control	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.1	5.93E-01	GXS	6.6	29753	5	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987576	PP_0840	cysE	serine O-acetyltransferase	1.6	2.68E-01	GXS	6.7	28206	2	Cytoplasmic	COG1045	Amino acid transport and metabolism	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	2.2	1.79E-01	control	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.1	8.11E-01	GXS	5.1	47738	2	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
26987592	PP_0856		hypothetical protein	4.7	2.58E-02	GXS	4.7	40737	2	Outer Membrane	COG1520	Function unknown	
26987593	PP_0857	engA	GTP-binding protein EngA	1.7	2.67E-01	control	9.2	54154	2	Cytoplasmic Membrane	COG1160	General function prediction only	
26987596	PP_0860		flavodoxin/nitric oxide synthase	1.1	8.73E-01	GXS	7.6	93734	5	Cytoplasmic Membrane	COG0369	Inorganic ion transport and metabolism	
26987597	PP_0861		TonB-dependent siderophore receptor	4.4	4.67E-02	GXS	4.8	84022	14	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26987600	PP_0864		ornithine decarboxylase	2.9	8.69E-02	GXS	4.7	41535	2	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26987619	PP_0883		outer membrane porin	2.3	1.60E-01	GXS	6.6	50256	5	Outer Membrane			
26987645	PP_0909		hypothetical protein	1.3	4.17E-01	GXS	6.4	38380	15	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	2.1	1.65E-01	GXS	4.4	47019	23	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.8	4.36E-01	GXS	5.8	78578	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987661	PP_0925		hypothetical protein	3.6	6.92E-01	GXS	5.8	31410	2	Unknown			
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	2.1	6.94E-02	GXS	6.2	51518	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987680	PP_0944	fumC	fumarate hydratase	1.9	2.42E-01	GXS	5.9	48541	22	Cytoplasmic	COG0114	Energy production and conversion	
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.4	9.60E-01	control	8.4	22938	4	Cytoplasmic	COG0040	Amino acid transport and metabolism	
26987707	PP_0971		hypothetical protein	1.8	6.49E-01	GXS	8.2	18030	3	Unknown	COG3631	General function prediction only	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.5	2.50E-01	control	5.1	107495	22	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	2.3	1.40E-01	control	7.4	52433	9	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.4	4.63E-01	control	9.7	41323	5	Cytoplasmic Membrane	COG0795	General function prediction only	
26987721	PP_0985		cold-shock domain-contain protein	2.9	1.42E-02	GXS	10.6	18586	3	Cytoplasmic	COG1278	Transcription	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	3.8	7.19E-02	GXS	6.4	40319	2	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	4.2	3.72E-02	control	5.7	46462	2	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	3.1	1.79E-02	GXS	5.6	84730	18	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.4	8.65E-01	control	7.0	36057	13	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	2.0	3.65E-03	GXS	6.4	65359	6	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	2.6	9.55E-02	GXS	6.5	33904	2	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	1.7	6.97E-01	control	7.3	54020	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.3	5.97E-01	GXS	6.2	45449	9	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.4	1.75E-01	control	10.1	33781	5	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.8	6.38E-02	control	9.9	30428	4	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	2.6	7.95E-02	GXS	6.7	41895	4	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	3.3	5.77E-02	GXS	5.9	49646	27	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.4	2.02E-01	GXS	6.8	55000	17	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.1	7.76E-01	control	6.7	25476	13	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.7	2.43E-01	GXS	5.4	25004	4	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.9	3.29E-01	GXS	5.1	61712	7	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.7	6.05E-01	GXS	7.0	51765	6	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.6	2.23E-01	GXS	5.2	58204	19	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.0	8.71E-01	GXS	4.7	140818	41	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987794	PP_1058		hypothetical protein	1.3	4.36E-01	GXS	9.5	117041	11	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987805	PP_1069		polar amino acid ABC transporter inner membrane subunit	1.1	7.69E-01	GXS	9.4	24744	3	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.3	4.06E-01	GXS	8.2	27464	6	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.1	9.63E-01	control	8.9	33428	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987815	PP_1079	argF	ornithine carbamoyltransferase	2.3	2.13E-01	GXS	5.7	34433	3	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	21.7	1.93E-03	GXS	4.4	17971	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.1	8.89E-01	control	4.9	21730	5	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.8	1.48E-01	control	5.1	45164	2	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987844	PP_1108		acylase	1.1	7.35E-01	control	8.7	88728	15	Periplasmic	COG2366	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	1.7	9.70E-02	control	7.6	32597	6	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	3.3	4.11E-02	GXS	5.0	24084	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	2.7	4.48E-02	GXS	9.3	15682	6	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	2.6	2.17E-01	control	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.5	9.87E-01	control	6.4	39402	2	Periplasmic	COG0683	Amino acid transport and metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.9	7.84E-02	GXS	4.8	105994	4	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987888	PP_1152		secretion protein HlyD family protein	1.4	5.31E-01	GXS	6.4	32353	2	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26987893	PP_1157		acetolactate synthase	1.2	6.27E-01	control	6.1	60059	8	Cytoplasmic	COG0028	Coenzyme metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.4	8.48E-02	GXS	5.7	106948	31	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987936	PP_1201		virulence factor family protein	2.8	7.83E-02	GXS	5.0	46885	3	Unknown	COG3946	Intracellular trafficking and secretion	
26987940	PP_1205	proS	prolyl-tRNA synthetase	2.5	1.57E-01	GXS	5.0	63623	6	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	3.3	5.05E-02	GXS	4.6	46120	17	Outer Membrane			
26987945	PP_1210		DNA-binding stress protein	2.4	1.03E-01	GXS	5.0	17861	5	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.0	8.91E-01	control	5.1	66568	15	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.5	2.03E-01	GXS	6.3	25310	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987956	PP_1221	tolA	biopolymer transport protein TolA	2.0	1.84E-01	GXS	9.8	40133	2	Outer Membrane	COG1196	Cell division and chromosome partitioning	
26987957	PP_1222	tolB	translocation protein TolB	2.8	2.52E-02	GXS	9.8	47431	8	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.8	2.15E-01	GXS	4.9	17833	11	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	3.3	2.29E-02	GXS	4.8	40784	3	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26988009	PP_1274		short chain dehydrogenase	1.8	1.04E-01	GXS	10.2	28618	5	Cytoplasmic	COG0300	General function prediction only	
26988026	PP_1291		PhoH family protein	1.5	4.87E-01	control	5.7	51856	3	Cytoplasmic	COG1875	General function prediction only	
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.7	1.46E-01	GXS	5.6	36424	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988033	PP_1298	aapQ	polar amino acid ABC transporter inner membrane subunit	2.3	2.83E-01	control	10.2	43229	3	Cytoplasmic Membrane	COG4597	Amino acid transport and metabolism	
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.2	7.88E-01	GXS	5.6	69049	4	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988044	PP_1309		hypothetical protein	1.6	1.42E-01	GXS	6.3	16018	8	Unknown	COG3105	Function unknown	
26988046	PP_1311		tryptophanyl-tRNA synthetase	2.4	4.67E-01	GXS	5.4	49297	2	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
26988050	PP_1315	rplM	50S ribosomal protein L13	2.1	9.28E-01	control	10.3	15862	3	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.9	2.05E-01	GXS	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.1	6.55E-01	GXS	7.1	29032	5	Unknown	COG2857	Energy production and conversion	
26988057	PP_1322		transport-associated protein	6.4	2.12E-02	GXS	9.8	20680	2	Periplasmic	COG2823	General function prediction only	
26988060	PP_1325		LppC family lipoprotein	2.2	1.13E-01	GXS	7.5	64637	12	Cytoplasmic Membrane	COG3107	General function prediction only	
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	1.6	9.18E-01	GXS	9.9	38127	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	3.9	2.45E-01	GXS	4.9	47444	2	Cytoplasmic	COG0849	Cell division and chromosome partitioning	

26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.1	6.43E-01	GXS	5	42236	2	Cytoplasmic	COG1364	Amino acid transport and metabolism		
26988093	PP_1359	fxsA	FxsA	1.2	4.18E-01	control	10.6	16958	1	Cytoplasmic Membrane	COG3030	General function prediction only		
26988095	PP_1361	groEL	chaperonin GroEL	1.1	5.76E-01	GXS	4.7	56743	12	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones		
26988096	PP_1362	pykA	pyruvate kinase	1.1	7.79E-01	GXS	6.7	52057	14	Cytoplasmic	COG0469	Carbohydrate transport and metabolism		
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.8	2.89E-01	GXS	4.8	67652	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26988106	PP_1372		hypothetical protein	1.8	2.56E-01	GXS	6.5	52321	3	Unknown	COG0433	Replication, recombination, and repair		
26988107	PP_1373		phosphate transporter	3.4	1.82E-01	GXS	9.6	52425	3	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism		
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.9	2.69E-01	GXS	5.1	52864	21	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.2	4.92E-01	control	5.3	112835	9	Cytoplasmic Membrane	COG0841	Defense mechanisms		
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	2.5	1.85E-01	GXS	6	41250	3	Unknown	COG0845	Cell envelope biogenesis, outer membrane		
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	1.2	5.25E-01	GXS	4.9	31783	3	Cytoplasmic	COG2513	Carbohydrate transport and metabolism		
26988152	PP_1419		outer membrane porin	4.2	2.93E-02	GXS	4.9	46644	6	Outer Membrane				
26988164	PP_1431	lepA	GTP-binding protein LepA	11.2	2.56E-02	control	5.5	66116	5	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane		
26988165	PP_1432	lepB	signal peptidase I	1.6	1.82E-01	GXS	9.2	32060	6	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion		
26988176	PP_1443	lon-1	ATP-dependent protease La	1.6	8.64E-01	GXS	6.4	89794	3	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones		
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.5	2.54E-01	GXS	6.0	86581	20	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism		
26988179	PP_1446		TonB-dependent receptor	3.1	1.12E-02	GXS	4.9	74207	3	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.8	6.88E-01	GXS	5.7	42575	7	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism		
26988192	PP_1459		CBS domain-containing protein	1.7	3.73E-01	GXS	4.7	44174	3	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism		
26988198	PP_1465	rplS	50S ribosomal protein L19	1.1	3.70E-01	GXS	11.0	13012	7	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis		
26988204	PP_1471	thrC	threonine synthase	1.8	2.82E-01	GXS	6.2	51645	9	Cytoplasmic	COG0498	Amino acid transport and metabolism		
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	2.9	1.12E-01	GXS	5.8	40626	3	Cytoplasmic	COG1902	Energy production and conversion		
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.5	2.76E-01	GXS	5.7	50918	4	Unknown	COG1012	Energy production and conversion		
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.5	3.80E-01	GXS	4.7	58605	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26988228	PP_1496	lysS	lysyl-tRNA synthetase	2.3	1.45E-01	GXS	5.0	57137	5	Cytoplasmic	COG1190	Translation, ribosomal structure and biogenesis		
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	2.2	9.04E-02	GXS	6.6	96963	4	Cytoplasmic	COG2352	Energy production and conversion		
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.9	9.70E-01	control	5.6	35858	6	Unknown	COG2171	Amino acid transport and metabolism		
26988323	PP_1591	rpsB	30S ribosomal protein S2	2.4	1.02E-01	GXS	9.3	27023	16	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis		
26988324	PP_1592	tsf	elongation factor Ts	4.3	2.47E-01	control	4.9	30432	3	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis		
26988331	PP_1599		surface antigen family outer membrane protein	1.4	9.76E-01	control	4.7	86513	9	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane		
26988342	PP_1610	pyrG	CTP synthetase	1.3	7.81E-01	GXS	5.8	59474	9	Cytoplasmic	COG0504	Nucleotide transport and metabolism		
26988344	PP_1612	eno	phosphopyruvate hydratase	1.7	3.62E-01	GXS	4.7	45490	4	Cytoplasmic	COG0148	Carbohydrate transport and metabolism		
26988354	PP_1622	nlpD	peptidase M23B	1.5	9.57E-01	GXS	11.0	27506	3	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane		
26988361	PP_1629	recA	recombinase A	3.2	3.67E-02	GXS	5.3	37545	5	Cytoplasmic	COG0468	DNA replication, recombination, and repair		
26988367	PP_1635		LuxR family two component transcriptional regulator	2.6	7.60E-02	GXS	4.8	23481	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	2.9	5.09E-02	GXS	4.8	16590	3	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion	
26988388	PP_1656	relA	(p)ppGpp synthetase I, SpoT/RelA	1.2	5.43E-01	control	7.9	83609	1	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
26988421	PP_1689		aromatic hydrocarbon degradation protein	4.1	3.27E-02	GXS	5.4	45693	7	Outer Membrane	COG2067	Lipid metabolism		
26988427	PP_1695		integral membrane sensor hybrid histidine kinase	1.3	3.63E-01	GXS	8.8	127309	8	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism	General function prediction only	
26988434	PP_1702	rdgC	recombination associated protein	1.3	5.44E-01	GXS	4.6	34283	2	Cytoplasmic	COG2974	DNA replication, recombination, and repair		
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.1	4.70E-01	GXS	4.8	26520	6	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones		
26988474	PP_1743	actP	acetate permease	6.1	2.14E-02	GXS	9.6	58972	4	Cytoplasmic Membrane	COG4147	General function prediction only		
26988483	PP_1752		hypothetical protein	1.3	3.07E-01	GXS	8.2	57637	5	Cytoplasmic	COG2326	Function unknown		
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.3	9.43E-01	control	4.7	102037	16	Cytoplasmic	COG0188	DNA replication, recombination, and repair		
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	3.2	4.78E-03	GXS	6.4	79133	2	Cytoplasmic	COG0128	Amino acid transport and metabolism		
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	3.2	4.14E-02	GXS	5.2	52989	3	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane		
26988511	PP_1780		mannosyltransferase	1.4	1.62E-01	GXS	5.8	180042	7	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane		
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	2.2	2.21E-01	GXS	6.4	40124	10	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane		
26988568	PP_1838		hypothetical protein	1.1	5.91E-01	control	6.8	76615	6	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane		
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.8	2.01E-01	GXS	9.2	60924	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription	Translation, ribosomal structure and biogenesis
26988602	PP_1872		aminotransferase AlaT	1.9	5.05E-01	GXS	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism		
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.2	6.51E-01	GXS	6.9	89194	16	Cytoplasmic Membrane	COG1960	Lipid metabolism		
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	2.2	1.29E-01	GXS	4.7	120904	25	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis		
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.6	1.02E-01	GXS	6.4	36497	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	2.1	2.12E-01	GXS	6.0	25470	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988645	PP_1916	fabF	3-oxoacyl-(acyl carrier protein) synthase II	1.6	9.50E-01	control	5.8	43152	3	Cytoplasmic Membrane	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.5	3.42E-01	GXS	5.9	43290	22	Cytoplasmic	COG1448	Amino acid transport and metabolism		
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	2.0	1.64E-01	GXS	5.6	56483	8	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.6	8.97E-01	control	4.8	38824	4	Cytoplasmic	COG0473	Amino acid transport and metabolism		
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.3	4.53E-01	GXS	5.3	40672	10	Cytoplasmic	COG0136	Amino acid transport and metabolism		
26988719	PP_1993		peptidoglycan-binding LysM	2.2	7.47E-02	GXS	3.9	96918	18	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion	
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	2.4	1.99E-01	GXS	7.8	32510	7	Cytoplasmic	COG0777	Lipid metabolism		
26988725	PP_2000	purF	amidophosphoribosyltransferase	2.1	2.04E-01	control	6.5	55400	11	Cytoplasmic	COG0034	Nucleotide transport and metabolism		
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	2.0	1.77E-01	GXS	5.4	43284	4	Cytoplasmic	COG0626	Amino acid transport and metabolism		
26988742	PP_2017	pepN	aminopeptidase N	1.1	5.46E-01	control	4.8	99573	9	Cytoplasmic	COG0308	Amino acid transport and metabolism		
26988805	PP_2080		NAD-glutamate dehydrogenase	1.4	1.76E-01	GXS	5.8	187043	53	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism		
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.2	3.18E-01	GXS	4.8	86015	17	Cytoplasmic	COG0574	Carbohydrate transport and metabolism		
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.1	9.05E-01	GXS	5.8	29111	3	Cytoplasmic Membrane				
26988814	PP_2089	oprF	OmpF family protein	1.4	4.25E-01	GXS	4.5	37012	29	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane		
26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	2.3	2.27E-01	GXS	8.2	35545	3	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism		
26988822	PP_2097		diguanylate cyclase with PAS/PAC sensor	4.9	4.43E-02	GXS	6.5	88173	3	Unknown	COG3706	Signal transduction mechanisms		
26988836	PP_2112	acnA	aconitate hydratase	2.2	2.74E-01	control	5.7	99147	3	Cytoplasmic	COG1048	Energy production and conversion		
26988854	PP_2130		soluble lytic transglycosylase	2.8	1.06E-02	GXS	9.9	75337	13	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane		
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.6	3.62E-01	GXS	5.9	77449	2	Cytoplasmic	COG1250	Lipid metabolism		
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.5	7.70E-02	GXS	7.7	53014	23	Cytoplasmic	COG0057	Carbohydrate transport and metabolism		
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	1.3	4.11E-01	GXS	7.7	50905	14	Cytoplasmic	COG1249	Energy production and conversion		
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.5	9.00E-01	control	5.3	26061	5	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane		
26988964	PP_2240		ABC transporter	1.7	5.89E-01	GXS	9.6	70269	3	Cytoplasmic Membrane	COG4178	General function prediction only		
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.4	5.87E-01	GXS	5.1	68646	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26989023	PP_2299	tig	trigger factor	2.1	2.97E-01	GXS	4.5	49190	6	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones		
26989024	PP_2300	clpP	ATP-dependent Clp protease proteolytic subunit	1.0	7.09E-01	GXS	5.6	23515	3	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion	
26989026	PP_2302	lon-2	ATP-dependent protease La	2.4	2.96E-01	control	5.9	88722	14	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones		
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.7	3.03E-01	GXS	4.8	68580	4	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones		
26989030	PP_2306		lipoprotein	3.2	4.18E-02	GXS	9.3	9997	3	Unknown				
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	1.4	4.65E-01	GXS	5.3	52127	5	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.4	6.53E-01	GXS	8.5	8801	3	Outer Membrane				
26989051	PP_2327	cysB	transcriptional regulator CysB	2.2	1.75E-01	GXS	6.7	35955	3	Cytoplasmic	COG0583	Transcription		
26989055	PP_2331		hypothetical protein	1.6	3.14E-01	GXS	7.9	57064	6	Cytoplasmic Membrane				
26989059	PP_2335		methylcitrate synthase	3.2	1.51E-02	GXS	6.7	41995	19	Cytoplasmic	COG0372	Energy production and conversion		
26989060	PP_2336		aconitate hydratase	1.1	7.75E-01	GXS	5.3	93961	33	Cytoplasmic	COG1048	Energy production and conversion		
26989061	PP_2337		hypothetical protein	2.6	1.10E-01	GXS	5.2	41312	9	Cytoplasmic	COG2828	Function unknown		
26989062	PP_2338	prpD	2-methylcitrate dehydratase	1.5	7.08E-01	GXS	7.1	54860	5	Cytoplasmic	COG2079	General function prediction only		
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	9.64E-01	GXS	5.0	93609	20	Cytoplasmic	COG1049	Energy production and conversion		
26989075	PP_2351		acetyl-CoA synthetase	2.3	5.62E-01	control	6.1	68868	3	Cytoplasmic	COG0365	Lipid metabolism		
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.1	8.29E-01	control	5.8	62191	3	Cytoplasmic	COG0155	Inorganic ion transport and metabolism		
26989103	PP_2379		electron transport protein SCO1/SenC	1.1	5.96E-01	control	8.5	24629	2	Unknown	COG1999	General function prediction only		
26989142	PP_2419		hypothetical protein	2.3	2.13E-02	GXS	10.2	47269	3	Cytoplasmic Membrane	COG3503	Function unknown		
26989186	PP_2463	cspA-2	cold shock protein CspA	2.6	3.16E-02	GXS	7.5	7711	3	Cytoplasmic	COG1278	Transcription		
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.2	5.32E-01	GXS	5.8	72697	11	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis		
26989189	PP_2466	infC	translation initiation factor IF-3	1.2	6.23E-01	GXS	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis		
26989191	PP_2468	rplT	50S ribosomal protein L20	1.0	4.77E-01	control	12.1	13280	3	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis		
26989289	PP_2569		major facilitator transporter	1.0	9.34E-01	GXS	9.0	60538	4	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism		

26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	6.1	1.69E-02	GXS	5.7	58659	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26989620	PP_2901		penicillin amidase family protein	2.4	5.95E-02	GXS	8	83333	6	Periplasmic	COG2366	General function prediction only			
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.8	2.84E-01	control	6.1	64654	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis			
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase	2.8	1.91E-01	GXS	8.0	59671	2	Unknown	COG0579	General function prediction only			
26989647	PP_2928		saccharopine dehydrogenase	3.5	2.83E-01	control	5.0	45363	2	Cytoplasmic	COG1748	Amino acid transport and metabolism			
26989846	PP_3127		lipopolysaccharide biosynthesis protein	2.5	1.31E-01	GXS	9.0	57141	7	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane			
26989851	PP_3132		polysaccharide biosynthesis protein	1.5	6.01E-01	control	9.7	49930	2	Cytoplasmic Membrane	COG2244	General function prediction only			
26989854	PP_3135		glycosyl transferase	1.5	5.71E-02	control	8.6	35887	5	Cytoplasmic	COG1216	General function prediction only			
26989864	PP_3145		hypothetical protein	3.8	1.88E-02	GXS	9.7	29885	9	Unknown					
26989874	PP_3155		outer membrane ferric siderophore receptor	3.6	3.23E-03	GXS	4.9	78211	10	Outer Membrane	COG4774	Inorganic ion transport and metabolism			
26990039	PP_3321		hypothetical protein	2.1	1.58E-01	GXS	6.1	19365	3	Unknown	COG4875	Function unknown			
26990043	PP_3325		outer membrane ferric siderophore receptor	2.6	1.17E-01	GXS	4.8	76226	17	Outer Membrane	COG4773	Inorganic ion transport and metabolism			
26990047	PP_3330		TonB-dependent siderophore receptor	3.0	3.77E-03	GXS	5.8	80740	11	Outer Membrane	COG4773	Inorganic ion transport and metabolism			
26990091	PP_3376	kguD	2-ketogluconate 6-phosphate reductase	1.3	4.50E-01	control	6.3	34561	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism	General function prediction only	
26990092	PP_3377		major facilitator transporter	1.4	7.42E-01	GXS	9.6	47449	2	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism			
26990128	PP_3415		LacI family transcription regulator	1.1	7.62E-01	control	7.6	36204	4	Unknown	COG1609	Transcription			
26990129	PP_3416	gnuK	carbohydrate kinase, thermoresistant glucokinase family	1.6	6.36E-01	GXS	5.7	19012	2	Unknown	COG3265	Carbohydrate transport and metabolism			
26990130	PP_3417	gntP	gluconate transporter	1.5	5.15E-01	GXS	8.9	47532	10	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism		
26990132	PP_3419		two component, sigma54 specific, transcriptional regulator, Fis family	2.0	1.58E-01	control	6.7	53669	2	Cytoplasmic	COG2204	Signal transduction mechanisms			
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.0	7.87E-01	control	6.2	59980	12	Cytoplasmic	COG1012	Energy production and conversion			
26990208	PP_3496		endoribonuclease L-PSP	1.5	3.21E-01	GXS	4.9	14327	2	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis			
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	2.0	1.32E-01	GXS	7.2	36863	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism		
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	1.3	1.42E-01	GXS	6.9	85338	11	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism			
26990290	PP_3578		phosphoglucomutase	1.2	6.24E-01	GXS	5.6	58620	1	Unknown	COG0033	Carbohydrate transport and metabolism			
26990294	PP_3582		RND efflux transporter	2.6	1.11E-02	GXS	5.2	53952	10	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion		
26990296	PP_3585		efflux transporter RND family, MFP subunit	2.1	1.37E-01	GXS	9.4	46468	7	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane			
26990298	PP_3587	tpx	redoxin domain protein	1.7	3.54E-01	GXS	4.7	17409	2	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones			
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	2.2	1.19E-01	GXS	5.9	43631	6	Cytoplasmic	COG1448	Amino acid transport and metabolism			
26990323	PP_3612		TonB-dependent siderophore receptor	3.1	2.11E-02	GXS	5.2	85491	14	Outer Membrane	COG4774	Inorganic ion transport and metabolism			
26990373	PP_3662		decarboxylase family protein	1.4	9.10E-01	GXS	6.7	50729	3	Cytoplasmic	COG1611	General function prediction only			
26990379	PP_3668		catalase/peroxidase HPI	1.4	2.04E-01	GXS	5.8	82061	12	Cytoplasmic	COG0376	Inorganic ion transport and metabolism			
26990399	PP_3691		DNA helicase-related protein	1.2	7.75E-01	control	5.0	245278	3	Unknown	COG1112	DNA replication, recombination, and repair			
26990407	PP_3699		hypothetical protein	1.6	8.89E-01	control	6.1	63413	3	Cytoplasmic	COG2849	Function unknown			
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.3	9.49E-01	control	4.9	129450	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms			
26990505	PP_3800		hypothetical protein	1.3	3.03E-01	GXS	4.6	20400	3	Unknown					
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.0	9.17E-01	control	5.3	30957	3	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane			
26990627	PP_3922		periplasmic protease	22.4	2.14E-01	control	9.8	37502	4	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion		
26990662	PP_3957		choline/carnitine/betaine transporter family protein	1.1	7.94E-01	GXS	7.6	72789	6	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane			
26990705	PP_4000	serS	seryl-tRNA synthetase	1.8	3.64E-01	control	5.1	46849	2	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis			
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	22.1	1.45E-01	control	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning			
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.3	6.01E-01	GXS	5.4	45695	6	Unknown	COG0538	Energy production and conversion			
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.1	7.14E-01	control	5.4	79899	29	Cytoplasmic	COG2838	Energy production and conversion			
26990721	PP_4016	purB	adenylosuccinate lyase	2.1	2.17E-01	GXS	5.9	50555	11	Cytoplasmic	COG0015	Nucleotide transport and metabolism			
26990738	PP_4035		NCS1 nucleoside transporter	3.1	2.87E-01	control	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism		
26990806	PP_4111	fusA	elongation factor G	1.1	8.01E-01	GXS	5.0	77832	7	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis			
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	4.4	5.21E-02	control	10.4	15085	2	Cytoplasmic Membrane	COG0838	Energy production and conversion			
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	2.2	1.54E-01	GXS	6.5	67609	4	Cytoplasmic	COG0649	Energy production and conversion			
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	2.0	3.50E-01	control	5.9	97582	4	Unknown	COG1034	Energy production and conversion			
26990832	PP_4138		NADPH-dependent FMN reductase	2.3	9.66E-02	GXS	8.7	20354	3	Cytoplasmic	COG0431	General function prediction only			
26990860	PP_4168		hypothetical protein	121.0	1.10E-04	control	5.6	12851	2	Cytoplasmic Membrane					
26990865	PP_4173		integral membrane sensor hybrid histidine kinase	1.6	2.52E-01	GXS	5.4	70995	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms			
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.3	3.30E-01	GXS	5.3	43264	2	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism		
26990871	PP_4179	htpG	heat shock protein 90	7.2	2.68E-02	GXS	5	71610	3	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones			
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.2	9.70E-01	control	6.2	30111	14	Cytoplasmic	COG0074	Energy production and conversion			
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.7	2.64E-01	GXS	6.1	41239	18	Cytoplasmic	COG0045	Energy production and conversion			
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.0	7.52E-01	GXS	6.3	49912	13	Cytoplasmic	COG1249	Energy production and conversion			
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	2.3	1.66E-01	GXS	5.1	42434	16	Cytoplasmic	COG0508	Energy production and conversion			
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.0	9.85E-01	GXS	6.5	106521	38	Cytoplasmic	COG0567	Energy production and conversion			
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.5	3.47E-01	control	6.2	63448	12	Cytoplasmic Membrane	COG1053	Energy production and conversion			
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.1	1.40E-02	GXS	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion			
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	8.9	1.33E-03	control	10.3	13813	3	Cytoplasmic Membrane	COG2009	Energy production and conversion			
26990886	PP_4194	gltA	type II citrate synthase	2.8	3.26E-02	GXS	7.0	47622	21	Cytoplasmic	COG0372	Energy production and conversion			
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2.8	7.03E-01	control	4.9	31237	6	Unknown	COG2025	Energy production and conversion			
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.3	3.40E-01	GXS	9.7	26361	7	Unknown	COG2086	Energy production and conversion			
26990903	PP_4211		RND efflux transporter	2.3	2.13E-02	GXS	8.2	51199	17	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion		
26990904	PP_4212		hypothetical protein	2.1	3.40E-01	GXS	7.1	62081	3	Cytoplasmic					
26990905	PP_4213		dipeptidase	1.7	3.65E-01	GXS	5.0	50104	15	Unknown	COG2355	Amino acid transport and metabolism			
26990906	PP_4214		aminotransferase, class V	2.1	1.10E-01	GXS	7.6	47747	10	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones			
26990908	PP_4216	pvdE	cyclic peptide transporter	3.7	1.57E-02	GXS	7.4	61169	11	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism		
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	6.1	1.04E-02	GXS	5.5	89725	46	Outer Membrane	COG4773	Inorganic ion transport and metabolism			
26990912	PP_4220		non-ribosomal peptide synthetase	2.6	4.07E-02	GXS	5.2	287552	23	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism			
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.2	5.85E-01	GXS	5.2	35613	8	Unknown	COG2010	Energy production and conversion			
26990966	PP_4275	zipA	cell division protein ZipA	1.0	9.13E-01	GXS	6.0	35312	13	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning			
26990980	PP_4289		hypothetical protein	1.6	3.20E-01	control	8.4	48415	3	Cytoplasmic Membrane	COG3748	Function unknown			
26991006	PP_4315		Ph2F family phenazine biosynthesis protein	2.8	7.36E-02	GXS	4.5	28437	4	Cytoplasmic	COG0384	General function prediction only			
26991007	PP_4316		2-hydroxyacid dehydrogenase	1.4	6.87E-01	GXS	6.3	32995	3	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism	General function prediction only	
26991021	PP_4331		hypothetical protein	1.1	9.34E-01	control	5.2	14696	2	Unknown					
26991026	PP_4336	motC	flagellar motor protein	1.2	5.91E-01	GXS	4.9	25930	2	Cytoplasmic Membrane	COG1291	Cell motility and secretion			
26991034	PP_4344	flhA	flagellar biosynthesis protein FlhA	3.2	8.44E-01	control	6.9	76003	2	Cytoplasmic Membrane	COG1298	Cell motility and secretion	Intracellular trafficking and secretion		
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	2.0	7.31E-01	control	10.1	17847	3	Cytoplasmic Membrane	COG1580	Cell motility and secretion			
26991090	PP_4401	bkdA1	3-methyl-2-oxobutanoate dehydrogenase	2.8	6.05E-01	GXS	6.0	45220	2	Cytoplasmic	COG1071	Energy production and conversion			
26991134	PP_4448		hypothetical protein	1.4	4.64E-01	GXS	6	66331	2	Cytoplasmic	COG0433	Replication, recombination, and repair			
26991159	PP_4473		aspartate kinase	1.5	4.01E-01	GXS	5.0	44605	5	Cytoplasmic	COG0527	Amino acid transport and metabolism			
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.3	2.77E-01	GXS	5.1	94711	8	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis			
26991161	PP_4475	astE	succinylglutamate desuccinylase	1.2	5.43E-01	GXS	6.2	37580	2	Cytoplasmic	COG2988	Amino acid transport and metabolism			
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.4	7.06E-01	GXS	5.4	51330	3	Cytoplasmic	COG1012	Energy production and conversion			
26991165	PP_4479	aruG	arginine N-succinyltransferase, beta subunit	2.7	9.04E-01	GXS	7.0	37782	2	Cytoplasmic	COG3138	Amino acid transport and metabolism			
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	2.3	1.20E-01	GXS	6.5	43490	6	Cytoplasmic	COG4992	Amino acid transport and metabolism			
26991173	PP_4487	acsA	acetyl-CoA synthetase	2.6	1.41E-02	GXS	6.4	71796	13	Cytoplasmic	COG0365	Lipid metabolism			
26991206	PP_4521		aerotaxis receptor	1.2	5.79E-01	GXS	6.4	56605	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.1	8.38E-01	GXS	10.3	48478	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription	Translation, ribosomal structure and biogenesis	
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.5	2.38E-01	GXS	5.7	42326	3	Cytoplasmic	COG0332	acyl-carrier-protein			
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	2.6	1.63E-01	GXS	8.3	146950	4	Cytoplasmic	COG1643	DNA replication, recombination, and repair			
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.6	3.32E-01	control	7.7	61812	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism		
26991255	PP_4571	cysK	cysteine synthase A	1.9	6.15E-01	GXS	5.5	34357	4	Cytoplasmic	COG0031	Amino acid transport and metabolism			
26991325	PP_4641	cstA	carbon starvation protein CstA	1.2	7.77E-01	GXS	9.0	73763	12	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms			
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.0	9.09E-01	GXS	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane			
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	1.6	6.34E-01	GXS	9.1	53016	3	Cytoplasmic Membrane	COG1271	Energy production and conversion			
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.5	5.48E-01	GXS	4.8	68764	3	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	4.0	4.28E-01	control	6.1	30321	5	Cytoplasmic	COG2084	Lipid metabolism			
26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.0	7.16E-01	GXS	6.0	54367	8	Cytoplasmic	COG1012	Energy production and conversion			
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	6.37E-01	GXS	5.4	36370	9	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism		

26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	1.0	6.17E-01	GXS	6.3	17784	3	Cytoplasmic	COG0440	Amino acid transport and metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	3.3	1.74E-01	control	6.8	62781	3	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991368	PP_4684		hypothetical protein	1.7	6.67E-01	GXS	5.1	56095	3	Cytoplasmic	COG2187	Function unknown	
26991381	PP_4697	pcnB	poly(A) polymerase	2.5	2.03E-01	GXS	9.6	52721	4	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.4	9.18E-01	GXS	6.8	61455	8	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	2.3	4.93E-01	control	6.5	71251	3	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	20.9	1.20E-01	control	5.6	107252	2	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.5	5.68E-02	control	4.9	75010	19	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.5	8.98E-01	control	6.8	91460	19	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP_4713	nusA	transcription elongation factor NusA	1.6	8.44E-01	GXS	4.3	54673	2	Cytoplasmic	COG0195	Transcription	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.3	5.35E-01	GXS	5.4	69722	17	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	2.0	4.73E-01	GXS	4.6	68800	5	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	1.7	3.62E-01	GXS	6.2	35615	4	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26991447	PP_4766		DEAD-box ATP dependent DNA helicase	1.0	4.27E-01	control	10.4	48823	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	2.0	9.60E-01	GXS	5.7	45178	2	Cytoplasmic	COG0001	Coenzyme metabolism	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.3	7.82E-01	control	5.6	96697	14	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	6.0	1.86E-02	GXS	6.1	22414	3	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991481	PP_4801	lipB	lipoate-protein ligase B	3.3	5.99E-01	GXS	6.0	23689	3	Cytoplasmic	COG0321	Coenzyme metabolism	
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	2.1	1.95E-01	GXS	6.6	42288	9	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane	
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	3.2	8.68E-02	GXS	6.1	45417	2	Cytoplasmic	COG0014	Amino acid transport and metabolism	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.1	6.80E-01	control	6.5	57695	5	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991518	PP_4838	oprC	TonB-dependent copper receptor	1.9	7.95E-02	GXS	6.2	74540	32	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991519	PP_4839		hypothetical protein	2.8	6.68E-03	GXS	9.6	50581	2	Cytoplasmic Membrane	COG3182	Function unknown	
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	2.1	2.04E-01	GXS	6.3	27400	4	Cytoplasmic	COG4221	General function prediction only	
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	1.4	3.87E-01	GXS	6.6	32427	6	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism	
26991556	PP_4876	rpsR	30S ribosomal protein S18	3.4	7.70E-02	GXS	11.3	8927	2	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.1	5.79E-01	GXS	7.9	96688	9	Cytoplasmic	COG0557	Transcription	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.8	1.28E-01	GXS	6.1	71958	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.1	6.06E-01	control	5.6	46833	5	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.2	4.88E-01	GXS	9.8	33001	13	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.6	1.73E-01	GXS	5.1	44762	10	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991572	PP_4894	hfq	RNA-binding protein Hfq	1.8	2.39E-01	GXS	9.0	9462	3	Cytoplasmic	COG1923	General function prediction only	
26991583	PP_4905		flagellar motor protein MotA	2.1	2.20E-01	control	6.2	30312	3	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991587	PP_4909	serB	phosphoserine phosphatase SerB	1.9	3.76E-01	GXS	5.1	45033	2	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991588	PP_4910		hypothetical protein	1.4	4.61E-01	GXS	4.7	53632	9	Cytoplasmic	COG3726	General function prediction only	
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	3.5	4.26E-01	control	6.2	83181	8	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26991593	PP_4915	parE	DNA topoisomerase IV subunit B	1.7	8.75E-01	control	6.2	69556	2	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.5	4.72E-01	GXS	7.6	66279	6	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991615	PP_4937		toluene tolerance protein	1.5	4.21E-01	control	10.4	25956	2	Cytoplasmic			
26991622	PP_4944		carbamoyltransferase	1.6	5.74E-01	control	7.2	65646	9	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	1.7	9.49E-01	control	6.3	142580	10	Cytoplasmic	COG4230	Energy production and conversion	
26991643	PP_4965	tktA	transketolase	1.5	2.59E-01	GXS	5.0	72463	17	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.1	7.10E-01	control	5.1	42779	4	Cytoplasmic	COG0192	Coenzyme metabolism	
26991653	PP_4975		thioesterase superfamily protein	1.7	2.93E-01	GXS	7.5	14902	5	Cytoplasmic	COG1607	Lipid metabolism	
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	3.3	8.40E-02	GXS	10.7	68073	12	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991676	PP_4999	pyrC	dihydroorotase	2.6	1.09E-01	GXS	5.4	44116	3	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	3.8	1.97E-02	GXS	5.7	49982	4	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	3.2	1.49E-01	GXS	10.9	26214	8	Cytoplasmic	COG3937	Function unknown	
26991688	PP_5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.5	8.71E-01	GXS	9.5	28397	2	Cytoplasmic	COG2226	Coenzyme metabolism	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.0	9.18E-01	GXS	4.9	69017	17	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	2.6	1.02E-01	GXS	8.3	95875	7	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.6	4.70E-02	GXS	6.4	92004	11	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.0	8.53E-01	control	5.3	67157	3	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.6	6.12E-02	GXS	5.1	51740	12	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991729	PP_5053	secB	preprotein translocase subunit SecB	3.4	5.66E-02	GXS	4.2	17754	5	Cytoplasmic	COG1952	Intracellular trafficking and secretion	
26991731	PP_5055		rhodanese domain-containing protein	1.1	6.16E-01	GXS	9.9	14839	3	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.1	7.60E-01	GXS	6.2	161772	19	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP_5077		sporulation domain protein	1.5	2.56E-01	GXS	7.1	55434	2	Unknown	COG3267	Intracellular trafficking and secretion	
26991760	PP_5084		penicillin-binding protein, 1A family	2.5	3.94E-02	GXS	7.2	89193	5	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP_5085	maeB	malic enzyme	1.2	6.34E-01	GXS	4.9	45127	9	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.6	5.40E-01	GXS	5.7	63668	8	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991766	PP_5090		sporulation domain protein	1.4	3.22E-01	GXS	10.6	24964	4	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991785	PP_5109	ftsX	hypothetical protein	1.4	9.20E-02	GXS	6.5	36984	5	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991794	PP_5118		rhodanese domain protein	3.1	4.67E-02	GXS	5.6	30750	5	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991799	PP_5123	coaD	phosphopantetheine adenylyltransferase	3.8	7.72E-02	GXS	7.9	17994	2	Cytoplasmic	COG0669	Coenzyme metabolism	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.2	3.12E-01	control	5.8	65671	8	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991821	PP_5145	ptsP	PTSINtr with GAF domain, PtsP	1.7	4.03E-01	control	5.3	83337	3	Cytoplasmic	COG3605	Signal transduction mechanisms	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	2.0	1.12E-01	GXS	6.3	44339	7	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991846	PP_5170	cysT	sulfate ABC transporter inner membrane subunit CysT	1.6	2.78E-01	GXS	9.6	29454	2	Cytoplasmic Membrane	COG0555	Posttranslational modification, protein turnover, chaperones	
26991849	PP_5173		acriflavin resistance protein	2.0	5.63E-01	GXS	5.4	112277	3	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991854	PP_5178	potH	binding-protein-dependent transport systems inner membrane component	19.8	2.09E-01	control	7.4	34422	2	Cytoplasmic Membrane	COG1176	Amino acid transport and metabolism	
26991859	PP_5183		glutamine synthetase	2.4	4.16E-02	GXS	4.8	50877	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991861	PP_5185	argA	N-acetylglutamate synthase	1.6	7.53E-01	GXS	5.9	47440	3	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.7	3.57E-01	control	6.3	104037	4	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991890	PP_5214	rho	transcription termination factor Rho	14.0	1.07E-02	GXS	8.2	47041	3	Cytoplasmic	COG1158	Transcription	
26991891	PP_5215	trx-2	thioredoxin	3.7	1.05E-01	GXS	4.8	11744	2	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
26991892	PP_5216	ppx	Ppx/GppA phosphatase	2.4	1.91E-01	control	6.9	55958	3	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991893	PP_5217	ppk	polyphosphate kinase	1.8	2.79E-01	GXS	7.8	81732	13	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.5	3.08E-01	GXS	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991967	PP_5291	pyrE	orotate phosphoribosyltransferase	1.3	5.66E-01	GXS	4.9	23079	2	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	1.7	2.31E-01	GXS	9.2	78603	8	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991982	PP_5306	exbB	ferric siderophore transport system protein ExbB	6.5	3.77E-02	control	9.5	33260	3	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26991983	PP_5307	exbD	biopolymer transport protein ExbD	2.4	9.92E-03	GXS	4.5	15269	5	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26991984	PP_5308	tonB	TonB family protein	2.1	1.52E-02	GXS	10.5	26022	5	Outer Membrane	COG0810	Cell envelope biogenesis, outer membrane	
26991989	PP_5313	hupA	histone family protein DNA-binding protein	11.5	3.14E-01	control	11.0	10551	4	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26992014	PP_5338	aspA	aspartate ammonia-lyase	4.2	7.25E-02	GXS	5.9	51562	3	Cytoplasmic	COG1027	Amino acid transport and metabolism	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.8	1.65E-02	GXS	5.3	65626	11	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	3.3	8.94E-03	GXS	6.5	51942	10	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.8	9.70E-02	GXS	7.2	30672	5	Cytoplasmic Membrane	COG4395	Function unknown	
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	1.6	4.33E-01	GXS	5.9	48114	3	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	2.0	3.34E-01	GXS	4.6	49359	12	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.8	1.29E-01	GXS	9.2	31464	9	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.3	6.76E-02	GXS	5.2	55352	24	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.7	2.77E-01	GXS	5.3	16898	7	Cytoplasmic Membrane	COG0711	Energy production and conversion	
24986476				1.1	9.94E-01	control			34				
24983268				1.4	4.39E-01	GXS			10				
24981839				1.3	8.18E-01	control			11				
148550051				1.3	4.37E-01	GXS			11				
313497930				1.8	1.82E-01	GXS			10				
313498866				3.6	3.49E-02	GXS			8				
24981833				1.7	2.83E-01	GXS			8				
15599454				1.4	5.59E-01	control			6				

313496770	2.2	1.15E-01	GXS	6
148545966	1.1	7.20E-01	GXS	5
313497915	4.4	5.92E-03	GXS	4
128169	3.2	7.32E-01	control	3
269200090	1.2	9.20E-01	GXS	3
24982804	3.8	4.41E-02	GXS	3
24982353	2.4	7.76E-02	GXS	3
339485705	536.7	9.02E-03	control	3
148547408	2.1	7.61E-01	GXS	3
24982932	2.4	1.07E-01	GXS	2
260663285	2.9	2.92E-02	GXS	2
148549576	4.2	2.70E-02	GXS	2
148546787	1.4	4.27E-01	GXS	2
300776150	3.2	5.00E-01	control	2
313500100	12.1	2.06E-01	control	2



1D-SDS-PAGE der Membranfraktion von mit Ethylenglycol bzw. Glyoxylsäure behandelten und unbehandelten Zellen von *P. putida* JM37. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP 0006	yidC	inner membrane protein translocase component YidC	1.3	4.09E-01	control	9.1	61919	12	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP 0011	dnaN	DNA polymerase III subunit beta	1.0	9.60E-01	control	4.9	40718	4	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP 0013	gyrB	DNA gyrase subunit B	2.8	2.24E-01	EG	5.8	90030	6	Unknown	COG0187	DNA replication, recombination, and repair	
26986802	PP 0057		major facilitator family transporter	1.7	2.66E-01	EG	9.3	58758	3	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26986803	PP 0058		phospholipid/glycerol acyltransferase	1.2	3.65E-01	control	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986805	PP 0060	glyS	glycyl-tRNA synthetase subunit beta	1.5	6.38E-01	EG	4.9	75112	6	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986808	PP 0063		lipid A biosynthesis lauroyl acyltransferase	1.5	5.59E-01	EG	10.1	32840	2	Cytoplasmic Membrane	COG1560	Cell envelope biogenesis, outer membrane	
26986836	PP 0091		lipoprotein	1.7	5.23E-01	EG	8.0	15672	2	Unknown			
26986848	PP 0103		cytochrome c oxidase, subunit II	2.3	2.57E-01	control	6.8	42059	1	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP 0111		electron transport protein SCO1/SenC	1.1	8.61E-01	EG	8.2	22960	2	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP 0116		lipoprotein	1.2	6.05E-01	control	7.4	25597	7	Unknown			
26986875	PP 0130		N-acetylmuramoyl-L-alanine amidase family protein	1.4	1.27E-01	control	9.6	29387	5	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986900	PP 0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.1	5.31E-01	control	7.3	50185	2	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP 0165		GGDEF domain-containing protein	1.0	8.71E-01	control	6.3	71284	7	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986924	PP 0180		cytochrome c family protein	1.1	5.62E-01	control	4.9	68013	3	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP 0184	argH	argininosuccinate lyase	1.1	8.40E-01	EG	5.4	52061	2	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP 0189	hemY	HemY domain protein	1.1	7.23E-01	control	9.6	46030	11	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP 0194	algP	alginate regulatory protein AlgP	1.3	9.49E-01	control	11.3	32300	3	Cytoplasmic			
26986943	PP 0199		hypothetical protein	1.4	6.52E-01	control	6.8	27782	3	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26986957	PP 0214	gabT	4-aminobutyrate aminotransferase	2.0	3.76E-01	EG	6.1	44824	7	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP 0234	oprE	outer membrane porin	1.1	7.09E-01	EG	5.4	48317	2	Outer Membrane			
26986997	PP 0255		17 kDa surface antigen	1.5	2.38E-01	control	10.4	15911	2	Cytoplasmic Membrane			
26987000	PP 0258		LysM domain/BON superfamily protein	2.6	1.18E-01	control	5.2	15616	5	Unknown	COG1652	Function unknown	
26987010	PP 0268	oprQ	outer membrane porin	1.1	8.08E-01	control	6.1	47787	10	Outer Membrane			
26987080	PP 0338	aceF	dihydrolipoamide acetyltransferase	1.6	2.94E-01	EG	5.3	55654	9	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP 0339	aceE	pyruvate dehydrogenase subunit E1	1.2	6.64E-01	EG	5.6	99332	36	Cytoplasmic	COG2609	Energy production and conversion	
26987129	PP 0387	rpoD	RNA polymerase sigma factor RpoD	1.8	7.14E-01	EG	4.6	69396	16	Cytoplasmic	COG0568	Transcription	
26987131	PP 0389	rpsU	30S ribosomal protein S21	1.6	9.83E-02	control	11.4	8370	3	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987138	PP 0396		hypothetical protein	1.5	6.04E-01	EG	7.0	50488	7	Cytoplasmic	COG2718	Function unknown	
26987139	PP 0397		serine protein kinase, PrkA	1.8	3.36E-01	EG	5.8	73782	21	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987159	PP 0418		GDSL family lipase	1.0	8.88E-01	control	4.4	67175	3	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987181	PP 0440	tuf	elongation factor Tu	1.4	6.12E-01	EG	5.0	43495	31	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP 0443	rplK	50S ribosomal protein L11	2.1	1.54E-01	EG	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP 0444	rplA	50S ribosomal protein L1	1.8	6.20E-01	EG	10.1	24251	4	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP 0445	rplJ	50S ribosomal protein L10	1.2	4.22E-01	control	10.2	17686	11	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP 0446	rplL	50S ribosomal protein L7/L12	1.4	3.15E-01	EG	4.4	12599	2	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP 0447	rpoB	DNA-directed RNA polymerase subunit beta	1.7	5.15E-01	EG	5.5	150992	48	Cytoplasmic	COG0085	Transcription	
26987190	PP 0449	rpsL	30S ribosomal protein S12	1.5	4.19E-01	EG	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP 0450	rpsG	30S ribosomal protein S7	1.3	5.29E-01	EG	10.8	17578	14	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP 0451	fusA	elongation factor G	1.7	4.43E-01	EG	4.9	78817	31	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987196	PP 0455	rplD	50S ribosomal protein L4	1.4	2.72E-01	control	10.3	21811	9	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP 0456	rplW	50S ribosomal protein L23	1.2	5.39E-01	EG	10.7	10900	2	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP 0457	rplB	50S ribosomal protein L2	1.3	2.93E-01	EG	11.7	29669	13	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP 0461	rplP	50S ribosomal protein L16	1.2	8.53E-01	control	11.9	15373	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP 0464	rplN	50S ribosomal protein L14	2.0	1.18E-01	EG	11.6	13410	9	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP 0466	rplE	50S ribosomal protein L5	1.1	9.12E-01	EG	10.3	20329	16	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP 0467	rpsN	30S ribosomal protein S14	1.5	1.49E-01	EG	12.3	11403	4	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP 0468	rpsH	30S ribosomal protein S8	2.0	5.64E-01	EG	10.2	13975	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP 0469	rplF	50S ribosomal protein L6	1.4	8.98E-01	EG	10.4	19143	4	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP 0470	rplR	50S ribosomal protein L18	1.6	1.61E-01	EG	10.9	12628	8	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP 0471	rpsE	30S ribosomal protein S5	1.3	3.71E-01	EG	10.6	17666	11	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP 0473	rplO	50S ribosomal protein L15	1.3	3.35E-01	EG	11.5	15189	8	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP 0474	secY	preprotein translocase subunit SecY	1.3	6.50E-01	EG	10.4	47853	5	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP 0476	rpsM	30S ribosomal protein S13	1.7	2.09E-01	EG	11.3	13256	6	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP 0477	rpsK	30S ribosomal protein S11	2.0	2.84E-01	EG	11.5	13660	4	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP 0478	rpsD	30S ribosomal protein S4	1.2	6.52E-01	EG	10.5	23056	11	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP 0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.2	9.07E-01	EG	4.7	36629	7	Cytoplasmic	COG0202	Transcription	
26987221	PP 0480	rplQ	50S ribosomal protein L17	1.2	5.85E-01	EG	11.3	14363	7	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP 0482		bacterioferritin	1.5	2.09E-01	control	4.6	17972	5	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987246	PP 0507		efflux ABC transporter ATP-binding protein	1.3	3.98E-01	control	7.2	25648	2	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987282	PP 0544		ethanolamine transproter	3.0	2.58E-01	EG	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987296	PP 0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.7	4.26E-01	EG	6.5	49088	4	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP 0564		hypothetical protein	1.4	4.56E-01	control	6.6	40223	4	Unknown	COG5345	Function unknown	
26987322	PP 0584		methyl-accepting chemotaxis transducer	1.2	2.88E-01	EG	5.0	69953	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987340	PP 0603	ileS	isoleucyl-tRNA synthetase	2.5	4.41E-01	EG	6.0	105800	2	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP 0622		competence lipoprotein ComL	1.2	4.00E-01	control	4.8	38410	6	Unknown	COG4105	General function prediction only	
26987362	PP 0626	ndh	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1.1	8.80E-01	control	9.0	47080	2	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26987416	PP 0680		ATP-dependent protease	2.3	3.42E-01	EG	4.5	89677	4	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987427	PP 0691	proB	gamma-glutamyl kinase	1.7	9.07E-01	EG	7.8	39661	5	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP 0707		MscS mechanosensitive ion channel	1.0	4.83E-01	EG	9.9	92124	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP 0711		isochorismatase superfamily hydrolase	1.6	8.10E-01	EG	5.3	23026	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987458	PP 0722	prsA	ribose-phosphate pyrophosphokinase	3.5	1.33E-01	EG	5.9	34192	4	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987460	PP 0724	lolB	outer membrane lipoprotein LolB	1.4	2.43E-01	EG	8.2	22895	3	Unknown	COG3017	Cell envelope biogenesis, outer membrane	
26987487	PP 0751	mqo-1	malate:quinone oxidoreductase	2.6	1.78E-01	EG	8.4	54282	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP 0753		lipoprotein	1.1	5.58E-01	control	9.5	20483	9	Unknown			
26987495	PP 0759		hypothetical protein	1.3	2.59E-01	control	7.0	29743	4	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP 0763		long-chain-fatty-acid--CoA ligase	1.5	8.94E-01	EG	5.5	62125	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987509	PP 0773		OmpA/MotB domain protein	1.1	8.33E-01	EG	9.5	24753	13	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987548	PP 0812	cyoA	ubiquinol oxidase subunit 2	1.2	3.88E-01	control	6.7	34557	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987570	PP 0834	yajC	preprotein translocase subunit YajC	2.2	2.63E-02	EG	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP 0835	secD	preprotein translocase subunit SecD	1.2	5.03E-01	control	9.6	66913	14	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987585	PP 0849	ndk	nucleoside diphosphate kinase	1.2	3.09E-01	EG	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP 0856		hypothetical protein	1.4	1.81E-01	control	4.7	40737	10	Outer Membrane	COG1520	Function unknown	
26987596	PP 0860		flavodoxin/nitric oxide synthase	1.3	3.25E-01	EG	7.6	93734	2	Cytoplasmic Membrane	COG0369	Inorganic ion transport and metabolism	
26987603	PP 0867		FecA-like outer membrane receptor	1.1	7.14E-01	control	4.9	88153	24	Outer Membrane	COG4772	Inorganic ion transport and metabolism	
26987619	PP 0883		outer membrane porin	1.1	9.59E-01	EG	6.6	50256	4	Outer Membrane			
26987645	PP 0909		hypothetical protein	1.0	8.97E-01	EG	6.4	38380	10	Unknown	COG3489	General function prediction only	
26987680	PP 0944	fumC	fumarate hydratase	1.1	7.59E-01	control	5.9	48541	15	Cytoplasmic	COG0114	Energy production and conversion	
26987695	PP 0959	ttg2B	hypothetical protein	1.2	5.56E-01	control	8.2	28489	2	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987713	PP 0977	valS	valyl-tRNA synthetase	1.2	9.71E-01	EG	5.1	107495	11	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987735	PP 0999	arcC	carbamate kinase	1.4	3.93E-01	EG	5.5	33423	2	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP 1000	argI	ornithine carbamoyltransferase	1.6	5.36E-01	EG	6.3	37911	8	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987738	PP 1002	arcD	arginine/ornithine antiporter	1.2	7.39E-01	EG	9.1	51061	2	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987742	PP 1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	1.1	3.65E-01	control	5.6	84730	31	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26987746	PP 1010	edd	phosphogluconate dehydratase	1.7	2.44E-01	EG	6.4	65359	4	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987758	PP 1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.9	1.39E-01	EG	6.8	55000	6	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987760	PP 1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.5	5.13E-01	EG	5.4	25004	5	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987767	PP 1031	guaB	inosine 5'-monophosphate dehydrogenase	182.0	5.42E-02	control	7.0	51765	2	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987806	PP 1070		polar amino acid ABC transporter inner membrane subunit	1.9	6.09E-01	control	8.2	27464	4	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP 1082	bfr	bacterioferritin	1.6	8.16E-02	control	4.4	17971	7	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP 1084		anti-oxidant AhpCTSA family protein	1.7	1.67E-01	EG	4.9	21730	6	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP 1088	argG	argininosuccinate synthase	5.1	3.63E-01	EG	5.1	45164	3	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP 1097	metG	methionyl-tRNA synthetase	2.4	3.91E-01	EG	5.5	75186	2	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987857	PP 1121		OmpA/MotB domain protein	1.3	5.90E-01	EG	5.0	24084	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987893	PP 1157		acetolactate synthase	2.2	2.14E-01	EG	6.1	60059	3	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26987914	PP 1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.9	1.00E+00	EG	5.7	106948	5	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987937	PP 1202		hypothetical protein	1.2	5.27E-01	control	9.7	95622	2	Cytoplasmic Membrane	COG2898	Function unknown	
26987940	PP 1205	proS	prolyl-tRNA synthetase	2.8	2.60E-01	EG	5.0	63623	2	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987945	PP 1210		DNA-binding stress protein	1.1	6.49E-01	control	5.0	17861	2	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP 1213	aspS	aspartyl-tRNA synthetase	1.6	3.53E-01	EG	5.1	66568	10	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	

26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.7	1.64E-01	EG	6.3	25310	4	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	2.2	1.48E-01	control	9.8	47431	10	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.5	2.68E-01	control	4.9	17833	12	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988050	PP_1315	rplM	50S ribosomal protein L13	5.1	1.05E-01	EG	10.3	15862	2	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.1	5.55E-01	EG	11.7	14592	4	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.5	5.16E-01	EG	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.1	7.78E-01	control	7.1	29032	6	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.2	1.23E-01	control	7.5	64637	21	Cytoplasmic Membrane	COG3107	General function prediction only	
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.3	9.38E-01	EG	5.0	42236	3	Cytoplasmic	COG1364	Amino acid transport and metabolism	
26988087	PP_1353		MscS mechanosensitive ion channel	1.0	7.80E-01	control	7.5	30804	2	Cytoplasmic Membrane	COG0668	Cell envelope biogenesis, outer membrane	
26988091	PP_1357		hypothetical protein	1.3	9.33E-01	EG	5.6	42364	2	Unknown			
26988096	PP_1362	pykA	pyruvate kinase	1.1	6.15E-01	EG	6.7	52057	13	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988100	PP_1366		transcriptional regulator MvaT, P16 subunit	1.0	9.65E-01	control	10.1	14184	2	Cytoplasmic			
26988117	PP_1383		BenF-like porin	1.1	8.75E-01	EG	6.8	46022	4	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.3	3.45E-01	control	5.1	52864	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.0	6.99E-01	EG	5.3	112835	6	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	1.1	8.94E-01	EG	6.0	41250	3	Unknown	COG0845	Cell envelope biogenesis, outer membrane	
26988164	PP_1431	lepA	GTP-binding protein LepA	2.6	3.73E-01	EG	5.5	66116	4	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.5	1.19E-01	control	9.2	32060	6	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988176	PP_1443	lon-1	ATP-dependent protease La	2.2	4.51E-01	EG	6.4	89794	3	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26988178	PP_1445	oprB-2	porin B	1.0	6.29E-01	control	6.0	49176	2	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.0	4.54E-01	control	5.7	42575	2	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988192	PP_1459		CBS domain-containing protein	2.9	8.98E-01	control	4.7	44174	2	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.2	6.11E-01	EG	11.0	13012	7	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	1.1	8.48E-01	EG	6.2	51645	7	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.3	7.10E-01	EG	5.7	50918	7	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.3	1.40E-01	control	4.7	58605	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988234	PP_1502		OmpA/MotB domain protein	1.0	7.50E-01	control	9.5	28964	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	9.95E-01	EG	9.3	27023	16	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.2	3.58E-01	control	4.7	86513	14	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.6	2.48E-01	EG	6.0	35135	2	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.5	8.09E-01	EG	5.8	59474	5	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.3	9.09E-01	EG	4.7	45490	3	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.4	8.60E-01	EG	11.0	27506	8	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	1.2	2.77E-01	control	4.8	16590	5	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.2	3.99E-01	EG	4.8	26520	9	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988474	PP_1743	actP	acetate permease	1.0	5.30E-01	control	9.6	58972	4	Cytoplasmic Membrane	COG4147	General function prediction only	
26988498	PP_1767	gyrA	DNA gyrase subunit A	2.4	4.80E-01	EG	4.7	102037	10	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988568	PP_1838		hypothetical protein	1.1	4.86E-01	EG	6.8	76615	6	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988588	PP_1858	efp	elongation factor P	1.4	4.16E-01	EG	4.5	21303	3	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.2	7.64E-01	EG	9.2	60924	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988602	PP_1872		aminotransferase AlaT	2.1	3.93E-01	EG	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.6	6.23E-01	EG	4.7	120904	13	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.1	8.58E-01	EG	6.4	36497	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.4	3.83E-01	EG	6.0	25470	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988696	PP_1970		lipoprotein	1.0	8.47E-01	control	4.9	22337	6	Unknown			
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.0	9.11E-01	EG	5.9	43290	9	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.0	7.75E-01	control	5.3	40672	5	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.6	2.10E-01	EG	7.8	32510	3	Cytoplasmic	COG0777	Lipid metabolism	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.9	4.10E-01	EG	6.5	55400	7	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988731	PP_2006		hypothetical protein	1.2	3.32E-01	control	5.1	63743	8	Unknown			
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.4	6.90E-01	EG	4.8	86015	11	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988814	PP_2089	oprF	OmpF family protein	1.0	7.31E-01	control	4.5	37012	36	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988830	PP_2105		hypothetical protein	1.0	9.86E-01	control	4.9	11370	2	Unknown	COG4575	Function unknown	
26988845	PP_2121		lipoprotein	1.1	4.97E-01	control	5.0	8131	2	Unknown			
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.5	7.05E-01	EG	7.7	53014	19	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	1.9	4.00E-01	EG	7.7	50905	3	Cytoplasmic	COG1249	Energy production and conversion	
26988913	PP_2189		hypothetical protein	1.2	7.09E-01	control	4.9	15175	2	Unknown	COG4575	Function unknown	
26988917	PP_2193		TonB-dependent siderophore receptor	1.2	6.84E-02	EG	4.8	89791	4	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.3	4.69E-01	EG	5.1	68646	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988988	PP_2264		extracellular solute-binding protein, family 1	2.1	2.44E-01	EG	5.6	65243	4	Unknown	COG1653	Carbohydrate transport and metabolism	
26989026	PP_2302	lon-2	ATP-dependent protease La	2.4	3.89E-01	EG	5.9	88722	10	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.1	6.75E-01	control	9.3	9997	3	Unknown			
26989033	PP_2309		hypothetical protein	1.8	9.56E-01	EG	12.2	14114	2	Cytoplasmic Membrane			
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.4	2.31E-01	control	8.5	8801	9	Outer Membrane			
26989055	PP_2331		hypothetical protein	1.2	7.06E-01	EG	7.9	57064	7	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.6	6.10E-01	EG	5.0	93609	11	Cytoplasmic	COG1049	Energy production and conversion	
26989146	PP_2423		hypothetical protein	1.3	9.85E-01	EG	9.8	34661	2	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26989170	PP_2447		hypothetical protein	1.0	9.34E-01	control	10.2	26784	2	Unknown			
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.4	7.19E-01	EG	5.8	72697	8	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP_2466	infC	translation initiation factor IF-3	1.2	8.83E-01	EG	10.0	20120	2	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.4	2.66E-01	EG	12.1	13280	4	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989297	PP_2578		hypothetical protein	1.1	9.88E-01	EG	9.5	19010	3	Unknown	COG3009	Function unknown	
26989381	PP_2662		hypothetical protein	63.3	2.66E-01	EG	4.3	42858	11	Outer Membrane			
26989398	PP_2679		quinoprotein ethanol dehydrogenase	198.1	3.05E-05	EG	9.1	64883	2	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	86.1	2.17E-05	EG	5.5	54903	6	Cytoplasmic	COG1012	Energy production and conversion	
26989572	PP_2853		hypothetical protein	1.0	6.71E-01	control	4.5	46020	10	Unknown			
26989647	PP_2928		saccharopine dehydrogenase	4.0	1.65E-01	EG	5.0	45363	2	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.2	3.98E-01	EG	9.0	57141	8	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989854	PP_3135		glycosyl transferase	1.2	4.68E-01	EG	8.6	35887	17	Cytoplasmic	COG1216	General function prediction only	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.0	5.36E-01	EG	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989893	PP_3174		aldo/keto reductase	1.8	4.55E-01	EG	6.5	36891	2	Cytoplasmic	COG0667	Energy production and conversion	
26990047	PP_3330		TonB-dependent siderophore receptor	1.3	1.48E-01	EG	5.8	80740	3	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	2.0	9.17E-03	EG	4.8	77137	6	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	1.2	4.94E-01	control	8.9	47532	11	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.7	4.34E-01	EG	6.2	59980	2	Cytoplasmic	COG1012	Energy production and conversion	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	2.0	2.50E-02	EG	7.2	36863	5	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990230	PP_3518		hypothetical protein	2.2	6.15E-01	control	10.4	51727	2	Extracellular			
26990294	PP_3582		RND efflux transporter	1.2	4.95E-01	control	5.2	53952	17	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	2.7	1.05E-01	EG	5.9	43631	3	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990323	PP_3612		TonB-dependent siderophore receptor	1.3	3.65E-01	EG	5.2	85491	26	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990373	PP_3662		decarboxylase family protein	1.7	9.03E-01	EG	6.7	50729	2	Cytoplasmic	COG1611	General function prediction only	
26990470	PP_3765		transcriptional regulator MvaT, P16 subunit	1.9	4.14E-01	EG	10.7	13559	2	Cytoplasmic			
26990499	PP_3794	pbpG	D-alanyl-D-alanine endopeptidase	1.5	8.32E-01	control	10.5	33802	3	Unknown	COG1686	Cell envelope biogenesis, outer membrane	
26990627	PP_3922		periplasmic protein	1.1	4.11E-01	EG	9.8	37502	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	5.0	3.01E-01	EG	5.4	79899	2	Cytoplasmic	COG2838	Energy production and conversion	
26990735	PP_4032		outer membrane lipoprotein Blc	4.1	1.09E-01	control	8.3	21093	2	Outer Membrane	COG3040	Cell envelope biogenesis, outer membrane	
26990738	PP_4035		NCS1 nucleoside transporter	1.1	5.77E-01	EG	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990806	PP_4111	fusA	elongation factor G	1.1	9.56E-01	EG	5.0	77832	4	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990810	PP_4116	aceA	isocitrate lyase	5.6	1.65E-05	EG	5.3	48633	2	Cytoplasmic	COG2224	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.0	9.42E-01	control	8.7	20354	2	Cytoplasmic	COG0431	General function prediction only	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	2.4	1.88E-01	EG	5.3	43264	3	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.1	7.99E-01	EG	6.2	30111	14	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.6	3.36E-01	EG	6.1	41239	19	Cytoplasmic	COG0045	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.3	8.44E-01	EG	7.5	26000	2	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.1	9.90E-01	EG	6.2	63448	5	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.0	8.84E-01	EG	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.2	9.79E-01	EG	10.3	13813	2	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.1	9.33E-01	EG	7.0	47622	7	Cytoplasmic	COG0372	Energy production and conversion	
26990890	PP_4198		OmpA/MotB domain protein	2.7	5.76E-01	EG	8.9	29694	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.6	9.89E-01	EG	4.9	31237	2	Unknown	COG2025	Energy production and conversion	

26990894	PP_4202		electron transfer flavoprotein, beta subunit	2.0	6.68E-01	EG	9.7	26361	5	Unknown	COG2086	Energy production and conversion			
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	1.3	6.76E-01	EG	9.6	53567	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones			
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.3	5.82E-01	EG	9.0	22637	3	Cytoplasmic	COG2993	Energy production and conversion			
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.2	3.87E-01	EG	5.2	35613	7	Unknown	COG2010	Energy production and conversion			
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	1.4	4.98E-01	EG	10.1	17847	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion			
26991173	PP_4487	acsA	acetyl-CoA synthetase	11.1	1.30E-01	EG	6.4	71796	2	Cytoplasmic	COG0365	Lipid metabolism			
26991206	PP_4521		aerotaxis receptor	2.3	1.89E-01	EG	6.4	56605	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion		Signal transduction mechanisms	
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	2.0	3.06E-01	EG	10.3	48478	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair		Transcription	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	2.1	5.79E-01	EG	7.7	61812	3	Cytoplasmic	COG0318	Lipid metabolism		Secondary metabolites biosynthesis, transport, and catabolism	
26991254	PP_4570		hypothetical protein	1.0	8.70E-01	EG	10.1	35846	5	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones			
26991255	PP_4571	cysK	cysteine synthase A	2.1	2.24E-01	EG	5.5	34357	3	Cytoplasmic	COG0031	Amino acid transport and metabolism			
26991325	PP_4641	cstA	carbon starvation protein CstA	1.1	8.46E-01	EG	9.0	73763	9	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms			
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.3	5.94E-01	control	4.8	14730	3	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane			
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.9	2.27E-01	EG	5.4	36370	10	Cytoplasmic	COG0059	Amino acid transport and metabolism		Coenzyme metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	2.4	1.84E-01	EG	6.8	62781	4	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase			
26991370	PP_4686		hypothetical protein	1.1	7.44E-01	control	6.2	32403	5	Periplasmic	COG3016	Function unknown			
26991381	PP_4697	pcnB	poly(A) polymerase	2.7	3.81E-01	EG	9.6	52721	2	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis			
26991386	PP_4702	acsB	acetyl-CoA synthetase	2.8	1.81E-01	EG	6.5	71251	4	Cytoplasmic	COG0365	Lipid metabolism			
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.7	3.53E-01	EG	4.9	75010	13	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis			
26991395	PP_4712	infB	translation initiation factor IF-2	2.9	4.77E-01	EG	6.8	91460	12	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis			
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.1	6.02E-01	EG	5.4	69722	8	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones			
26991410	PP_4727	dnaK	molecular chaperone DnaK	2.8	8.07E-02	EG	4.6	68800	4	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones			
26991418	PP_4735	lctP	L-lactate transport	2.3	6.72E-02	control	9.3	58955	4	Cytoplasmic Membrane	COG1620	Energy production and conversion			
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	1.3	4.23E-01	control	8.5	56126	3	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane			
26991478	PP_4798		lytic murein transglycosylase	1.4	1.81E-01	EG	7.7	48000	6	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane			
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.9	1.15E-01	EG	6.6	42288	4	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane			
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	1.6	1.63E-01	control	5.0	31015	3	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones			
26991518	PP_4838	oprC	TonB-dependent copper receptor	1.3	7.45E-01	EG	6.2	74540	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism			
26991519	PP_4839		hypothetical protein	1.1	7.58E-01	EG	9.6	50581	2	Cytoplasmic Membrane	COG3182	Function unknown			
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	1.3	3.79E-01	EG	6.3	27400	2	Cytoplasmic	COG4221	General function prediction only			
26991556	PP_4876	rpsR	30S ribosomal protein S18	1.0	8.30E-01	EG	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis			
26991557	PP_4877	rpsF	30S ribosomal protein S6	1.1	5.27E-01	control	4.7	16373	2	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis			
26991559	PP_4880	vacB	ribonuclease R	2.2	2.09E-01	EG	7.9	96688	6	Cytoplasmic	COG0557	Transcription			
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.2	2.92E-01	EG	6.1	71958	16	Cytoplasmic Membrane	COG0840	Cell motility and secretion		Signal transduction mechanisms	
26991567	PP_4889	purA	adenylosuccinate synthetase	1.0	6.77E-01	control	5.6	46833	2	Cytoplasmic	COG0104	Nucleotide transport and metabolism			
26991569	PP_4891	hflC	HflC protein	1.0	9.42E-01	EG	9.8	33001	13	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones			
26991570	PP_4892	hflK	HflK protein	2.8	2.49E-01	EG	5.1	44762	5	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones			
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.6	3.26E-01	EG	8.6	31547	4	Cytoplasmic Membrane	COG0688	Lipid metabolism			
26991589	PP_4911		hypothetical protein	1.3	2.78E-01	control	8.5	27337	2	Periplasmic	COG3009	Function unknown			
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	265.4	9.32E-02	EG	6.2	83181	2	Cytoplasmic	COG0188	DNA replication, recombination, and repair			
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.2	4.06E-01	control	7.6	66279	6	Cytoplasmic Membrane	COG1132	Defense mechanisms			
26991616	PP_4938		glycosyl transferase	1.4	8.78E-01	EG	9.4	41783	4	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane			
26991622	PP_4944		carbamoyltransferase	1.7	5.00E-01	EG	7.2	65646	6	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones			
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.1	9.19E-01	control	5.6	38453	4	Cytoplasmic	COG0191	Carbohydrate transport and metabolism			
26991643	PP_4965	tktA	transketolase	1.8	4.34E-01	EG	5.0	72463	9	Cytoplasmic	COG0021	Carbohydrate transport and metabolism			
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.6	4.77E-01	EG	5.1	42779	4	Cytoplasmic	COG0192	Coenzyme metabolism			
26991660	PP_4983		amine oxidase	1.9	2.43E-01	EG	10.2	65923	8	Unknown	COG1231	Amino acid transport and metabolism			
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	2.2	6.23E-01	EG	5.7	49982	6	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones			
26991688	PP_5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.1	8.25E-01	EG	9.5	28397	2	Cytoplasmic	COG2226	Coenzyme metabolism			
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.2	3.78E-01	control	4.9	69017	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion		Signal transduction mechanisms	
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.0	9.57E-01	EG	8.3	95875	6	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane			
26991720	PP_5044		GTP-binding protein TypA	1.8	6.39E-01	EG	5.3	67157	3	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms			
26991722	PP_5046	glnA	glutamine synthetase, type I	1.7	4.54E-01	EG	5.1	51740	12	Cytoplasmic	COG0174	Amino acid transport and metabolism			
26991729	PP_5053	secB	preprotein translocase subunit SecB	1.6	5.22E-01	EG	4.2	17754	2	Cytoplasmic	COG1952	Intracellular trafficking and secretion			
26991731	PP_5055		rhodanese domain-containing protein	1.4	6.67E-01	EG	9.9	14839	2	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism			
26991753	PP_5077		sporulation domain protein	1.3	7.92E-01	EG	7.1	55434	3	Unknown	COG3267	Intracellular trafficking and secretion			
26991760	PP_5084		penicillin-binding protein, 1A family	1.7	8.71E-02	EG	7.2	89193	2	Extracellular	COG5009	Cell envelope biogenesis, outer membrane			
26991761	PP_5085	maeB	malic enzyme	2.0	2.92E-01	EG	4.9	45127	8	Cytoplasmic	COG0281	Energy production and conversion			
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.1	9.26E-01	EG	5.7	63668	2	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis			
26991766	PP_5090		sporulation domain protein	1.4	2.47E-01	EG	10.6	24964	4	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning			
26991772	PP_5096		hypothetical protein	1.5	5.13E-01	EG	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown			
26991785	PP_5109	ftsX	hypothetical protein	1.1	6.78E-01	control	6.5	36984	2	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning			
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	4.1	2.48E-01	EG	5.8	65671	3	Cytoplasmic	COG0129	Amino acid transport and metabolism		Carbohydrate transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.7	2.70E-01	EG	6.3	44339	8	Cytoplasmic	COG0111	Amino acid transport and metabolism			
26991861	PP_5185	argA	N-acetylglutamate synthase	1.2	6.55E-01	EG	5.9	47440	2	Cytoplasmic	COG0548	Amino acid transport and metabolism			
26991868	PP_5192	gcvP-2	glycine dehydrogenase	2.9	5.37E-01	EG	6.3	104037	2	Cytoplasmic	COG1003	Amino acid transport and metabolism			
26991890	PP_5214	rho	transcription termination factor Rho	1.5	7.32E-01	EG	8.2	47041	4	Cytoplasmic	COG1158	Transcription			
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.6	3.33E-01	control	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis			
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	2.8	5.02E-01	EG	9.2	78603	4	Cytoplasmic	COG0317	Signal transduction mechanisms		Transcription	
26991989	PP_5313	hupA	histone family protein DNA-binding protein	1.3	9.58E-01	EG	11.0	10551	3	Cytoplasmic	COG0776	DNA replication, recombination, and repair			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.8	5.76E-01	EG	5.3	65626	9	Cytoplasmic	COG5016	Energy production and conversion			
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.6	6.39E-01	EG	6.5	51942	8	Cytoplasmic	COG0439	Lipid metabolism			
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	3.3	1.49E-01	EG	5.9	48114	2	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane			
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	9.44E-01	EG	4.6	49359	12	Cytoplasmic	COG0055	Energy production and conversion			
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.2	7.47E-01	EG	9.2	31464	10	Cytoplasmic	COG0224	Energy production and conversion			
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.6	1.81E-01	EG	5.2	55352	16	Cytoplasmic	COG0056	Energy production and conversion			
148545484	Pput_0228	gabD	succinate-semialdehyde dehydrogenase I	1.9	4.42E-01	EG	5.3	51548	8	Cytoplasmic	COG1012	Energy production and conversion			
148545505	Pput_0249		outer membrane porin	1.1	7.32E-01	control	5.4	48366	16	Outer Membrane					
148545562	Pput_0307		AsmA family protein	1.2	2.07E-01	EG	6.1	80211	9	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane			
148545637	Pput_0382		malate synthase G	1.3	5.34E-01	EG	5.8	78248	2	Cytoplasmic	COG2225	Energy production and conversion			
148545690	Pput_0438		organic solvent tolerance protein	1.3	2.73E-01	control	4.8	105822	26	Outer Membrane	COG1452	Cell envelope biogenesis, outer membrane			
148545717	Pput_0465	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.0	8.58E-01	EG	6.8	36249	4	Cytoplasmic	COG0002	Amino acid transport and metabolism			
148545733	Pput_0481		DNA-directed RNA polymerase subunit beta'	1.4	7.77E-01	EG	7.2	154769	52	Cytoplasmic	COG0086	Transcription			
148545789	Pput_0539		OmpW family protein	1.2	2.62E-01	control	5.2	24190	10	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane			
148545791	Pput_0541		hypothetical protein	1.1	5.68E-01	control	9.7	45825	12	Cytoplasmic Membrane	COG0577	Defense mechanisms			
148545797	Pput_0547		hypothetical protein	1.3	6.95E-01	EG	8.5	16877	2	Unknown	COG3126	Function unknown			
148545834	Pput_0584		aldehyde dehydrogenase	3.9	2.81E-02	EG	5.9	55223	18	Cytoplasmic	COG1012	Energy production and conversion			
148545859	Pput_0609		alpha-2-macroglobulin domain-containing protein	1.0	9.43E-01	EG	5.2	178356	7	Unknown	COG2373	General function prediction only			
148545865	Pput_0615		hypothetical protein	1.3	6.21E-01	EG	9.5	21405	6	Unknown					
148545886	Pput_0636		beta alanine--pyruvate transaminase	1.4	6.23E-01	EG	6.8	48577	5	Cytoplasmic	COG0161	Coenzyme metabolism			
148545890	Pput_0640		hypothetical protein	1.4	9.82E-01	EG	9.7	83607	2	Unknown	COG3008	General function prediction only			
148545951	Pput_0705		putative ABC transporter ATP-binding protein	2.2	6.58E-01	EG	5.3	61844	7	Cytoplasmic	COG0488	General function prediction only			
148545966	Pput_0720	rplU	50S ribosomal protein L21	1.5	5.04E-01	EG	10.7	11632	5	Cytoplasmic	COG0261	Translation, ribosomal structure and biogenesis			
148546001	Pput_0755		50S ribosomal protein L25/general stress protein Ctc	4.0	1.67E-01	EG	6.0	21298	2	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis			
148546005	Pput_0759		TPR repeat-containing protein	1.4	4.78E-01	control	4.6	63914	2	Cytoplasmic	COG5010	Intracellular trafficking and secretion			
148546038	Pput_0792		hypothetical protein	1.1	3.12E-01	EG	5.0	67997	19	Outer Membrane					
148546039	Pput_0793		hypothetical protein	1.8	3.15E-01	EG	9.5	50556	6	Unknown					
148546135	Pput_0891		TonB-dependent siderophore receptor	1.1	7.96E-01	EG	4.8	81988	3	Outer Membrane	COG4774	Inorganic ion transport and metabolism			
148546195	Pput_0952		hypothetical protein	1.2	5.27E-01	EG	4.4	47132	22	Outer Membrane	COG3487	Inorganic ion transport and metabolism			
148546281	Pput_1038		arginine deiminase	1.3	5.80E-01	EG	5.8	46419	14	Cytoplasmic	COG2235	Amino acid transport and metabolism			
148546286	Pput_1043		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	1.4	8.81E-01	EG	6.3	94800	4	Outer Membrane	COG1629	Inorganic ion transport and metabolism			
148546290	Pput_1047		type I glyceraldehyde-3-phosphate dehydrogenase	1.1	7.41E-01	control	7.0	36013	8	Cytoplasmic	COG0057	Carbohydrate transport and metabolism			
148546300	Pput_1057		carbohydrate-selective porin OprB	1.1	5.17E-01	control	6.1	49588	24	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane			
148546315	Pput_1072	guaA	GMP synthase	1.4	5.27E-01	EG	5.3	58146	10	Cytoplasmic	COG0519	Nucleotide transport and metabolism			
148546321	Pput_1078		phosphoribosylformylglycinamidine synthase	1.8	4.18E-01	EG	4.7	140744	19	Cytoplasmic	COG0046	Nucleotide transport and metabolism			
148546342	Pput_1099		membrane carboxypeptidase (penicillin-binding protein)-like protein	1.1	6.59E-01	control	9.5	116866	7	Unknown	COG0744	Cell envelope biogenesis, outer membrane			
148546352	Pput_1109		ABC transporter-like protein	1.6	6.56E-01	EG	7.9	26871	2	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism			
148546390	Pput_1147		penicillin amidase	1.1	3.03E-01	control	8.5	88721	19	Periplasmic	COG2366	General function prediction only			
148546401	Pput_1158		OmpA/MotB domain-containing protein	1.2	7.11E-01	EG	4.5	24650	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane			
148546410	Pput_1167		17 kDa surface antigen	1.1	8.94E-01	EG	9.3	15682	8	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane			
148546458	Pput_1215		outer membrane protein H1	1.1	6.18E-01	control	6.5	21492	2	Outer Membrane					

148546461	Pput_1218		C4-dicarboxylate transporter DctA	1.3	5.04E-01	control	9.0	46240	2	Cytoplasmic Membrane	COG1301	Energy production and conversion		
148546473	Pput_1230		virulence factor family protein	1.3	2.85E-01	EG	5.0	46965	2	Unknown	COG3946	Intracellular trafficking and secretion		
148546478	Pput_1235		outer membrane porin	1.2	4.34E-01	control	4.6	46148	22	Outer Membrane				
148546511	Pput_1268		hypothetical protein	1.0	7.43E-01	control	4.8	40802	8	Unknown	COG3317	Cell envelope biogenesis, outer membrane		
148546632	Pput_1392		TolC family type I secretion outer membrane protein	1.2	1.19E-01	EG	5.4	50379	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
148546674	Pput_1434	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	3.6	1.22E-01	EG	6.3	43478	4	Cytoplasmic	COG4992	Amino acid transport and metabolism		
148546681	Pput_1441	alaS	alanyl-tRNA synthetase	1.5	8.81E-01	EG	5.2	97206	5	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis		
148546791	Pput_1552		PhzF family phenazine biosynthesis protein	1.5	5.53E-01	EG	4.6	28510	2	Cytoplasmic	COG0384	General function prediction only		
148546831	Pput_1593	zipA	cell division protein ZipA	1.1	4.86E-01	control	5.7	32849	10	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning		
148546880	Pput_1642		class V aminotransferase	1.2	3.60E-01	control	8.7	47665	4	Cytoplasmic	COG0520	Posttranslational modification, protein turnover, chaperones		
148546881	Pput_1643		peptidase M19, renal dipeptidase	2.2	2.65E-02	EG	5.9	51410	4	Unknown	COG2355	Amino acid transport and metabolism		
148546882	Pput_1644		hypothetical protein	2.5	3.24E-01	EG	7.0	61848	2	Cytoplasmic				
148546903	Pput_1665	sucA	2-oxoglutarate dehydrogenase E1 component	1.0	8.24E-01	control	6.5	106519	20	Cytoplasmic	COG0567	Energy production and conversion		
148546904	Pput_1666		dihydrolipoamide succinyltransferase	1.2	9.24E-01	EG	5.0	42436	12	Cytoplasmic	COG0508	Energy production and conversion		
148546916	Pput_1678		TonB-dependent siderophore receptor	1.0	8.57E-01	EG	5.5	90426	49	Outer Membrane	COG4773	Inorganic ion transport and metabolism		
148546920	Pput_1682		hypothetical protein	1.9	1.55E-01	EG	7.2	39496	5	Cytoplasmic				
148546921	Pput_1683		RND efflux system outer membrane lipoprotein	1.2	6.12E-01	EG	5.5	51518	3	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
148546924	Pput_1686		hypothetical protein	1.4	4.57E-01	EG	4.3	9411	2	Unknown				
148547052	Pput_1817		adenylosuccinate lyase	1.1	8.57E-01	EG	6.2	52497	4	Cytoplasmic	COG0015	Nucleotide transport and metabolism		
148547137	Pput_1907		hypothetical protein	1.2	4.69E-01	control	5.9	12488	2	Unknown				
148547224	Pput_2002		multi-sensor hybrid histidine kinase	1.5	8.90E-01	EG	4.9	129353	5	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms		
148547283	Pput_2061		catalase/peroxidase HPI	1.3	8.87E-01	EG	5.9	82005	12	Cytoplasmic	COG0376	Inorganic ion transport and metabolism		
148547407	Pput_2186		RND family efflux transporter MFP subunit	1.2	7.99E-01	EG	9.2	46606	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane		
148547426	Pput_2205		Pyrrolo-quinoline quinone	1.4	4.58E-01	EG	6.8	85340	8	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism		
148547579	Pput_2358		alpha/beta hydrolase fold family protein	1.4	7.91E-01	EG	8.7	32000	2	Cytoplasmic	COG0596	General function prediction only		
148547631	Pput_2410		TonB-dependent receptor	1.5	4.90E-01	EG	5.2	77047	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
148547633	Pput_2412		TonB-dependent siderophore receptor	1.3	2.63E-01	EG	5.5	79564	24	Outer Membrane	COG4773	Inorganic ion transport and metabolism		
148547639	Pput_2419		TonB-dependent siderophore receptor	1.6	3.14E-01	EG	4.8	76203	6	Outer Membrane	COG4773	Inorganic ion transport and metabolism		
148547806	Pput_2589		hypothetical protein	1.0	9.53E-01	EG	4.4	40855	11	Unknown				
148547850	Pput_2634		hypothetical protein	1.2	6.81E-01	EG	5.7	18527	3	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport		
148548356	Pput_3146		general substrate transporter	1.1	8.44E-01	EG	9.0	60590	9	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism		
148548404	Pput_3196		TonB-dependent siderophore receptor	1.1	4.36E-01	EG	4.8	87178	18	Outer Membrane	COG4773	Inorganic ion transport and metabolism		
148548436	Pput_3228		hypothetical protein	1.2	4.68E-01	control	8.1	10935	3	Unknown				
148548651	Pput_3443	cysB	transcriptional regulator CysB	1.2	6.96E-01	EG	6.9	35897	4	Cytoplasmic	COG0583	Transcription		
148548667	Pput_3459		methyl-accepting chemotaxis sensory transducer	1.4	1.42E-01	control	5.3	52116	10	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms	
148548785	Pput_3579		VacJ family lipoprotein	1.3	4.08E-01	control	5.1	26108	6	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane		
148548816	Pput_3610		lytic transglycosylase catalytic subunit	1.4	6.89E-01	EG	9.9	74631	13	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane		
148548833	Pput_3627	acnA	aconitate hydratase	1.2	9.32E-01	EG	5.4	99221	9	Cytoplasmic	COG1048	Energy production and conversion		
148548866	Pput_3660		NAD-glutamate dehydrogenase	1.6	7.71E-01	EG	5.7	182512	34	Cytoplasmic	COG2902	Amino acid transport and metabolism		
148548922	Pput_3716		hypothetical protein	1.5	5.26E-01	EG	10.1	16394	2	Cytoplasmic Membrane				
148548931	Pput_3725	pepN	aminopeptidase N	1.3	9.58E-01	EG	4.8	99527	6	Cytoplasmic	COG0308	Amino acid transport and metabolism		
148548974	Pput_3768		peptidoglycan-binding LysM	1.1	6.75E-01	control	3.9	97202	18	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion	
148548989	Pput_3783	gltX	glutamyl-tRNA synthetase	1.7	1.15E-01	EG	5.6	56451	4	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
148549028	Pput_3822	fadE	acyl-CoA dehydrogenase	1.1	8.36E-01	control	6.6	88807	12	Cytoplasmic Membrane	COG1960	Lipid metabolism		
148549110	Pput_3904		lipopolysaccharide biosynthesis protein	1.2	8.37E-01	EG	7.8	41683	2	Unknown	COG3524	Cell envelope biogenesis, outer membrane		
148549168	Pput_3962		hypothetical protein	2.1	4.76E-01	EG	7.8	57585	7	Cytoplasmic	COG2326	Function unknown		
148549188	Pput_3982		VacJ family lipoprotein	1.1	3.47E-01	control	5.4	30772	4	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane		
148549236	Pput_4030		aromatic hydrocarbon degradation membrane protein	1.3	4.97E-01	EG	6.1	46106	15	Outer Membrane	COG2067	Lipid metabolism		
148549449	Pput_4243		NADH:flavin oxidoreductase/NADH oxidase	1.8	8.72E-02	EG	5.8	40498	2	Cytoplasmic	COG1902	Energy production and conversion		
148549481	Pput_4275		TonB-dependent receptor	1.2	6.40E-01	EG	4.9	74714	29	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
148549491	Pput_4285		pyridoxine 5'-phosphate synthase	2.1	4.30E-01	EG	5.8	26011	2	Cytoplasmic	COG0854	Coenzyme metabolism		
148549557	Pput_4352		methyl-accepting chemotaxis sensory transducer	1.2	5.39E-01	EG	4.8	67728	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
148549568	Pput_4363	groEL	chaperonin GroEL	1.2	8.92E-01	EG	4.7	56729	15	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones		
148549606	Pput_4402		transport-associated	1.1	6.25E-01	control	9.5	20708	7	Periplasmic	COG2823	General function prediction only		
148549619	Pput_4415		hypothetical protein	1.5	1.73E-02	EG	6.3	16046	6	Unknown	COG3105	Function unknown		
148549732	Pput_4530		3-hydroxyisobutyrate dehydrogenase	1.3	6.96E-01	control	6.1	30308	3	Cytoplasmic	COG2084	Lipid metabolism		
148549733	Pput_4531		methylmalonate-semialdehyde dehydrogenase	1.0	8.14E-01	control	6.1	54376	6	Cytoplasmic	COG1012	Energy production and conversion		
148549748	Pput_4546		hypothetical protein	1.1	6.45E-01	control	8.7	27275	3	Unknown	COG3071	Coenzyme metabolism		
148549776	Pput_4574	rpsO	30S ribosomal protein S15	2.3	8.21E-02	control	10.8	10030	3	Cytoplasmic	COG0184	Translation, ribosomal structure and biogenesis		
148549799	Pput_4597		SmpA/OmlA domain-containing protein	1.4	2.62E-01	control	4.4	19526	5	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane		
148549872	Pput_4670		rare lipoprotein B	1.2	4.48E-01	control	7.4	22436	10	Unknown	COG2980	Cell envelope biogenesis, outer membrane		
148549918	Pput_4716		TonB-dependent copper receptor	1.0	9.68E-01	EG	6.2	74527	53	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
148549935	Pput_4733		DNA-binding transcriptional activator OsmE	2.2	2.02E-02	control	6.8	12405	2	Unknown				
148549945	Pput_4743		inner-membrane translocator	1.2	8.06E-01	EG	10.1	46677	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism		
148549988	Pput_4786		hypothetical protein	1.1	6.75E-01	control	4.6	53602	5	Cytoplasmic	COG3726	General function prediction only		
148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	1.2	8.38E-01	EG	5.4	51447	6	Cytoplasmic	COG0499	Coenzyme metabolism		
148550055	Pput_4853		DEAD/DEAH box helicase domain-containing protein	1.7	6.29E-01	EG	10.7	68197	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription	
148550083	Pput_4881		poly(hydroxyalkanoate) granule-associated protein	1.5	1.01E-01	EG	11.0	26226	8	Cytoplasmic	COG3937	Function unknown		
148550117	Pput_4915		glycogen/starch/alpha-glucan phosphorylase	1.3	8.54E-01	EG	6.5	91943	10	Cytoplasmic	COG0058	Carbohydrate transport and metabolism		
148550151	Pput_4949	gltB	glutamate synthase subunit alpha	1.8	6.28E-01	EG	6.3	161781	11	Cytoplasmic	COG0069	Amino acid transport and metabolism		
148550326	Pput_5126		polyphosphate kinase	2.2	8.86E-01	EG	7.1	83794	7	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism		
148550461	Pput_5261		import inner membrane translocase subunit Tim44	1.0	8.39E-01	EG	7.2	31998	3	Cytoplasmic Membrane	COG4395	Function unknown		
148550499	Pput_5299		F0F1 ATP synthase subunit B	1.1	3.99E-01	EG	5.4	16912	7	Cytoplasmic Membrane	COG0711	Energy production and conversion		
170723478	PputW619_4317		TonB-dependent siderophore receptor	1.0	6.05E-01	EG	4.8	81702	18	Outer Membrane	COG4774	Inorganic ion transport and metabolism		
104784199		Pseudomonas entomophila L48	putative putrescine ABC transporter ATP-binding protein	5.7	3.69E-01	EG			2					
269139009		Edwardsiella tarda EIB202	multifunctional: proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase/transcriptional repressor	3.0	1.13E-01	EG			2					
313498846		Pseudomonas putida BIRD-1	Hypothetical protein, conserved	2.8	3.27E-02	control			8					
313107588		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030037	2.2	5.43E-01	EG			5					
313498241		Pseudomonas putida BIRD-1	GalU	2.0	6.41E-01	EG			2					
339485939		Pseudomonas putida S16	leucyl aminopeptidase	1.7	5.52E-01	EG			7					
24986476		Pseudomonas putida KT2440	carbamoyl-phosphate synthase, large subunit	1.7	4.56E-01	EG			23					
313107572		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030021	1.7	2.88E-01	EG			3					
15599454		Pseudomonas aeruginosa PAO1	50S ribosomal protein L22	1.6	1.74E-01	EG			7					
104779763		Pseudomonas entomophila L48	50S ribosomal protein L29	1.6	7.10E-02	control			3					
167035543		Pseudomonas putida GB-1	extracellular solute-binding protein	1.5	2.64E-01	EG			6					
313107574		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030023	1.5	5.97E-01	EG			7					
24981839		Pseudomonas putida KT2440	ribosomal protein S3	1.4	4.36E-01	EG			9					
24981833		Pseudomonas putida KT2440	ribosomal protein L3	1.4	7.73E-01	EG			8					
254241390		Pseudomonas aeruginosa 2192	hypothetical protein PA2G_02085	1.4	2.81E-01	control			8					
24983268		Pseudomonas putida KT2440	ribosomal protein S1	1.4	5.59E-01	EG			9					
313497389		Pseudomonas putida BIRD-1	Pgl	1.3	1.86E-01	EG			7					
24982932		Pseudomonas putida KT2440	ribosomal protein S16	1.3	3.23E-01	control			2					
313107581		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030030	1.2	6.67E-01	EG			11					
339486576		Pseudomonas putida S16	TM helix repeat-containing protein	1.2	1.82E-01	control			4					
313497435		Pseudomonas putida BIRD-1	Polar amino acid ABC transporter, inner membrane subunit	1.2	4.70E-01	control			3					
313500902		Pseudomonas putida BIRD-1	TolC family type I secretion outer membrane protein	1.2	3.11E-01	control			15					
104782659		Pseudomonas entomophila L48	dihydrolipoamide dehydrogenase	1.1	9.44E-01	EG			11					
313107576		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030025	1.1	5.73E-01	control			18					
83644329		Hahella chejuensis KCTC 2396	putative Ser protein kinase	1.1	5.73E-01	EG			1					
313107578		Pseudomonas aeruginosa 39016	hypothetical protein PA39016_001030027	1.1	6.93E-01	EG			7					
146307255		Pseudomonas mendocina ymp	copper-translocating P-type ATPase	1.0	8.41E-01	control			7					
313500331		Pseudomonas putida BIRD-1	Quinoprotein glucose dehydrogenase A	1.0	9.87E-01	EG			31					
339485833		Pseudomonas putida S16	preprotein translocase subunit SecF	1.0	8.34E-01	control			3					

5.1.2.3 Membranfraktion_P_putida_JM37_GXS_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	2.9	9.45E-04	GXS	9.1	61919	17	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.0	7.45E-01	GXS	4.9	40718	4	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.2	4.98E-01	control	5.8	90030	3	Unknown	COG0187	DNA replication, recombination, and repair	
26986771	PP_0026		CDF family cobalt/cadmium/zinc transporter	1.3	9.67E-01	control	5.5	32393	2	Cytoplasmic Membrane	COG1230	Inorganic ion transport and metabolism	
26986802	PP_0057		major facilitator family transporter	7.6	2.64E-04	GXS	9.3	58758	6	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26986803	PP_0058		phospholipid/glycerol acyltransferase	2.7	1.48E-02	GXS	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986851	PP_0106		cytochrome c oxidase, subunit III	27.2	8.02E-04	GXS	8.7	33623	2	Cytoplasmic Membrane	COG1845	Energy production and conversion	
26986852	PP_0107		hypothetical protein	3.2	4.22E-02	GXS	7.1	37216	3	Cytoplasmic Membrane	COG3346	Function unknown	
26986856	PP_0111		electron transport protein SCO1/SenC	3.7	8.51E-04	GXS	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	2.6	3.25E-03	control	7.4	25597	4	Unknown			
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.1	2.36E-01	GXS	9.6	29387	5	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986887	PP_0142		hypothetical protein	50.1	9.93E-02	GXS	5.3	40379	2	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26986890	PP_0145		sodium-dependent inorganic phosphate (Pi) transporter	15.4	4.12E-02	GXS	9.8	59817	2	Cytoplasmic Membrane	COG1283	Inorganic ion transport and metabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	3.8	1.33E-02	GXS	7.3	50185	8	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986928	PP_0184	argH	argininosuccinate lyase	1.2	8.12E-01	control	5.4	52061	2	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	1.2	7.74E-01	GXS	11.3	32300	3	Cytoplasmic			
26986943	PP_0199		hypothetical protein	2.6	5.57E-02	GXS	6.8	27782	3	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.2	4.66E-01	control	5.2	51549	6	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.5	3.59E-01	control	6.1	44824	4	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986969	PP_0226		polar amino acid ABC transporter inner membrane subunit	2.3	3.43E-02	GXS	9.1	24515	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	3.8	1.94E-02	control	5.4	48317	3	Outer Membrane			
26986990	PP_0247	envZ	integral membrane sensor signal transduction histidine kinase	1.9	2.79E-01	GXS	6.1	48808	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986997	PP_0255		17 kDa surface antigen	1.3	1.39E-01	GXS	10.4	15911	2	Cytoplasmic Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	3.4	2.16E-02	control	5.2	15616	4	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	15.6	1.56E-04	control	6.1	47787	7	Outer Membrane			
26987023	PP_0281		polar amino acid ABC transporter inner membrane subunit	9.6	4.45E-02	GXS	9.8	24644	2	Cytoplasmic Membrane	COG4215	Amino acid transport and metabolism	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.2	3.70E-01	control	5.3	55654	7	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.3	5.14E-01	control	5.6	99332	34	Cytoplasmic	COG2609	Energy production and conversion	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.2	8.43E-01	control	4.6	69396	10	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	6.1	7.67E-03	control	11.4	8370	2	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987138	PP_0396		hypothetical protein	1.5	2.40E-01	GXS	7.0	50488	6	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.4	4.06E-01	control	5.8	73782	17	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987150	PP_0409		PAS/PAC sensor signal transduction histidine kinase	55.7	3.87E-04	GXS	5.4	89442	2	Cytoplasmic Membrane	COG4585	Signal transduction mechanisms	
26987159	PP_0418		GDSL family lipase	1.6	1.99E-01	GXS	4.4	67175	4	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987181	PP_0440	tuf	elongation factor Tu	1.3	2.04E-01	control	5.0	43495	27	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	2.8	6.26E-02	control	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.6	4.15E-01	control	10.1	24251	4	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.8	1.23E-01	control	10.2	17686	9	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.9	1.14E-01	control	5.5	150992	34	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	2.9	3.93E-02	control	7.2	154797	29	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	7.6	1.78E-02	control	11.7	13727	2	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	3.7	1.89E-02	control	10.8	17578	10	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.4	1.37E-01	control	4.9	78817	25	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	2.8	2.13E-02	control	10.3	21811	8	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	5.2	1.03E-02	control	11.7	29669	12	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	2.0	3.92E-01	control	11.9	15373	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.9	7.10E-02	control	11.6	13410	8	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	3.9	1.52E-02	control	10.3	20329	9	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	3.7	7.74E-03	control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	8.4	4.02E-03	control	10.2	13975	4	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	4.0	1.64E-01	control	10.4	19143	4	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	5.9	9.34E-03	control	10.9	12628	5	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	2.6	2.03E-02	control	10.6	17666	7	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	5.3	1.04E-02	control	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	3.7	2.35E-03	GXS	10.4	47853	9	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	6.2	1.49E-02	control	11.3	13256	5	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	5.8	3.71E-02	control	11.5	13660	3	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	4.1	8.52E-03	control	10.5	23056	10	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	2.0	3.56E-02	GXS	4.7	36629	4	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.7	1.76E-01	control	11.3	14363	6	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	130.5	2.91E-04	control	4.6	17972	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	1.1	7.11E-01	control	7.2	25648	2	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.0	6.18E-02	control	5.9	55268	10	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.3	3.43E-01	control	6.5	49088	2	Cytoplasmic	COG0439	Lipid metabolism	
26987299	PP_0561	dipZ	thiol:disulfide interchange protein precursor	5.9	4.41E-03	GXS	8.1	62470	2	Cytoplasmic Membrane	COG4232	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26987302	PP_0564		hypothetical protein	3.6	4.15E-03	GXS	6.6	40223	7	Unknown	COG5345	Function unknown	
26987322	PP_0584		methyl-accepting chemotaxis transducer	2.6	5.91E-02	GXS	5.0	69953	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987334	PP_0596		beta alanine--pyruvate transaminase	1.7	3.99E-01	control	6.8	48529	2	Cytoplasmic	COG0161	Coenzyme metabolism	
26987359	PP_0622		competence lipoprotein ComL	1.2	2.90E-01	control	4.8	38410	6	Unknown	COG4105	General function prediction only	
26987362	PP_0626	ndh	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1.1	9.14E-01	control	9.0	47080	2	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.1	9.11E-01	control	6.2	44897	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.8	3.19E-01	control	5.3	61860	3	Cytoplasmic	COG0488	General function prediction only	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.6	2.97E-01	GXS	7.8	39661	3	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987447	PP_0711		isochorismatase superfamily hydrolase	1.6	2.51E-01	GXS	5.3	23026	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987460	PP_0724	lolB	outer membrane lipoprotein LolB	1.8	9.71E-02	control	8.2	22895	2	Unknown	COG3017	Cell envelope biogenesis, outer membrane	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.3	4.03E-01	GXS	8.4	54282	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.5	9.95E-02	control	9.5	20483	10	Unknown			
26987495	PP_0759		hypothetical protein	1.1	9.10E-01	control	7.0	29743	5	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	2.5	1.23E-01	GXS	5.5	62125	5	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987502	PP_0766		hypothetical protein	1.1	5.49E-01	GXS	9.6	50572	7	Unknown			
26987509	PP_0773		OmpA/MotB domain protein	1.5	8.95E-02	GXS	9.5	24753	15	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987521	PP_0785		sulfate transport protein CysZ	9.7	6.86E-04	GXS	9.6	27308	2	Cytoplasmic Membrane	COG2981	Amino acid transport and metabolism	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	10.3	7.15E-05	GXS	6.7	34557	15	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	2.3	1.45E-03	GXS	9.6	11902	3	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	3.0	3.21E-04	GXS	9.6	66913	18	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	15.4	7.12E-05	control	5.3	15044	2	Extracellular	COG0105	Nucleotide transport and metabolism	

26987592	PP_0856		hypothetical protein	2.5	1.29E-02	control	4.7	40737	10	Outer Membrane	COG1520	Function unknown
26987603	PP_0867		FecA-like outer membrane receptor	10.7	2.79E-04	control	4.9	88153	21	Outer Membrane	COG4772	Inorganic ion transport and metabolism
26987619	PP_0883		outer membrane porin	2.0	1.18E-01	control	6.6	50256	6	Outer Membrane		
26987623	PP_0887		integral membrane sensor signal transduction histidine kinase	9.2	1.30E-03	GXS	6.1	49523	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms
26987645	PP_0909		hypothetical protein	2.3	2.29E-02	GXS	6.4	38380	11	Unknown	COG3489	General function prediction only
26987646	PP_0910		hypothetical protein	5.0	1.04E-01	GXS	5.3	51201	3	Unknown	COG3488	Energy production and conversion
26987650	PP_0914		GGDEF domain-containing protein	9.7	9.41E-04	GXS	5.8	78578	10	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.2	4.87E-01	control	6.2	51518	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis
26987680	PP_0944	fumC	fumarate hydratase	1.0	7.70E-01	GXS	5.9	48541	15	Cytoplasmic	COG0114	Energy production and conversion
26987695	PP_0959	ttg2B	hypothetical protein	8.2	2.72E-03	GXS	8.2	28489	5	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism
26987713	PP_0977	valS	valyl-tRNA synthetase	1.3	1.87E-01	GXS	5.1	107495	11	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis
26987716	PP_0980	pepA	leucyl aminopeptidase	1.2	8.06E-01	control	7.4	52433	6	Cytoplasmic	COG0260	Amino acid transport and metabolism
26987718	PP_0982		permease YjgP/YjgQ family protein	3.7	1.31E-03	GXS	9.7	41323	6	Cytoplasmic Membrane	COG0795	General function prediction only
26987719	PP_0983		permease YjgP/YjgQ family protein	5.6	1.82E-02	GXS	7.1	38733	3	Cytoplasmic Membrane	COG0795	General function prediction only
26987735	PP_0999	arcC	carbamate kinase	2.5	1.33E-01	control	5.5	33423	2	Cytoplasmic	COG0549	Amino acid transport and metabolism
26987736	PP_1000	argI	ornithine carbamoyltransferase	3.0	3.14E-02	control	6.3	37911	7	Cytoplasmic	COG0078	Amino acid transport and metabolism
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.9	4.98E-02	GXS	9.1	51061	3	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism
26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	4.2	1.20E-03	control	5.6	84730	27	Outer Membrane	COG1629	Inorganic ion transport and metabolism
26987746	PP_1010	edd	phosphogluconate dehydratase	1.5	2.60E-01	control	6.4	65359	4	Cytoplasmic	COG0129	Amino acid transport and metabolism Carbohydrate transport and metabolism
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	12.9	1.20E-02	GXS	7.3	54020	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	2.1	4.80E-03	GXS	10.1	33781	3	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	17.8	3.38E-02	GXS	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism
26987755	PP_1019	oprB-1	porin B	2.4	1.63E-01	control	5.9	49646	2	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.2	6.25E-01	GXS	6.8	55000	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.1	5.15E-01	GXS	6.7	25476	5	Unknown	COG0363	Carbohydrate transport and metabolism
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	2.7	2.42E-02	control	5.4	25004	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism
26987768	PP_1032	guaA	GMP synthase	1.2	5.60E-01	GXS	5.2	58204	7	Cytoplasmic	COG0519	Nucleotide transport and metabolism
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	5.8	8.45E-03	GXS	8.2	27464	8	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.9	1.74E-01	control	8.9	33428	2	Periplasmic	COG0834	Amino acid transport and metabolism Signal transduction mechanisms
26987818	PP_1082	bfr	bacterioferritin	45.3	2.69E-04	control	4.4	17971	7	Cytoplasmic	COG2193	Inorganic ion transport and metabolism
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.1	6.67E-01	GXS	4.9	21730	5	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
26987857	PP_1121		OmpA/MotB domain protein	1.9	1.01E-01	control	5.0	24084	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987858	PP_1122		OmpA/MotB domain protein	1.6	3.18E-02	control	4.7	27345	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	3.0	4.20E-02	GXS	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism
26987888	PP_1152		secretion protein HlyD family protein	7.7	2.40E-04	GXS	6.4	32353	4	Cytoplasmic Membrane	COG1566	Defense mechanisms
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	3.0	1.19E-01	GXS	5.7	106948	3	Cytoplasmic	COG0209	Nucleotide transport and metabolism
26987935	PP_1200	kup	Kup system potassium uptake protein	4.7	1.43E-02	GXS	7.9	68568	2	Cytoplasmic Membrane	COG3158	Inorganic ion transport and metabolism
26987937	PP_1202		hypothetical protein	3.5	2.65E-03	GXS	9.7	95622	6	Cytoplasmic Membrane	COG2898	Function unknown
26987940	PP_1205	proS	prolyl-tRNA synthetase	2.2	2.06E-01	GXS	5.0	63623	3	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis
26987945	PP_1210		DNA-binding stress protein	1.3	3.62E-01	GXS	5.0	17861	2	Cytoplasmic	COG0783	Inorganic ion transport and metabolism
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.2	6.39E-01	GXS	5.1	66568	8	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	3.1	4.44E-03	GXS	6.3	25310	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion
26987957	PP_1222	tolB	translocation protein TolB	1.5	3.68E-02	control	9.8	47431	9	Unknown	COG0823	Intracellular trafficking and secretion
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.6	6.26E-02	control	4.9	17833	14	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987980	PP_1245		hypothetical protein	5.8	1.43E-03	GXS	9.4	31144	5	Unknown		
26988051	PP_1316	rpsI	30S ribosomal protein S9	2.9	8.65E-02	control	11.7	14592	5	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	3.4	1.05E-03	GXS	8.4	45901	4	Cytoplasmic Membrane	COG1290	Energy production and conversion
26988060	PP_1325		LppC family lipoprotein	1.8	1.17E-02	control	7.5	64637	17	Cytoplasmic Membrane	COG3107	General function prediction only
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	3.3	1.31E-01	GXS	9.9	38127	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.0	5.20E-01	control	5.0	42236	3	Cytoplasmic	COG1364	Amino acid transport and metabolism
26988084	PP_1350		multi-sensor signal transduction histidine kinase	2.7	5.05E-02	GXS	6.8	75271	2	Cytoplasmic Membrane	COG5000	Signal transduction mechanisms
26988093	PP_1359	fxsA	FxsA	3.4	1.07E-02	GXS	10.6	16958	2	Cytoplasmic Membrane	COG3030	General function prediction only
26988096	PP_1362	pykA	pyruvate kinase	1.2	6.63E-01	control	6.7	52057	7	Cytoplasmic	COG0469	Carbohydrate transport and metabolism
26988100	PP_1366		transcriptional regulator MvaT, P16 subunit	2.2	3.97E-01	GXS	10.1	14184	2	Cytoplasmic		
26988107	PP_1373		phosphate transporter	4.4	6.97E-03	GXS	9.6	52425	5	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism
26988117	PP_1383		BenF-like porin	1.6	6.15E-01	control	6.8	46022	2	Outer Membrane		
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.2	5.48E-01	control	5.1	52864	22	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	4.6	4.01E-04	GXS	5.3	112835	14	Cytoplasmic Membrane	COG0841	Defense mechanisms
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	1.3	7.26E-01	GXS	6.0	41250	3	Unknown	COG0845	Cell envelope biogenesis, outer membrane
26988165	PP_1432	lepB	signal peptidase I	3.8	1.17E-03	GXS	9.2	32060	10	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.4	2.66E-01	GXS	5.7	42575	2	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism
26988198	PP_1465	rplS	50S ribosomal protein L19	6.8	9.17E-04	control	11.0	13012	6	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis
26988204	PP_1471	thrC	threonine synthase	1.7	8.58E-02	GXS	6.2	51645	7	Cytoplasmic	COG0498	Amino acid transport and metabolism
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.6	1.29E-01	GXS	5.7	50918	8	Unknown	COG1012	Energy production and conversion
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	5.3	1.94E-03	GXS	4.7	58605	22	Cytoplasmic Membrane	COG0840	Cell motility and secretion Signal transduction mechanisms
26988234	PP_1502		OmpA/MotB domain protein	2.5	1.05E-02	control	9.5	28964	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.3	5.65E-01	control	9.3	27023	14	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis
26988331	PP_1599		surface antigen family outer membrane protein	2.9	5.17E-03	control	4.7	86513	13	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane
26988342	PP_1610	pyrG	CTP synthetase	1.9	1.94E-01	GXS	5.8	59474	5	Cytoplasmic	COG0504	Nucleotide transport and metabolism
26988344	PP_1612	eno	phosphopyruvate hydratase	5.5	9.98E-03	control	4.7	45490	2	Cytoplasmic	COG0148	Carbohydrate transport and metabolism
26988354	PP_1622	nlpD	peptidase M23B	1.1	7.12E-01	GXS	11.0	27506	8	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane
26988361	PP_1629	recA	recombinase A	3.2	7.10E-02	GXS	5.3	37545	4	Cytoplasmic	COG0468	DNA replication, recombination, and repair
26988378	PP_1646		alkyl hydroperoxide reductase/thiol specific antioxidant/ Mal allergen	2.6	3.74E-03	GXS	4.8	16590	4	Periplasmic	COG0526	Posttranslational modification, protein turnover, chaperones Energy production and conversion
26988382	PP_1650	gacS	multi-sensor hybrid histidine kinase	10.3	2.28E-03	GXS	5.4	100653	8	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms
26988384	PP_1652		sensor histidine kinase	154.5	4.49E-03	GXS	7.3	52141	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms
26988407	PP_1675	cobD	cobalamin biosynthesis protein	4.0	3.56E-02	GXS	8.3	33221	3	Cytoplasmic Membrane	COG1270	Coenzyme metabolism
26988427	PP_1695		integral membrane sensor hybrid histidine kinase	11.5	9.82E-03	GXS	8.8	127309	4	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism General function prediction only
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.4	4.05E-01	GXS	4.8	26520	10	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones
26988474	PP_1743	actP	acetate permease	3.6	2.04E-04	GXS	9.6	58972	6	Cytoplasmic Membrane	COG4147	General function prediction only
26988498	PP_1767	gyrA	DNA gyrase subunit A	3.3	4.21E-01	control	4.7	102037	3	Cytoplasmic	COG0188	DNA replication, recombination, and repair
26988550	PP_1820		benzoate transporter	11.7	5.63E-03	GXS	9.2	41143	2	Cytoplasmic Membrane	COG3135	Secondary metabolites biosynthesis, transport, and catabolism
26988568	PP_1838		hypothetical protein	5.6	9.81E-04	GXS	6.8	76615	17	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane
26988588	PP_1858	efp	elongation factor P	3.0	1.58E-02	control	4.5	21303	2	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.8	2.97E-01	control	9.2	60924	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair Transcription
26988602	PP_1872		aminotransferase AlaT	1.9	2.19E-01	GXS	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism
26988608	PP_1878		hypothetical protein	4.7	2.13E-02	GXS	7.3	29093	2	Cytoplasmic		
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	3.6	1.28E-01	control	4.7	120904	8	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis

26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.8	1.52E-02	GXS	6.4	36497	7	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	8.2	8.49E-03	control	6.0	25470	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988696	PP_1970		lipoprotein	2.1	6.28E-03	control	4.9	22337	5	Unknown			
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.2	4.90E-01	GXS	5.9	43290	6	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	2.5	5.18E-02	GXS	5.3	40672	5	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.2	6.06E-01	control	7.8	32510	3	Cytoplasmic	COG0777	Lipid metabolism	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.0	4.78E-01	GXS	6.5	55400	5	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988731	PP_2006		hypothetical protein	1.0	9.92E-01	control	5.1	63743	6	Unknown			
26988744	PP_2019		hypothetical protein	2.8	2.96E-03	GXS	6.6	87732	5	Cytoplasmic Membrane	COG1033	General function prediction only	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.1	5.47E-01	GXS	4.8	86015	10	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988814	PP_2089	oprF	OmpF family protein	1.2	6.65E-01	GXS	4.5	37012	38	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988830	PP_2105		hypothetical protein	5.4	1.87E-05	GXS	4.9	11370	3	Unknown	COG4575	Function unknown	
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	1.5	3.36E-01	GXS	6.0	57068	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988845	PP_2121		lipoprotein	7.2	7.46E-04	control	5.0	8131	2	Unknown			
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.4	6.00E-01	control	7.7	53014	14	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988880	PP_2156	lolE	lipoprotein releasing system, transmembrane protein, LolC/E family	17.2	1.63E-03	GXS	9.5	44220	5	Cytoplasmic Membrane	COG4591	Cell envelope biogenesis, outer membrane	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.2	5.13E-01	GXS	5.3	26061	5	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988892	PP_2168	tal	transaldolase B	1.9	9.34E-01	control	5.0	33615	2	Unknown	COG0176	Carbohydrate transport and metabolism	
26988913	PP_2189		hypothetical protein	4.3	3.64E-02	GXS	4.9	15175	2	Unknown	COG4575	Function unknown	
26988973	PP_2249		methyl-accepting chemotaxis transducer	4.1	8.39E-03	GXS	5.1	68646	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988988	PP_2264		extracellular solute-binding protein, family 1	1.8	6.09E-02	GXS	5.6	65243	6	Unknown	COG1653	Carbohydrate transport and metabolism	
26989026	PP_2302	lon-2	ATP-dependent protease La	3.8	2.75E-01	control	5.9	88722	3	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	4.2	9.21E-03	control	9.3	9997	3	Unknown			
26989033	PP_2309		hypothetical protein	3.8	1.36E-03	GXS	12.2	14114	3	Cytoplasmic Membrane			
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	2.9	2.96E-02	control	8.5	8801	5	Outer Membrane			
26989051	PP_2327	cysB	transcriptional regulator CysB	1.6	4.33E-01	control	6.7	35955	3	Cytoplasmic	COG0583	Transcription	
26989055	PP_2331		hypothetical protein	3.5	1.13E-03	GXS	7.9	57064	11	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.6	2.43E-01	control	5.0	93609	5	Cytoplasmic	COG1049	Energy production and conversion	
26989103	PP_2379		electron transport protein SCO1/SenC	8.6	6.70E-04	GXS	8.5	24629	3	Unknown	COG1999	General function prediction only	
26989146	PP_2423		hypothetical protein	2.7	1.59E-02	GXS	9.8	34661	4	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26989166	PP_2443		serine/threonine transporter SstT	6.5	5.21E-02	GXS	7.3	42012	3	Cytoplasmic Membrane	COG3633	Amino acid transport and metabolism	
26989170	PP_2447		hypothetical protein	2.2	1.85E-01	GXS	10.2	26784	6	Unknown			
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.2	6.32E-01	control	5.8	72697	4	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	5.5	3.10E-02	control	12.1	13280	4	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989297	PP_2578		hypothetical protein	2.0	5.75E-03	control	9.5	19010	3	Unknown	COG3009	Function unknown	
26989572	PP_2853		hypothetical protein	10.9	1.11E-04	control	4.5	46020	8	Unknown			
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	8.8	6.47E-03	GXS	5.7	58659	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989809	PP_3090		OmpA domain-containing protein	30.8	9.56E-03	GXS	9.0	93143	4	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	8.7	4.97E-03	GXS	6.8	138655	12	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	3.5	7.44E-03	GXS	5.7	26868	5	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	2.3	6.67E-03	GXS	9.0	57141	11	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989854	PP_3135		glycosyl transferase	3.1	8.46E-03	control	8.6	35887	16	Cytoplasmic	COG1216	General function prediction only	
26989873	PP_3154		hypothetical protein	1.1	5.33E-01	GXS	6.5	23974	2	Unknown			
26990047	PP_3330		TonB-dependent siderophore receptor	9.8	8.14E-05	control	5.8	80740	3	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	168.3	6.51E-04	control	4.8	77137	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990063	PP_3348		GGDEF domain-containing protein	8.4	2.38E-03	GXS	6.8	41944	2	Cytoplasmic Membrane	COG2199	Signal transduction mechanisms	
26990130	PP_3417	gntP	gluconate transporter	2.1	1.62E-02	GXS	8.9	47532	11	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.7	2.13E-01	control	7.2	36863	3	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990294	PP_3582		RND efflux transporter	3.0	4.65E-03	control	5.2	53952	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.3	5.44E-01	GXS	5.9	43631	2	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990323	PP_3612		TonB-dependent siderophore receptor	26.6	3.97E-04	control	5.2	85491	17	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990373	PP_3662		decarboxylase family protein	2.1	1.28E-01	GXS	6.7	50729	2	Cytoplasmic	COG1611	General function prediction only	
26990499	PP_3794	pbpG	D-alanyl-D-alanine endopeptidase	1.5	8.29E-01	control	10.5	33802	2	Unknown	COG1686	Cell envelope biogenesis, outer membrane	
26990542	PP_3837		SURF4 domain-containing protein	2.2	4.35E-01	GXS	9.7	14885	2	Cytoplasmic Membrane	COG2259	Function unknown	
26990635	PP_3930		17 kDa surface antigen	3.0	6.42E-04	GXS	12.0	11808	3	Cytoplasmic Membrane			
26990695	PP_3990		hypothetical protein	4.5	3.38E-02	GXS	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	7.1	6.07E-02	GXS	6.4	91296	5	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	5.2	3.58E-02	GXS	5.4	79899	4	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	3.3	6.30E-02	GXS	5.9	50555	6	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	7.3	2.78E-03	GXS	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990806	PP_4111	fusA	elongation factor G	1.1	9.65E-01	control	5.0	77832	3	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	17.5	9.47E-03	GXS	6.1	37637	2	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.5	3.47E-01	control	8.7	20354	3	Cytoplasmic	COG0431	General function prediction only	
26990851	PP_4158	kdpD	osmosensitive K+ channel signal transduction histidine kinase	14.8	2.22E-02	GXS	7.2	96700	3	Cytoplasmic Membrane	COG2205	Signal transduction mechanisms	
26990860	PP_4168		hypothetical protein	4.1	9.83E-04	GXS	5.6	12851	4	Cytoplasmic Membrane			
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.0	6.82E-03	control	6.2	30111	10	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.8	3.66E-02	control	6.1	41239	17	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	2.6	2.23E-03	control	6.3	49912	5	Cytoplasmic	COG1249	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.1	9.85E-01	control	6.5	106521	18	Cytoplasmic	COG0567	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	8.44E-01	control	6.2	63448	4	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.8	6.31E-02	GXS	9.0	13579	3	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	3.1	6.01E-02	GXS	10.3	13813	3	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.5	2.14E-01	GXS	7.0	47622	7	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.3	8.93E-01	control	9.7	26361	5	Unknown	COG2086	Energy production and conversion	
26990944	PP_4253	ccoP-1	cytochrome c oxidase, cbb3-type, subunit III	1.8	1.80E-01	GXS	5.3	33915	2	Unknown	COG2010	Energy production and conversion	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	2.2	2.75E-02	GXS	9.6	53567	3	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.9	2.17E-02	GXS	9.0	22637	7	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	4.1	2.44E-04	GXS	5.2	35613	10	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	6.7	2.58E-02	GXS	8.5	53406	5	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26991011	PP_4321	dsbE	periplasmic protein thiol--disulphide oxidoreductase DsbE	5.4	8.50E-03	GXS	6.5	19892	2	Cytoplasmic Membrane	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26991021	PP_4331		hypothetical protein	5.0	8.87E-03	GXS	5.2	14696	2	Unknown			
26991026	PP_4336	motC	flagellar motor protein	3.3	3.04E-02	GXS	4.9	25930	2	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991034	PP_4344	flhA	flagellar biosynthesis protein FlhA	43.7	1.12E-03	GXS	6.9	76003	3	Cytoplasmic Membrane	COG1298	Cell motility and secretion	Intracellular trafficking and secretion
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	6.2	2.22E-03	GXS	10.1	17847	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
26991072	PP_4383	flgI	flagellar basal body P-ring protein	4.2	1.89E-01	GXS	8.5	38182	2	Periplasmic	COG1706	Cell motility and secretion	
26991157	PP_4471	mgtE	magnesium transporter	7.2	2.44E-03	GXS	4.3	53584	5	Cytoplasmic Membrane	COG2239	Inorganic ion transport and metabolism	
26991190	PP_4505		integral membrane sensor signal transduction histidine kinase	4.7	1.39E-03	GXS	8.5	49718	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	

26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	35.5	1.56E-04	control	5.4	50393	15	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	2.9	3.16E-03	GXS	6.4	56605	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	3.8	1.28E-02	GXS	7.7	61812	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991254	PP_4570		hypothetical protein	3.2	8.90E-04	GXS	10.1	35846	7	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991255	PP_4571	cysK	cysteine synthase A	1.3	3.82E-01	GXS	5.5	34357	2	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991266	PP_4582		hypothetical protein	9.5	3.10E-02	GXS	9.5	18552	2	Cytoplasmic Membrane			
26991325	PP_4641	cstA	carbon starvation protein CstA	3.1	2.03E-03	GXS	9.0	73763	13	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	2.4	6.90E-03	GXS	4.8	14730	5	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	2.9	2.66E-03	GXS	9.1	53016	5	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	4.5	1.91E-02	GXS	4.8	68764	3	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	1.4	5.56E-01	control	6.1	30321	2	Cytoplasmic	COG2084	Lipid metabolism	
26991353	PP_4669		OmpA/MotB domain protein	7.3	1.00E-01	GXS	9.9	18241	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991361	PP_4677	pssA-2	CDP-diacylglycerol--serine O-phosphatidyltransferase	2.3	1.13E-01	GXS	9.2	30359	2	Cytoplasmic Membrane	COG1183	Lipid metabolism	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	7.20E-01	control	5.4	36370	3	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991366	PP_4682		hypothetical protein	1.0	9.05E-01	control	8.2	27215	3	Unknown	COG4783	General function prediction only	
26991367	PP_4683	mrcB	penicillin-binding protein 1B	6.4	2.70E-03	GXS	9.5	85156	4	Cytoplasmic Membrane	COG0744	Cell envelope biogenesis, outer membrane	
26991370	PP_4686		hypothetical protein	3.1	9.10E-03	control	6.2	32403	2	Periplasmic	COG3016	Function unknown	
26991372	PP_4688		transport system permease	15.1	1.71E-02	GXS	10.5	35814	3	Cytoplasmic Membrane	COG0609	Inorganic ion transport and metabolism	
26991388	PP_4704		hypothetical protein	3.5	5.41E-02	GXS	5.6	107252	3	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.0	8.58E-01	GXS	4.9	75010	9	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	2.2	1.44E-01	control	6.8	91460	5	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	4.2	2.91E-03	GXS	5.4	69722	24	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991418	PP_4735	lctP	L-lactate transport	4.4	2.84E-02	GXS	9.3	58955	4	Cytoplasmic Membrane	COG1620	Energy production and conversion	
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	5.9	1.87E-03	GXS	8.5	56126	7	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane	
26991478	PP_4798		lytic murein transglycosylase	1.2	3.33E-01	GXS	7.7	48000	4	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	2.0	6.21E-02	GXS	6.6	42288	4	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane	
26991499	PP_4819		Zinc finger-domain-containing protein	3.9	7.11E-01	GXS	4.5	49827	2	Cytoplasmic			
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	1.8	5.05E-02	GXS	5.0	31015	5	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991518	PP_4838	oprC	TonB-dependent copper receptor	8.7	7.42E-03	control	6.2	74540	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991519	PP_4839		hypothetical protein	9.7	1.28E-04	GXS	9.6	50581	9	Cytoplasmic Membrane	COG3182	Function unknown	
26991556	PP_4876	rpsR	30S ribosomal protein S18	2.2	2.84E-01	control	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.3	7.30E-01	control	7.9	96688	2	Cytoplasmic	COG0557	Transcription	
26991561	PP_4882		binding-protein-dependent transport systems inner membrane component	21.4	1.10E-02	GXS	10.2	56334	2	Cytoplasmic Membrane	COG1178	Inorganic ion transport and metabolism	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	4.6	1.46E-03	GXS	6.1	71958	24	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991569	PP_4891	hflC	HflC protein	1.7	1.92E-02	GXS	9.8	33001	18	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	2.1	8.07E-04	GXS	5.1	44762	6	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991583	PP_4905		flagellar motor protein MotA	3.8	6.57E-05	GXS	6.2	30312	5	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.5	1.67E-01	control	8.6	31547	3	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991589	PP_4911		hypothetical protein	1.5	1.19E-01	GXS	8.5	27337	5	Periplasmic	COG3009	Function unknown	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	3.7	1.01E-03	GXS	7.6	66279	13	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991616	PP_4938		glycosyl transferase	1.1	7.24E-01	control	9.4	41783	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26991622	PP_4944		carbamoyltransferase	1.7	3.56E-01	control	7.2	65646	3	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.1	6.99E-01	GXS	5.1	42779	3	Cytoplasmic	COG0192	Coenzyme metabolism	
26991660	PP_4983		amine oxidase	1.1	8.43E-01	control	10.2	65923	5	Unknown	COG1231	Amino acid transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	2.4	4.06E-01	control	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991682	PP_5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	1.4	5.48E-01	GXS	9.6	62722	2	Cytoplasmic	COG3243	Lipid metabolism	
26991701	PP_5025	mdoH	glucosyltransferase MdoH	3.5	1.71E-03	GXS	8.3	95875	12	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.3	7.76E-01	control	6.4	92004	5	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.7	2.74E-01	control	5.3	67157	2	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.4	3.91E-01	control	5.1	51740	7	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991729	PP_5053	secB	preprotein translocase subunit SecB	1.9	1.41E-01	GXS	4.2	17754	2	Cytoplasmic	COG1952	Intracellular trafficking and secretion	
26991731	PP_5055		rhodanese domain-containing protein	2.5	1.46E-03	GXS	9.9	14839	5	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991743	PP_5067		potassium efflux protein KefA	2.9	5.96E-03	GXS	8.9	122371	8	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26991760	PP_5084		penicillin-binding protein, 1A family	2.3	3.93E-02	GXS	7.2	89193	7	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP_5085	maeB	malic enzyme	1.1	7.55E-01	control	4.9	45127	7	Cytoplasmic	COG0281	Energy production and conversion	
26991766	PP_5090		sporulation domain protein	3.6	8.65E-03	GXS	10.6	24964	4	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	3.2	8.98E-03	GXS	9.9	21599	3	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	1.9	1.09E-01	GXS	6.5	36984	5	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991809	PP_5133		hypothetical protein	9.9	1.38E-03	GXS	7.1	50655	2	Cytoplasmic Membrane			
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.0	7.42E-01	GXS	6.3	44339	6	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991845	PP_5169	cysW	sulfate ABC transporter inner membrane subunit CysW	1.9	7.81E-01	GXS	8.3	31513	2	Cytoplasmic Membrane	COG4208	Inorganic ion transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	1.8	5.03E-03	GXS	5.4	112277	6	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991854	PP_5178	potH	binding-protein-dependent transport systems inner membrane component	7.7	4.03E-02	GXS	7.4	34422	2	Cytoplasmic Membrane	COG1176	Amino acid transport and metabolism	
26991861	PP_5185	argA	N-acetylglutamate synthase	1.9	1.99E-01	GXS	5.9	47440	2	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.3	7.11E-01	control	6.9	55958	2	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991958	PP_5282	rpmB	50S ribosomal protein L28	4.4	1.32E-02	control	12.3	8922	3	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991982	PP_5306	exbB	ferric siderophore transport system protein ExbB	15.8	8.96E-04	GXS	9.5	33260	3	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26991983	PP_5307	exbD	biopolymer transport protein ExbD	14.4	2.24E-04	GXS	4.5	15269	5	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26991984	PP_5308	tonB	TonB family protein	3.6	9.65E-03	GXS	10.5	26022	3	Outer Membrane	COG0810	Cell envelope biogenesis, outer membrane	
26991997	PP_5321	phoR	PAS/PAC sensor signal transduction histidine kinase	5.7	5.01E-03	GXS	7.3	49063	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.0	1.85E-01	GXS	5.3	65626	5	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.3	2.70E-01	GXS	6.5	51942	6	Cytoplasmic	COG0439	Lipid metabolism	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	6.86E-01	control	4.6	49359	7	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.3	7.21E-01	control	9.2	31464	10	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.3	3.22E-01	control	5.2	55352	19	Cytoplasmic	COG0056	Energy production and conversion	
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	5.6	2.10E-01	GXS	6.7	31712	2	Cytoplasmic Membrane	COG0356	Energy production and conversion	
148545333	Pput_0076	glyS	glycyl-tRNA synthetase subunit beta	1.1	5.49E-01	control	4.9	75107	2	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
148545376	Pput_0119		cytochrome c oxidase subunit II	11.0	4.46E-05	GXS	6.8	42031	8	Cytoplasmic Membrane	COG1622	Energy production and conversion	
148545406	Pput_0149		multi-sensor signal transduction histidine kinase	30.4	1.79E-02	GXS	6.8	66107	2	Cytoplasmic Membrane	COG5002	Signal transduction mechanisms	
148545414	Pput_0157		ABC transporter auxiliary component-like protein	1.9	1.76E-01	GXS	9.7	23114	2	Unknown	COG3218	General function prediction only	
148545441	Pput_0184		diguanylate cyclase/phosphodiesterase	2.9	8.14E-03	GXS	6.3	71316	16	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
148545459	Pput_0202		cytochrome c, class I	5.5	1.81E-04	GXS	4.9	69292	2	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
148545468	Pput_0211		HemY domain-containing protein	3.2	8.47E-04	GXS	9.6	46008	15	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
148545505	Pput_0249		outer membrane porin	2.9	1.96E-02	control	5.4	48366	16	Outer Membrane			
148545562	Pput_0307		AsmA family protein	2.6	2.83E-02	GXS	6.1	80211	13	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
148545690	Pput_0438		organic solvent tolerance protein	3.0	1.07E-04	control	4.8	105822	21	Outer Membrane	COG1452	Cell envelope biogenesis, outer membrane	
148545699	Pput_0447		binding-protein-dependent transport systems inner membrane component	2.5	1.50E-02	GXS	9.5	45770	4	Cytoplasmic Membrane	COG1176	Amino acid transport and metabolism	

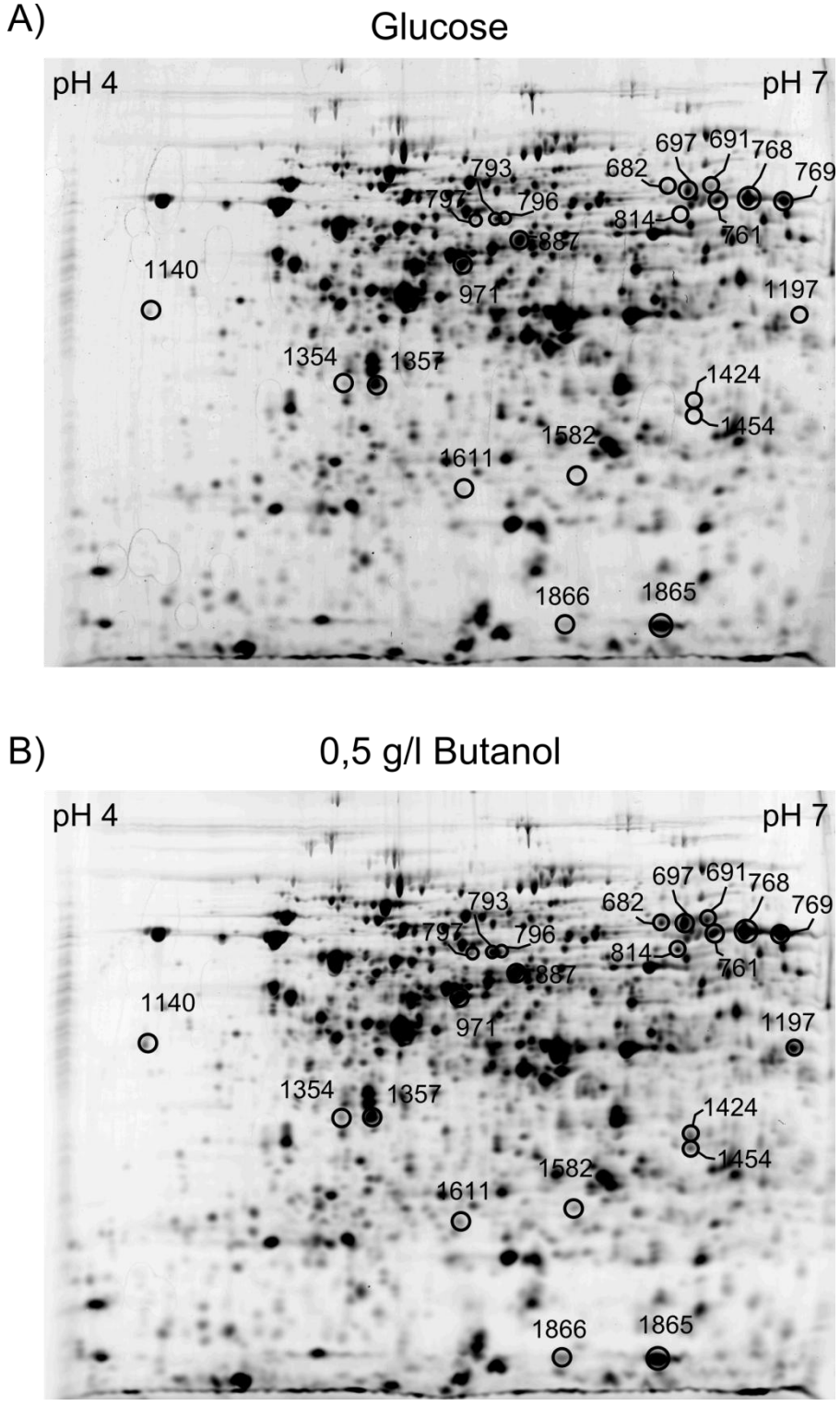
148545717	Pput_0465	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.3	3.87E-01	GXS	6.8	36249	3	Cytoplasmic	COG0002	Amino acid transport and metabolism	
148545789	Pput_0539		OmpW family protein	11.7	2.36E-03	control	5.2	24190	10	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
148545791	Pput_0541		hypothetical protein	2.8	9.35E-03	GXS	9.7	45825	17	Cytoplasmic Membrane	COG0577	Defense mechanisms	
148545797	Pput_0547		hypothetical protein	1.4	6.40E-01	GXS	8.5	16877	3	Unknown	COG3126	Function unknown	
148545859	Pput_0609		alpha-2-macroglobulin domain-containing protein	1.2	1.65E-01	GXS	5.2	178356	10	Unknown	COG2373	General function prediction only	
148545865	Pput_0615		hypothetical protein	3.6	2.06E-02	control	9.5	21405	6	Unknown			
148545890	Pput_0640		hypothetical protein	2.1	8.95E-02	GXS	9.7	83607	3	Unknown	COG3008	General function prediction only	
148545925	Pput_0675		fimbrial protein pilin	10.9	5.25E-02	GXS	7.3	13687	3	Extracellular	COG4969	Cell motility and secretion	Intracellular trafficking and secretion
148545986	Pput_0740		mechanosensitive ion channel MscS	5.7	2.20E-03	GXS	9.3	86463	8	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
148546038	Pput_0792		hypothetical protein	5.2	8.94E-05	control	5.0	67997	17	Outer Membrane			
148546111	Pput_0867		hypothetical protein	3.0	1.05E-02	GXS	9.0	18117	5	Outer Membrane	COG3134	Function unknown	
148546134	Pput_0890		flavodoxin/nitric oxide synthase	6.8	3.16E-03	GXS	8.2	93954	6	Cytoplasmic Membrane	COG0369	Inorganic ion transport and metabolism	
148546135	Pput_0891		TonB-dependent siderophore receptor	5.6	2.94E-04	control	4.8	81988	17	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
148546188	Pput_0945		multidrug efflux protein	2.4	2.04E-01	GXS	4.9	110332	4	Cytoplasmic Membrane	COG0841	Defense mechanisms	
148546195	Pput_0952		hypothetical protein	1.1	6.14E-01	control	4.4	47132	21	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
148546281	Pput_1038		arginine deiminase	1.3	3.69E-01	control	5.8	46419	12	Cytoplasmic	COG2235	Amino acid transport and metabolism	
148546290	Pput_1047		type I glyceraldehyde-3-phosphate dehydrogenase	1.5	1.14E-01	GXS	7.0	36013	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
148546300	Pput_1057		carbohydrate-selective porin OprB	1.7	3.42E-02	control	6.1	49588	20	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
148546321	Pput_1078		phosphoribosylformylglycinamidine synthase	1.8	2.87E-02	control	4.7	140744	11	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
148546342	Pput_1099		membrane carboxypeptidase (penicillin-binding protein)-like protein	3.1	1.19E-02	GXS	9.5	116866	15	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
148546390	Pput_1147		penicillin amidase	1.3	1.88E-02	GXS	8.5	88721	19	Periplasmic	COG2366	General function prediction only	
148546410	Pput_1167		17 kDa surface antigen	1.4	1.55E-01	GXS	9.3	15682	8	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
148546421	Pput_1178		diguanylate cyclase/phosphodiesterase	9.7	6.33E-03	GXS	6.8	82740	4	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
148546431	Pput_1188		PAS/PAC/GAF sensor-containing diguanylate cyclase/phosphodiesterase	4.0	1.63E-03	GXS	5.5	95733	3	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
148546458	Pput_1215		outer membrane protein H1	6.2	1.87E-04	control	6.5	21492	2	Outer Membrane			
148546461	Pput_1218		C4-dicarboxylate transporter DctA	4.8	1.14E-02	GXS	9.0	46240	8	Cytoplasmic Membrane	COG1301	Energy production and conversion	
148546473	Pput_1230		virulence factor family protein	4.9	6.15E-03	GXS	5.0	46965	9	Unknown	COG3946	Intracellular trafficking and secretion	
148546478	Pput_1235		outer membrane porin	1.2	5.42E-01	control	4.6	46148	20	Outer Membrane			
148546511	Pput_1268		hypothetical protein	2.1	4.76E-02	control	4.8	40802	8	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
148546787	Pput_1548		TPR repeat-containing protein	2.0	2.27E-02	GXS	4.8	43184	3	Cytoplasmic Membrane	COG4235	Posttranslational modification, protein turnover, chaperones	
148546791	Pput_1552		PhzF family phenazine biosynthesis protein	1.8	6.46E-02	GXS	4.6	28510	3	Cytoplasmic	COG0384	General function prediction only	
148546817	Pput_1579		hypothetical protein	7.7	6.50E-04	GXS	8.4	48033	4	Cytoplasmic Membrane	COG3748	Function unknown	
148546831	Pput_1593	zipA	cell division protein ZipA	2.7	2.35E-03	GXS	5.7	32849	12	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
148546880	Pput_1642		class V aminotransferase	1.1	4.11E-01	GXS	8.7	47665	4	Cytoplasmic	COG0520	Posttranslational modification, protein turnover, chaperones	
148546881	Pput_1643		peptidase M19, renal dipeptidase	4.3	3.59E-03	GXS	5.9	51410	7	Unknown	COG2355	Amino acid transport and metabolism	
148546882	Pput_1644		hypothetical protein	5.3	5.46E-02	GXS	7.0	61848	3	Cytoplasmic			
148546904	Pput_1666		dihydrolipoamide succinyltransferase	1.3	6.12E-01	control	5.0	42436	8	Cytoplasmic	COG0508	Energy production and conversion	
148546910	Pput_1672		hypothetical protein	8.2	6.16E-02	GXS	10.7	19547	2	Cytoplasmic Membrane			
148546911	Pput_1673		peptidase	8.9	2.78E-04	GXS	10.1	44906	6	Cytoplasmic Membrane	COG3182	Function unknown	
148546916	Pput_1678		TonB-dependent siderophore receptor	2.9	8.31E-04	control	5.5	90426	49	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
148546919	Pput_1681		cyclic peptide transporter	65.7	5.64E-04	GXS	6.8	62270	4	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
148546920	Pput_1682		hypothetical protein	1.0	8.47E-01	control	7.2	39496	4	Cytoplasmic			
148546924	Pput_1686		hypothetical protein	1.7	2.14E-01	GXS	4.3	9411	4	Unknown			
148546955	Pput_1717		binding-protein-dependent transport systems inner membrane component	7.2	9.68E-02	GXS	7.1	39298	3	Cytoplasmic Membrane	COG4174	General function prediction only	
148547137	Pput_1907		hypothetical protein	1.9	1.67E-02	control	5.9	12488	2	Unknown			
148547143	Pput_1913		putative periplasmic protease	4.6	1.01E-02	GXS	9.8	37486	9	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
148547224	Pput_2002		multi-sensor hybrid histidine kinase	3.7	1.30E-02	GXS	4.9	129353	19	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
148547283	Pput_2061		catalase/peroxidase HPI	3.3	3.48E-02	control	5.9	82005	9	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
148547407	Pput_2186		RND family efflux transporter MFP subunit	2.6	2.25E-03	GXS	9.2	46606	10	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
148547408	Pput_2187		acriflavin resistance protein	11.7	2.72E-03	GXS	6.6	111397	5	Cytoplasmic Membrane	COG0841	Defense mechanisms	
148547426	Pput_2205		Pyrrolo-quinoline quinone	3.1	3.08E-03	GXS	6.8	85340	20	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
148547633	Pput_2412		TonB-dependent siderophore receptor	6.0	3.28E-03	control	5.5	79564	18	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
148547639	Pput_2419		TonB-dependent siderophore receptor	39.3	5.39E-04	control	4.8	76203	3	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
148547786	Pput_2569		hypothetical protein	1.4	4.46E-01	control	9.3	24404	9	Unknown			
148547789	Pput_2572		undecaprenyl-phosphate galactose phosphotransferase	8.7	1.20E-03	GXS	9.1	53342	6	Cytoplasmic Membrane	COG2148	Cell envelope biogenesis, outer membrane	
148547791	Pput_2574		glycosyl transferase family protein	2.5	1.81E-02	GXS	9.2	43209	5	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
148547806	Pput_2589		hypothetical protein	1.6	6.84E-02	control	4.4	40855	10	Unknown			
148547850	Pput_2634		hypothetical protein	1.3	3.58E-01	GXS	5.7	18527	4	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
148548356	Pput_3146		general substrate transporter	2.2	6.47E-03	GXS	9.0	60590	9	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
148548404	Pput_3196		TonB-dependent siderophore receptor	24.6	3.23E-04	control	4.8	87178	15	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
148548436	Pput_3228		hypothetical protein	2.5	6.24E-02	control	8.1	10935	3	Unknown			
148548667	Pput_3459		methyl-accepting chemotaxis sensory transducer	3.0	2.50E-02	GXS	5.3	52116	17	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
148548673	Pput_3465		PpiC-type peptidyl-prolyl cis-trans isomerase	6.8	5.73E-03	GXS	4.8	68554	4	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
148548706	Pput_3498		ABC transporter	3.5	3.49E-04	GXS	9.2	68774	5	Cytoplasmic Membrane	COG4178	General function prediction only	
148548794	Pput_3588		LolC/E family lipoprotein releasing system, transmembrane protein	9.3	2.31E-03	GXS	9.6	45680	4	Cytoplasmic Membrane	COG4591	Cell envelope biogenesis, outer membrane	
148548816	Pput_3610		lytic transglycosylase catalytic subunit	1.6	4.39E-01	control	9.9	74631	9	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
148548833	Pput_3627	acnA	aconitate hydratase	1.8	5.58E-01	control	5.4	99221	3	Cytoplasmic	COG1048	Energy production and conversion	
148548866	Pput_3660		NAD-glutamate dehydrogenase	2.8	8.00E-02	control	5.7	182512	22	Cytoplasmic	COG2902	Amino acid transport and metabolism	
148548922	Pput_3716		hypothetical protein	6.8	5.84E-04	GXS	10.1	16394	4	Cytoplasmic Membrane			
148548931	Pput_3725	pepN	aminopeptidase N	1.7	1.13E-01	control	4.8	99527	3	Cytoplasmic	COG0308	Amino acid transport and metabolism	
148548974	Pput_3768		peptidoglycan-binding LysM	1.9	2.14E-02	GXS	3.9	97202	25	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
148549168	Pput_3962		hypothetical protein	1.2	8.90E-01	control	7.8	57585	3	Cytoplasmic	COG2326	Function unknown	
148549226	Pput_4020		phospholipid/glycerol acyltransferase	8.8	4.87E-03	GXS	9.4	68479	4	Cytoplasmic Membrane	COG0204	Lipid metabolism	
148549236	Pput_4030		aromatic hydrocarbon degradation membrane protein	3.5	1.59E-02	control	6.1	46106	11	Outer Membrane	COG2067	Lipid metabolism	
148549385	Pput_4179		putative membrane-associated zinc metalloprotease	29.9	1.96E-03	GXS	9.6	48116	3	Cytoplasmic Membrane	COG0750	Cell envelope biogenesis, outer membrane	
148549449	Pput_4243		NADH:flavin oxidoreductase/NADH oxidase	1.1	6.34E-01	GXS	5.8	40498	2	Cytoplasmic	COG1902	Energy production and conversion	
148549460	Pput_4254		sodium/hydrogen exchanger	2.9	9.50E-02	GXS	8.1	64491	3	Cytoplasmic Membrane	COG0025	Inorganic ion transport and metabolism	
148549468	Pput_4262		transporter-associated region	7.2	7.70E-03	GXS	4.8	44197	5	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism	
148549481	Pput_4275		TonB-dependent receptor	4.3	4.05E-03	control	4.9	74714	24	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
148549491	Pput_4285		pyridoxine 5'-phosphate synthase	13.2	9.67E-04	control	5.8	26011	2	Cytoplasmic	COG0854	Coenzyme metabolism	
148549557	Pput_4352		methyl-accepting chemotaxis sensory transducer	3.3	3.03E-03	GXS	4.8	67728	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
148549568	Pput_4363	groEL	chaperonin GroEL	2.3	3.64E-03	control	4.7	56729	11	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
148549576	Pput_4371		mechanosensitive ion channel MscS	3.9	2.28E-03	GXS	7.5	30558	4	Cytoplasmic Membrane	COG0668	Cell envelope biogenesis, outer membrane	
148549606	Pput_4402		transport-associated	1.9	1.48E-01	control	9.5	20708	8	Periplasmic	COG2823	General function prediction only	
148549609	Pput_4405		ubiquinol--cytochrome c reductase, cytochrome c1	2.5	2.83E-02	GXS	7.0	29040	7	Unknown	COG2857	Energy production and conversion	
148549619	Pput_4415		hypothetical protein	1.8	1.11E-01	GXS	6.3	16046	7	Unknown	COG3105	Function unknown	
148549733	Pput_4531		methylmalonate-semialdehyde dehydrogenase	1.4	2.70E-01	GXS	6.1	54376	5	Cytoplasmic	COG1012	Energy production and conversion	

148549762	Pput_4560		multi-sensor signal transduction histidine kinase	10.5	2.49E-02	GXS	6.3	109257	4	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism	General function prediction only
148549776	Pput_4574	rpsO	30S ribosomal protein S15	14.4	1.04E-02	control	10.8	10030	2	Cytoplasmic	COG0184	Translation, ribosomal structure and biogenesis	
148549799	Pput_4597		SmpA/OmlA domain-containing protein	1.0	8.54E-01	control	4.4	19526	7	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
148549872	Pput_4670		rare lipoprotein B	2.8	7.75E-03	control	7.4	22436	10	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
148549901	Pput_4699		integral membrane sensor hybrid histidine kinase	21.7	9.18E-04	GXS	6.6	101532	6	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
148549918	Pput_4716		TonB-dependent copper receptor	3.3	4.02E-03	control	6.2	74527	46	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
148549935	Pput_4733		DNA-binding transcriptional activator OsmE	2.0	1.14E-01	control	6.8	12405	2	Unknown			
148549937	Pput_4735		AsmA family protein	4.9	4.29E-03	GXS	9.5	73480	8	Cytoplasmic Membrane	COG2982	Cell envelope biogenesis, outer membrane	
148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	1.4	2.51E-01	control	5.4	51447	2	Cytoplasmic	COG0499	Coenzyme metabolism	
148550055	Pput_4853		DEAD/DEAH box helicase domain-containing protein	4.4	1.61E-01	control	10.7	68197	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
148550083	Pput_4881		poly(hydroxyalkanoate) granule-associated protein	22.9	1.77E-03	control	11.0	26226	6	Cytoplasmic	COG3937	Function unknown	
148550099	Pput_4897		polar amino acid ABC transporter inner membrane subunit	6.4	1.02E-02	GXS	9.0	35027	5	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
148550151	Pput_4949	gltB	glutamate synthase subunit alpha	2.9	1.02E-01	control	6.3	161781	4	Cytoplasmic	COG0069	Amino acid transport and metabolism	
148550152	Pput_4950		sporulation domain-containing protein	1.7	1.47E-01	GXS	6.8	55866	3	Cytoplasmic	COG3267	Intracellular trafficking and secretion	
148550315	Pput_5115		ABC transporter-like protein	1.8	2.06E-01	GXS	7.8	98720	2	Cytoplasmic Membrane	COG1131	Defense mechanisms	
148550413	Pput_5213		hypothetical protein	9.2	1.21E-02	GXS	4.9	26240	3	Unknown			
148550499	Pput_5299		F0F1 ATP synthase subunit B	2.0	3.68E-02	GXS	5.4	16912	7	Cytoplasmic Membrane	COG0711	Energy production and conversion	
170721482	PputW619_2301		L-lactate transport	4.4	5.65E-02	GXS	9.3	59045	4	Cytoplasmic Membrane	COG1620	Energy production and conversion	
313497034				135.4	1.18E-03	GXS			4				
325277153				28.4	1.03E-02	GXS			2				
313498419				17.4	2.63E-03	GXS			2				
313107587				14.3	3.84E-02	GXS			2				
313496479				11.1	7.12E-03	GXS			2				
167034812				8.3	2.39E-02	GXS			3				
325271311				7.3	1.23E-02	GXS			3				
313497159				7.1	3.50E-02	GXS			2				
313500902				6.5	2.06E-03	control			13				
269200098				6.4	1.50E-03	GXS			6				
254241390				6.1	1.75E-03	GXS			21				
313107579				6.0	2.07E-03	GXS			3				
313496550				5.9	6.21E-05	GXS			8				
15599454				5.8	9.09E-03	control			4				
167031919				5.2	2.81E-03	control			2				
24982932				4.8	9.25E-04	control			2				
313499081				3.8	1.35E-02	GXS			4				
313497205				3.6	3.04E-03	GXS			4				
313497435				3.5	2.13E-02	GXS			2				
313500027				3.5	8.82E-03	GXS			4				
146307255				3.5	6.71E-04	GXS			10				
128169				3.4	5.07E-02	control			2				
313496366				3.3	3.75E-04	GXS			7				
313499955				3.3	8.34E-03	GXS			27				
313107574				3.2	5.65E-02	control			5				
313500996				3.0	8.29E-03	GXS			6				
269200090				3.0	3.22E-02	GXS			4				
24981833				3.0	8.04E-02	control			6				
313500331				3.0	6.44E-04	GXS			37				
24986476				3.0	8.93E-03	control			11				
313500889				2.9	3.93E-03	GXS			12				
313107576				2.9	2.19E-03	GXS			30				
313107572				2.5	4.18E-03	GXS			3				
339486576				2.5	1.04E-03	GXS			5				
104779763				2.4	3.48E-02	control			2				
24982083				2.3	4.39E-02	control			4				
167032148				2.3	2.41E-03	GXS			7				
24981839				2.0	2.38E-01	control			6				
167036003				2.0	6.19E-02	GXS			9				
313107588				1.7	2.94E-01	GXS			3				
167035543				1.7	1.16E-01	control			4				
313107578				1.6	1.89E-01	GXS			6				
24983268				1.5	9.12E-02	control			7				
146305341				1.3	7.93E-01	control			3				
134294113				1.3	9.81E-01	control			2				
313107581				1.0	6.82E-01	GXS			8				

5.2 Teilprojekt Butanol

5.2.1 Schüttelkolben

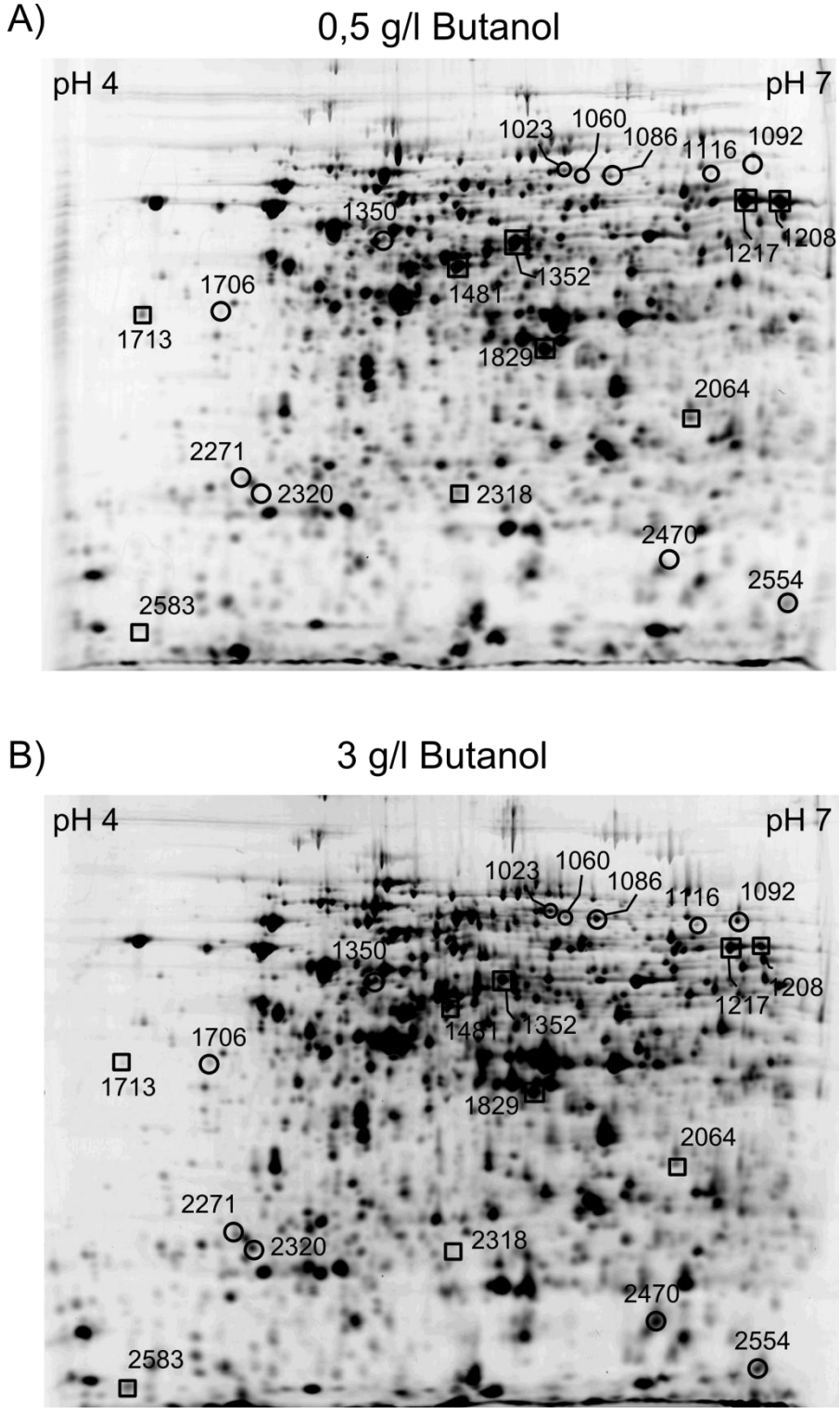
5.2.1.1 2D-DIGE-Analyse



Differenziell regulierte Spots zwischen mit 0,5 g/l Butanol behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 0,5 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.2.1.1 2D_DIGE_P_putida_KT2440_0.5g_BuOH_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
682	26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	3.5	2.67E-03	0,5g BuOH	6.4	69567	2	3%	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
682	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.5	2.67E-03	0,5g BuOH	6.4	71796	15	25%	Cytoplasmic	COG0365	Lipid metabolism	
691	26991574	PP_4896	mutL	DNA mismatch repair protein	2.8	2.70E-03	0,5g BuOH	6.7	69745	15	27%	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
691	26988482	PP_1751	mnmC	5-methylaminomethyl-2-thiouridine methyltransferase	2.8	2.70E-03	0,5g BuOH	6.5	71190	2	4%	Cytoplasmic	COG4121	Function unknown	
691	26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	2.8	2.70E-03	0,5g BuOH	6.4	69567	8	14%	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
691	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.8	2.70E-03	0,5g BuOH	6.4	71796	30	50%	Cytoplasmic	COG0365	Lipid metabolism	
697	26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	3.2	2.02E-03	0,5g BuOH	6.4	69567	4	8%	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
697	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.2	2.02E-03	0,5g BuOH	6.4	71796	30	59%	Cytoplasmic	COG0365	Lipid metabolism	
697	26987746	PP_1010	edd	phosphogluconate dehydratase	3.2	2.02E-03	0,5g BuOH	6.4	65359	4	7%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
761	26987746	PP_1010	edd	phosphogluconate dehydratase	2.3	6.11E-03	0,5g BuOH	6.4	65359	22	38%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
761	26990840	PP_4147		peptide ABC transporter periplamic peptide-binding protein	2.3	6.11E-03	0,5g BuOH	7.2	69637	22	35%	Periplasmic	COG4166	Amino acid transport and metabolism	
761	26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	2.3	6.11E-03	0,5g BuOH	6.5	67609	22	39%	Cytoplasmic	COG0649	Energy production and conversion	
761	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.3	6.11E-03	0,5g BuOH	7.0	69173	17	33%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
768	26990493	PP_3788		non-ribosomal peptide synthetase	3.3	1.71E-02	0,5g BuOH	6.7	56336	5	10%	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
768	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	3.3	1.71E-02	0,5g BuOH	7.0	69173	37	59%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
769	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.4	9.27E-03	0,5g BuOH	7.0	69173	28	48%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
793	26986947	PP_0203		hypothetical protein	2.4	4.18E-04	0,5g BuOH	5.9	62682	5	9%	Unknown	COG0624	Amino acid transport and metabolism	
793	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.4	4.18E-04	0,5g BuOH	5.5	63339	15	23%	Cytoplasmic	COG1960	Lipid metabolism	
793	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.4	4.18E-04	0,5g BuOH	5.7	61082	19	36%	Cytoplasmic	COG0644	Energy production and conversion	
793	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.4	4.18E-04	0,5g BuOH	5.3	52585	6	14%	Cytoplasmic	COG2204	Signal transduction mechanisms	
793	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.4	4.18E-04	0,5g BuOH	7.0	69173	4	11%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
796	26990069	PP_3354		acyl-CoA dehydrogenase, ferrulic acid biotransformation protein	2.2	2.50E-04	0,5g BuOH	5.6	62339	5	11%	Cytoplasmic	COG1960	Lipid metabolism	
796	26986947	PP_0203		hypothetical protein	2.2	2.50E-04	0,5g BuOH	5.9	62682	18	41%	Unknown	COG0624	Amino acid transport and metabolism	
796	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.2	2.50E-04	0,5g BuOH	5.5	63339	31	56%	Cytoplasmic	COG1960	Lipid metabolism	
796	26987499	PP_0763		long-chain-fatty-acid--CoA ligase	2.2	2.50E-04	0,5g BuOH	5.5	62125	2	3%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
796	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.2	2.50E-04	0,5g BuOH	5.7	61082	20	35%	Cytoplasmic	COG0644	Energy production and conversion	
796	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.2	2.50E-04	0,5g BuOH	5.3	52585	17	48%	Cytoplasmic	COG2204	Signal transduction mechanisms	
796	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.2	2.50E-04	0,5g BuOH	7.0	69173	6	16%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
797	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.5	7.76E-04	0,5g BuOH	5.5	63339	23	41%	Cytoplasmic	COG1960	Lipid metabolism	
797	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.5	7.76E-04	0,5g BuOH	5.7	61082	26	47%	Cytoplasmic	COG0644	Energy production and conversion	
797	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.5	7.76E-04	0,5g BuOH	5.3	52585	7	15%	Cytoplasmic	COG2204	Signal transduction mechanisms	
797	26987410	PP_0674		ABC transporter ATP-binding protein	2.5	7.76E-04	0,5g BuOH	5.3	61860	3	6%	Cytoplasmic	COG0488	General function prediction only	
797	26986947	PP_0203		hypothetical protein	2.5	7.76E-04	0,5g BuOH	5.9	62682	14	29%	Unknown	COG0624	Amino acid transport and metabolism	
814	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	9.2	3.37E-05	0,5g BuOH	6.5	106521	3	3%	Cytoplasmic	COG0567	Energy production and conversion	
814	26991425	PP_4742	hsdS	type I restriction-modification system, S subunit	9.2	3.37E-05	0,5g BuOH	6.5	62995	2	4%	Cytoplasmic	COG0732	Defense mechanisms	
814	26987543	PP_0807		anaerobic nitric oxide reductase transcription regulator	9.2	3.37E-05	0,5g BuOH	6.3	57234	2	3%	Cytoplasmic	COG3604	Transcription	Signal transduction mechanisms
814	26990265	PP_3553		acyl-CoA synthetase	9.2	3.37E-05	0,5g BuOH	6.4	59576	19	39%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
814	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	9.2	3.37E-05	0,5g BuOH	7.0	69173	2	4%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
814	26987608	PP_0872	prfC	peptide chain release factor 3	9.2	3.37E-05	0,5g BuOH	6.2	59713	7	13%	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
887	26992056	PP_5380	copA	copper resistance protein A	4.3	4.91E-03	0,5g BuOH	6.0	74225	3	4%	Periplasmic	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
887	26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	4.3	4.91E-03	0,5g BuOH	5.4	55551	2	4%	Cytoplasmic	COG2204	Signal transduction mechanisms	
887	26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	4.3	4.91E-03	0,5g BuOH	5.6	51255	5	13%	Cytoplasmic	COG0065	Amino acid transport and metabolism	
887	26989399	PP_2680		aldehyde dehydrogenase family protein	4.3	4.91E-03	0,5g BuOH	5.5	54903	23	46%	Cytoplasmic	COG1012	Energy production and conversion	
971	26987824	PP_1088	argG	argininosuccinate synthase	3.9	1.93E-02	0,5g BuOH	5.1	45164	7	17%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
971	26990810	PP_4116	aceA	isocitrate lyase	3.9	1.93E-02	0,5g BuOH	5.3	48633	21	40%	Cytoplasmic	COG2224	Energy production and conversion	
971	26988046	PP_1311		tryptophanyl-tRNA synthetase	3.9	1.93E-02	0,5g BuOH	5.4	49297	3	8%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
971	26989399	PP_2680		aldehyde dehydrogenase family protein	3.9	1.93E-02	0,5g BuOH	5.5	54903	5	15%	Cytoplasmic	COG1012	Energy production and conversion	
971	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	3.9	1.93E-02	0,5g BuOH	5.4	50393	3	7%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1140	26989381	PP_2662		hypothetical protein	4.5	3.95E-02	0,5g BuOH	4.3	42858	8	23%	Outer Membrane			
1140	26990810	PP_4116	aceA	isocitrate lyase	4.5	3.95E-02	0,5g BuOH	5.3	48633	4	9%	Cytoplasmic	COG2224	Energy production and conversion	
1197	26990459	PP_3754		beta-ketothiolase	6.7	3.07E-05	0,5g BuOH	6.9	40988	14	36%	Cytoplasmic	COG0183	Lipid metabolism	
1197	26988351	PP_1619	truD	tRNA pseudouridine synthase D	6.7	3.07E-05	0,5g BuOH	6.9	38439	4	11%	Cytoplasmic	COG0585	Function unknown	
1197	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	6.7	3.07E-05	0,5g BuOH	6.2	45449	2	6%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1197	26987028	PP_0286	mutY	A/G-specific adenine glycosylase	6.7	3.07E-05	0,5g BuOH	6.8	39758	2	6%	Cytoplasmic	COG1194	DNA replication, recombination, and repair	
1354	26988324	PP_1592	tsf	elongation factor Ts	1.8	6.07E-04	0,5g BuOH	4.9	30432	5	17%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
1354	26987980	PP_1245		hypothetical protein	1.8	6.07E-04	0,5g BuOH	9.4	31144	2	10%	Unknown			
1354	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.8	6.07E-04	0,5g BuOH	4.9	31237	5	20%	Unknown	COG2025	Energy production and conversion	
1354	26991771	PP_5095	proC-2	pyrroline-5-carboxylate reductase	1.8	6.07E-04	0,5g BuOH	4.7	28258	2	8%	Cytoplasmic	COG0345	Amino acid transport and metabolism	
1357	26988324	PP_1592	tsf	elongation factor Ts	1.8	3.03E-03	0,5g BuOH	4.9	30432	4	13%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
1357	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.8	3.03E-03	0,5g BuOH	4.9	31237	8	34%	Unknown	COG2025	Energy production and conversion	
1357	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.8	3.03E-03	0,5g BuOH	4.9	31237	18	80%	Unknown	COG2025	Energy production and conversion	
1424	26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	3.2	2.87E-05	0,5g BuOH	6.5	27422	3	13%	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
1424	26987198	PP_0457	rplB	50S ribosomal protein L2	3.2	2.87E-05	0,5g BuOH	11.7	29669	2	5%	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
1424	26990465	PP_3760		MCP methyltransferase, CheR-type	3.2	2.87E-05	0,5g BuOH	6.4	31647	2	5%	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
1424	26989649	PP_2930		L-serine dehydratase	3.2	2.87E-05	0,5g BuOH	6.6	31890	3	10%	Cytoplasmic	COG1171	Amino acid transport and metabolism	
1424	26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	3.2	2.87E-05	0,5g BuOH	6.5	29780	2	8%	Cytoplasmic	COG0388	General function prediction only	
1445	26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	7.6	2.06E-05	0,5g BuOH	6.3	30088	6	24%	Cytoplasmic	COG1250	Lipid metabolism	
1445	26990956	PP_4265	anr	transcriptional regulator Anr	7.6	2.06E-05	0,5g BuOH	6.5	27221	2	8%	Cytoplasmic	COG0664	Signal transduction mechanisms	
1445	26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	7.6	2.06E-05	0,5g BuOH	6.5	30686	4	14%	Cytoplasmic	COG2904	Function unknown	
1445	26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	7.6	2.06E-05	0,5g BuOH	6.5	29780	4	15%	Cytoplasmic	COG0388	General function prediction only	
1445	26988515	PP_1784	rmlD	dTDP-4-dehydrorhamnose reductase	7.6	2.06E-05	0,5g BuOH	6.7	32131	2	6%	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
1582	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	2.7	1.91E-03	0,5g BuOH	6.0	26030	8	36%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
1582	26987219	PP_0478	rpsD	30S ribosomal protein S4	2.7	1.91E-03	0,5g BuOH	10.5	23056	2	10%	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
1582	26989384	PP_2665	agmR	LuxR family two component transcriptional regulator	2.7	1.91E-03	0,5g BuOH	5.9	24536	4	18%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
1582	26988239	PP_1507		hypothetical protein	2.7	1.91E-03	0,5g BuOH	6.0	23544	2	11%	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones	
1582	26987954	PP_1219	tolQ	biopolymer transport protein TolQ	2.7	1.91E-03	0,5g BuOH	6.3	25310	2	11%	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
1611	26989392	PP_2673		pentapeptide repeat-containing protein	3.7	1.47E-02	0,5g BuOH	5.3	23569	10	46%	Extracellular	COG1357	Function unknown	
1611	26987219	PP_0478	rpsD	30S ribosomal protein S4	3.7	1.47E-02	0,5g BuOH	10.5	23056	5	24%	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
1865	26991550	PP_4870		azurin	1.9	3.54E-02	0,5g BuOH	6.9	16028	6	39%	Periplasmic	COG3241	Energy production and conversion	
1865	26988633	PP_1903		protein tyrosine phosphatase	1.9	3.54E-02	0,5g BuOH	6.3	16761	2	11%	Cytoplasmic	COG0394	Signal transduction mechanisms	
1865	26987953	PP_1218		hypothetical protein	1.9	3.54E-02	0,5g BuOH	6.5	17205	4	27%	Cytoplasmic	COG0824	General function prediction only	
1865	26987166	PP_0425		OsmC family protein	1.9	3.54E-02	0,5g BuOH	6.3	15143	4	24%	Unknown	COG1765	Posttranslational modification, protein turnover, chaperones	
1866	26989156	PP_2433		hypothetical protein	2.4	9.29E-03	0,5g BuOH	5.7	18025	2	10%	Cytoplasmic	COG5642	Function unknown	
1866	26987214	PP_0473	rplO	50S ribosomal protein L15	2.4	9.29E-03	0,5g BuOH	11.5	15189	2	17%	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
1866	26991489	PP_4809		iojap-like protein	2.4	9.29E-03	0,5g BuOH	5.6	15617	2	14%	Cytoplasmic	COG0799	Function unknown	

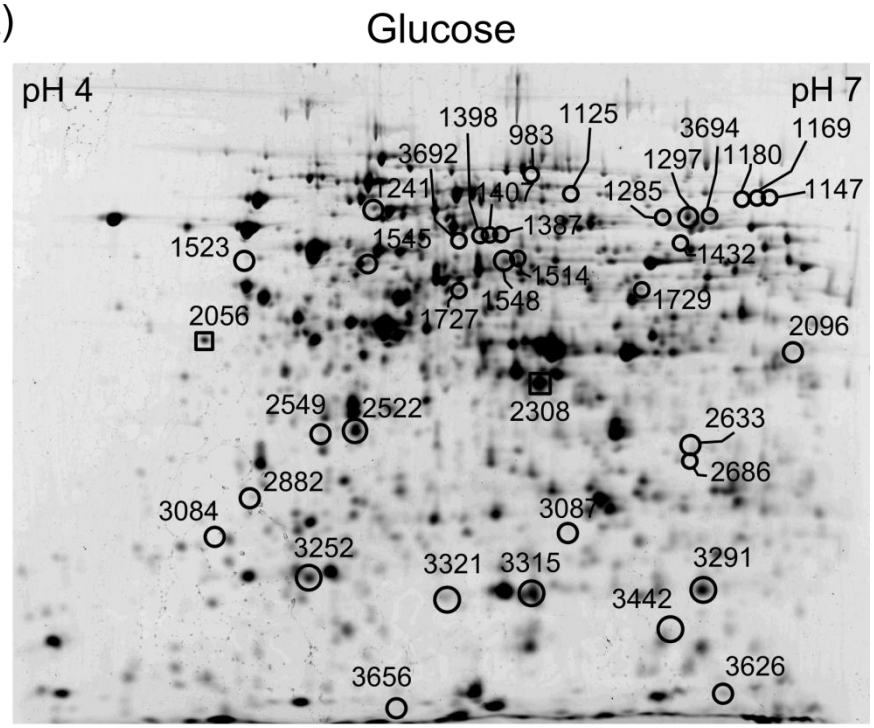


Differenziell regulierte Spots zwischen mit 0,5 g/l und 3 g/l Butanol behandelten Zellen von *P. putida* KT2440. A) zeigt das Gelbild einer mit 0,5 g/l Butanol, B) das Gelbild einer mit 3 g/l behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 3 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

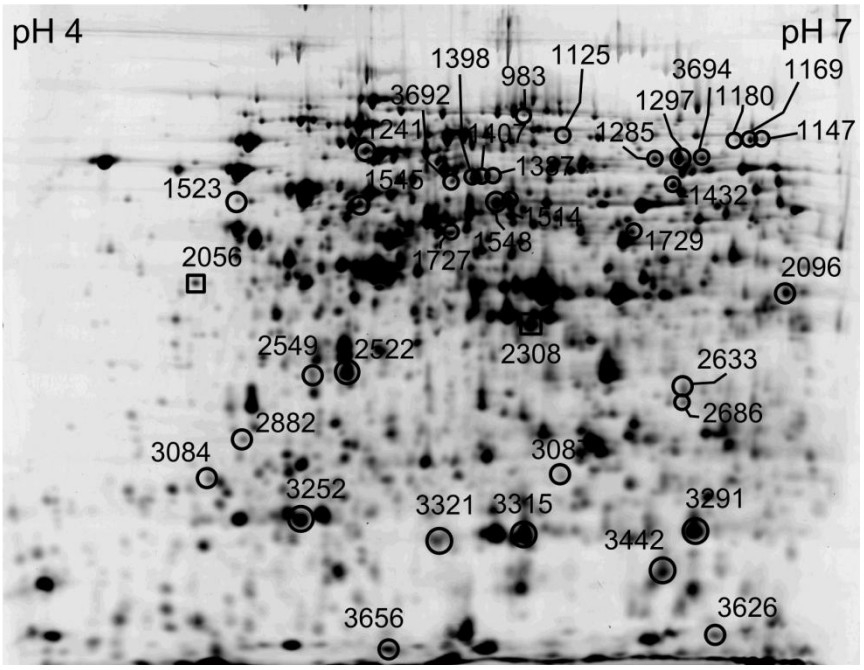
5.2.1.1 2D_DIGE_P_putida_KT2440_0.5g_vs_3g_BuOH_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
1023	26990379	PP_3668		catalase/peroxidase HPI	2.0	7.04E-03	3gBuOH	5.8	82061	12	18%	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
1023	26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	2.0	7.04E-03	3gBuOH	5.7	83310	2	3%	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
1060	26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	3.2	1.95E-03	3gBuOH	5.9	77449	11	15%	Cytoplasmic	COG1250	Lipid metabolism	
1068	26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	3.5	1.94E-03	3gBuOH	5.9	77449	16	24%	Cytoplasmic	COG1250	Lipid metabolism	
1092	26986860	PP_0115	katE	hydroperoxidase II	13.0	4.93E-04	3gBuOH	6.7	78105	22	35%	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
1116	26991434	PP_4753		N-methylproline demethylase	2.4	9.76E-04	3gBuOH	6.5	75215	3	4%	Cytoplasmic	COG1902	Energy production and conversion	
1208	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	0.3	2.33E-02	0.5gBuOH	7.0	69173	23	36%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1217	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	0.5	3.29E-02	0.5gBuOH	7.0	69173	29	44%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1350	26989818	PP_3099		hypothetical protein	1.8	1.13E-02	3gBuOH	4.9	56072	22	42%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and	vesicular transport
1352	26989399	PP_2680		aldehyde dehydrogenase family protein	0.4	6.70E-03	0.5gBuOH	5.5	54903	7	17%	Cytoplasmic	COG1012	Energy production and conversion	
1481	26990810	PP_4116	aceA	isocitrate lyase	0.3	4.00E-03	0.5gBuOH	5.3	48633	23	41%	Cytoplasmic	COG2224	Energy production and conversion	
1481	26988046	PP_1311		tryptophanyl-tRNA synthetase	0.3	4.00E-03	0.5gBuOH	5.4	49297	2	5%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
1706	26989807	PP_3088		hypothetical protein	1.8	1.78E-03	3gBuOH	4.4	39853	6	17%	Unknown	COG3515	Intracellular trafficking, secretion, and	vesicular transport
1713	26989381	PP_2662		hypothetical protein	0.2	4.42E-03	0.5gBuOH	4.3	42858	4	8%	Outer Membrane			
1829	26990488	PP_3783		hypothetical protein	0.5	4.48E-04	0.5gBuOH	5.8	34938	9	23%	Cytoplasmic			
1829	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	0.5	4.48E-04	0.5gBuOH	6.4	40068	3	8%	Periplasmic	COG0687	Amino acid transport and metabolism	
2064	26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	0.5	5.66E-03	0.5gBuOH	6.5	29780	3	9%	Cytoplasmic	COG0388	General function prediction only	
2064	26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	0.5	5.66E-03	0.5gBuOH	6.3	30088	7	32%	Cytoplasmic	COG1250	Lipid metabolism	
2064	26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	0.5	5.66E-03	0.5gBuOH	6.5	30686	4	14%	Cytoplasmic	COG2904	Function unknown	
2271	26989842	PP_3123		3-oxoacid CoA-transferase subunit B	2.5	5.40E-04	3gBuOH	4.4	23239	2	9%	Cytoplasmic	COG2057	Lipid metabolism	
2318	26989392	PP_2673		pentapeptide repeat-containing protein	0.4	9.26E-03	0.5gBuOH	5.3	23569	6	25%	Extracellular	COG1357	Function unknown	
2470	26987533	PP_0797		hypothetical protein	3.6	2.50E-02	3gBuOH	6.8	19982	3	20%	Cytoplasmic			
2583	26991312	PP_4628	mioC	flavodoxin	0.4	1.34E-03	3gBuOH	4.1	15937	3	16%	Unknown	COG0716	Energy production and conversion	
2583	26986881	PP_0136		inhibitor of vertebrate lysozyme	0.4	1.34E-03	3gBuOH	4.4	17512	2	13%	Periplasmic			

A)



B)

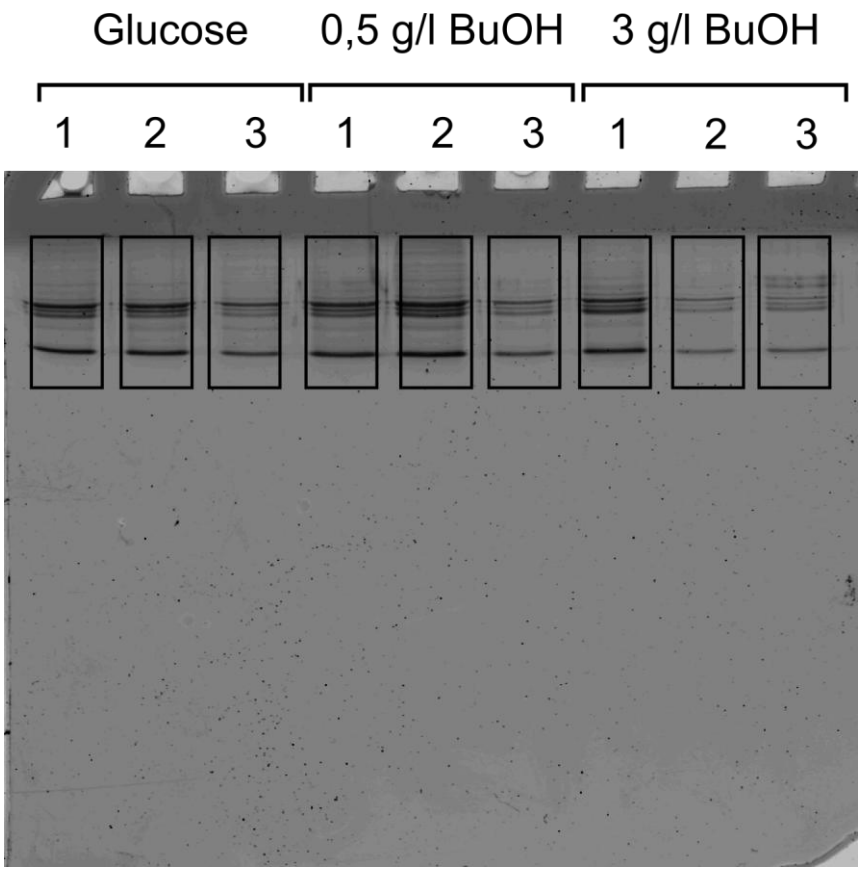


Differenziell regulierte Spots zwischen mit 3 g/l Butanol behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 3 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
983	26987189	PP 0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.8	7.14E-05	3g BuOH	7.2	154797	4	3%	Cytoplasmic	COG0086	Transcription	
983	26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.8	7.14E-05	3g BuOH	5.6	96697	7	9%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
983	26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.8	7.14E-05	3g BuOH	5.6	99332	2	2%	Cytoplasmic	COG2609	Energy production and conversion	
983	26989814	PP_3095		chaperone-associated ATPase	1.8	7.14E-05	3g BuOH	6.1	96474	22	26%	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
1125	26988137	PP_1403	bglX	periplasmic beta-glucosidase	3.5	1.08E-04	3g BuOH	6.1	83414	2	2%	Periplasmic	COG1472	Carbohydrate transport and metabolism	
1125	26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	3.5	1.08E-04	3g BuOH	5.9	77449	19	32%	Cytoplasmic	COG1250	Lipid metabolism	
1147	26990333	PP_3622		isoquinoline 1-oxidoreductase, beta subunit	3.1	8.01E-04	3g BuOH	7.0	80889	2	3%	Cytoplasmic Membrane	COG1529	Energy production and conversion	
1147	26991986	PP 5310	recG	ATP-dependent DNA helicase RecG	3.1	8.01E-04	3g BuOH	6.8	76452	11	15%	Cytoplasmic	COG1200	DNA replication, recombination, and repair	Transcription
1147	26986860	PP_0115	katE	hydroperoxidase II	3.1	8.01E-04	3g BuOH	6.7	78105	10	16%	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
1169	26990333	PP_3622		isoquinoline 1-oxidoreductase, beta subunit	7.7	1.33E-04	3g BuOH	7.0	80889	14	21%	Cytoplasmic Membrane	COG1529	Energy production and conversion	
1169	26986860	PP_0115	katE	hydroperoxidase II	7.7	1.33E-04	3g BuOH	6.7	78105	26	42%	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
1180	26986860	PP_0115	katE	hydroperoxidase II	3.5	5.77E-04	3g BuOH	6.7	78105	20	34%	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
1241	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2	1.74E-04	3g BuOH	5.3	55654	8	21%	Cytoplasmic	COG0508	Energy production and conversion	
1241	26986841	PP_0096	prlC	oligopeptidase A	2	1.74E-04	3g BuOH	5.0	75721	11	18%	Cytoplasmic	COG0339	Amino acid transport and metabolism	
1241	26990871	PP 4179	htpG	heat shock protein 90	2	1.74E-04	3g BuOH	5.0	71610	39	55%	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
1285	26990871	PP_4179	htpG	heat shock protein 90	2.7	1.16E-03	3g BuOH	5.0	71610	4	8%	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
1285	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.7	1.16E-03	3g BuOH	6.4	71796	18	36%	Cytoplasmic	COG0365	Lipid metabolism	
1297	26987746	PP_1010	edd	phosphogluconate dehydratase	2.4	1.43E-03	3g BuOH	6.4	65359	2	3%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1297	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.4	1.43E-03	3g BuOH	6.4	71796	22	43%	Cytoplasmic	COG0365	Lipid metabolism	
1387	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	1.8	1.17E-03	3g BuOH	5.5	63339	13	20%	Cytoplasmic	COG1960	Lipid metabolism	
1387	26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.8	1.17E-03	3g BuOH	5.5	62125	17	40%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1387	26990764	PP 4063		AMP-binding domain protein	1.8	1.17E-03	3g BuOH	5.6	61594	6	11%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1387	26991380	PP 4696		two component, sigma54 specific, transcriptional regulator, Fis family	1.8	1.17E-03	3g BuOH	5.3	52585	3	8%	Cytoplasmic	COG2204	Signal transduction mechanisms	
1387	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	1.8	1.17E-03	3g BuOH	5.7	61082	6	10%	Cytoplasmic	COG0644	Energy production and conversion	
1398	26986947	PP_0203		hypothetical protein	2.5	1.13E-03	3g BuOH	5.9	62682	9	22%	Unknown	COG0624	Amino acid transport and metabolism	
1398	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.5	1.13E-03	3g BuOH	5.5	63339	17	32%	Cytoplasmic	COG1960	Lipid metabolism	
1398	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.5	1.13E-03	3g BuOH	5.7	61082	31	60%	Cytoplasmic	COG0644	Energy production and conversion	
1398	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.5	1.13E-03	3g BuOH	5.3	52585	7	19%	Cytoplasmic	COG2204	Signal transduction mechanisms	
1407	26986947	PP 0203		hypothetical protein	2.3	2.27E-04	3g BuOH	5.9	62682	19	33%	Unknown	COG0624	Amino acid transport and metabolism	
1407	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.3	2.27E-04	3g BuOH	5.5	63339	21	32%	Cytoplasmic	COG1960	Lipid metabolism	
1407	26987499	PP_0763		long-chain-fatty-acid--CoA ligase	2.3	2.27E-04	3g BuOH	5.5	62125	4	7%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1407	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.3	2.27E-04	3g BuOH	5.7	61082	20	38%	Cytoplasmic	COG0644	Energy production and conversion	
1407	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.3	2.27E-04	3g BuOH	5.3	52585	14	30%	Cytoplasmic	COG2204	Signal transduction mechanisms	
1432	26987608	PP_0872	prfC	peptide chain release factor 3	8.5	8.48E-05	3g BuOH	6.2	59713	3	5%	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
1432	26990265	PP_3553		acyl-CoA synthetase	8.5	8.48E-05	3g BuOH	6.4	59576	14	24%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1432	26990895	PP 4203		electron-transferring-flavoprotein dehydrogenase	8.5	8.48E-05	3g BuOH	5.7	61082	3	8%	Cytoplasmic	COG0644	Energy production and conversion	
1514	26991954	PP 5278		aldehyde dehydrogenase family protein	1.9	6.14E-04	3g BuOH	5.5	53053	13	30%	Cytoplasmic	COG1012	Energy production and conversion	
1514	26988522	PP_1791		aldolase/synthase	1.9	6.14E-04	3g BuOH	5.9	58534	7	17%	Cytoplasmic	COG0119	Amino acid transport and metabolism	
1523	146306885	not in database		Ribosomal Protein	2	1.06E-03	3g BuOH			2	4%				
1523	26991860	PP_5184		glutamine synthetase	2	1.06E-03	3g BuOH	4.5	50974	10	31%	Cytoplasmic	COG0174	Amino acid transport and metabolism	
1545	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.9	7.44E-04	3g BuOH	4.9	54767	13	26%	Cytoplasmic	COG1951	Energy production and conversion	
1545	26989818	PP_3099		hypothetical protein	1.9	7.44E-04	3g BuOH	4.9	56072	33	66%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
1548	26989399	PP_2680		aldehyde dehydrogenase family protein	2.5	2.50E-02	3g BuOH	5.5	54903	24	66%	Cytoplasmic	COG1012	Energy production and conversion	
1548	26988711	PP 1985	leuC	isopropylmalate isomerase large subunit	2.5	2.50E-02	3g BuOH	5.6	51255	5	13%	Cytoplasmic	COG0065	Amino acid transport and metabolism	
1727	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.9	7.87E-03	3g BuOH	5.4	50393	5	13%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1727	26990524	PP_3819	gor	glutathione reductase	1.9	7.87E-03	3g BuOH	5.2	49180	2	5%	Cytoplasmic	COG1249	Energy production and conversion	
1727	26990810	PP_4116	aceA	isocitrate lyase	1.9	7.87E-03	3g BuOH	5.3	48633	10	22%	Cytoplasmic	COG2224	Energy production and conversion	
1727	26990705	PP_4000	serS	seryl-tRNA synthetase	1.9	7.87E-03	3g BuOH	5.1	46849	2	5%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
1727	26991065	PP_4376	fliD	flagellar cap protein FliD	1.9	7.87E-03	3g BuOH	5.2	46522	10	29%	Extracellular	COG1345	Cell motility and secretion	
1729	26989786	PP_3067		hypothetical protein	2.5	1.22E-04	3g BuOH	6.6	48836	3	7%	Cytoplasmic			
1729	26987407	PP 0671	glyA	serine hydroxymethyltransferase	2.5	1.22E-04	3g BuOH	6.2	44897	3	6%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
1729	26988486	PP_1755	fumC-2	fumarate hydratase	2.5	1.22E-04	3g BuOH	6.4	49131	11	20%	Cytoplasmic	COG0114	Energy production and conversion	
1729	26991399	PP_4716	glmM	phosphoglucosamine mutase	2.5	1.22E-04	3g BuOH	6.0	47744	4	9%	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
1729	26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	2.5	1.22E-04	3g BuOH	6.4	79133	2	3%	Cytoplasmic	COG0128	Amino acid transport and metabolism	
2056	26987941	PP_1206	oprD	outer membrane porin	0.5	3.60E-02	Control	4.6	46120	8	20%	Outer Membrane			
2096	26990459	PP_3754		beta-ketothiolase	3.9	2.11E-04	3g BuOH	6.9	40988	11	28%	Cytoplasmic	COG0183	Lipid metabolism	
2096	26988351	PP_1619	truD	tRNA pseudouridine synthase D	3.9	2.11E-04	3g BuOH	6.9	38439	7	21%	Cytoplasmic	COG0585	Function unknown	
2096	26990878	PP 4186	sucC	succinyl-CoA synthetase subunit beta	3.9	2.11E-04	3g BuOH	6.1	41239	5	16%	Cytoplasmic	COG0045	Energy production and conversion	
2096	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	3.9	2.11E-04	3g BuOH	6.2	45449	4	13%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
2308	26987175	PP_0434	anmK	anhydro-N-acetylmuramic acid kinase	0.5	1.74E-03	Control	5.8	38235	2	7%	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
2308	26990488	PP_3783		hypothetical protein	0.5	1.74E-03	Control	5.8	34938	14	45%	Cytoplasmic			
2308	26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	0.5	1.74E-03	Control	5.6	35858	2	7%	Unknown	COG2171	Amino acid transport and metabolism	
2308	26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	0.5	1.74E-03	Control	6.3	36692	6	20%	Periplasmic	COG1613	Inorganic ion transport and metabolism	
2308	26990488	PP_3783		hypothetical protein	0.5	1.74E-03	Control	5.8	34938	21	82%	Cytoplasmic			
2308	26990893	PP 4201		electron transfer flavoprotein, alpha subunit	0.5	1.74E-03	Control	4.9	31237	10	61%	Unknown	COG2025	Energy production and conversion	
2522	26988324	PP 1592	tsf	elongation factor Ts	2	9.40E-04	3g BuOH	4.9	30432	11	33%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
2522	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2	9.40E-04	3g BuOH	4.9	31237	4	15%	Unknown	COG2025	Energy production and conversion	
2522	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2	9.40E-04	3g BuOH	4.9	31237	19	87%	Unknown	COG2025	Energy production and conversion	
2549	26988324	PP_1592	tsf	elongation factor Ts	2	5.64E-04	3g BuOH	4.9	30432	3	9%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
2549	26987980	PP_1245		hypothetical protein	2	5.64E-04	3g BuOH	9.4	31144	2	8%	Unknown			
2549	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2	5.64E-04	3g BuOH	4.9	31237	4	15%	Unknown	COG2025	Energy production and conversion	
2549	26991771	PP_5095	proC-2	pyrroline-5-carboxylate reductase	2	5.64E-04	3g BuOH	4.7	28258	2	8%	Cytoplasmic	COG0345	Amino acid transport and metabolism	
2633	26989609	PP 2890	xthA	exonuclease III	1.8	4.33E-05	3g BuOH	6.7	30951	2	7%	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
2633	26986929	PP_0185	prpA	LytTR family two component transcriptional regulator	1.8	4.33E-05	3g BuOH	6.5	27422	3	13%	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
2633	26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	1.8	4.33E-05	3g BuOH	6.5	30686	2	8%	Cytoplasmic	COG2904	Function unknown	
2633	26989649	PP_2930		L-serine dehydratase	1.8	4.33E-05	3g BuOH	6.6	31890	3	10%	Cytoplasmic	COG1171	Amino acid transport and metabolism	
2633	26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	1.8	4.33E-05	3g BuOH	6.5	29780	2	8%	Cytoplasmic	COG0388	General function prediction only	
2686	26987193	PP_0452	tuf	elongation factor Tu	4.6	5.38E-05	3g BuOH	5.0	43478	3	15%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
2686	26987755	PP 1019	oprB-1	porin B	4.6	5.38E-05	3g BuOH	5.9	49646	2	9%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
2686	26987595	PP 0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	4.6	5.38E-05	3g BuOH	6.5	29780	4	15%	Cytoplasmic	COG0388	General function prediction only	
2686	26988814	PP_2089	oprF	OmpF family protein	4.6	5.38E-05	3g BuOH	4.5	37012	2	9%	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
2686	26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	4.6	5.38E-05	3g BuOH	6.3	30088	6	31%	Cytoplasmic	COG1250	Lipid metabolism	
2686	26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	4.6	5.38E-05	3g BuOH	6.1	41239	2	10%	Cytoplasmic	COG0045	Energy production and conversion	
2686	26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	4.6	5.38E-05	3g BuOH	5.8	40626	2	13%	Cytoplasmic	COG1902	Energy production and conversion	
2686	26987941	PP_1206	oprD	outer membrane porin	4.6	5.38E-05	3g BuOH	4.6	46120	2	11%	Outer Membrane			
2686	26991641	PP_4963	pgk	phosphoglycerate kinase	4.6	5.38E-05	3g BuOH	4.9	40005	2	11%	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
2882	26990878	PP 4186	sucC	succinyl-CoA synthetase subunit beta	1.9	7.56E-05	3g BuOH	6.1	41239	3	13%	Cytoplasmic	COG0045	Energy production and conversion	
2882	26987941	PP_1206	oprD	outer membrane porin	1.9	7.56E-05	3g BuOH	4.6	46120	2	11%	Outer Membrane			
2882	26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.9	7.56E-05	3g BuOH	5.8	40626	2	13%	Cytoplasmic	COG1902	Energy production and conversion	
2882	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.9	7.56E-05	3g BuOH	4.9	31237	2	14%	Unknown	COG2025	Energy production and conversion	
2882	26988234	PP_1502		OmpA/MotB domain protein	1.9	7.56E-05	3g BuOH	9.5	28964	2	10%	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
2882	26987193	PP_0452	tuf	elongation factor Tu	1.9	7.56E-05	3g BuOH	5.0	43478	5	22%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
2882	26987755	PP_1019	oprB-1	porin B	1.9	7.56E-05	3g BuOH	5.9	49646	2	9%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
2882	26988814	PP 2089	oprF	OmpF family protein	1.9	7.56E-05	3g BuOH	4.5	37012	3	9%	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
2882	26991006	PP_4315		PhzF family phenazine biosynthesis protein	1.9	7.56E-05	3g BuOH	4.5	28437	4	15%	Cytoplasmic	COG0384	General function prediction only	
3078	26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	2.7	6.62E-03	3g BuOH	6.0	26030	10	47%	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only

3078	26988239	PP_1507		hypothetical protein	2.7	6.62E-03	3g BuOH	6.0	23544	3	17%	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones
3084	26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	4.2	1.16E-02	3g BuOH	5.0	42236	4	6%	Cytoplasmic	COG1364	Amino acid transport and metabolism
3252	26987820	PP_1084		anti-oxidant AhpCTSA family protein	2.2	5.97E-04	3g BuOH	4.9	21730	2	12%	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
3252	26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	2.2	5.97E-04	3g BuOH	4.8	20507	11	71%	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
3252	26987156	PP_0415	rpe	ribulose-phosphate 3-epimerase	2.2	5.97E-04	3g BuOH	5.6	27672	3	13%	Cytoplasmic	COG0036	Carbohydrate transport and metabolism
3252	26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	2.2	5.97E-04	3g BuOH	4.8	20507	14	80%	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
3252	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2.2	5.97E-04	3g BuOH	4.9	31237	6	44%	Unknown	COG2025	Energy production and conversion
3252	26987156	PP_0415	rpe	ribulose-phosphate 3-epimerase	2.2	5.97E-04	3g BuOH	5.6	27672	6	25%	Cytoplasmic	COG0036	Carbohydrate transport and metabolism
3291	26991658	PP_4981		hypothetical protein	2.3	3.32E-04	3g BuOH	8.8	22129	2	7%	Unknown	COG2353	Function unknown
3291	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2.3	3.32E-04	3g BuOH	4.9	31237	3	26%	Unknown	COG2025	Energy production and conversion
3291	26991658	PP_4981		hypothetical protein	2.3	3.32E-04	3g BuOH	8.8	22129	11	60%	Unknown	COG2353	Function unknown
3315	26988957	PP_2233		isochorismatase superfamily hydrolase	1.9	2.83E-03	3g BuOH	6.0	19296	2	10%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
3315	26992091	PP_5416	atpH	F0F1 ATP synthase subunit delta	1.9	2.83E-03	3g BuOH	5.7	19197	3	16%	Cytoplasmic	COG0712	Energy production and conversion
3315	26989808	PP_3089		hypothetical protein	1.9	2.83E-03	3g BuOH	5.3	19453	6	38%	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport
3321	207094127	not in database			1.9	2.87E-04	3g BuOH			2	54%			
3321	26987651	PP_0915	sodB	superoxide dismutase	1.9	2.87E-04	3g BuOH	5.8	21938	2	7%	Periplasmic	COG0605	Inorganic ion transport and metabolism
3442	26987533	PP_0797		hypothetical protein	3.9	2.97E-04	3g BuOH	6.8	19982	2	13%	Cytoplasmic		
3442	26987533	PP_0797		hypothetical protein	3.9	2.97E-04	3g BuOH	6.8	19982	8	49%	Cytoplasmic		
3442	26991236	PP_4552	phaJ1	MaoC domain protein dehydratase	3.9	2.97E-04	3g BuOH	6.3	17135	4	41%	Unknown	COG2030	Lipid metabolism
3442	26990893	PP_4201		electron transfer flavoprotein, alpha subunit	3.9	2.97E-04	3g BuOH	4.9	31237	3	22%	Unknown	COG2025	Energy production and conversion
3442	26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	3.9	2.97E-04	3g BuOH	6.3	17784	2	10%	Cytoplasmic	COG0440	Amino acid transport and metabolism
3626	26988856	PP_2132		universal stress protein	1.8	5.64E-04	3g BuOH	6.6	16209	2	14%	Unknown	COG0589	Signal transduction mechanisms
3656	26987221	PP_0480	rplQ	50S ribosomal protein L17	5.7	2.67E-04	3g BuOH	11.3	14363	2	10%	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis
3656	26988051	PP_1316	rpsI	30S ribosomal protein S9	5.7	2.67E-04	3g BuOH	11.7	14592	2	14%	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis
3656	26989959	PP_3241		hypothetical protein	5.7	2.67E-04	3g BuOH	6.0	18261	4	26%	Unknown	COG3652	Function unknown
3656	26991554	PP_4874	rplI	50S ribosomal protein L9	5.7	2.67E-04	3g BuOH	5.3	15466	5	24%	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis
3656	26987190	PP_0449	rpsL	30S ribosomal protein S12	5.7	2.67E-04	3g BuOH	11.7	13727	2	16%	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis
3656	26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	5.7	2.67E-04	3g BuOH	5.3	16898	3	21%	Cytoplasmic Membrane	COG0711	Energy production and conversion
3692	26990489	PP_3784		hypothetical protein	3	2.43E-04	3g BuOH	5.4	41070	10	23%	Unknown	COG0251	Translation, ribosomal structure and biogenesis
3692	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	3	2.43E-04	3g BuOH	5.5	63339	10	14%	Cytoplasmic	COG1960	Lipid metabolism
3692	26986947	PP_0203		hypothetical protein	3	2.43E-04	3g BuOH	5.9	62682	3	5%	Unknown	COG0624	Amino acid transport and metabolism
3692	26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	3	2.43E-04	3g BuOH	5.7	61082	24	41%	Cytoplasmic	COG0644	Energy production and conversion
3694	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.4	7.18E-04	3g BuOH	6.4	71796	4	7%	Cytoplasmic	COG0365	Lipid metabolism

5.2.1.2 Membranproteom-Analyse



1D-SDS-PAGE der Membranfraktion von mit 0,5 g/l bzw. 3 g/l Butanol behandelten und unbehandelten Zellen von *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.2.1.2 Membranfraktion_P_putida_KT2440_0.5g_3g_BuOH_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.9	6.16E-02	0,5 g Butanol	9.1	61919	12	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986790	PP_0045		CzcC family cobalt/zinc/cadmium efflux transporter outer membrane protein	1.8	4.26E-01	0,5 g Butanol	9.6	45844	2	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26986791	PP_0046		porin	1.2	6.70E-01	0,5 g Butanol	5.0	49397	22	Outer Membrane			
26986803	PP_0058		phospholipid/glycerol acyltransferase	3.3	8.53E-02	0,5 g Butanol	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	3.4	2.10E-02	0,5 g Butanol	7.3	50185	6	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	3.4	5.86E-02	0,5 g Butanol	6.3	71284	2	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	4.3	8.06E-02	0,5 g Butanol	7.8	51116	7	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	4.7	5.30E-02	0,5 g Butanol	7.7	78583	8	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986933	PP_0189	hemY	HemY domain protein	1.5	2.12E-01	0,5 g Butanol	9.6	46030	8	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	4.5	2.06E-01	0,5 g Butanol	11.3	32300	3	Cytoplasmic			
26986977	PP_0234	oprE	outer membrane porin	1.4	2.73E-01	0,5 g Butanol	5.4	48317	25	Outer Membrane			
26987010	PP_0268	oprQ	outer membrane porin	1.4	2.98E-01	0,5 g Butanol	6.1	47787	10	Outer Membrane			
26987029	PP_0287		AsmA family protein	3.9	1.00E-01	0,5 g Butanol	6.0	80277	3	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	4.9	1.92E-02	0,5 g Butanol	8.5	58780	2	Cytoplasmic Membrane			
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.4	7.58E-01	0,5 g Butanol	5.3	55654	2	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	2.1	1.74E-03	0,5 g Butanol	5.6	99332	4	Cytoplasmic	COG2609	Energy production and conversion	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.3	3.82E-01	0,5 g Butanol	11.4	8370	6	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987159	PP_0418		GDSL family lipase	2.3	1.29E-01	0,5 g Butanol	4.4	67175	7	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987184	PP_0443	rplK	50S ribosomal protein L11	1.3	3.46E-01	0,5 g Butanol	10.5	14866	4	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.2	8.54E-01	3 g Butanol	10.1	24251	4	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.4	4.98E-01	0,5 g Butanol	10.2	17686	8	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	1.9	5.32E-01	0,5 g Butanol	4.4	12599	2	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.9	6.80E-02	0,5 g Butanol	5.5	150992	13	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.3	4.48E-01	0,5 g Butanol	7.2	154797	34	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.8	2.16E-01	0,5 g Butanol	11.7	13727	2	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.6	3.17E-01	0,5 g Butanol	10.8	17578	12	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.8	2.22E-02	0,5 g Butanol	4.9	78817	18	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.3	1.64E-01	0,5 g Butanol	5.0	43478	23	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	1.4	7.29E-01	0,5 g Butanol	10.5	11753	2	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.3	4.83E-01	0,5 g Butanol	10.3	21811	5	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.8	8.30E-01	3 g Butanol	10.7	10900	4	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	2.6	1.76E-01	0,5 g Butanol	11.7	29669	11	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	4.2	1.14E-01	0,5 g Butanol	11.9	15373	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.7	1.01E-01	0,5 g Butanol	11.6	13410	9	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.4	3.80E-01	0,5 g Butanol	10.3	20329	9	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.6	2.41E-01	0,5 g Butanol	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.5	2.66E-01	0,5 g Butanol	10.2	13975	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.4	6.28E-01	3 g Butanol	10.4	19143	5	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.2	5.53E-01	3 g Butanol	10.9	12628	5	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.2	4.86E-01	0,5 g Butanol	10.6	17666	9	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.8	1.77E-01	0,5 g Butanol	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.8	1.51E-01	0,5 g Butanol	10.4	47853	4	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.2	4.72E-01	0,5 g Butanol	11.3	13256	8	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.3	3.78E-01	0,5 g Butanol	11.5	13660	5	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.7	1.72E-01	0,5 g Butanol	10.5	23056	12	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	2.1	5.48E-02	0,5 g Butanol	4.7	36629	4	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	3.4	6.00E-02	0,5 g Butanol	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.3	3.98E-01	3 g Butanol	4.6	17972	16	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.9	2.13E-01	0,5 g Butanol	4.8	24196	6	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.3	6.24E-01	0,5 g Butanol	5.9	55268	3	Cytoplasmic	COG1012	Energy production and conversion	
26987302	PP_0564		hypothetical protein	1.5	1.93E-01	0,5 g Butanol	6.6	40223	5	Unknown	COG5345	Function unknown	
26987308	PP_0570		alpha-2-macroglobulin domain protein	3.1	1.63E-01	0,5 g Butanol	5.2	178472	2	Unknown	COG2373	General function prediction only	
26987322	PP_0584		methyl-accepting chemotaxis transducer	2.9	4.19E-02	0,5 g Butanol	5.0	69953	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	3.9	5.48E-02	0,5 g Butanol	6.6	83475	7	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26987359	PP_0622		competence lipoprotein ComL	3.5	3.84E-02	0,5 g Butanol	4.8	38410	7	Unknown	COG4105	General function prediction only	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.5	1.65E-01	0,5 g Butanol	6.2	44897	3	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	3.1	1.18E-01	0,5 g Butanol	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	2.4	1.86E-01	0,5 g Butanol	4.6	63994	4	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	3.4	2.15E-02	0,5 g Butanol	8.4	54282	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.7	1.79E-01	0,5 g Butanol	9.5	20483	6	Unknown			
26987495	PP_0759		hypothetical protein	3.7	1.70E-02	0,5 g Butanol	7.0	29743	4	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987501	PP_0765		hypothetical protein	1.4	1.72E-01	0,5 g Butanol	5.0	67937	14	Outer Membrane			
26987509	PP_0773		OmpA/MotB domain protein	1.7	3.68E-01	0,5 g Butanol	9.5	24753	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.7	1.02E-01	0,5 g Butanol	6.7	34557	12	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	1.9	1.15E-01	0,5 g Butanol	7.8	74391	8	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	2.2	7.12E-02	0,5 g Butanol	9.6	66913	19	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	2.2	7.41E-02	0,5 g Butanol	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.0	8.30E-01	0,5 g Butanol	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP_0856		hypothetical protein	3.1	4.97E-02	0,5 g Butanol	4.7	40737	9	Outer Membrane	COG1520	Function unknown	
26987617	PP_0881	dppB	alkaline phosphatase	3.4	1.27E-01	0,5 g Butanol	8.4	36980	2	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987619	PP_0883		outer membrane porin	1.2	6.25E-01	0,5 g Butanol	6.6	50256	7	Outer Membrane			
26987645	PP_0909		hypothetical protein	3.8	5.27E-02	0,5 g Butanol	6.4	38380	5	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	2.4	1.21E-01	0,5 g Butanol	4.4	47019	7	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987651	PP_0915	sodB	superoxide dismutase	1.5	2.58E-01	0,5 g Butanol	5.8	21938	2	Periplasmic	COG0605	Inorganic ion transport and metabolism	
26987696	PP_0960	ttg2C	hypothetical protein	1.8	1.31E-01	0,5 g Butanol	4.6	16953	4	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	3.6	4.51E-02	0,5 g Butanol	5.1	107495	3	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987718	PP_0982		permease YjgP/YjgQ family protein	2.3	1.38E-01	0,5 g Butanol	9.7	41323	3	Cytoplasmic Membrane	COG0795	General function prediction only	

26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.1	9.02E-01	0,5 g Butanol	7.0	36057	9	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.1	8.87E-01	0,5 g Butanol	6.4	65359	6	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	4.7	1.34E-01	0,5 g Butanol	7.3	54020	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.6	2.89E-01	0,5 g Butanol	6.2	45449	5	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.6	4.67E-02	0,5 g Butanol	10.1	33781	6	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.5	1.39E-01	0,5 g Butanol	9.9	30428	3	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.1	5.96E-01	0,5 g Butanol	6.7	41895	9	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.7	7.99E-02	0,5 g Butanol	5.9	49646	34	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.4	3.18E-01	0,5 g Butanol	6.8	55000	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.5	4.92E-01	0,5 g Butanol	6.7	25476	6	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.3	4.06E-01	0,5 g Butanol	5.4	25004	2	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987796	PP_1060		glutamate synthase, large subunit	2.7	2.11E-01	0,5 g Butanol	8.1	59136	2	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.1	9.38E-01	3 g Butanol	8.2	27464	3	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	1.4	3.26E-01	3 g Butanol	4.4	17971	15	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.6	7.89E-02	0,5 g Butanol	4.9	21730	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987844	PP_1108		acylase	2.7	2.51E-02	0,5 g Butanol	8.7	88728	16	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.4	4.19E-01	3 g Butanol	5.0	24084	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.2	6.03E-01	3 g Butanol	9.3	15682	6	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987941	PP_1206	oprD	outer membrane porin	1.7	2.83E-02	0,5 g Butanol	4.6	46120	18	Outer Membrane			
26987944	PP_1209		cold-shock domain-contain protein	2.6	1.49E-01	0,5 g Butanol	11.4	10246	2	Cytoplasmic	COG1278	Transcription	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	2.6	6.05E-04	0,5 g Butanol	5.1	66568	7	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	3.9	1.27E-01	0,5 g Butanol	6.3	25310	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.9	2.81E-01	0,5 g Butanol	9.8	47431	4	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.0	9.58E-01	3 g Butanol	4.9	17833	14	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	2.9	2.59E-02	0,5 g Butanol	4.8	40784	4	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987980	PP_1245		hypothetical protein	3.5	3.52E-03	0,5 g Butanol	9.4	31144	10	Unknown			
26988044	PP_1309		hypothetical protein	3.4	2.11E-01	0,5 g Butanol	6.3	16018	4	Unknown	COG3105	Function unknown	
26988050	PP_1315	rplM	50S ribosomal protein L13	1.6	3.66E-01	0,5 g Butanol	10.3	15862	4	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.6	1.42E-01	0,5 g Butanol	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	3.3	5.57E-02	0,5 g Butanol	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	3.2	7.59E-02	0,5 g Butanol	7.1	29032	4	Unknown	COG2857	Energy production and conversion	
26988057	PP_1322		transport-associated protein	2.0	6.82E-02	0,5 g Butanol	9.8	20680	4	Periplasmic	COG2823	General function prediction only	
26988060	PP_1325		LppC family lipoprotein	1.9	1.16E-01	0,5 g Butanol	7.5	64637	19	Cytoplasmic Membrane	COG3107	General function prediction only	
26988068	PP_1334	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	1.2	5.47E-01	0,5 g Butanol	10.0	39307	2	Cytoplasmic Membrane	COG0472	Cell envelope biogenesis, outer membrane	
26988095	PP_1361	groEL	chaperonin GroEL	1.8	2.19E-01	3 g Butanol	4.7	56743	16	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	2.4	9.07E-01	3 g Butanol	6.7	52057	2	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	4.1	3.05E-02	0,5 g Butanol	4.8	67652	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	2.7	5.68E-02	0,5 g Butanol	9.6	52425	3	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988117	PP_1383		BenF-like porin	2.0	8.47E-02	0,5 g Butanol	6.8	46022	11	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	2.1	9.32E-02	3 g Butanol	5.1	52864	23	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.8	2.80E-01	3 g Butanol	5.3	112835	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988152	PP_1419		outer membrane porin	1.2	4.88E-01	0,5 g Butanol	4.9	46644	11	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	1.9	9.39E-02	0,5 g Butanol	9.2	32060	5	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.5	3.93E-01	0,5 g Butanol	6.0	86581	3	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	3.5	1.51E-02	0,5 g Butanol	9.0	45563	2	Cytoplasmic Membrane			
26988194	PP_1461	ffh	signal recognition particle protein	1.5	7.79E-01	0,5 g Butanol	10.7	58232	2	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.1	7.03E-01	0,5 g Butanol	11.0	13012	6	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	3.1	9.12E-02	0,5 g Butanol	6.2	51645	2	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	2.3	4.70E-02	0,5 g Butanol	4.7	58605	8	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988234	PP_1502		OmpA/MotB domain protein	84.7	4.76E-04	3 g Butanol	9.5	28964	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988235	PP_1503		hypothetical protein	53.3	5.86E-03	3 g Butanol	9.1	16837	2	Unknown			
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.4	3.52E-01	0,5 g Butanol	9.3	27023	17	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	2.1	5.16E-02	0,5 g Butanol	4.7	86513	16	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.3	3.04E-01	0,5 g Butanol	4.7	45490	2	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.8	1.61E-01	0,5 g Butanol	11.0	27506	4	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.9	1.22E-01	0,5 g Butanol	5.4	45693	10	Outer Membrane	COG2067	Lipid metabolism	
26988474	PP_1743	actP	acetate permease	3.0	2.58E-02	3 g Butanol	9.6	58972	3	Cytoplasmic Membrane	COG4147	General function prediction only	
26988568	PP_1838		hypothetical protein	3.0	1.07E-02	0,5 g Butanol	6.8	76615	11	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	2.8	3.74E-04	0,5 g Butanol	4.7	120904	8	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	2.1	4.72E-02	0,5 g Butanol	5.9	43290	6	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	2.4	1.18E-01	0,5 g Butanol	3.9	96918	14	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	2.8	1.66E-01	0,5 g Butanol	7.8	32510	2	Cytoplasmic	COG0777	Lipid metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.4	2.08E-01	0,5 g Butanol	4.8	86015	5	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.9	4.38E-02	0,5 g Butanol	5.8	29111	3	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.1	8.36E-01	3 g Butanol	4.5	37012	31	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988845	PP_2121		lipoprotein	3.3	1.97E-01	3 g Butanol	5.0	8131	2	Unknown			
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.2	5.85E-01	0,5 g Butanol	7.7	53014	9	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.9	2.53E-01	0,5 g Butanol	5.3	26061	8	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.7	9.26E-01	3 g Butanol	5.1	68646	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	6.4	2.36E-02	0,5 g Butanol	5.3	52127	9	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.2	8.18E-01	3 g Butanol	8.5	8801	4	Outer Membrane			
26989055	PP_2331		hypothetical protein	3.4	9.18E-02	0,5 g Butanol	7.9	57064	4	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	6.97E-01	0,5 g Butanol	5.0	93609	8	Cytoplasmic	COG1049	Energy production and conversion	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.5	4.01E-01	0,5 g Butanol	5.8	62191	2	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989191	PP_2468	rplT	50S ribosomal protein L20	4.1	1.81E-01	0,5 g Butanol	12.1	13280	6	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989381	PP_2662		hypothetical protein	5.3	9.27E-02	0,5 g Butanol	4.3	42858	14	Outer Membrane			
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11.3	2.31E-02	0,5 g Butanol	7.0	69173	6	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	4.5	3.71E-02	0,5 g Butanol	5.5	54903	13	Cytoplasmic	COG1012	Energy production and conversion	

5.2.1.2 Membranfraktion_P_putida_KT2440_0.5g_3g_BuOH_Tabelle

26989810	PP_3091		hypothetical protein	1.3	4.82E-01	0,5 g Butanol	6.8	138655	2	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and	vesicular transport
26989818	PP_3099		hypothetical protein	17.1	5.03E-04	3 g Butanol	4.9	56072	26	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and	vesicular transport
26989819	PP_3100		hypothetical protein	17.7	3.26E-04	3 g Butanol	7.7	21741	2	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and	vesicular transport
26990092	PP_3377		major facilitator transporter	1.2	9.44E-01	0,5 g Butanol	9.6	47449	3	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	1.5	2.10E-01	0,5 g Butanol	8.9	47532	10	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990294	PP_3582		RND efflux transporter	1.6	2.50E-01	0,5 g Butanol	5.2	53952	15	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990413	PP_3705		hypothetical protein	3.6	1.01E-01	0,5 g Butanol	9.0	43629	2	Cytoplasmic Membrane			
26990459	PP_3754		beta-ketothiolase	3.7	1.38E-01	0,5 g Butanol	6.9	40988	3	Cytoplasmic	COG0183	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	2.8	2.09E-01	0,5 g Butanol	4.9	129450	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	3.4	8.87E-04	0,5 g Butanol	6.4	41164	2	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777		hypothetical protein	9.1	2.30E-03	0,5 g Butanol	5.2	31324	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	2.1	8.61E-02	0,5 g Butanol	6.2	27714	3	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	3.4	3.00E-02	0,5 g Butanol	7.0	53071	10	Cytoplasmic	COG0635	Coenzyme metabolism	
26990488	PP_3783		hypothetical protein	9.2	3.51E-03	0,5 g Butanol	5.8	34938	4	Cytoplasmic			
26990489	PP_3784		hypothetical protein	2.4	4.78E-02	0,5 g Butanol	5.4	41070	5	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	6.8	7.15E-03	0,5 g Butanol	6.5	50495	3	Cytoplasmic			
26990491	PP_3786		aminotransferase	32.0	4.71E-01	0,5 g Butanol	6.4	44067	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990493	PP_3788		non-ribosomal peptide synthetase	23.4	2.46E-02	0,5 g Butanol	6.7	56336	2	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990627	PP_3922		periplasmic protease	2.0	3.04E-02	0,5 g Butanol	9.8	37502	3	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990695	PP_3990		hypothetical protein	1.3	7.95E-01	0,5 g Butanol	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	4.8	2.21E-01	0,5 g Butanol	6.4	91296	3	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.6	2.26E-01	3 g Butanol	5.4	79899	6	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	15.2	6.11E-02	0,5 g Butanol	5.9	50555	3	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990810	PP_4116	aceA	isocitrate lyase	7.1	2.16E-02	0,5 g Butanol	5.3	48633	5	Cytoplasmic	COG2224	Energy production and conversion	
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	2.3	8.32E-02	0,5 g Butanol	10.4	15085	5	Cytoplasmic Membrane	COG0838	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	3.6	4.70E-02	0,5 g Butanol	6.5	67609	2	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.3	1.87E-01	0,5 g Butanol	5.9	97582	3	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	3.3	2.60E-02	0,5 g Butanol	6.1	37637	4	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.4	3.82E-01	0,5 g Butanol	6.2	30111	8	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.3	3.22E-01	0,5 g Butanol	6.1	41239	15	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.3	3.39E-01	0,5 g Butanol	6.3	49912	5	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.9	5.59E-02	0,5 g Butanol	5.1	42434	6	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.2	3.93E-02	0,5 g Butanol	6.5	106521	8	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.9	1.74E-01	0,5 g Butanol	7.5	26000	2	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	3.3	6.28E-02	0,5 g Butanol	6.2	63448	3	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	3.6	1.29E-01	3 g Butanol	9.0	13579	5	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	2.2	1.70E-01	0,5 g Butanol	10.3	13813	2	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.2	4.77E-01	0,5 g Butanol	9.7	26361	5	Unknown	COG2086	Energy production and conversion	
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.2	4.13E-01	0,5 g Butanol	5.5	89725	14	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	3.5	3.05E-02	0,5 g Butanol	9.6	53567	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	3.1	1.72E-02	0,5 g Butanol	5.2	35613	8	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	2.7	6.92E-02	0,5 g Butanol	8.5	53406	4	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	1.5	2.32E-01	0,5 g Butanol	6.0	35312	9	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991012	PP_4322	ccmF	cytochrome c-type biogenesis protein CcmF	3.8	8.60E-02	0,5 g Butanol	9.7	72089	2	Cytoplasmic Membrane	COG1138	Posttranslational modification, protein turnover, chaperones	
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	5.0	7.37E-02	0,5 g Butanol	10.1	17847	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
26991067	PP_4378	fliC	flagellin FliC	1.2	7.67E-01	3 g Butanol	4.2	67846	2	Extracellular	COG1344	Cell motility and secretion	
26991159	PP_4473		aspartate kinase	1.4	7.88E-01	0,5 g Butanol	5.0	44605	2	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.1	9.07E-01	0,5 g Butanol	5.1	94711	2	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991173	PP_4487	acsA	acetyl-CoA synthetase	1.9	1.91E-01	0,5 g Butanol	6.4	71796	11	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.0	8.06E-01	0,5 g Butanol	5.4	50393	25	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.1	9.95E-01	0,5 g Butanol	10.3	48478	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991254	PP_4570		hypothetical protein	3.6	6.26E-02	0,5 g Butanol	10.1	35846	3	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991266	PP_4582		hypothetical protein	2.1	1.22E-01	0,5 g Butanol	9.5	18552	2	Cytoplasmic Membrane			
26991325	PP_4641	cstA	carbon starvation protein CstA	1.6	1.28E-01	0,5 g Butanol	9.0	73763	8	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991353	PP_4669		OmpA/MotB domain protein	4.2	3.86E-02	0,5 g Butanol	9.9	18241	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.5	1.36E-01	0,5 g Butanol	5.4	36370	7	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	1.6	5.43E-01	0,5 g Butanol	6.3	17784	2	Cytoplasmic	COG0440	Amino acid transport and metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.4	3.66E-01	0,5 g Butanol	6.8	62781	2	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991395	PP_4712	infB	translation initiation factor IF-2	1.1	9.48E-01	3 g Butanol	6.8	91460	7	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.9	6.71E-02	0,5 g Butanol	5.4	69722	18	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.8	1.10E-02	0,5 g Butanol	4.6	68800	6	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991414	PP_4731	omlA	SmpA/OmlA domain protein	2.8	5.30E-03	0,5 g Butanol	4.4	19586	2	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	5.4	7.91E-02	0,5 g Butanol	8.5	56126	2	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane	
26991475	PP_4795		rare lipoprotein B	2.6	1.17E-03	0,5 g Butanol	6.1	22414	8	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991478	PP_4798		lytic murein transglycosylase	3.6	1.19E-02	0,5 g Butanol	7.7	48000	5	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991484	PP_4804		rare lipoprotein A family	4.8	9.72E-02	0,5 g Butanol	10.0	35869	2	Unknown	COG0797	Cell envelope biogenesis, outer membrane	
26991556	PP_4876	rpsR	30S ribosomal protein S18	2.3	1.65E-02	0,5 g Butanol	11.3	8927	5	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991557	PP_4877	rpsF	30S ribosomal protein S6	1.3	5.85E-01	0,5 g Butanol	4.7	16373	2	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.2	8.80E-01	3 g Butanol	7.9	96688	2	Cytoplasmic	COG0557	Transcription	
26991569	PP_4891	hflC	HflC protein	1.6	2.44E-01	0,5 g Butanol	9.8	33001	11	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	5.2	7.25E-02	0,5 g Butanol	5.1	44762	2	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991572	PP_4894	hfq	RNA-binding protein Hfq	1.0	8.70E-01	0,5 g Butanol	9.0	9462	2	Cytoplasmic	COG1923	General function prediction only	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.8	2.40E-01	0,5 g Butanol	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991588	PP_4910		hypothetical protein	2.6	4.75E-02	0,5 g Butanol	4.7	53632	7	Cytoplasmic	COG3726	General function prediction only	
26991599	PP_4921		NCS1 nucleoside transporter	2.6	8.47E-02	0,5 g Butanol	8.1	44950	2	Cytoplasmic Membrane	COG1457	Nucleotide transport and metabolism	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.2	9.80E-01	3 g Butanol	5.2	52637	10	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	2.1	5.31E-02	0,5 g Butanol	7.6	66279	2	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.8	2.03E-02	0,5 g Butanol	5.1	42779	3	Cytoplasmic	COG0192	Coenzyme metabolism	

5.2.1.2 Membranfraktion_P_putida_KT2440_0.5g_3g_BuOH_Tabelle

26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.1	6.13E-01	0,5 g Butanol	5.7	49982	2	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.9	5.10E-01	0,5 g Butanol	10.9	26214	3	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	4.2	2.89E-02	0,5 g Butanol	4.9	69017	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	2.9	1.18E-01	0,5 g Butanol	8.3	95875	6	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991720	PP_5044		GTP-binding protein TypA	1.8	2.49E-01	0,5 g Butanol	5.3	67157	4	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.7	2.81E-02	0,5 g Butanol	5.1	51740	9	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991731	PP_5055		rhodanese domain-containing protein	2.6	6.59E-02	0,5 g Butanol	9.9	14839	2	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	4.7	1.69E-03	0,5 g Butanol	6.2	161772	6	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	1.5	1.49E-01	0,5 g Butanol	4.9	45127	5	Cytoplasmic	COG0281	Energy production and conversion	
26991766	PP_5090		sporulation domain protein	2.3	2.63E-01	0,5 g Butanol	10.6	24964	2	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	1.1	6.09E-01	0,5 g Butanol	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	2.4	7.87E-02	0,5 g Butanol	6.5	36984	2	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991815	PP_5139	cadA-2	heavy metal translocating P-type ATPase	1.2	4.90E-01	0,5 g Butanol	6.5	79328	3	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	2.6	6.50E-02	0,5 g Butanol	6.3	44339	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.9	3.43E-02	0,5 g Butanol	12.3	8922	3	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991980	PP_5304		lipoprotein	4.1	3.62E-02	0,5 g Butanol	5.1	26284	2	Unknown			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.8	5.00E-02	0,5 g Butanol	5.3	65626	8	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	2.1	2.78E-02	0,5 g Butanol	6.5	51942	5	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.8	1.21E-01	3 g Butanol	7.2	30672	6	Cytoplasmic Membrane	COG4395	Function unknown	
26992055	PP_5379	copB	copper resistance B precursor	2.0	5.23E-02	0,5 g Butanol	5.0	40230	8	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	6.88E-01	3 g Butanol	4.6	49359	10	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.3	5.61E-01	0,5 g Butanol	9.2	31464	4	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.3	5.39E-01	0,5 g Butanol	5.2	55352	12	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	2.2	2.79E-02	0,5 g Butanol	5.3	16898	8	Cytoplasmic Membrane	COG0711	Energy production and conversion	
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	3.1	2.86E-01	0,5 g Butanol	6.7	31712	2	Cytoplasmic Membrane	COG0356	Energy production and conversion	
313496770				1.8	1.32E-01	0,5 g Butanol			13				
313498866				1.5	1.45E-01	0,5 g Butanol			11				
24983268				1.7	2.72E-02	0,5 g Butanol			11				
24981833				1.1	6.86E-01	0,5 g Butanol			8				
24981839				1.8	1.99E-01	0,5 g Butanol			8				
148550051				1.9	3.20E-03	0,5 g Butanol			6				
15599454				2.1	1.03E-01	0,5 g Butanol			5				
24986476				1.8	5.26E-02	0,5 g Butanol			5				
24982083				1.3	6.66E-01	0,5 g Butanol			5				
339485705				3.3	4.04E-02	0,5 g Butanol			4				
262385099				2.5	1.51E-02	0,5 g Butanol			3				
24982932				1.4	4.56E-01	0,5 g Butanol			2				
148549576				1.6	2.02E-01	0,5 g Butanol			2				
104779763				3.4	6.00E-02	0,5 g Butanol			2				
170722689				1.7	9.58E-01	0,5 g Butanol			2				
128169				1.4	4.63E-01	3 g Butanol			2				

5.2.1.2 Membranfraktion_P_putida_KT2440_0.5g_BuOH_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.1	6.50E-01	control	9.1	61919	13	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.3	6.69E-01	control	4.9	40718	2	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986790	PP_0045		CzcC family cobalt/zinc/cadmium efflux transporter outer membrane protein	1.0	6.31E-01	0,5 g BuOH	9.6	45844	2	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26986791	PP_0046		porin	1.1	5.71E-01	control	5.0	49397	23	Outer Membrane			
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.1	6.22E-01	0,5 g BuOH	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986856	PP_0111		electron transport protein SCO1/SenC	1.4	2.97E-01	0,5 g BuOH	8.2	22960	3	Cytoplasmic Membrane	COG1999	General function prediction only	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.0	9.54E-01	control	7.3	50185	7	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.3	4.98E-01	control	6.3	71284	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.2	7.03E-01	0,5 g BuOH	7.8	51116	7	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.1	9.89E-01	control	7.7	78583	10	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986933	PP_0189	hemY	HemY domain protein	1.0	9.66E-01	control	9.6	46030	7	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	1.0	9.18E-01	0,5 g BuOH	11.3	32300	4	Cytoplasmic			
26986977	PP_0234	oprE	outer membrane porin	1.0	9.26E-01	control	5.4	48317	30	Outer Membrane			
26987010	PP_0268	oprQ	outer membrane porin	1.0	9.00E-01	control	6.1	47787	12	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.4	3.31E-01	0,5 g BuOH	6.0	80277	5	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	3.2	2.19E-02	0,5 g BuOH	8.5	58780	2	Cytoplasmic Membrane			
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.3	6.40E-01	control	5.3	55654	3	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.2	7.58E-01	control	5.6	99332	6	Cytoplasmic	COG2609	Energy production and conversion	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.0	7.84E-01	0,5 g BuOH	11.4	8370	6	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987159	PP_0418		GDSL family lipase	1.1	7.33E-01	0,5 g BuOH	4.4	67175	8	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987184	PP_0443	rplK	50S ribosomal protein L11	1.3	7.80E-01	control	10.5	14866	7	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.5	6.70E-01	control	10.1	24251	4	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.2	7.41E-01	control	10.2	17686	9	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	1.2	6.72E-01	control	4.4	12599	3	Unknown	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.1	9.62E-01	control	5.5	150992	17	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.3	8.34E-01	control	7.2	154797	35	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.2	4.12E-01	control	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.1	6.72E-01	control	10.8	17578	15	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.1	5.23E-01	0,5 g BuOH	4.9	78817	21	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.1	6.67E-01	0,5 g BuOH	5.0	43478	25	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	1.2	6.95E-01	control	10.5	11753	2	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.2	8.37E-01	control	10.3	21811	8	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.6	3.89E-01	control	10.7	10900	4	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.1	7.73E-01	control	11.7	29669	12	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.1	8.39E-01	control	11.9	15373	6	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.4	3.04E-01	control	11.6	13410	11	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.3	5.05E-01	control	10.3	20329	12	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.3	1.40E-01	control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.3	4.01E-01	control	10.2	13975	6	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.8	5.85E-01	control	10.4	19143	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.5	3.18E-01	control	10.9	12628	6	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.4	3.49E-01	control	10.6	17666	9	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.6	2.77E-01	control	11.5	15189	7	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.2	6.84E-01	control	10.4	47853	7	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.4	1.51E-01	control	11.3	13256	8	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.5	2.70E-02	control	11.5	13660	5	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.2	5.55E-01	control	10.5	23056	15	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.0	7.55E-01	0,5 g BuOH	4.7	36629	6	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.2	7.67E-01	control	11.3	14363	5	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.2	5.26E-01	control	4.6	17972	16	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987236	PP_0496		amino acid carrier protein	1.2	5.66E-01	control	9.0	51685	2	Cytoplasmic Membrane	COG1115	Amino acid transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.1	8.91E-01	0,5 g BuOH	4.8	24196	5	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.8	3.06E-01	0,5 g BuOH	5.9	55268	2	Cytoplasmic	COG1012	Energy production and conversion	
26987302	PP_0564		hypothetical protein	1.0	9.92E-01	control	6.6	40223	5	Unknown	COG5345	Function unknown	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.2	7.28E-01	control	5.0	69953	17	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	1.2	4.05E-01	0,5 g BuOH	6.6	83475	8	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26987359	PP_0622		competence lipoprotein ComL	1.6	1.02E-01	0,5 g BuOH	4.8	38410	8	Unknown	COG4105	General function prediction only	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.2	5.33E-01	control	6.2	44897	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	1.0	7.37E-01	0,5 g BuOH	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	1.1	8.26E-01	0,5 g BuOH	4.6	63994	4	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.2	8.70E-01	control	8.4	54282	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.0	9.70E-01	control	9.5	20483	6	Unknown			
26987495	PP_0759		hypothetical protein	1.2	3.25E-01	0,5 g BuOH	7.0	29743	3	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987501	PP_0765		hypothetical protein	1.4	3.50E-02	control	5.0	67937	18	Outer Membrane			
26987509	PP_0773		OmpA/MotB domain protein	1.5	3.82E-01	0,5 g BuOH	9.5	24753	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.3	1.72E-01	0,5 g BuOH	6.7	34557	12	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	1.1	5.91E-01	0,5 g BuOH	7.8	74391	8	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.0	9.32E-01	control	9.6	66913	21	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.1	9.65E-01	0,5 g BuOH	4.8	32758	4	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.2	6.71E-01	control	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP_0856		hypothetical protein	1.4	3.10E-01	0,5 g BuOH	4.7	40737	8	Outer Membrane	COG1520	Function unknown	
26987617	PP_0881	dppB	alkaline phosphatase	1.2	8.00E-01	control	8.4	36980	2	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987619	PP_0883		outer membrane porin	1.6	1.19E-01	control	6.6	50256	10	Outer Membrane			
26987645	PP_0909		hypothetical protein	1.4	2.89E-01	0,5 g BuOH	6.4	38380	7	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.1	8.70E-01	0,5 g BuOH	4.4	47019	6	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987651	PP_0915	sodB	superoxide dismutase	1.0	8.95E-01	0,5 g BuOH	5.8	21938	2	Periplasmic	COG0605	Inorganic ion transport and metabolism	
26987696	PP_0960	ttg2C	hypothetical protein	1.2	4.02E-01	0,5 g BuOH	4.6	16953	4	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	

26987713	PP_0977	valS	valyl-tRNA synthetase	1.8	3.09E-02	0,5 g BuOH	5.1	107495	2	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.3	3.09E-01	0,5 g BuOH	9.7	41323	3	Cytoplasmic Membrane	COG0795	General function prediction only	
26987719	PP_0983		permease YjgP/YjgQ family protein	1.3	4.33E-01	0,5 g BuOH	7.1	38733	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.5	4.53E-01	control	7.0	36057	9	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.2	5.29E-01	control	6.4	65359	5	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	1.2	7.89E-01	0,5 g BuOH	7.3	54020	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.2	6.43E-01	control	6.2	45449	4	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.5	8.80E-02	control	10.1	33781	8	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.3	2.10E-01	control	9.9	30428	3	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.5	2.23E-01	control	6.7	41895	8	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.2	1.76E-01	control	5.9	49646	42	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.1	9.78E-01	control	6.8	55000	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.1	8.19E-01	control	6.7	25476	6	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.2	8.47E-01	control	5.4	25004	4	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987796	PP_1060		glutamate synthase, large subunit	1.1	8.85E-01	control	8.1	59136	3	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.0	9.39E-01	control	8.2	27464	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	1.2	4.73E-01	control	4.4	17971	15	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.2	6.15E-01	0,5 g BuOH	4.9	21730	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987844	PP_1108		acylase	1.2	3.45E-01	0,5 g BuOH	8.7	88728	16	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.1	8.09E-01	control	5.0	24084	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.4	4.15E-01	0,5 g BuOH	9.3	15682	5	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.2	6.53E-01	control	5.7	106948	2	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987923	PP_1188	dctA	C4-dicarboxylate transporter DctA	1.2	2.35E-01	0,5 g BuOH	8.8	46298	2	Cytoplasmic Membrane	COG1301	Energy production and conversion	
26987941	PP_1206	oprD	outer membrane porin	1.4	2.27E-01	control	4.6	46120	22	Outer Membrane			
26987944	PP_1209		cold-shock domain-contain protein	1.5	4.50E-01	0,5 g BuOH	11.4	10246	2	Cytoplasmic	COG1278	Transcription	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.1	6.40E-01	0,5 g BuOH	5.1	66568	7	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.1	7.99E-01	control	6.3	25310	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.3	4.34E-01	control	9.8	47431	4	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.0	9.11E-01	control	4.9	17833	16	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	1.1	4.64E-01	0,5 g BuOH	4.8	40784	4	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987980	PP_1245		hypothetical protein	1.1	3.52E-01	control	9.4	31144	10	Unknown			
26987984	PP_1249		hypothetical protein	1.4	4.41E-01	control	9.3	6714	2	Unknown			
26988044	PP_1309		hypothetical protein	1.6	7.12E-01	control	6.3	16018	3	Unknown	COG3105	Function unknown	
26988050	PP_1315	rplM	50S ribosomal protein L13	1.4	3.16E-01	control	10.3	15862	4	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.5	9.02E-02	control	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.1	4.88E-01	0,5 g BuOH	8.4	45901	4	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.0	9.64E-01	control	7.1	29032	5	Unknown	COG2857	Energy production and conversion	
26988057	PP_1322		transport-associated protein	1.2	2.28E-01	control	9.8	20680	4	Periplasmic	COG2823	General function prediction only	
26988060	PP_1325		LppC family lipoprotein	1.1	5.46E-01	0,5 g BuOH	7.5	64637	22	Cytoplasmic Membrane	COG3107	General function prediction only	
26988068	PP_1334	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	1.0	9.79E-01	0,5 g BuOH	10.0	39307	2	Cytoplasmic Membrane	COG0472	Cell envelope biogenesis, outer membrane	
26988087	PP_1353		MscS mechanosensitive ion channel	1.1	5.39E-01	0,5 g BuOH	7.5	30804	2	Cytoplasmic Membrane	COG0668	Cell envelope biogenesis, outer membrane	
26988093	PP_1359	fxsA	FxsA	1.2	7.37E-01	control	10.6	16958	3	Cytoplasmic Membrane	COG3030	General function prediction only	
26988095	PP_1361	groEL	chaperonin GroEL	1.2	6.50E-01	control	4.7	56743	13	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.0	9.47E-01	0,5 g BuOH	4.8	67652	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	1.0	9.09E-01	control	9.6	52425	4	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988117	PP_1383		BenF-like porin	1.8	8.63E-02	control	6.8	46022	12	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.4	2.67E-02	0,5 g BuOH	5.1	52864	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.5	6.27E-02	0,5 g BuOH	5.3	112835	2	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988152	PP_1419		outer membrane porin	1.0	7.29E-01	0,5 g BuOH	4.9	46644	10	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	1.2	2.76E-01	control	9.2	32060	4	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.0	8.73E-01	0,5 g BuOH	6.0	86581	4	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	1.0	9.10E-01	0,5 g BuOH	9.0	45563	3	Cytoplasmic Membrane			
26988194	PP_1461	ffh	signal recognition particle protein	1.1	9.15E-01	0,5 g BuOH	10.7	58232	2	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.3	5.83E-01	control	11.0	13012	8	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	1.1	6.73E-01	0,5 g BuOH	6.2	51645	3	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.1	9.49E-01	control	4.7	58605	8	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.7	5.51E-01	control	9.3	27023	19	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.2	1.56E-01	0,5 g BuOH	4.7	86513	18	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.4	5.69E-01	control	4.7	45490	2	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.0	9.29E-01	control	11.0	27506	5	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.1	5.12E-01	control	5.4	45693	11	Outer Membrane	COG2067	Lipid metabolism	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.2	8.07E-01	0,5 g BuOH	4.8	26520	4	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988474	PP_1743	actP	acetate permease	4.5	2.18E-02	0,5 g BuOH	9.6	58972	2	Cytoplasmic Membrane	COG4147	General function prediction only	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.1	7.89E-01	control	6.4	40124	2	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988568	PP_1838		hypothetical protein	1.2	3.84E-01	0,5 g BuOH	6.8	76615	10	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.3	7.38E-01	control	4.7	120904	9	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.0	8.42E-01	control	5.9	43290	8	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.3	9.76E-01	control	4.8	38824	2	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.2	7.77E-01	control	3.9	96918	15	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.4	5.95E-01	control	7.8	32510	2	Cytoplasmic	COG0777	Lipid metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.0	7.52E-01	0,5 g BuOH	4.8	86015	3	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.1	6.50E-01	0,5 g BuOH	5.8	29111	3	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.0	9.91E-01	control	4.5	37012	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.2	9.01E-01	control	7.7	53014	13	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.2	9.24E-01	control	5.3	26061	8	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.0	6.26E-01	0,5 g BuOH	5.1	68646	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	1.1	8.03E-01	control	5.3	52127	13	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.0	8.09E-01	0,5 g BuOH	8.5	8801	9	Outer Membrane			

26989055	PP_2331		hypothetical protein	1.2	5.29E-01	0,5 g BuOH	7.9	57064	5	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	6.07E-01	0,5 g BuOH	5.0	93609	8	Cytoplasmic	COG1049	Energy production and conversion	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.3	4.88E-01	control	5.8	62191	3	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989189	PP_2466	infC	translation initiation factor IF-3	1.4	8.09E-01	control	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.2	9.66E-01	0,5 g BuOH	12.1	13280	7	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989381	PP_2662		hypothetical protein	2.2	2.23E-01	0,5 g BuOH	4.3	42858	14	Outer Membrane			
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	15.2	2.07E-02	0,5 g BuOH	7.0	69173	6	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	11.6	5.37E-03	0,5 g BuOH	5.5	54903	13	Cytoplasmic	COG1012	Energy production and conversion	
26989810	PP_3091		hypothetical protein	1.4	4.14E-01	0,5 g BuOH	6.8	138655	2	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	1.0	8.98E-01	0,5 g BuOH	5.7	26868	2	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989818	PP_3099		hypothetical protein	1.6	3.94E-01	0,5 g BuOH	4.9	56072	4	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989887	PP_3168	benF	benzoate-specific porin	2.3	1.31E-01	control	5.6	45611	3	Outer Membrane			
26990092	PP_3377		major facilitator transporter	1.4	3.58E-01	0,5 g BuOH	9.6	47449	3	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	1.3	2.41E-01	control	8.9	47532	10	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990294	PP_3582		RND efflux transporter	1.1	6.28E-01	0,5 g BuOH	5.2	53952	15	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990296	PP_3585		efflux transporter RND family, MFP subunit	1.5	9.68E-01	0,5 g BuOH	9.4	46468	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990459	PP_3754		beta-ketothiolase	150.9	3.06E-02	0,5 g BuOH	6.9	40988	3	Cytoplasmic	COG0183	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.0	8.80E-01	control	4.9	129450	5	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	1.1	9.15E-01	control	6.4	41164	4	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777		hypothetical protein	1.2	5.48E-01	0,5 g BuOH	5.2	31324	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	1.1	7.73E-01	0,5 g BuOH	6.2	27714	3	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	1.3	6.72E-01	control	7.0	53071	11	Cytoplasmic	COG0635	Coenzyme metabolism	
26990488	PP_3783		hypothetical protein	1.0	8.91E-01	control	5.8	34938	4	Cytoplasmic			
26990489	PP_3784		hypothetical protein	1.1	9.24E-01	control	5.4	41070	7	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	1.2	3.78E-01	0,5 g BuOH	6.5	50495	3	Cytoplasmic			
26990491	PP_3786		aminotransferase	1.1	6.36E-01	control	6.4	44067	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990493	PP_3788		non-ribosomal peptide synthetase	1.2	5.81E-01	0,5 g BuOH	6.7	56336	2	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990627	PP_3922		periplasmic protease	1.2	4.87E-01	0,5 g BuOH	9.8	37502	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	1.2	3.25E-01	0,5 g BuOH	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.9	1.19E-01	control	5.4	79899	7	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.2	9.28E-01	0,5 g BuOH	5.9	50555	3	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990810	PP_4116	aceA	isocitrate lyase	9.2	2.35E-02	0,5 g BuOH	5.3	48633	5	Cytoplasmic	COG2224	Energy production and conversion	
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	1.1	9.44E-01	control	10.4	15085	5	Cytoplasmic Membrane	COG0838	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.1	5.32E-01	0,5 g BuOH	6.5	67609	2	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.0	8.43E-01	control	5.9	97582	4	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	1.1	7.74E-01	0,5 g BuOH	6.1	37637	3	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.1	8.40E-01	control	6.2	30111	7	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.1	9.79E-01	control	6.1	41239	17	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.1	9.41E-01	control	6.3	49912	6	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.5	6.43E-01	control	5.1	42434	5	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.4	3.98E-01	control	6.5	106521	10	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	2.1	2.89E-01	control	7.5	26000	2	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.0	8.71E-01	0,5 g BuOH	6.2	63448	5	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.0	9.82E-01	control	9.0	13579	5	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.1	4.54E-01	0,5 g BuOH	10.3	13813	2	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990891	PP_4199		lipoprotein	1.5	9.13E-01	0,5 g BuOH	5.3	13080	2	Unknown			
26990894	PP_4202		electron transfer flavoprotein, beta subunit	2.0	1.14E-01	0,5 g BuOH	9.7	26361	5	Unknown	COG2086	Energy production and conversion	
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.1	9.04E-01	0,5 g BuOH	5.5	89725	11	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990944	PP_4253	ccoP-1	cytochrome c oxidase, cbb3-type, subunit III	1.0	9.33E-01	control	5.3	33915	3	Unknown	COG2010	Energy production and conversion	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	2.4	4.41E-02	0,5 g BuOH	9.6	53567	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.7	8.59E-02	0,5 g BuOH	5.2	35613	9	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	1.2	9.22E-01	control	8.5	53406	4	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	1.3	3.28E-01	control	6.0	35312	11	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991012	PP_4322	ccmF	cytochrome c-type biogenesis protein CcmF	1.5	3.79E-01	0,5 g BuOH	9.7	72089	2	Cytoplasmic Membrane	COG1138	Posttranslational modification, protein turnover, chaperones	
26991048	PP_4359	fliL	flagellar basal body-associated protein FliL	1.1	8.87E-01	0,5 g BuOH	10.1	17847	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
26991067	PP_4378	fliC	flagellin FliC	1.2	9.25E-01	control	4.2	67846	2	Extracellular	COG1344	Cell motility and secretion	
26991159	PP_4473		aspartate kinase	1.1	6.79E-01	control	5.0	44605	2	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	5.4	8.90E-03	0,5 g BuOH	6.4	71796	9	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.0	7.19E-01	0,5 g BuOH	5.4	50393	30	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.2	6.93E-01	0,5 g BuOH	10.3	48478	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991254	PP_4570		hypothetical protein	1.0	9.14E-01	0,5 g BuOH	10.1	35846	5	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991266	PP_4582		hypothetical protein	1.1	8.01E-01	control	9.5	18552	2	Cytoplasmic Membrane			
26991325	PP_4641	cstA	carbon starvation protein CstA	1.2	2.50E-01	control	9.0	73763	9	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.8	2.19E-01	control	4.8	68764	2	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991353	PP_4669		OmpA/MotB domain protein	1.1	6.04E-01	0,5 g BuOH	9.9	18241	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.2	4.64E-01	0,5 g BuOH	5.4	36370	7	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	1.0	9.63E-01	control	6.3	17784	2	Cytoplasmic	COG0440	Amino acid transport and metabolism	
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.1	8.47E-01	control	6.8	62781	3	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.2	7.51E-01	control	4.9	75010	2	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.3	8.75E-01	control	6.8	91460	7	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.0	9.96E-01	control	5.4	69722	21	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.1	4.94E-01	0,5 g BuOH	4.6	68800	7	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991414	PP_4731	omlA	SmpA/OmlA domain protein	1.0	9.23E-01	control	4.4	19586	2	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	1.3	9.43E-01	0,5 g BuOH	8.5	56126	3	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane	
26991475	PP_4795		rare lipoprotein B	1.0	8.36E-01	control	6.1	22414	10	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991478	PP_4798		lytic murein transglycosylase	2.1	5.32E-02	0,5 g BuOH	7.7	48000	4	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991484	PP_4804		rare lipoprotein A family	1.4	1.72E-01	0,5 g BuOH	10.0	35869	2	Unknown	COG0797	Cell envelope biogenesis, outer membrane	
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	1.2	7.53E-01	control	5.0	31015	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	

26991556	PP_4876	rpsR	30S ribosomal protein S18	1.1	6.64E-01	control	11.3	8927	6	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991557	PP_4877	rpsF	30S ribosomal protein S6	1.1	7.23E-01	0,5 g BuOH	4.7	16373	2	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.4	5.88E-01	0,5 g BuOH	7.9	96688	2	Cytoplasmic	COG0557	Transcription	
26991569	PP_4891	hflC	HflC protein	1.1	6.23E-01	control	9.8	33001	10	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.3	7.09E-01	0,5 g BuOH	5.1	44762	2	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991572	PP_4894	hfq	RNA-binding protein Hfq	1.4	9.15E-01	control	9.0	9462	2	Cytoplasmic	COG1923	General function prediction only	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.4	2.09E-01	0,5 g BuOH	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991588	PP_4910		hypothetical protein	1.0	8.04E-01	0,5 g BuOH	4.7	53632	8	Cytoplasmic	COG3726	General function prediction only	
26991589	PP_4911		hypothetical protein	1.3	5.40E-01	0,5 g BuOH	8.5	27337	2	Periplasmic	COG3009	Function unknown	
26991599	PP_4921		NCS1 nucleoside transporter	1.3	3.23E-01	control	8.1	44950	2	Cytoplasmic Membrane	COG1457	Nucleotide transport and metabolism	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.2	6.00E-01	control	5.2	52637	12	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.2	2.94E-01	0,5 g BuOH	7.6	66279	4	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.1	4.47E-01	0,5 g BuOH	5.1	42779	4	Cytoplasmic	COG0192	Coenzyme metabolism	
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	1.8	8.29E-01	control	10.7	68073	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.4	8.45E-01	control	5.7	49982	2	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.0	8.91E-01	0,5 g BuOH	10.9	26214	2	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.3	5.12E-01	control	4.9	69017	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.2	7.75E-01	control	8.3	95875	6	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991720	PP_5044		GTP-binding protein TypA	1.0	8.12E-01	0,5 g BuOH	5.3	67157	5	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.1	7.03E-01	control	5.1	51740	7	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991731	PP_5055		rhodanese domain-containing protein	1.1	7.46E-01	control	9.9	14839	3	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.2	4.83E-01	0,5 g BuOH	6.2	161772	7	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	1.1	5.03E-01	control	4.9	45127	5	Cytoplasmic	COG0281	Energy production and conversion	
26991766	PP_5090		sporulation domain protein	1.1	7.84E-01	control	10.6	24964	3	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	1.1	5.98E-01	0,5 g BuOH	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	1.1	6.61E-01	0,5 g BuOH	6.5	36984	3	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991815	PP_5139	cadA-2	heavy metal translocating P-type ATPase	1.0	8.22E-01	control	6.5	79328	3	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.4	6.11E-01	control	6.3	44339	3	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.1	6.09E-01	0,5 g BuOH	12.3	8922	3	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991980	PP_5304		lipoprotein	1.2	6.78E-01	control	5.1	26284	2	Unknown			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.2	8.72E-01	control	5.3	65626	12	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.2	6.74E-01	control	6.5	51942	6	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.0	8.98E-01	control	7.2	30672	4	Cytoplasmic Membrane	COG4395	Function unknown	
26992055	PP_5379	copB	copper resistance B precursor	1.1	7.52E-01	control	5.0	40230	10	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	7.68E-01	control	4.6	49359	12	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.1	8.90E-01	control	9.2	31464	5	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.1	9.28E-01	control	5.2	55352	12	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.1	4.89E-01	0,5 g BuOH	5.3	16898	9	Cytoplasmic Membrane	COG0711	Energy production and conversion	
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	2.3	5.59E-01	0,5 g BuOH	6.7	31712	2	Cytoplasmic Membrane	COG0356	Energy production and conversion	
313496770				1.1	6.38E-01	control			15				
313498866				1.0	9.05E-01	control			11				
24981839				1.1	9.90E-01	control			10				
24981833				1.4	7.01E-01	control			9				
24982083				1.9	5.81E-01	control			7				
15599454				1.2	5.77E-01	control			6				
339485705				1.2	5.29E-01	control			5				
24982932				1.3	5.18E-01	control			2				
148549148				1.1	6.05E-01	0,5 g BuOH			9				
148550051				1.0	7.15E-01	0,5 g BuOH			5				
24986476				1.2	4.38E-01	0,5 g BuOH			5				
262385099				1.2	4.03E-01	0,5 g BuOH			3				
128169				1.2	9.23E-01	0,5 g BuOH			2				
104779763				1.3	4.12E-01	0,5 g BuOH			2				

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	2.1	2.81E-02	control	9.1	61919	10	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986775	PP_0030		sensor histidine kinase	3.2	1.06E-01	control	6.35	52113.4	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986791	PP_0046		porin	1.3	1.29E-01	control	5.04	49397.3	21	Outer Membrane			
26986803	PP_0058		phospholipid/glycerol acyltransferase	4.9	7.10E-02	control	10.03	29093.8	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986856	PP_0111		electron transport protein SCO1/SenC	3.0	1.56E-01	control	8.18	22960.2	2	Cytoplasmic Membrane	COG1999	General function prediction only	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	4.8	5.70E-03	control	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	3.2	1.01E-01	control	7.79	51116.4	3	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	5.6	5.58E-02	control	7.7	78583	9	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986933	PP_0189	hemY	HemY domain protein	1.6	3.01E-01	control	9.57	46030.2	8	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	4.5	1.61E-01	control	11.31	32300.1	4	Cytoplasmic			
26986977	PP_0234	oprE	outer membrane porin	1.5	2.35E-01	control	5.43	48316.7	30	Outer Membrane			
26987010	PP_0268	oprQ	outer membrane porin	1.4	2.40E-01	control	6.12	47786.5	11	Outer Membrane			
26987029	PP_0287		AsmA family protein	2.7	1.10E-01	control	5.96	80276.5	4	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.0	1.89E-01	control	5.27	55653.7	4	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	3.4	5.83E-02	control	5.6	99332	5	Cytoplasmic	COG2609	Energy production and conversion	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.1	8.13E-01	3 g Butanol	11.44	8369.7	5	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987159	PP_0418		GDSL family lipase	2.1	1.28E-01	control	4.43	67174.9	8	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987184	PP_0443	rplK	50S ribosomal protein L11	1.5	4.79E-01	control	10.48	14866	6	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.3	7.62E-01	control	10.12	24250.8	4	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.7	2.77E-01	control	10.16	17686.2	8	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	2.1	1.64E-01	control	5.52	150991.5	11	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.7	4.04E-01	control	7.21	154796.9	31	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	2.3	7.89E-02	control	11.7	13726.8	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.8	1.18E-01	control	10.8	17578.3	13	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.8	1.07E-01	control	4.88	78817.1	20	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.3	2.04E-01	control	5.02	43478.4	21	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.6	3.97E-01	control	10.34	21810.8	9	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.2	8.02E-01	3 g Butanol	10.67	10899.6	5	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	3.1	9.53E-02	control	11.72	29669	11	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	4.8	7.79E-02	control	11.92	15373.1	4	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	2.5	2.73E-02	control	11.6	13410	10	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	2.0	1.51E-01	control	10.34	20328.5	8	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	2.2	4.34E-02	control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.9	8.61E-02	control	10.16	13975.2	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.0	9.23E-01	control	10.37	19142.9	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.7	1.95E-01	control	10.88	12627.5	7	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.8	1.66E-01	control	10.63	17666.4	8	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987213	PP_0472	rpmD	50S ribosomal protein L30	1.6	6.35E-02	control	10.6	6452	2	Cytoplasmic	COG1841	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	3.1	5.61E-02	control	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	2.7	5.69E-02	control	10.4	47853	7	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.8	5.10E-02	control	11.3	13256	6	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	2.1	8.81E-02	control	11.48	13659.6	5	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	2.0	4.17E-02	control	10.5	23056	15	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	2.1	9.99E-02	control	4.65	36629.3	4	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	4.6	5.75E-02	control	11.3	14363	5	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.1	3.51E-01	3 g Butanol	4.55	17972.3	17	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.8	8.54E-02	control	4.77	24196.4	4	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.9	6.38E-02	3 g Butanol	5.9	55268	2	Cytoplasmic	COG1012	Energy production and conversion	
26987302	PP_0564		hypothetical protein	1.6	1.60E-01	control	6.58	40223.2	3	Unknown	COG5345	Function unknown	
26987322	PP_0584		methyl-accepting chemotaxis transducer	3.9	3.66E-02	control	5.0	69953	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	3.9	9.21E-02	control	6.58	83474.6	6	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26987359	PP_0622		competence lipoprotein ComL	2.3	1.02E-01	control	4.81	38409.6	5	Unknown	COG4105	General function prediction only	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.4	3.17E-01	control	6.19	44896.8	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	2.9	2.08E-01	control	9.89	92123.5	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	1.9	2.58E-01	control	4.61	63994	3	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	2.2	3.49E-01	control	8.42	54281.9	4	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.9	2.08E-01	control	9.48	20483.1	6	Unknown			
26987495	PP_0759		hypothetical protein	3.3	1.96E-02	control	7.0	29743	2	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987501	PP_0765		hypothetical protein	2.3	1.43E-02	control	5.0	67937	16	Outer Membrane			
26987509	PP_0773		OmpA/MotB domain protein	1.1	6.35E-01	control	9.51	24753.4	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.3	3.90E-01	control	6.69	34556.6	9	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	1.7	8.48E-02	control	7.84	74391.2	8	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	2.3	6.68E-02	control	9.55	66913	20	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	2.0	4.66E-02	control	4.8	32758	4	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.2	6.15E-01	control	5.27	15043.9	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP_0856		hypothetical protein	2.2	1.96E-01	control	4.66	40736.5	6	Outer Membrane	COG1520	Function unknown	
26987619	PP_0883		outer membrane porin	2.0	7.62E-02	control	6.59	50256.1	10	Outer Membrane			
26987645	PP_0909		hypothetical protein	3.7	7.78E-02	control	6.37	38380.3	5	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	2.3	2.92E-01	control	4.37	47018.9	3	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.5	4.61E-01	control	6.99	36056.7	11	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.7	1.86E-01	control	6.43	65359.3	4	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	2.1	2.71E-01	control	7.33	54020	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.4	3.87E-01	control	6.17	45448.5	4	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	2.3	9.02E-03	control	10.1	33781	6	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	2.4	4.01E-03	control	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	2.0	1.63E-01	control	6.67	41895.1	6	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	2.2	4.14E-02	control	5.9	49646	39	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	2.0	1.63E-01	control	6.75	55000.3	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.8	2.93E-01	control	6.72	25476.1	6	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.6	3.49E-01	control	5.36	25003.9	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.0	8.85E-01	3 g Butanol	8.16	27464.2	4	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	1.1	4.25E-01	3 g Butanol	4.44	17971.4	17	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.3	1.60E-01	control	4.86	21729.5	2	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.4	4.41E-01	control	5.13	45164	2	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987844	PP_1108		acylase	2.4	5.99E-02	control	8.7	88728	8	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.2	6.93E-01	3 g Butanol	4.95	24083.7	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.6	2.28E-01	3 g Butanol	9.25	15681.7	6	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987941	PP_1206	oprD	outer membrane porin	2.5	2.91E-02	control	4.6	46120	24	Outer Membrane			

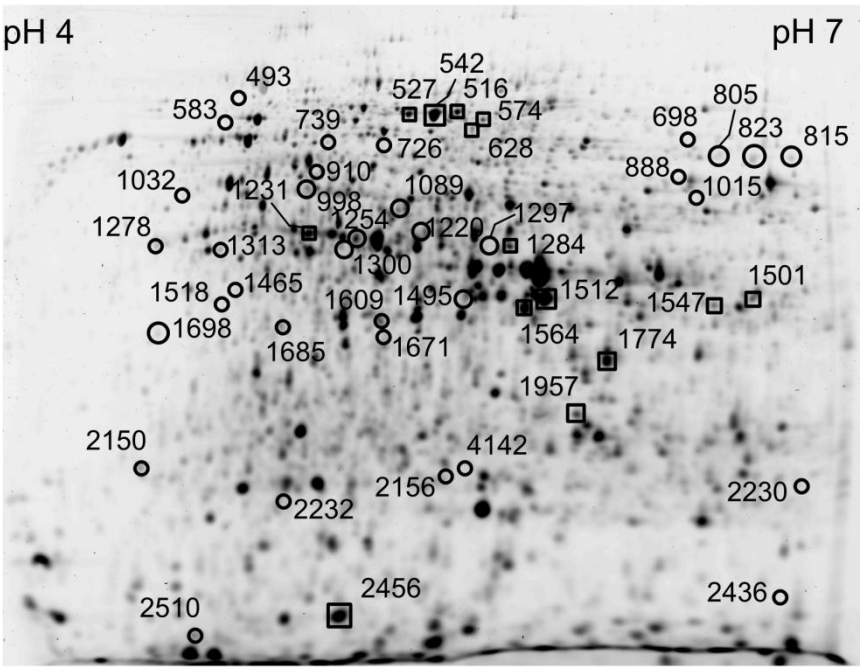
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.4	2.07E-01	control	5.14	66567.5	3	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis
26987957	PP_1222	tolB	translocation protein TolB	3.0	7.48E-02	control	9.77	47430.5	2	Unknown	COG0823	Intracellular trafficking and secretion
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.0	9.46E-01	control	4.88	17832.8	16	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26987973	PP_1238		lipoprotein	3.0	2.54E-02	control	4.8	40784	4	Unknown	COG3317	Cell envelope biogenesis, outer membrane
26987980	PP_1245		hypothetical protein	3.9	2.44E-03	control	9.4	31144	10	Unknown		
26987984	PP_1249		hypothetical protein	3.4	2.72E-02	control	9.3	6714	2	Unknown		
26988044	PP_1309		hypothetical protein	3.1	6.52E-01	control	6.25	16018.1	2	Unknown	COG3105	Function unknown
26988050	PP_1315	rplM	50S ribosomal protein L13	1.3	6.03E-01	control	10.27	15862.3	3	Unknown	COG0102	Translation, ribosomal structure and biogenesis
26988051	PP_1316	rpsI	30S ribosomal protein S9	2.3	4.38E-03	control	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	3.8	3.36E-02	control	8.4	45901	2	Cytoplasmic Membrane	COG1290	Energy production and conversion
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	2.7	1.09E-01	control	7.11	29032.3	6	Unknown	COG2857	Energy production and conversion
26988057	PP_1322		transport-associated protein	2.2	1.06E-01	control	9.81	20679.7	2	Periplasmic	COG2823	General function prediction only
26988060	PP_1325		LppC family lipoprotein	1.7	1.87E-01	control	7.5	64636.9	17	Cytoplasmic Membrane	COG3107	General function prediction only
26988068	PP_1334	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	1.6	2.30E-01	control	9.95	39306.6	2	Cytoplasmic Membrane	COG0472	Cell envelope biogenesis, outer membrane
26988093	PP_1359	fxsA	FxsA	2.4	1.45E-01	control	10.56	16958	2	Cytoplasmic Membrane	COG3030	General function prediction only
26988095	PP_1361	groEL	chaperonin GroEL	1.5	3.51E-01	3 g Butanol	4.69	56742.8	17	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones
26988096	PP_1362	pykA	pyruvate kinase	1.1	5.42E-01	control	6.68	52057.2	2	Cytoplasmic	COG0469	Carbohydrate transport and metabolism
26988105	PP_1371		methyl-accepting chemotaxis transducer	4.0	3.90E-02	control	4.8	67652	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion
26988107	PP_1373		phosphate transporter	2.7	6.34E-02	control	9.6	52425	4	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism
26988117	PP_1383		BenF-like porin	4.2	5.56E-04	control	6.8	46022	12	Outer Membrane		
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	2.8	3.39E-02	3 g Butanol	5.1	52864	23	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	2.7	7.88E-02	3 g Butanol	5.32	112834.7	6	Cytoplasmic Membrane	COG0841	Defense mechanisms
26988152	PP_1419		outer membrane porin	1.3	4.11E-01	control	4.85	46643.5	11	Outer Membrane		
26988165	PP_1432	lepB	signal peptidase I	2.4	4.93E-02	control	9.2	32060	5	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.5	4.93E-01	control	6.04	86580.6	4	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism
26988191	PP_1458		metabolite-proton symporter	3.0	3.07E-02	control	9.0	45563	3	Cytoplasmic Membrane		
26988194	PP_1461	ffh	signal recognition particle protein	2.1	5.13E-01	control	10.67	58231.7	2	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion
26988198	PP_1465	rplS	50S ribosomal protein L19	1.5	4.01E-01	control	10.96	13012	7	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis
26988204	PP_1471	thrC	threonine synthase	2.8	4.89E-02	control	6.2	51645	2	Cytoplasmic	COG0498	Amino acid transport and metabolism
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	2.8	6.24E-02	control	4.7	58605	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion
26988234	PP_1502		OmpA/MotB domain protein	128.1	1.91E-05	3 g Butanol	9.5	28964	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26988323	PP_1591	rpsB	30S ribosomal protein S2	2.6	2.53E-01	control	9.25	27022.8	18	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis
26988331	PP_1599		surface antigen family outer membrane protein	2.0	8.82E-02	control	4.71	86513.3	13	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane
26988344	PP_1612	eno	phosphopyruvate hydratase	1.1	6.80E-01	control	4.67	45489.9	2	Cytoplasmic	COG0148	Carbohydrate transport and metabolism
26988354	PP_1622	nlpD	peptidase M23B	1.9	1.15E-01	control	11.01	27505.8	2	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane
26988421	PP_1689		aromatic hydrocarbon degradation protein	2.2	5.22E-02	control	5.4	45693	10	Outer Membrane	COG2067	Lipid metabolism
26988474	PP_1743	actP	acetate permease	17.1	5.49E-02	3 g Butanol	9.6	58972	3	Cytoplasmic Membrane	COG4147	General function prediction only
26988568	PP_1838		hypothetical protein	2.6	7.91E-02	control	6.81	76614.7	7	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	4.4	1.71E-01	control	4.71	120904.4	6	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	2.4	1.10E-01	control	5.89	43289.9	7	Cytoplasmic	COG1448	Amino acid transport and metabolism
26988719	PP_1993		peptidoglycan-binding LysM	2.7	1.20E-01	control	3.85	96918.4	12	Unknown	COG3170	Cell motility and secretion
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.2	9.30E-01	control	4.78	86015.1	3	Cytoplasmic	COG0574	Carbohydrate transport and metabolism
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.9	7.87E-02	control	5.84	29111.4	3	Cytoplasmic Membrane		
26988814	PP_2089	oprF	OmpF family protein	1.1	9.80E-01	3 g Butanol	4.49	37011.5	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26988845	PP_2121		lipoprotein	4.2	1.55E-01	3 g Butanol	5.02	8131.2	2	Unknown		
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.5	4.89E-01	control	7.72	53013.8	9	Cytoplasmic	COG0057	Carbohydrate transport and metabolism
26988887	PP_2163	vacJ	VacJ family lipoprotein	2.2	3.29E-01	control	5.34	26061.3	8	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	5.3	4.18E-02	control	5.3	52127	9	Unknown	COG0840	Cell motility and secretion
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.1	8.27E-01	3 g Butanol	8.5	8800.7	10	Outer Membrane		
26989055	PP_2331		hypothetical protein	2.8	1.08E-01	control	7.92	57064.4	4	Cytoplasmic Membrane		
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.2	6.60E-01	3 g Butanol	4.97	93609.1	6	Cytoplasmic	COG1049	Energy production and conversion
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.9	2.30E-01	control	5.76	62190.8	3	Cytoplasmic	COG0155	Inorganic ion transport and metabolism
26989189	PP_2466	infC	translation initiation factor IF-3	1.1	5.99E-01	3 g Butanol	9.96	20120.3	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis
26989191	PP_2468	rplT	50S ribosomal protein L20	4.2	7.70E-02	control	12.13	13279.7	4	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis
26989381	PP_2662		hypothetical protein	2.4	5.01E-01	control	4.3	42857.9	12	Outer Membrane		
26989399	PP_2680		aldehyde dehydrogenase family protein	3.5	1.42E-01	3 g Butanol	5.51	54903.3	3	Cytoplasmic	COG1012	Energy production and conversion
26989811	PP_3092		hypothetical protein	1.4	5.56E-01	3 g Butanol	5.72	26867.6	2	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport
26989818	PP_3099		hypothetical protein	16.2	3.40E-04	3 g Butanol	4.9	56072	27	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport
26989819	PP_3100		hypothetical protein	16.5	2.58E-03	3 g Butanol	7.7	21741	2	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport
26989887	PP_3168	benF	benzoate-specific porin	7.6	1.90E-02	control	5.6	45611	3	Outer Membrane		
26990092	PP_3377		major facilitator transporter	1.6	4.12E-01	control	9.58	47448.5	2	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism
26990130	PP_3417	gntP	gluconate transporter	2.1	5.24E-03	control	8.9	47532	9	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism
26990294	PP_3582		RND efflux transporter	1.4	4.31E-01	control	5.21	53951.8	11	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane
26990466	PP_3761		multi-sensor hybrid histidine kinase	3.4	9.44E-02	control	4.86	129450.2	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms
26990480	PP_3775		sarcosine oxidase	4.5	5.09E-02	control	6.4	41164	4	Cytoplasmic	COG0665	Amino acid transport and metabolism
26990482	PP_3777		hypothetical protein	8.0	2.86E-02	control	5.2	31324	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	1.9	1.53E-01	control	6.24	27714.4	3	Cytoplasmic	COG0345	Amino acid transport and metabolism
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	4.8	3.29E-02	control	7.0	53071	10	Cytoplasmic	COG0635	Coenzyme metabolism
26990488	PP_3783		hypothetical protein	8.6	4.98E-03	control	5.8	34938	3	Cytoplasmic		
26990489	PP_3784		hypothetical protein	3.3	3.30E-02	control	5.4	41070	4	Unknown	COG0251	Translation, ribosomal structure and biogenesis
26990627	PP_3922		periplasmic protease	1.7	3.45E-01	control	9.78	37501.8	3	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones
26990695	PP_3990		hypothetical protein	1.2	5.57E-01	control	8.41	24356.4	2	Cytoplasmic Membrane	COG0670	General function prediction only
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.2	6.62E-01	control	5.37	79899.2	8	Cytoplasmic	COG2838	Energy production and conversion
26990721	PP_4016	purB	adenylosuccinate lyase	2.3	1.69E-01	control	5.93	50555.2	2	Cytoplasmic	COG0015	Nucleotide transport and metabolism
26990813	PP_4119	nuoA	NADH dehydrogenase subunit A	2.4	1.36E-01	control	10.38	15084.7	5	Cytoplasmic Membrane	COG0838	Energy production and conversion
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.7	2.52E-01	control	5.94	97581.5	3	Unknown	COG1034	Energy production and conversion
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	1.7	2.01E-01	control	6.11	37637.3	4	Cytoplasmic Membrane	COG1005	Energy production and conversion
26990871	PP_4179	htpG	heat shock protein 90	2.0	9.47E-01	control	5	71610.3	3	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.5	1.61E-01	control	6.24	30110.6	7	Cytoplasmic	COG0074	Energy production and conversion
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.4	3.38E-01	control	6.12	41239.1	15	Cytoplasmic	COG0045	Energy production and conversion
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.4	5.03E-01	control	6.26	49912.1	7	Cytoplasmic	COG1249	Energy production and conversion
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	2.6	1.41E-01	control	5.08	42434.4	4	Cytoplasmic	COG0508	Energy production and conversion
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.7	7.86E-02	control	6.54	106520.9	5	Cytoplasmic	COG0567	Energy production and conversion
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	2.0	4.36E-03	control	6.2	63448	4	Cytoplasmic Membrane	COG1053	Energy production and conversion
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	3.2	1.50E-01	3 g Butanol	9.04	13578.9	4	Cytoplasmic Membrane	COG2142	Energy production and conversion
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	2.1	1.41E-01	control	10.3	13812.7	2	Cytoplasmic Membrane	COG2009	Energy production and conversion
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.6	2.55E-01	3 g Butanol	9.66	26360.5	4	Unknown	COG2086	Energy production and conversion
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.4	3.16E-01	control	5.45	89724.7	14	Outer Membrane	COG4773	Inorganic ion transport and metabolism
26990944	PP_4253	ccoP-1	cytochrome c oxidase, cbb3-type, subunit III	1.7	1.66E-01	control	5.34	33915.1	7	Unknown	COG2010	Energy production and conversion

26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	1.6	3.10E-01	control	9.55	53566.6	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	2.4	2.20E-01	control	5.17	35613.1	2	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	4.6	7.23E-02	control	8.45	53405.6	3	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	2.1	1.09E-01	control	6.02	35311.5	10	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991067	PP_4378	fliC	flagellin FliC	1.7	6.92E-01	control	4.19	67846.1	2	Extracellular	COG1344	Cell motility and secretion	
26991173	PP_4487	acsA	acetyl-CoA synthetase	2.5	1.79E-01	3 g Butanol	6.35	71796.1	5	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.0	7.75E-01	control	5.42	50393.3	27	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.1	8.59E-01	control	10.25	48477.7	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991254	PP_4570		hypothetical protein	3.4	1.04E-01	control	10.11	35846	5	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991266	PP_4582		hypothetical protein	2.3	1.35E-01	control	9.5	18552.3	2	Cytoplasmic Membrane			
26991325	PP_4641	cstA	carbon starvation protein CstA	2.0	2.53E-02	control	9.0	73763	8	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991353	PP_4669		OmpA/MotB domain protein	4.3	3.27E-02	control	9.9	18241	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.5	1.15E-01	control	5.44	36370.2	6	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991363	PP_4679	ilvH	acetolactate synthase 3 regulatory subunit	1.8	3.60E-01	control	6.27	17784.3	2	Cytoplasmic	COG0440	Amino acid transport and metabolism	
26991395	PP_4712	infB	translation initiation factor IF-2	1.2	9.61E-01	control	6.82	91460.2	8	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.9	7.65E-02	control	5.38	69722.3	22	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991414	PP_4731	omlA	SmpA/OmlA domain protein	3.1	6.52E-03	control	4.4	19586	2	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991475	PP_4795		rare lipoprotein B	2.7	7.63E-03	control	6.1	22414	8	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991556	PP_4876	rpsR	30S ribosomal protein S18	3.3	1.53E-03	control	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991569	PP_4891	hflC	HflC protein	1.9	1.34E-01	control	9.82	33001.2	9	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991588	PP_4910		hypothetical protein	3.0	8.59E-02	control	4.67	53631.7	4	Cytoplasmic	COG3726	General function prediction only	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.2	5.94E-01	control	5.24	52637	10	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.9	8.19E-02	control	7.63	66279.1	3	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.6	1.47E-01	control	5.14	42779	3	Cytoplasmic	COG0192	Coenzyme metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.6	9.99E-01	control	5.74	49981.7	2	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	5.2	2.62E-02	control	4.9	69017	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	4.4	1.12E-01	control	8.26	95875.1	3	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991720	PP_5044		GTP-binding protein TypA	1.5	9.15E-01	control	5.28	67157.1	4	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.6	1.07E-01	control	5.07	51740.1	6	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991731	PP_5055		rhodanese domain-containing protein	3.3	1.11E-01	control	9.85	14839.3	3	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	2.8	3.81E-02	control	6.2	161772	2	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	1.6	6.46E-02	control	4.9	45127	5	Cytoplasmic	COG0281	Energy production and conversion	
26991766	PP_5090		sporulation domain protein	2.6	1.61E-01	control	10.58	24963.7	2	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	1.6	3.67E-01	control	9.85	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	2.3	1.09E-01	control	6.54	36983.6	2	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991815	PP_5139	cadA-2	heavy metal translocating P-type ATPase	1.3	4.69E-01	control	6.47	79327.9	3	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	2.0	3.73E-01	control	6.3	44338.5	3	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.9	6.62E-02	control	12.29	8922.4	3	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991980	PP_5304		lipoprotein	4.1	1.07E-02	control	5.1	26284	2	Unknown			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.2	1.77E-01	control	5.33	65625.9	7	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	2.7	6.98E-02	control	6.45	51941.8	5	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.7	1.86E-01	3 g Butanol	7.17	30671.5	6	Cytoplasmic Membrane	COG4395	Function unknown	
26992055	PP_5379	copB	copper resistance B precursor	2.2	4.03E-02	control	5.0	40230	9	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	9.18E-01	control	4.63	49358.8	10	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.4	8.38E-01	control	9.22	31464.1	5	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.5	3.90E-01	control	5.16	55351.8	12	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	2.1	5.02E-02	control	5.3	16898	9	Cytoplasmic Membrane	COG0711	Energy production and conversion	
15599454				2.8	6.54E-02	control			5				
24982932				1.9	1.10E-01	control			2				
148550051				1.5	1.14E-01	control			2				
148547806				1.6	1.16E-01	control			8				
313496770				2.0	1.31E-01	control			13				
24986476				1.7	1.71E-01	control			3				
262385099				1.9	1.71E-01	control			3				
24981839				2.2	1.78E-01	control			10				
104779763				2.7	2.51E-01	control			2				
148549148				1.6	2.57E-01	control			8				
24982083				2.7	3.38E-01	control			6				
24981833				1.6	4.54E-01	control			7				
170722689				1.3	9.87E-01	control			2				
128169				1.6	4.27E-01	3 g Butanol			3				

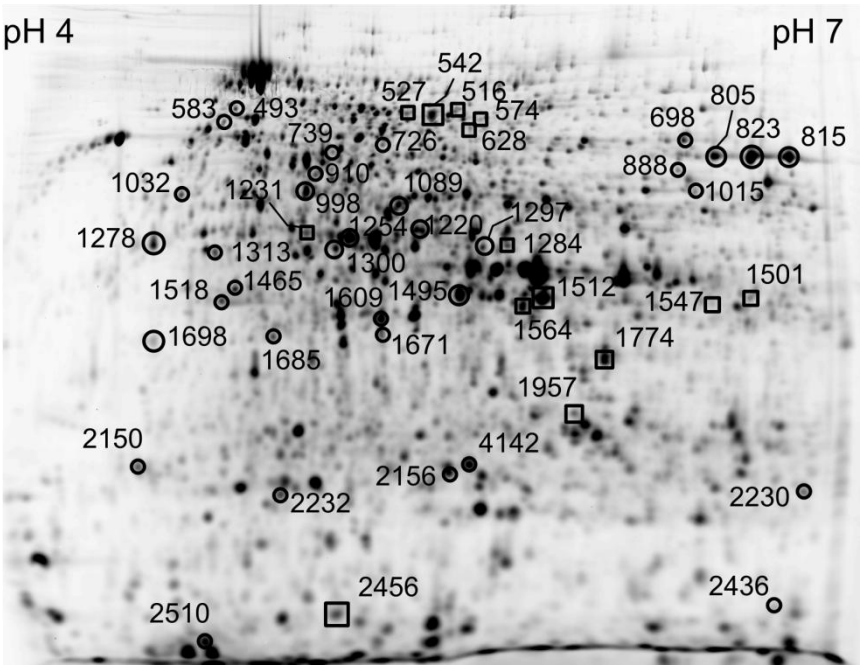
5.2.3 Bioreaktor

5.2.3.1 2D-DIGE-Analyse

A)



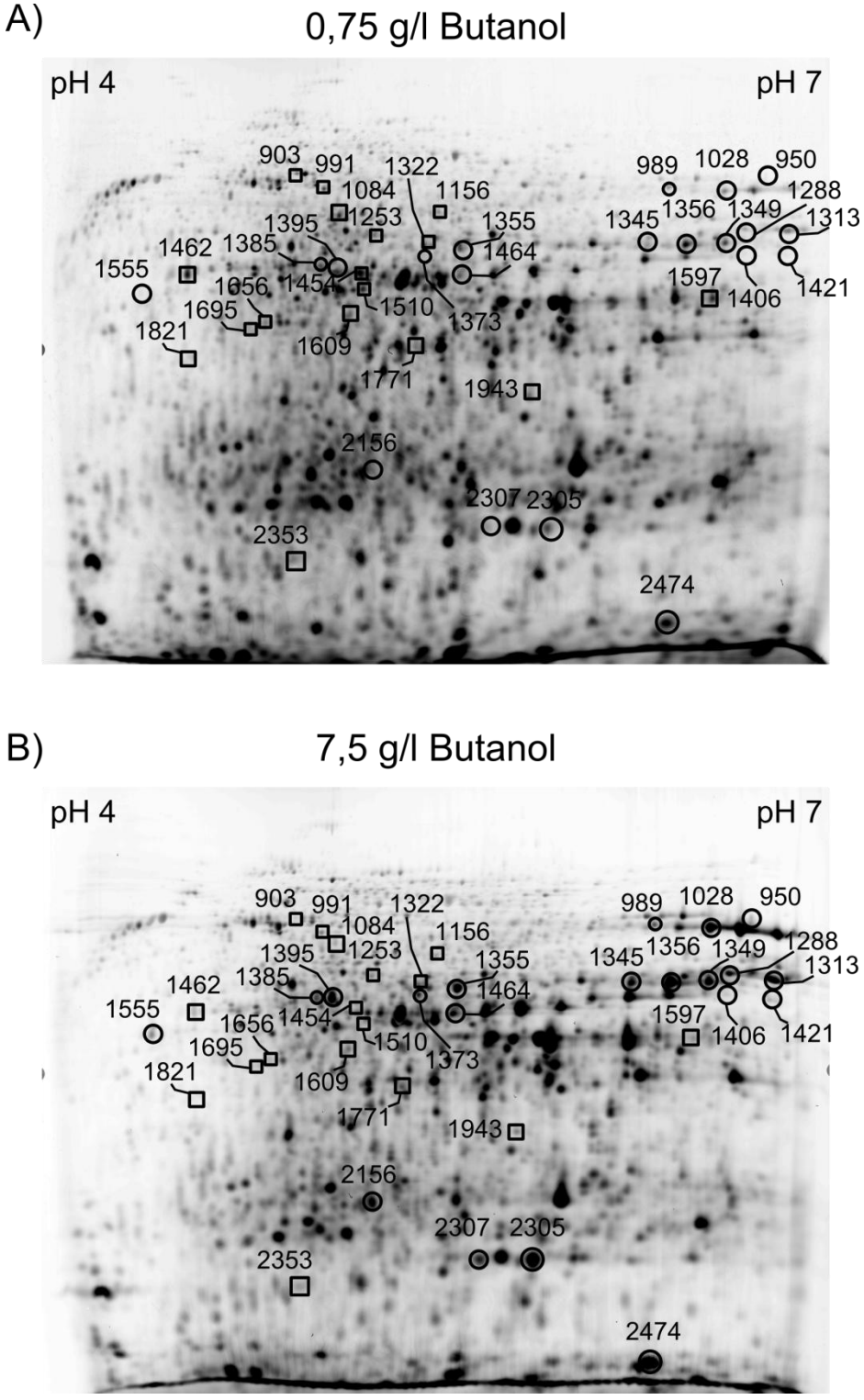
B)



Differenziell regulierte Spots zwischen mit 0,75 g/l Butanol (im Feedmedium) behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 0,75 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.2.3.1 2D_DIGE_P_putida_KT2440_0.75g_BuOH_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
516	26988393	PP_1661		dehydrogenase subunit	4.1	1.29E-02	control	5.5	81020	24	34%	Extracellular	COG2303	Amino acid transport and metabolism	
527	26988393	PP_1661		dehydrogenase subunit	3.3	1.69E-02	control	5.5	81020	28	40%	Extracellular	COG2303	Amino acid transport and metabolism	
542	26988393	PP_1661		dehydrogenase subunit	4.8	4.52E-03	control	5.5	81020	23	39%	Extracellular	COG2303	Amino acid transport and metabolism	
574	26988393	PP_1661		dehydrogenase subunit	2.5	7.37E-03	control	5.5	81020	23	33%	Extracellular	COG2303	Amino acid transport and metabolism	
628	26992056	PP_5380	copA	copper resistance protein A	2.0	7.75E-03	control	6.0	74225	8	10%	Periplasmic	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
698	26991173	PP_4487	acsA	acetyl-CoA synthetase	6.0	1.54E-02	0,75 g BuOH	6.4	71796	12	19%	Cytoplasmic	COG0365	Lipid metabolism	
805	26987746	PP_1010	edd	phosphogluconate dehydratase	7.4	3.41E-02	0,75 g BuOH	6.4	65359	3	8%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
805	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	7.4	3.41E-02	0,75 g BuOH	7.0	69173	24	37%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
815	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	14.0	2.94E-02	0,75 g BuOH	7.0	69173	20	31%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
823	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	14.0	2.64E-02	0,75 g BuOH	7.0	69173	25	36%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
888	374320134	not in database		succinate dehydrogenase flavoprotein subunit	8.0	1.59E-02	0,75 g BuOH			4	6%				
888	26990265	PP_3553		acyl-CoA synthetase	8.0	1.59E-02	0,75 g BuOH	6.4	59576	7	13%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
910	26991739	PP_5063	betB	betaine aldehyde dehydrogenase	2.2	3.72E-03	0,75 g BuOH	4.8	52986	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
998	308069359	not in database		glutamine synthetase	3.1	1.65E-02	0,75 g BuOH			4	11%				
998	26988391	PP_1659		hypothetical protein	3.1	1.65E-02	0,75 g BuOH	5.9	48336	5	11%	Periplasmic			
998	304406967	not in database		RNA binding S1 domain protein	3.1	1.65E-02	0,75 g BuOH			3	7%				
998	26991410	PP_4727	dnaK	molecular chaperone DnaK	3.1	1.65E-02	0,75 g BuOH	4.6	68800	4	6%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
1032	26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	5.0	1.08E-02	0,75 g BuOH	4.6	69396	3	5%	Cytoplasmic	COG0568	Transcription	
1089	26990705	PP_4000	serS	seryl-tRNA synthetase	2.7	3.56E-02	0,75 g BuOH	5.1	46849	4	9%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
1089	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.7	3.56E-02	0,75 g BuOH	5.2	55352	13	24%	Cytoplasmic	COG0056	Energy production and conversion	
1089	262039014	not in database		glucose-6-phosphate isomerase	2.7	3.56E-02	0,75 g BuOH			2	5%				
1089	26991936	PP_5260		hypothetical protein	2.7	3.56E-02	0,75 g BuOH	5.1	51372	9	19%	Cytoplasmic	COG5383	Function unknown	
1089	26987948	PP_1213	aspS	aspartyl-tRNA synthetase	2.7	3.56E-02	0,75 g BuOH	5.1	66568	2	3%	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
1220	253576627	not in database		6-phosphogluconate dehydrogenase	3.3	9.30E-03	0,75 g BuOH			3	6%				
1220	304407346	not in database		Glutamate dehydrogenase (NADP(+))	3.3	9.30E-03	0,75 g BuOH			2	5%				
1231	26988391	PP_1659		hypothetical protein	2.2	1.78E-02	control	5.9	48336	14	40%	Periplasmic			
1231	26987193	PP_0452	tuf	elongation factor Tu	2.2	1.78E-02	control	5.0	43478	2	5%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1231	26989818	PP_3099		hypothetical protein	2.2	1.78E-02	control	4.9	56072	2	4%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
1231	26988344	PP_1612	eno	phosphopyruvate hydratase	2.2	1.78E-02	control	4.7	45490	2	4%	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
1254	26991761	PP_5085	maeB	malic enzyme	2.6	1.11E-02	0,75 g BuOH	4.9	45127	2	5%	Cytoplasmic	COG0281	Energy production and conversion	
1254	310830363	not in database		ranslation elongation factor Tu	2.6	1.11E-02	0,75 g BuOH			12	30%				
1254	26987193	PP_0452	tuf	elongation factor Tu	2.6	1.11E-02	0,75 g BuOH	5.0	43478	8	28%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1254	26988391	PP_1659		hypothetical protein	2.6	1.11E-02	0,75 g BuOH	5.9	48336	5	14%	Periplasmic			
1278	26991077	PP_4388	flgE	flagellar hook protein FlgE	4.3	2.89E-03	0,75 g BuOH	4.3	45796	6	20%	Extracellular	COG1749	Cell motility and secretion	
1284	26990737	PP_4034		allantoate amidohydrolase	2.4	4.29E-02	control	5.7	45010	3	7%	Cytoplasmic	COG0624	Amino acid transport and metabolism	
1284	26988732	PP_2007		P-47-related protein	2.4	4.29E-02	control	5.8	44707	10	27%	Unknown			
1297	26990719	PP_4014	mnmA	tRNA-specific 2-thiouridylase MnmA	3.1	7.62E-03	0,75 g BuOH	5.5	41489	2	5%	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
1300	26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	3.5	4.19E-04	0,75 g BuOH	4.7	36629	2	5%	Cytoplasmic	COG0202	Transcription	
1300	26987193	PP_0452	tuf	elongation factor Tu	3.5	4.19E-04	0,75 g BuOH	5.0	43478	4	10%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1300	261404073	not in database		phosphoglycerate kinase	3.5	4.19E-04	0,75 g BuOH			3	8%				
1300	26991903	PP_5227	lysA-2	diaminopimelate decarboxylase	3.5	4.19E-04	0,75 g BuOH	4.9	45213	9	18%	Cytoplasmic	COG0019	Amino acid transport and metabolism	
1313	261409493	not in database		DNA-directed RNA polymerase subunit alpha	3.0	3.68E-03	0,75 g BuOH			8	27%				
1313	26987941	PP_1206	oprD	outer membrane porin	3.0	3.68E-03	0,75 g BuOH	4.6	46120	6	12%	Outer Membrane			
1465	26987973	PP_1238		lipoprotein	6.3	1.64E-04	0,75 g BuOH	4.8	40784	6	17%	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
1495	350549527	not in database		Ketol-acid reductoisomerase	4.0	5.76E-03	0,75 g BuOH			3	12%				
1501	26989418	PP_2699		hypothetical protein	2.4	6.98E-03	control	6.5	40451	10	28%	Cytoplasmic			
1501	26989059	PP_2335		methylcitrate synthase	2.4	6.98E-03	control	6.7	41995	2	6%	Cytoplasmic	COG0372	Energy production and conversion	
1501	148547037	not in database		phenylhydantoinase	2.4	6.98E-03	control			2	4%				
1512	26987735	PP_0999	arcC	carbamate kinase	1.9	3.96E-02	control	5.5	33423	2	6%	Cytoplasmic	COG0549	Amino acid transport and metabolism	
1512	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.9	3.96E-02	control	6.4	40068	13	35%	Periplasmic	COG0687	Amino acid transport and metabolism	
1518	26991828	PP_5152		SdiA-regulated domain protein	5.6	6.73E-03	0,75 g BuOH	4.5	33795	7	22%	Cytoplasmic Membrane	COG3204	Function unknown	
1547	26988393	PP_1661		dehydrogenase subunit	3.1	3.39E-04	control	5.5	81020	4	5%	Extracellular	COG2303	Amino acid transport and metabolism	
1564	26990488	PP_3783		hypothetical protein	2.3	3.61E-02	control	5.8	34938	7	23%	Cytoplasmic			
1564	26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	2.3	3.61E-02	control	6.3	38659	7	20%	Cytoplasmic	COG0620	Amino acid transport and metabolism	
1564	26990544	PP_3839		alcohol dehydrogenase	2.3	3.61E-02	control	5.7	35397	2	7%	Cytoplasmic	COG1064	General function prediction only	
1609	26988324	PP_1592	tsf	elongation factor Ts	1.9	2.48E-02	0,75 g BuOH	4.9	30432	3	9%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
1609	26990421	PP_3713	catA	catechol 1,2-dioxygenase	1.9	2.48E-02	0,75 g BuOH	5.1	34249	6	19%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
1609	26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.9	2.48E-02	0,75 g BuOH	5.6	36424	8	23%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
1609	26989181	PP_2458	rbsK	ribokinase	1.9	2.48E-02	0,75 g BuOH	5.1	31151	2	6%	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
1671	26990421	PP_3713	catA	catechol 1,2-dioxygenase	3.3	4.35E-02	0,75 g BuOH	5.1	34249	3	10%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
1671	26987522	PP_0786	trxB	thioredoxin reductase	3.3	4.35E-02	0,75 g BuOH	5.1	33841	3	9%	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
1685	308068312	not in database		Vegetative protein 296	3.8	6.02E-03	0,75 g BuOH			4	16%				
1698	26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	2.6	5.70E-03	0,75 g BuOH	4.2	29130	4	12%	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
1698	26991828	PP_5152		SdiA-regulated domain protein	2.6	5.70E-03	0,75 g BuOH	4.5	33795	2	6%	Cytoplasmic Membrane	COG3204	Function unknown	
1774	26988537	PP_1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase	1.8	2.15E-02	control	6.0	30469	3	9%	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
1774	26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.8	2.15E-02	control	6.2	30111	3	9%	Cytoplasmic	COG0074	Energy production and conversion	
1957	26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	2.1	3.88E-02	control	6.2	32979	3	12%	Cytoplasmic	COG0685	Amino acid transport and metabolism	
2142	26991689	PP_5012		hypothetical protein	7.1	4.35E-02	0,75 g BuOH	5.4	22983	2	7%	Unknown	COG3165	Function unknown	
2150	26989102	PP_2378	yhgI	yhgI protein	2.1	4.90E-02	0,75 g BuOH	4.3	20955	2	9%	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
2232	26987297	PP_0559	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	2.3	1.25E-03	0,75 g BuOH	4.7	16186	2	17%	Unknown	COG0511	Lipid metabolism	
2456	26987686	PP_0950	ptsN	PTS IIA-like nitrogen-regulatory protein PtsN	3.7	7.34E-03	control	4.8	16772	3	18%	Cytoplasmic	COG1762	Carbohydrate transport and metabolism	Signal transduction mechanisms
2456	26988392	PP_1660		hypothetical protein	3.7	7.34E-03	control	5.1	19178	2	10%	Cytoplasmic Membrane			
2510	26989394	PP_2675		cytochrome c-type protein	4.4	2.40E-03	0,75 g BuOH	4.9	16280	3	20%	Unknown	COG2010	Energy production and conversion	

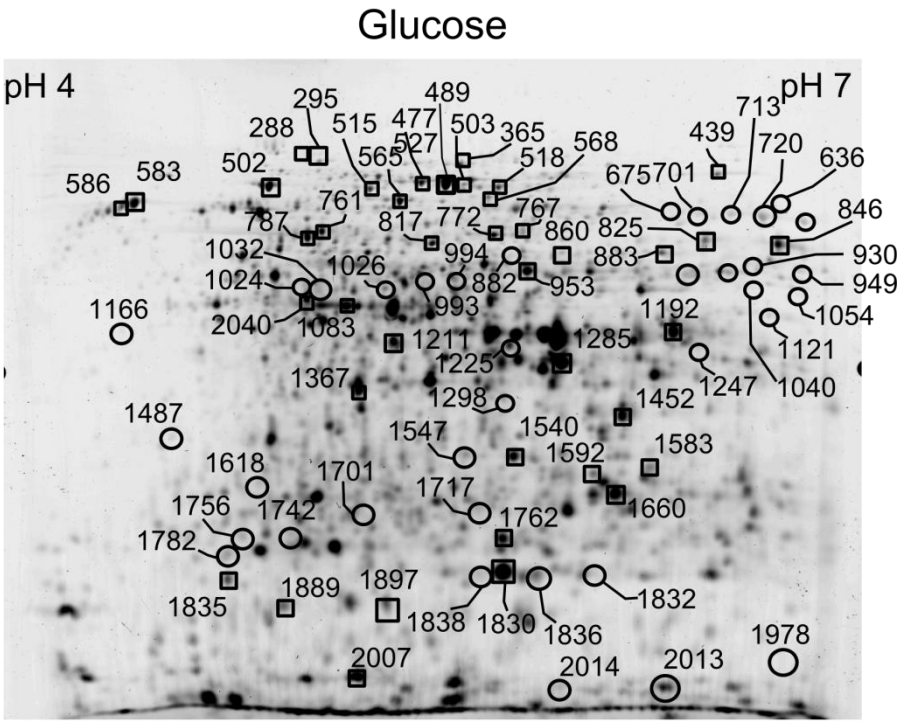


Differenziell regulierte Spots zwischen mit 0,75 g/l und 7,5 g/l Butanol (im Feedmedium) behandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 7,5 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

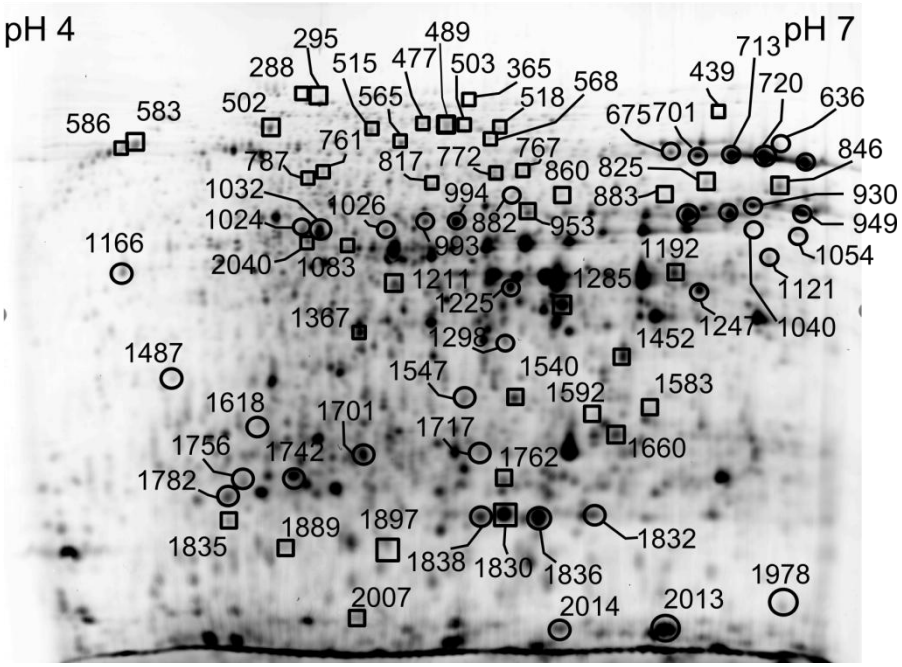
5.2.3.1 2D_DIGE_P_putida_KT2440_0.75g_7.5g_BuOH_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
950	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	28.0	1.12E-02	7,5 g BuOH	7.0	69173	19	25%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
989	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.8	3.73E-03	7,5 g BuOH	6.4	71796	8	13%	Cytoplasmic	COG0365	Lipid metabolism	
991	26987192	PP_0451	fusA	elongation factor G	2.1	4.26E-03	0,75 g BuOH	4.9	78817	32	59%	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
1028	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	4.4	4.70E-02	7,5 g BuOH	7.0	69173	14	21%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1084	26988095	PP_1361	groEL	chaperonin GroEL	4.4	4.61E-02	0,75 g BuOH	4.7	56743	19	35%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1084	26991160	PP_4474	alaS	alanyl-tRNA synthetase	4.4	4.61E-02	0,75 g BuOH	5.1	94711	9	9%	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
1156	26990379	PP_3668		catalase/peroxidase HPI	4.5	4.67E-02	0,75 g BuOH	5.8	82061	6	10%	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
1156	26988988	PP_2264		extracellular solute-binding protein, family 1	4.5	4.67E-02	0,75 g BuOH	5.6	65243	31	64%	Unknown	COG1653	Carbohydrate transport and metabolism	
1253	26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.9	2.17E-02	0,75 g BuOH	4.8	48526	5	11%	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
1253	26988391	PP_1659		hypothetical protein	1.9	2.17E-02	0,75 g BuOH	5.9	48336	3	7%	Periplasmic			
1288	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.6	2.67E-02	7,5 g BuOH	7.0	69173	13	20%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1313	26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	7.7	3.15E-02	7,5 g BuOH	7.4	62241	5	10%	Cytoplasmic	COG3243	Lipid metabolism	
1313	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	7.7	3.15E-02	7,5 g BuOH	7.0	69173	26	36%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1322	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.8	3.84E-02	0,75 g BuOH	5.2	55352	7	14%	Cytoplasmic	COG0056	Energy production and conversion	
1322	26988163	PP_1430	algY	protease Do	2.8	3.84E-02	0,75 g BuOH	6.6	52617	3	5%	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
1322	26991936	PP_5260		hypothetical protein	2.8	3.84E-02	0,75 g BuOH	5.1	51372	2	4%	Cytoplasmic	COG5383	Function unknown	
1322	26990705	PP_4000	serS	seryl-tRNA synthetase	2.8	3.84E-02	0,75 g BuOH	5.1	46849	3	6%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
1322	26987948	PP_1213	aspS	aspartyl-tRNA synthetase	2.8	3.84E-02	0,75 g BuOH	5.1	66568	10	15%	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
1345	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.5	4.35E-02	7,5 g BuOH	7.0	69173	6	13%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1349	26988393	PP_1661		dehydrogenase subunit	4.8	1.15E-02	7,5 g BuOH	5.5	81020	3	3%	Extracellular	COG2303	Amino acid transport and metabolism	
1349	26987967	PP_1232		hypothetical protein	4.8	1.15E-02	7,5 g BuOH	6.9	53219	15	32%	Unknown	COG4783	General function prediction only	
1349	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	4.8	1.15E-02	7,5 g BuOH	7.0	69173	16	24%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1349	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	4.8	1.15E-02	7,5 g BuOH	6.5	49088	10	22%	Cytoplasmic	COG0439	Lipid metabolism	
1355	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	5.9	1.36E-02	7,5 g BuOH	5.8	65671	7	9%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1355	26988163	PP_1430	algY	protease Do	5.9	1.36E-02	7,5 g BuOH	6.6	52617	4	6%	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
1355	26990810	PP_4116	aceA	isocitrate lyase	5.9	1.36E-02	7,5 g BuOH	5.3	48633	21	38%	Cytoplasmic	COG2224	Energy production and conversion	
1356	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.7	2.08E-02	7,5 g BuOH	7.0	69173	18	32%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1356	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	6.7	2.08E-02	7,5 g BuOH	6.5	49088	7	17%	Cytoplasmic	COG0439	Lipid metabolism	
1373	26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	3.8	5.08E-03	7,5 g BuOH	5.7	49982	2	4%	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
1373	26986756	PP_0011	dnaN	DNA polymerase III subunit beta	3.8	5.08E-03	7,5 g BuOH	4.9	40718	2	5%	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
1373	26990810	PP_4116	aceA	isocitrate lyase	3.8	5.08E-03	7,5 g BuOH	5.3	48633	12	24%	Cytoplasmic	COG2224	Energy production and conversion	
1373	26991319	PP_4635		trans-2-enoyl-CoA reductase	3.8	5.08E-03	7,5 g BuOH	5.0	44265	6	14%	Cytoplasmic	COG3007	Function unknown	
1385	26990810	PP_4116	aceA	isocitrate lyase	4.0	4.50E-02	7,5 g BuOH	5.3	48633	2	5%	Cytoplasmic	COG2224	Energy production and conversion	
1385	26991395	PP_4712	infB	translation initiation factor IF-2	4.0	4.50E-02	7,5 g BuOH	6.8	91460	2	3%	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
1385	26989399	PP_2680		aldehyde dehydrogenase family protein	4.0	4.50E-02	7,5 g BuOH	5.5	54903	9	20%	Cytoplasmic	COG1012	Energy production and conversion	
1395	26988095	PP_1361	groEL	chaperonin GroEL	8.1	3.12E-03	7,5 g BuOH	4.7	56743	3	5%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1395	26989399	PP_2680		aldehyde dehydrogenase family protein	8.1	3.12E-03	7,5 g BuOH	5.5	54903	10	24%	Cytoplasmic	COG1012	Energy production and conversion	
1406	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	16.0	2.10E-02	7,5 g BuOH	7.0	69173	11	22%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1421	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	19.0	1.91E-02	7,5 g BuOH	7.0	69173	13	23%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1454	308070977	not in database			2.9	6.98E-03	0,75 g BuOH			5	19%				
1454	26991761	PP_5085	maeB	malic enzyme	2.9	6.98E-03	0,75 g BuOH	4.9	45127	2	6%	Cytoplasmic	COG0281	Energy production and conversion	
1454	194365230	not in database			2.9	6.98E-03	0,75 g BuOH			4	9%				
1454	26988391	PP_1659		hypothetical protein	2.9	6.98E-03	0,75 g BuOH	5.9	48336	16	45%	Periplasmic			
1454	26987193	PP_0452	tuf	elongation factor Tu	2.9	6.98E-03	0,75 g BuOH	5.0	43478	6	15%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1462	317055545	not in database			4.4	6.90E-03	0,75 g BuOH			2	9%				
1462	26991077	PP_4388	flgE	flagellar hook protein FlgE	4.4	6.90E-03	0,75 g BuOH	4.3	45796	7	25%	Extracellular	COG1749	Cell motility and secretion	
1464	26990737	PP_4034		allantoate amidohydrolase	1.9	2.35E-02	7,5 g BuOH	5.7	45010	2	4%	Cytoplasmic	COG0624	Amino acid transport and metabolism	
1464	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.9	2.35E-02	7,5 g BuOH	5.4	45695	8	18%	Unknown	COG0538	Energy production and conversion	
1464	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	1.9	2.35E-02	7,5 g BuOH	7.0	69173	3	5%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1464	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.9	2.35E-02	7,5 g BuOH	6.3	49912	3	6%	Cytoplasmic	COG1249	Energy production and conversion	
1510	26987181	PP_0440	tuf	elongation factor Tu	2.3	1.57E-02	0,75 g BuOH	5.0	43495	2	5%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1510	26991903	PP_5227	lysA-2	diaminopimelate decarboxylase	2.3	1.57E-02	0,75 g BuOH	4.9	45213	3	6%	Cytoplasmic	COG0019	Amino acid transport and metabolism	
1555	26989381	PP_2662		hypothetical protein	18.0	3.30E-02	7,5 g BuOH	4.3	42858	8	24%	Outer Membrane			
1597	26987736	PP_1000	argI	ornithine carbamoyltransferase	2.4	2.77E-03	0,75 g BuOH	6.3	37911	3	8%	Cytoplasmic	COG0078	Amino acid transport and metabolism	
1609	26991068	PP_4379		beta-ketoacyl-acyl-carrier-protein synthase I	1.8	8.52E-03	0,75 g BuOH	4.8	33207	2	6%	Cytoplasmic	COG0332	acyl-carrier-protein	
1609	261407994	not in database			1.8	8.52E-03	0,75 g BuOH			2	5%				
1656	26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	3.0	2.55E-03	0,75 g BuOH	5.0	93609	2	3%	Cytoplasmic	COG1049	Energy production and conversion	
1656	26988095	PP_1361	groEL	chaperonin GroEL	3.0	2.55E-03	0,75 g BuOH	4.7	56743	2	4%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1695	26991828	PP_5152		SdiA-regulated domain protein	4.4	2.08E-03	0,75 g BuOH	4.5	33795	3	9%	Cytoplasmic Membrane	COG3204	Function unknown	
1771	26990421	PP_3713	catA	catechol 1,2-dioxygenase	2.1	4.19E-02	0,75 g BuOH	5.1	34249	2	7%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
1771	26989181	PP_2458	rbsK	ribokinase	2.1	4.19E-02	0,75 g BuOH	5.1	31151	2	6%	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
1821	26988094	PP_1360	groES	co-chaperonin GroES	2.5	7.26E-03	0,75 g BuOH	5.2	10224	2	19%	Cytoplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
1821	26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	2.5	7.26E-03	0,75 g BuOH	4.2	29130	7	29%	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
1943	26987959	PP_1224		hypothetical protein	2.3	1.14E-02	0,75 g BuOH	8.3	28730	7	38%	Unknown	COG1729	Function unknown	
1943	253577368	not in database			2.3	1.14E-02	0,75 g BuOH			3	12%				
2156	26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	3.1	1.73E-02	7,5 g BuOH	6.2	27714	3	9%	Cytoplasmic	COG0345	Amino acid transport and metabolism	
2156	26989399	PP_2680		aldehyde dehydrogenase family protein	3.1	1.73E-02	7,5 g BuOH	5.5	54903	3	6%	Cytoplasmic	COG1012	Energy production and conversion	
2305	26988957	PP_2233		isochorismatase superfamily hydrolase	4.3	8.01E-04	7,5 g BuOH	6.0	19296	6	29%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
2307	26988957	PP_2233		isochorismatase superfamily hydrolase	3.4	2.60E-02	7,5 g BuOH	6.0	19296	6	20%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
2353	26989845	PP_3126		polysaccharide export protein	2.5	2.66E-02	0,75 g BuOH	4.9	19528	3	15%	Unknown	COG1596	Cell wall membrane envelope biogenesis	
2474	26991550	PP_4870		azurin	4.7	1.09E-02	7,5 g BuOH	6.9	16028	4	23%	Periplasmic	COG3241	Energy production and conversion	

A)



B)



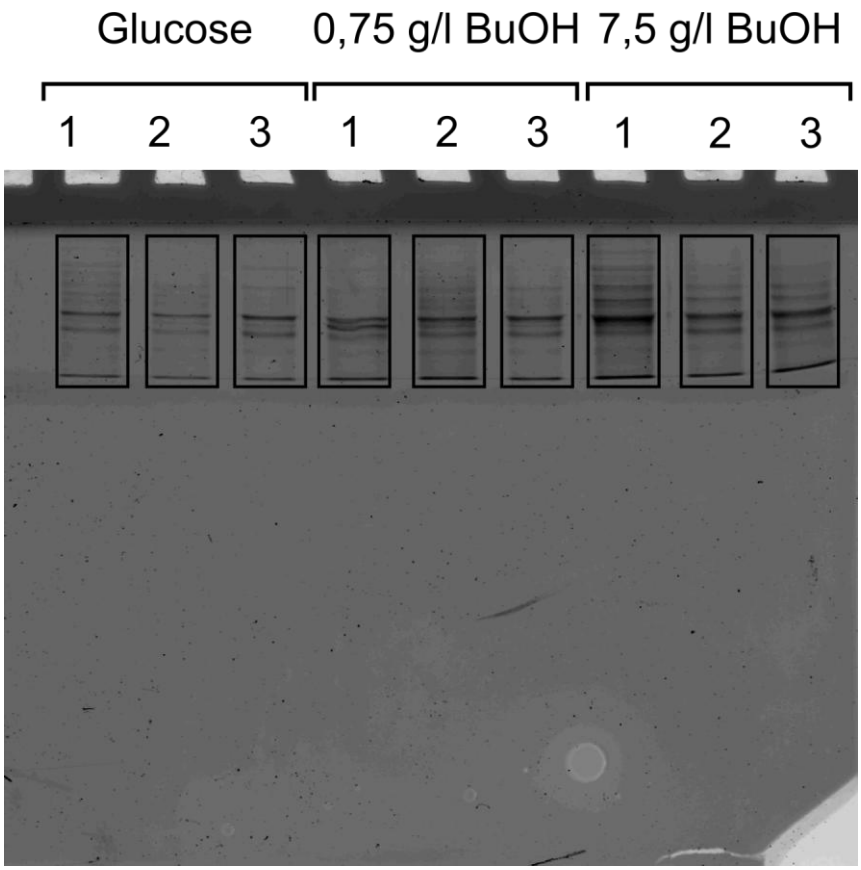
Differenziell regulierte Spots zwischen mit 7,5 g/l Butanol (im Feedmedium) behandelten und unbehandelten Zellen von *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in mit 7,5 g/l Butanol behandelten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden.

5.2.3.1 2D_DIGE_P_putida_KT2440_7.5g_BuOH_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
288	26987529	PP_0793	fruB	phosphoenolpyruvate-protein phosphotransferase	17.0	3.46E-03	7,5 g/l BuOH	4.8	101497	2	3%	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
363	26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	3.3	1.38E-02	control	5.2	94861	18	19%	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
439	26988451	PP_1719	prc	carboxyl-terminal protease	7.8	1.25E-02	control	7.1	79096	10	13%	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
477	26988393	PP_1661		dehydrogenase subunit	5.1	5.30E-04	control	5.5	81020	10	12%	Extracellular	COG2303	Amino acid transport and metabolism	
489	26988393	PP_1661		dehydrogenase subunit	11.0	5.50E-05	control	5.5	81020	22	27%	Extracellular	COG2303	Amino acid transport and metabolism	
502	26991410	PP_4727	dnaK	molecular chaperone DnaK	2.7	2.24E-02	control	4.6	68800	17	24%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
503	26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	6.5	7.74E-03	control	5.0	93609	3	3%	Cytoplasmic	COG1049	Energy production and conversion	
503	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	6.5	7.74E-03	control	5.4	79899	18	23%	Cytoplasmic	COG2838	Energy production and conversion	
515	26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	2.1	3.69E-02	control	4.9	75010	5	7%	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
518	26988393	PP_1661		dehydrogenase subunit	3.5	2.62E-03	control	5.5	81020	9	11%	Extracellular	COG2303	Amino acid transport and metabolism	
565	26990871	PP_4179	htpG	heat shock protein 90	4.2	2.26E-03	control	5.0	71610	17	21%	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
568	26992056	PP_5380	copA	copper resistance protein A	2.9	7.25E-03	control	6.0	74225	12	17%	Periplasmic	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
568	26991067	PP_4378	fliC	flagellin FliC	2.9	7.25E-03	control	4.2	67846	2	4%	Extracellular	COG1344	Cell motility and secretion	
583	26991067	PP_4378	fliC	flagellin FliC	8.5	1.73E-02	control	4.2	67846	9	15%	Extracellular	COG1344	Cell motility and secretion	
586	26991067	PP_4378	fliC	flagellin FliC	3.8	4.10E-02	control	4.2	67846	10	19%	Extracellular	COG1344	Cell motility and secretion	
636	26991173	PP_4487	acsA	acetyl-CoA synthetase	19.0	1.51E-02	7,5 g/l BuOH	6.4	71796	9	14%	Cytoplasmic	COG0365	Lipid metabolism	
675	26991173	PP_4487	acsA	acetyl-CoA synthetase	5.3	7.76E-03	7,5 g/l BuOH	6.4	71796	8	13%	Cytoplasmic	COG0365	Lipid metabolism	
701	26991173	PP_4487	acsA	acetyl-CoA synthetase	7.4	9.32E-03	7,5 g/l BuOH	6.4	71796	2	3%	Cytoplasmic	COG0365	Lipid metabolism	
701	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	7.4	9.32E-03	7,5 g/l BuOH	7.0	69173	13	19%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
713	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	28.0	2.09E-03	7,5 g/l BuOH	7.0	69173	14	21%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
720	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	30.0	4.04E-03	7,5 g/l BuOH	7.0	69173	19	25%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
736	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	37.0	5.34E-03	7,5 g/l BuOH	7.0	69173	20	27%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
761	26988095	PP_1361	groEL	chaperonin GroEL	6.6	3.55E-02	control	4.7	56743	19	35%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
761	26991160	PP_4474	alaS	alanyl-tRNA synthetase	6.6	3.55E-02	control	5.1	94711	9	9%	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
767	26986947	PP_0203		hypothetical protein	3.1	2.68E-02	control	5.9	62682	2	4%	Unknown	COG0624	Amino acid transport and metabolism	
767	26990379	PP_3668		catalase/peroxidase HPI	3.1	2.68E-02	control	5.8	82061	5	8%	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
767	26991928	PP_5252		amidohydrolase 3	3.1	2.68E-02	control	6.4	72743	15	21%	Unknown	COG1574	General function prediction only	
772	26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	2.2	3.95E-02	control	5.3	52585	3	6%	Cytoplasmic	COG2204	Signal transduction mechanisms	
772	26986947	PP_0203		hypothetical protein	2.2	3.95E-02	control	5.9	62682	15	24%	Unknown	COG0624	Amino acid transport and metabolism	
772	26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.2	3.95E-02	control	5.5	63339	7	11%	Cytoplasmic	COG1960	Lipid metabolism	
787	26988095	PP_1361	groEL	chaperonin GroEL	4.6	1.87E-02	control	4.7	56743	17	32%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
817	26990379	PP_3668		catalase/peroxidase HPI	7.0	1.19E-02	control	5.8	82061	6	10%	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
817	26988988	PP_2264		extracellular solute-binding protein, family 1	7.0	1.19E-02	control	5.6	65243	31	64%	Unknown	COG1653	Carbohydrate transport and metabolism	
825	26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	3.0	1.01E-02	control	7.1	60366	11	16%	Periplasmic	COG0747	Amino acid transport and metabolism	
846	26991385	PP_4701	pgi	glucose-6-phosphate isomerase	3.4	7.32E-03	control	6.8	61455	2	3%	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
846	26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	3.4	7.32E-03	control	7.1	60366	18	29%	Periplasmic	COG0747	Amino acid transport and metabolism	
860	26987283	PP_0545		aldehyde dehydrogenase family protein	2.7	3.40E-02	control	5.9	55268	4	18%	Cytoplasmic	COG1012	Energy production and conversion	
860	26991173	PP_4487	acsA	acetyl-CoA synthetase	2.7	3.40E-02	control	6.4	71796	4	6%	Cytoplasmic	COG0365	Lipid metabolism	
860	26989399	PP_2680		aldehyde dehydrogenase family protein	2.7	3.40E-02	control	5.5	54903	4	8%	Cytoplasmic	COG1012	Energy production and conversion	
860	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	2.7	3.40E-02	control	6.2	63448	10	16%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
882	26989399	PP_2680		aldehyde dehydrogenase family protein	10.0	4.43E-02	7,5 g/l BuOH	5.5	54903	9	19%	Cytoplasmic	COG1012	Energy production and conversion	
882	26990265	PP_3553		acyl-CoA synthetase	10.0	4.43E-02	7,5 g/l BuOH	6.4	59576	3	6%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
882	26987139	PP_0397		serine protein kinase, PrkA	10.0	4.43E-02	7,5 g/l BuOH	5.8	73782	2	3%	Cytoplasmic	COG2766	Signal transduction mechanisms	
883	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	8.0	1.01E-02	control	6.3	49912	11	28%	Cytoplasmic	COG1249	Energy production and conversion	
930	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.3	2.71E-02	7,5 g/l BuOH	7.0	69173	13	20%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
949	26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	12.0	3.38E-02	7,5 g/l BuOH	7.4	62241	5	10%	Cytoplasmic	COG3243	Lipid metabolism	
949	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	12.0	3.38E-02	7,5 g/l BuOH	7.0	69173	26	36%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
953	26987737	PP_1001	arcA	arginine deiminase	2.8	5.82E-03	control	5.7	46462	24	64%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
953	26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	2.8	5.82E-03	control	5.7	50918	6	16%	Unknown	COG1012	Energy production and conversion	
986	26988393	PP_1661		dehydrogenase subunit	8.0	6.70E-03	7,5 g/l BuOH	5.5	81020	3	3%	Extracellular	COG2303	Amino acid transport and metabolism	
986	26987967	PP_1232		hypothetical protein	8.0	6.70E-03	7,5 g/l BuOH	6.9	53219	15	32%	Unknown	COG4783	General function prediction only	
986	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	8.0	6.70E-03	7,5 g/l BuOH	7.0	69173	16	24%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
986	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	8.0	6.70E-03	7,5 g/l BuOH	6.5	49088	10	22%	Cytoplasmic	COG0439	Lipid metabolism	
993	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.6	1.47E-02	7,5 g/l BuOH	5.8	65671	7	9%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
993	26988393	PP_1661		dehydrogenase subunit	2.6	1.47E-02	7,5 g/l BuOH	5.5	81020	5	7%	Extracellular	COG2303	Amino acid transport and metabolism	
993	26990705	PP_4000	serS	seryl-tRNA synthetase	2.6	1.47E-02	7,5 g/l BuOH	5.1	46849	2	5%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
993	26990810	PP_4116	aceA	isocitrate lyase	2.6	1.47E-02	7,5 g/l BuOH	5.3	48633	15	28%	Cytoplasmic	COG2224	Energy production and conversion	
994	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	5.2	9.20E-03	7,5 g/l BuOH	5.8	65671	7	9%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
994	26988163	PP_1430	algY	protease Do	5.2	9.20E-03	7,5 g/l BuOH	6.6	52617	4	6%	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
994	26990810	PP_4116	aceA	isocitrate lyase	5.2	9.20E-03	7,5 g/l BuOH	5.3	48633	21	38%	Cytoplasmic	COG2224	Energy production and conversion	
995	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11.0	3.64E-03	7,5 g/l BuOH	7.0	69173	18	32%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
995	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	11.0	3.64E-03	7,5 g/l BuOH	6.5	49088	7	17%	Cytoplasmic	COG0439	Lipid metabolism	
1024	26990810	PP_4116	aceA	isocitrate lyase	4.5	3.27E-02	7,5 g/l BuOH	5.3	48633	2	5%	Cytoplasmic	COG2224	Energy production and conversion	
1024	26991395	PP_4712	infB	translation initiation factor IF-2	4.5	3.27E-02	7,5 g/l BuOH	6.8	91460	2	3%	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
1024	26989399	PP_2680		aldehyde dehydrogenase family protein	4.5	3.27E-02	7,5 g/l BuOH	5.5	54903	9	20%	Cytoplasmic	COG1012	Energy production and conversion	
1026	26990810	PP_4116	aceA	isocitrate lyase	2.4	4.84E-03	7,5 g/l BuOH	5.3	48633	10	19%	Cytoplasmic	COG2224	Energy production and conversion	
1026	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2.4	4.84E-03	7,5 g/l BuOH	4.9	54767	12	20%	Cytoplasmic	COG1951	Energy production and conversion	
1026	26988075	PP_1341	ftsA	cell division protein FtsA	2.4	4.84E-03	7,5 g/l BuOH	4.9	47444	8	19%	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
1026	26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	2.4	4.84E-03	7,5 g/l BuOH	5.7	49982	5	10%	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
1026	26986756	PP_0011	dnaN	DNA polymerase III subunit beta	2.4	4.84E-03	7,5 g/l BuOH	4.9	40718	15	40%	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
1032	26988095	PP_1361	groEL	chaperonin GroEL	8.7	2.12E-03	7,5 g/l BuOH	4.7	56743	3	5%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1032	26989399	PP_2680		aldehyde dehydrogenase family protein	8.7	2.12E-03	7,5 g/l BuOH	5.5	54903	10	24%	Cytoplasmic	COG1012	Energy production and conversion	
1040	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11.0	2.39E-02	7,5 g/l BuOH	7.0	69173	11	22%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1054	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11.0	3.44E-02	7,5 g/l BuOH	7.0	69173	13	23%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1083	308070977	not in database			5.3	9.14E-04	control			5	19%				
1083	26991761	PP_5085	maeB	malic enzyme	5.3	9.14E-04	control	4.9	45127	2	6%	Cytoplasmic	COG0281	Energy production and conversion	
1083	194365230	not in database			5.3	9.14E-04	control			4	9%				
1083	26988391	PP_1659		hypothetical protein	5.3	9.14E-04	control	5.9	48336	16	45%	Periplasmic			
1083	26987193	PP_0452	tuf	elongation factor Tu	5.3	9.14E-04	control	5.0	43478	6	15%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1121	26990127	PP_3414		methyl-accepting chemotaxis transducer/sensory box protein	2.8	3.45E-02	7,5 g/l BuOH	6.8	48686	7	14%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1121	26987736	PP_1000	argI	ornithine carbamoyltransferase	2.8	3.45E-02	7,5 g/l BuOH	6.3	37911	2	9%	Cytoplasmic	COG0078	Amino acid transport and metabolism	
1121	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	2.8	3.45E-02	7,5 g/l BuOH	7.0	69173	3	6%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1166	26989381	PP_2662		hypothetical protein	25.0	2.15E-02	7,5 g/l BuOH	4.3	42858	8	24%	Outer Membrane			
1192	26987736	PP_1000	argI	ornithine carbamoyltransferase	2.3	2.09E-02	control	6.3	37911	21	52%	Cytoplasmic	COG0078	Amino acid transport and metabolism	
1211	26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	2.0	4.17E-03	control	5.0	35225	3	9%	Cytoplasmic	COG0113	Coenzyme metabolism	
1211	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	2.0	4.17E-03	control	6.2	45449	5	13%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1211	26987153	PP_0412		polyamine ABC transporter periplasmic protein	2.0	4.17E-03	control	5.3	37801	6	17%	Periplasmic	COG0687	Amino acid transport and metabolism	
1225	26990480	PP_3775		sarcosine oxidase	3.9	2.83E-03	7,5 g/l BuOH	6.4	41164	4	11%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1225	26991547	PP_4867		extracellular ligand-binding receptor	3.9	2.83E-03	7,5 g/l BuOH	6.2	40270	3	8%	Periplasmic	COG0683	Amino acid transport and metabolism	
1225	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	3.9	2.83E-03	7,5 g/l BuOH	6.2	45449	7	16%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1225	26990810	PP_4116	aceA	isocitrate lyase	3.9	2.83E-03	7,5 g/l BuOH	5.3	48633	13	20%	Cytoplasmic	COG2224	Energy production and conversion	
1247	26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	7.1	2.14E-02	7,5 g/l BuOH	7.7	50905	3	6%	Cytoplasmic	COG1249	Energy production and conversion	
1247	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	7.1	2.14E-02	7,5 g/l BuOH	7.0	69173	9	14%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1247	26990765	PP_4064	ivd	acyl-CoA dehydrogenase domain-containing protein	7.1	2.14E-02	7,5 g/l BuOH	7.2	46572	2	4%	Cytoplasmic	COG1960	Lipid metabolism	
1285	26987735	PP_0999	arcC	carbamate kinase	2.8	2.88E-02	control	5.5	33423	3	9%	Cytoplasmic	COG0549	Amino acid transport and metabolism	
1285	26991754	PP_5078	aroB	3-dehydroquinate synthase	2.8	2.88E-02	control	6.0	39485	3	8%	Cytoplasmic	COG0337	Amino acid transport and metabolism	

1285	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	2.8	2.88E-02	control	6.4	40068	14	30%	Periplasmic	COG0687	Amino acid transport and metabolism				
1285	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	2.8	2.88E-02	control	6.2	45449	10	20%	Periplasmic	COG1653	Carbohydrate transport and metabolism				
1367	26988324	PP_1592	tsf	elongation factor Ts	2.0	4.32E-02	control	4.9	30432	16	46%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis				
1367	26987193	PP_0452	tuf	elongation factor Tu	2.0	4.32E-02	control	5.0	43478	2	5%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis				
1367	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	2.0	4.32E-02	control	6.4	40068	2	6%	Periplasmic	COG0687	Amino acid transport and metabolism				
1398	26988324	PP_1592	tsf	elongation factor Ts	2.5	2.72E-03	7,5 g/l BuOH	4.9	30432	3	13%	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis				
1398	26991794	PP_5118		rhodanese domain protein	2.5	2.72E-03	7,5 g/l BuOH	5.6	30750	4	13%	Cytoplasmic	COG2897	Inorganic ion transport and metabolism				
1452	26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	2.0	2.95E-02	control	6.2	59980	2	3%	Cytoplasmic	COG1012	Energy production and conversion				
1452	26988537	PP_1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase	2.0	2.95E-02	control	6.0	30469	4	12%	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane				
1452	26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.0	2.95E-02	control	6.2	30111	10	27%	Cytoplasmic	COG0074	Energy production and conversion				
1540	26992070	PP_5395		hypothetical protein	1.9	4.39E-02	control	5.6	31623	9	24%	Cytoplasmic	COG1568	General function prediction only				
1547	26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.0	4.07E-03	7,5 g/l BuOH	6.2	44897	2	4%	Cytoplasmic	COG0112	Amino acid transport and metabolism				
1547	26992070	PP_5395		hypothetical protein	2.0	4.07E-03	7,5 g/l BuOH	5.6	31623	5	19%	Cytoplasmic	COG1568	General function prediction only				
1547	26990252	PP_3540	mvaB	hydroxymethylglutaryl-CoA lyase	2.0	4.07E-03	7,5 g/l BuOH	5.4	31341	5	18%	Cytoplasmic	COG0119	Amino acid transport and metabolism				
1583	26991941	PP_5265	xpt	xanthine phosphoribosyltransferase	3.0	3.21E-02	control	6.1	20386	5	25%	Cytoplasmic	COG0503	Nucleotide transport and metabolism				
1583	26990740	PP_4038		dihydropyrimidine dehydrogenase	3.0	3.21E-02	control	5.1	46093	3	8%	Cytoplasmic	COG0167	Nucleotide transport and metabolism				
1583	26991954	PP_5278		aldehyde dehydrogenase family protein	3.0	3.21E-02	control	5.5	53053	2	4%	Cytoplasmic	COG1012	Energy production and conversion				
1583	26990095	PP_3380	ptxS	PtxS family transcriptional regulator	3.0	3.21E-02	control	6.9	36789	6	17%	Cytoplasmic	COG1609	Transcription				
1583	26988464	PP_1733	minD	septum site-determining protein MinD	3.0	3.21E-02	control	6.2	29650	7	24%	Cytoplasmic	COG2894	Cell division and chromosome partitioning				
1583	26990265	PP_3553		acyl-CoA synthetase	3.0	3.21E-02	control	6.4	59576	2	4%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism			
1592	26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	3.1	9.21E-03	control	6.2	32979	4	13%	Cytoplasmic	COG0685	Amino acid transport and metabolism				
1618	26987505	PP_0769		histidine kinase	3.7	6.91E-03	7,5 g/l BuOH	4.6	25229	3	11%	Cytoplasmic	COG0642	Signal transduction mechanisms				
1618	26990810	PP_4116	aceA	isocitrate lyase	3.7	6.91E-03	7,5 g/l BuOH	5.3	48633	7	12%	Cytoplasmic	COG2224	Energy production and conversion				
1660	26986978	PP_0235	lsfA	peroxidase	4.0	3.23E-02	control	6.0	23948	4	22%	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones				
1660	26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	4.0	3.23E-02	control	6.2	27714	4	14%	Cytoplasmic	COG0345	Amino acid transport and metabolism				
1660	26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	4.0	3.23E-02	control	9.2	31464	2	7%	Cytoplasmic	COG0224	Energy production and conversion				
1701	26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	6.1	9.90E-05	7,5 g/l BuOH	6.2	27714	3	9%	Cytoplasmic	COG0345	Amino acid transport and metabolism				
1701	26989399	PP_2680		aldehyde dehydrogenase family protein	6.1	9.90E-05	7,5 g/l BuOH	5.5	54903	3	6%	Cytoplasmic	COG1012	Energy production and conversion				
1707	26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	5.1	1.88E-02	7,5 g/l BuOH	8.2	35545	5	9%	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism				
1707	26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	5.1	1.88E-02	7,5 g/l BuOH	6.2	27714	2	6%	Cytoplasmic	COG0345	Amino acid transport and metabolism				
1707	26989399	PP_2680		aldehyde dehydrogenase family protein	5.1	1.88E-02	7,5 g/l BuOH	5.5	54903	3	4%	Cytoplasmic	COG1012	Energy production and conversion				
1742	26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	9.6	9.72E-05	7,5 g/l BuOH	9.2	31464	2	7%	Cytoplasmic	COG0224	Energy production and conversion				
1756	26987591	PP_0855		hypothetical protein	6.0	3.07E-02	7,5 g/l BuOH	4.6	22514	4	23%	Unknown	COG2976	Function unknown				
1756	26989399	PP_2680		aldehyde dehydrogenase family protein	6.0	3.07E-02	7,5 g/l BuOH	5.5	54903	2	5%	Cytoplasmic	COG1012	Energy production and conversion				
1762	26988024	PP_1289		hypothetical protein	3.1	2.17E-02	control	6.5	29332	3	9%	Unknown	COG3022	Function unknown				
1762	26987447	PP_0711		isochorismatase superfamily hydrolase	3.1	2.17E-02	control	5.3	23026	7	38%	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism				
1762	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	3.1	2.17E-02	control	6.7	41895	2	5%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism				
1782	26987276	PP_0538	ppa	inorganic pyrophosphatase	2.6	3.17E-03	7,5 g/l BuOH	4.6	19189	5	31%	Cytoplasmic	COG0221	Energy production and conversion				
1830	26987651	PP_0915	sodB	superoxide dismutase	2.6	2.98E-02	control	5.8	21938	4	20%	Periplasmic	COG0605	Inorganic ion transport and metabolism				
1830	26988957	PP_2233		isochorismatase superfamily hydrolase	2.6	2.98E-02	control	6.0	19296	2	10%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism				
1830	26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	2.6	2.98E-02	control	7.8	32510	2	8%	Cytoplasmic	COG0777	Lipid metabolism				
1832	26988957	PP_2233		isochorismatase superfamily hydrolase	3.5	2.60E-03	7,5 g/l BuOH	6.0	19296	7	61%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism				
1836	26988957	PP_2233		isochorismatase superfamily hydrolase	3.2	3.13E-02	7,5 g/l BuOH	6.0	19296	6	29%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism				
1838	26988957	PP_2233		isochorismatase superfamily hydrolase	5.6	3.69E-05	7,5 g/l BuOH	6.0	19296	6	20%	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism				
1889	26989845	PP_3126		polysaccharide export protein	2.9	1.26E-02	control	4.9	19528	3	15%	Unknown	COG1596	Cell wall	membrane	envelope biogenesis		
1897	26991979	PP_5303		endoribonuclease	2.1	4.16E-02	control	4.8	13508	3	24%	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis				
1897	26987945	PP_1210		DNA-binding stress protein	2.1	4.16E-02	control	5.0	17861	13	83%	Cytoplasmic	COG0783	Inorganic ion transport and metabolism				
1978	26991457	PP_4776		AsnC family transcriptional regulator	9.9	4.66E-03	7,5 g/l BuOH	6.8	17871	4	22%	Cytoplasmic	COG1522	Transcription				
1978	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	9.9	4.66E-03	7,5 g/l BuOH	7.0	69173	3	6%	Periplasmic	COG4993	Carbohydrate transport and metabolism				
2007	26987686	PP_0950	ptsN	PTS IIA-like nitrogen-regulatory protein PtsN	6.1	1.95E-03	control	4.8	16772	3	18%	Cytoplasmic	COG1762	Carbohydrate transport and metabolism	Signal transduction mechanisms			
2013	26991550	PP_4870		azurin	5.6	6.97E-05	7,5 g/l BuOH	6.9	16028	4	23%	Periplasmic	COG3241	Energy production and conversion				
2014	26991550	PP_4870		azurin	3.2	7.31E-06	7,5 g/l BuOH	6.9	16028	2	7%	Periplasmic	COG3241	Energy production and conversion				
2014	26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	3.2	7.31E-06	7,5 g/l BuOH	5.6	69049	2	3%	Cytoplasmic	COG2895	Inorganic ion transport and metabolism				
2040	26988344	PP_1612	eno	phosphopyruvate hydratase	3.9	2.50E-02	control	4.7	45490	10	23%	Cytoplasmic	COG0148	Carbohydrate transport and metabolism				
2040	26989399	PP_2680		aldehyde dehydrogenase family protein	3.9	2.50E-02	control	5.5	54903	2	3%	Cytoplasmic	COG1012	Energy production and conversion				

5.2.3.2 Membranproteom-Analyse



1D-SDS-PAGE der Membranfraktion von mit 0,75 g/l bzw. 7,5 g/l Butanol behandelten und unbehandelten Zellen von *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.2.3.2 Membranfraktion_P_putida_KT2440_0.75g_7.5g_BuOH_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.2	5.67E-01	7,5 g/l BuOH	9.1	61919	13	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.4	2.74E-01	0,75 g/l BuOH	4.9	40718	6	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.2	6.72E-01	7,5 g/l BuOH	5.8	90030	9	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.5	1.36E-01	0,75 g/l BuOH	6.1	31236	5	Cytoplasmic			
26986775	PP_0030		sensor histidine kinase	2.5	8.46E-02	7,5 g/l BuOH	6.4	52113	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986802	PP_0057		major facilitator family transporter	1.7	1.66E-01	7,5 g/l BuOH	9.3	58758	3	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.1	7.47E-01	0,75 g/l BuOH	4.9	75112	9	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.2	5.44E-01	7,5 g/l BuOH	4.8	36024	2	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.2	9.87E-01	7,5 g/l BuOH	6.4	44046	2	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986841	PP_0096	prlC	oligopeptidase A	1.0	9.30E-01	0,75 g/l BuOH	5.0	75721	12	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	2.0	8.45E-03	0,75 g/l BuOH	6.8	26001	5	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.0	9.44E-01	0,75 g/l BuOH	6.8	42059	7	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.7	1.94E-01	7,5 g/l BuOH	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.0	8.49E-01	7,5 g/l BuOH	7.4	25597	4	Unknown			
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	3.1	6.14E-02	7,5 g/l BuOH	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.3	4.70E-01	7,5 g/l BuOH	6.3	71284	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	2.0	2.77E-01	7,5 g/l BuOH	7.7	78583	12	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986928	PP_0184	argH	argininosuccinate lyase	1.0	9.17E-01	7,5 g/l BuOH	5.4	52061	4	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.8	4.04E-01	7,5 g/l BuOH	9.6	46030	10	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	2.3	5.00E-01	0,75 g/l BuOH	11.3	32300	3	Cytoplasmic			
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.2	3.38E-01	0,75 g/l BuOH	5.2	51549	10	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.5	2.34E-01	0,75 g/l BuOH	6.1	44824	7	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.1	6.79E-01	7,5 g/l BuOH	5.4	48317	19	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.5	4.15E-01	0,75 g/l BuOH	5.2	15616	7	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.1	8.95E-01	7,5 g/l BuOH	6.1	47787	6	Outer Membrane			
26987030	PP_0288		major facilitator superfamily MFS_1	8.8	4.32E-02	7,5 g/l BuOH	8.5	58780	4	Cytoplasmic Membrane			
26987063	PP_0321		threonine aldolase	1.4	3.43E-01	0,75 g/l BuOH	5.4	38068	5	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	2.1	9.28E-02	0,75 g/l BuOH	4.7	24565	2	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.5	1.51E-01	0,75 g/l BuOH	5.3	55654	12	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	2.2	1.56E-02	0,75 g/l BuOH	5.6	99332	26	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.6	2.80E-01	7,5 g/l BuOH	5.3	109432	3	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987089	PP_0347		hypothetical protein	1.8	2.86E-01	7,5 g/l BuOH	7.4	53779	2	Cytoplasmic			
26987098	PP_0356	glcB	malate synthase G	4.6	1.39E-03	7,5 g/l BuOH	5.8	78346	9	Cytoplasmic	COG2225	Energy production and conversion	
26987108	PP_0366	bioD	dithiobiotin synthetase	2.0	7.25E-02	0,75 g/l BuOH	5.3	23871	2	Cytoplasmic	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	6.01E-01	0,75 g/l BuOH	5.8	65541	12	Cytoplasmic	COG1960	Lipid metabolism	
26987117	PP_0375		prolyl oligopeptidase family protein	6.6	2.18E-03	7,5 g/l BuOH	6.0	67549	3	Cytoplasmic	COG1506	Amino acid transport and metabolism	
26987118	PP_0376	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	3.2	3.38E-02	7,5 g/l BuOH	6.5	42507	3	Cytoplasmic	COG0535	General function prediction only	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	4.5	8.58E-03	7,5 g/l BuOH	6.8	29075	7	Cytoplasmic	COG5424	Coenzyme metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.3	3.60E-01	7,5 g/l BuOH	4.6	69396	8	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.7	1.74E-01	0,75 g/l BuOH	11.4	8370	2	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987137	PP_0395		SpoVR family protein	1.0	9.37E-01	0,75 g/l BuOH	5.4	61330	2	Cytoplasmic	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	1.2	4.85E-01	0,75 g/l BuOH	7.0	50488	3	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.2	4.60E-01	0,75 g/l BuOH	5.8	73782	30	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987158	PP_0417	trpE	anthranilate synthase component I	1.4	4.77E-01	0,75 g/l BuOH	4.8	54406	2	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
26987159	PP_0418		GDSL family lipase	1.3	8.90E-01	0,75 g/l BuOH	4.4	67175	6	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.6	2.24E-01	0,75 g/l BuOH	6.8	36277	6	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987181	PP_0440	tuf	elongation factor Tu	1.7	1.57E-01	0,75 g/l BuOH	5.0	43495	3	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	1.4	3.89E-01	0,75 g/l BuOH	10.5	14866	4	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	3.1	5.48E-01	0,75 g/l BuOH	10.1	24251	6	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.4	2.22E-01	7,5 g/l BuOH	10.2	17686	5	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.0	8.78E-01	7,5 g/l BuOH	5.5	150992	58	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.1	4.74E-01	7,5 g/l BuOH	7.2	154797	43	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.1	9.27E-01	0,75 g/l BuOH	11.7	13727	2	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.6	4.02E-01	7,5 g/l BuOH	10.8	17578	9	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.2	4.65E-01	0,75 g/l BuOH	4.9	78817	46	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.6	1.79E-01	0,75 g/l BuOH	5.0	43478	45	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.9	2.54E-01	0,75 g/l BuOH	10.3	21811	5	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.5	3.72E-01	7,5 g/l BuOH	11.7	29669	13	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.5	5.27E-01	7,5 g/l BuOH	11.9	15373	4	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.2	2.64E-01	7,5 g/l BuOH	11.6	13410	12	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	2.3	5.67E-01	0,75 g/l BuOH	10.3	20329	10	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.2	8.95E-01	0,75 g/l BuOH	12.3	11403	2	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.4	9.70E-01	0,75 g/l BuOH	10.2	13975	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	3.0	4.15E-01	0,75 g/l BuOH	10.4	19143	4	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.5	2.24E-01	0,75 g/l BuOH	10.9	12628	6	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.1	9.33E-01	0,75 g/l BuOH	10.6	17666	10	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	2.0	6.97E-01	0,75 g/l BuOH	11.5	15189	8	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.8	4.65E-01	7,5 g/l BuOH	10.4	47853	7	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.2	6.99E-01	0,75 g/l BuOH	11.3	13256	4	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.6	7.20E-02	0,75 g/l BuOH	11.5	13660	4	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.1	4.66E-01	7,5 g/l BuOH	10.5	23056	12	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.1	6.28E-01	0,75 g/l BuOH	4.7	36629	10	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.1	3.57E-01	7,5 g/l BuOH	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	3.5	2.87E-01	7,5 g/l BuOH	4.6	17972	18	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987224	PP_0483	uvrA	excinuclease ABC subunit A	2.5	1.45E-01	7,5 g/l BuOH	7.0	104378	2	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
26987282	PP_0544		ethanolamine transproter	1.3	7.96E-01	0,75 g/l BuOH	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.6	1.66E-01	0,75 g/l BuOH	5.9	55268	19	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.7	1.73E-01	0,75 g/l BuOH	6.5	49088	8	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	3.4	1.78E-01	7,5 g/l BuOH	6.6	40223	5	Unknown	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	1.2	6.27E-01	7,5 g/l BuOH	5.3	71043	2	Unknown	COG1166	Amino acid transport and metabolism	
26987314	PP_0576		lipoprotein	1.2	9.51E-01	7,5 g/l BuOH	9.5	21449	2	Unknown			
26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	3.2	3.56E-02	0,75 g/l BuOH	7.5	47782	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.0	8.92E-01	0,75 g/l BuOH	5.0	69953	20	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.1	8.09E-01	7,5 g/l BuOH	5.9	53498	6	Cytoplasmic	COG1012	Energy production and conversion	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.0	9.49E-01	0,75 g/l BuOH	6.0	105800	11	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.2	6.60E-01	0,75 g/l BuOH	5.2	94861	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.2	5.04E-01	0,75 g/l BuOH	6.2	44897	13	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.1	9.28E-01	7,5 g/l BuOH	5.3	61860	14	Cytoplasmic	COG0488	General function prediction only	

26987411	PP_0675	gdhA	glutamate dehydrogenase	1.0	7.85E-01	0,75 g/l BuOH	6.5	48871	4	Unknown	COG0334	Amino acid transport and metabolism	
26987416	PP_0680		ATP-dependent protease	1.2	5.47E-01	0,75 g/l BuOH	4.5	89677	5	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.4	7.73E-01	0,75 g/l BuOH	7.8	39661	3	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	1.8	2.77E-01	7,5 g/l BuOH	9.9	92124	8	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	2.0	1.58E-01	0,75 g/l BuOH	5.3	23026	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	1.5	6.52E-01	7,5 g/l BuOH	10.5	31284	2	Cytoplasmic	COG2326	Function unknown	
26987455	PP_0719		GTP-dependent nucleic acid-binding protein EngD	1.3	6.16E-01	0,75 g/l BuOH	4.7	39962	2	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.3	5.61E-01	0,75 g/l BuOH	6.4	23242	4	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.1	8.73E-01	7,5 g/l BuOH	5.9	34192	3	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	3.2	1.69E-02	7,5 g/l BuOH	8.4	54282	8	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.4	6.25E-01	0,75 g/l BuOH	9.5	20483	4	Unknown			
26987495	PP_0759		hypothetical protein	1.8	6.52E-02	0,75 g/l BuOH	7.0	29743	3	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.0	1.00E+00	7,5 g/l BuOH	5.5	62125	7	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.1	8.57E-01	0,75 g/l BuOH	5.0	67937	21	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.3	6.12E-01	0,75 g/l BuOH	9.6	50572	9	Unknown			
26987504	PP_0768		response regulator/hypothetical protein	1.1	8.44E-01	0,75 g/l BuOH	8.4	59272	4	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987509	PP_0773		OmpA/MotB domain protein	3.7	3.14E-01	7,5 g/l BuOH	9.5	24753	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987526	PP_0790		signaling modulator of AmpD, AmpE	1.8	4.08E-01	7,5 g/l BuOH	7.8	31007	2	Cytoplasmic Membrane	COG3725	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	5.4	3.86E-02	7,5 g/l BuOH	6.7	34557	5	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	5.1	1.06E-01	7,5 g/l BuOH	7.8	74391	2	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987553	PP_0817		aminotransferase	2.7	1.10E-01	7,5 g/l BuOH	8.1	44996	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	1.5	9.42E-01	7,5 g/l BuOH	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.9	2.23E-01	7,5 g/l BuOH	9.6	66913	15	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.4	3.93E-01	7,5 g/l BuOH	4.8	32758	4	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.0	7.31E-01	0,75 g/l BuOH	6.6	29753	2	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.0	8.56E-01	0,75 g/l BuOH	6.2	44468	7	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987617	PP_0881	dppB	alkaline phosphatase	1.1	6.92E-01	7,5 g/l BuOH	8.4	36980	2	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	4.3	2.15E-02	0,75 g/l BuOH	7.1	60366	2	Periplasmic	COG0747	Amino acid transport and metabolism	
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.0	8.02E-01	0,75 g/l BuOH	4.9	54767	6	Cytoplasmic	COG1951	Energy production and conversion	
26987649	PP_0913		hypothetical protein	2.3	6.21E-01	0,75 g/l BuOH	4.4	47019	5	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.2	5.72E-01	7,5 g/l BuOH	5.8	78578	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987661	PP_0925		hypothetical protein	1.3	2.20E-01	0,75 g/l BuOH	5.8	31410	2	Unknown			
26987666	PP_0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.1	5.34E-01	0,75 g/l BuOH	4.8	52678	4	Cytoplasmic	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.1	7.31E-01	0,75 g/l BuOH	6.2	51518	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987689	PP_0953		ABC transporter ATP-binding protein	1.1	6.84E-01	7,5 g/l BuOH	7.0	26579	2	Cytoplasmic	COG1137	General function prediction only	
26987696	PP_0960	ttg2C	hypothetical protein	2.5	9.40E-02	7,5 g/l BuOH	4.6	16953	3	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.0	9.73E-01	0,75 g/l BuOH	5.1	107495	11	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.1	6.33E-01	0,75 g/l BuOH	7.4	52433	14	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.8	2.43E-01	7,5 g/l BuOH	9.7	41323	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987719	PP_0983		permease YjgP/YjgQ family protein	2.7	5.34E-01	7,5 g/l BuOH	7.1	38733	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	1.5	3.12E-01	0,75 g/l BuOH	6.4	40319	4	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	2.1	1.36E-02	0,75 g/l BuOH	5.5	33423	3	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	3.6	2.82E-02	0,75 g/l BuOH	6.3	37911	18	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	2.2	8.18E-02	0,75 g/l BuOH	5.7	46462	22	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.0	8.75E-01	7,5 g/l BuOH	9.1	51061	3	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	7.1	5.41E-03	0,75 g/l BuOH	7.0	36057	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	4.7	1.60E-02	0,75 g/l BuOH	6.4	65359	7	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	5.1	2.82E-02	0,75 g/l BuOH	6.5	33904	4	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987749	PP_1013		integral membrane sensor signal transduction histidine kinase	1.2	6.68E-01	0,75 g/l BuOH	7.3	54020	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26987750	PP_1014		hypothetical protein	1.4	3.84E-01	0,75 g/l BuOH	6.4	45472	3	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.3	3.62E-01	0,75 g/l BuOH	6.2	45449	21	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.2	4.25E-01	7,5 g/l BuOH	10.1	33781	9	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.1	5.75E-01	7,5 g/l BuOH	9.9	30428	4	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.3	7.21E-01	7,5 g/l BuOH	6.7	41895	17	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.6	5.30E-01	0,75 g/l BuOH	5.9	49646	31	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.3	4.52E-01	0,75 g/l BuOH	6.8	55000	10	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	2.4	1.03E-01	0,75 g/l BuOH	6.7	25476	4	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	2.2	9.21E-02	0,75 g/l BuOH	5.4	25004	4	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.1	6.74E-01	0,75 g/l BuOH	5.1	61712	15	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.9	1.69E-01	0,75 g/l BuOH	7.0	51765	5	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.6	2.27E-01	0,75 g/l BuOH	5.2	58204	10	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.0	9.62E-01	0,75 g/l BuOH	4.7	140818	23	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.1	5.90E-01	7,5 g/l BuOH	8.2	27464	3	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	2.4	3.65E-01	0,75 g/l BuOH	8.9	33428	4	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987818	PP_1082	bfr	bacterioferritin	5.2	1.79E-01	7,5 g/l BuOH	4.4	17971	12	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	2.4	5.63E-02	0,75 g/l BuOH	4.9	21730	12	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.1	4.74E-01	0,75 g/l BuOH	5.1	45164	6	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.3	3.67E-01	7,5 g/l BuOH	5.5	75186	6	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987844	PP_1108		acylase	1.0	9.39E-01	0,75 g/l BuOH	8.7	88728	6	Periplasmic	COG2366	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	3.4	2.81E-02	0,75 g/l BuOH	7.6	32597	4	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	1.3	6.00E-01	0,75 g/l BuOH	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.8	4.72E-01	0,75 g/l BuOH	4.7	27345	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	3.1	1.79E-01	7,5 g/l BuOH	9.3	15682	8	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987877	PP_1141	braC	extracellular ligand-binding receptor	2.5	4.04E-02	0,75 g/l BuOH	6.4	39402	7	Periplasmic	COG0683	Amino acid transport and metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.1	9.19E-01	0,75 g/l BuOH	4.8	105994	4	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987893	PP_1157		acetolactate synthase	1.2	3.12E-01	7,5 g/l BuOH	6.1	60059	2	Cytoplasmic	COG0028	Coenzyme metabolism	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.4	4.08E-01	0,75 g/l BuOH	4.5	46989	2	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.5	3.29E-01	7,5 g/l BuOH	5.7	106948	24	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987920	PP_1185	oprH	outer membrane protein H1	15.2	1.13E-01	7,5 g/l BuOH	6.8	21501	5	Outer Membrane			
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.0	8.69E-01	7,5 g/l BuOH	5.0	63623	5	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.2	6.56E-01	7,5 g/l BuOH	4.6	46120	21	Outer Membrane			
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.1	8.07E-01	7,5 g/l BuOH	5.1	66568	16	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	2.7	3.59E-01	7,5 g/l BuOH	6.3	25310	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987955	PP_1220	tolR	biopolymer transport protein TolR	4.2	1.74E-01	7,5 g/l BuOH	9.4	16247	2	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	2.2	2.30E-02	7,5 g/l BuOH	9.8	47431	6	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.1	8.39E-01	7,5 g/l BuOH	4.9	17833	12	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.9	1.37E-01	0,75 g/l BuOH	5.1	26916	2	Cytoplasmic	COG0152	Nucleotide transport and metabolism	
26987980	PP_1245		hypothetical protein	1.9	6.47E-01	0,75 g/l BuOH	9.4	31144	2	Unknown			
26988026	PP_1291		PhoH family protein	2.0	2.58E-01	0,75 g/l BuOH	5.7	51856	4	Cytoplasmic	COG1875	General function prediction only	

26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	6.4	6.51E-05	0,75 g/l BuOH	5.6	36424	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.2	9.89E-01	7,5 g/l BuOH	5.6	69049	6	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988049	PP_1314		aldo/keto reductase family oxidoreductase	1.7	2.14E-01	0,75 g/l BuOH	6.5	38777	2	Cytoplasmic	COG0667	Energy production and conversion	
26988050	PP_1315	rplM	50S ribosomal protein L13	1.2	6.11E-01	0,75 g/l BuOH	10.3	15862	2	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.4	4.96E-01	7,5 g/l BuOH	11.7	14592	4	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.9	1.84E-01	7,5 g/l BuOH	8.4	45901	5	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.4	5.55E-01	7,5 g/l BuOH	7.1	29032	6	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.1	8.49E-01	7,5 g/l BuOH	7.5	64637	10	Cytoplasmic Membrane	COG3107	General function prediction only	
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.2	5.00E-01	0,75 g/l BuOH	5.3	53602	2	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.5	7.20E-01	0,75 g/l BuOH	6.6	46750	2	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	1.1	7.04E-01	0,75 g/l BuOH	9.9	38127	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	1.7	2.14E-01	0,75 g/l BuOH	4.9	47444	5	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988076	PP_1342	ftsZ	cell division protein FtsZ	1.1	9.47E-01	7,5 g/l BuOH	4.7	41830	3	Cytoplasmic	COG0206	Cell division and chromosome partitioning	
26988093	PP_1359	fxsA	FxsA	1.3	3.89E-01	7,5 g/l BuOH	10.6	16958	2	Cytoplasmic Membrane	COG3030	General function prediction only	
26988095	PP_1361	groEL	chaperonin GroEL	1.0	9.79E-01	0,75 g/l BuOH	4.7	56743	13	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	2.0	2.19E-01	0,75 g/l BuOH	6.7	52057	12	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.1	5.08E-01	7,5 g/l BuOH	4.8	67652	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	1.5	3.61E-01	7,5 g/l BuOH	9.6	52425	2	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.1	7.72E-01	7,5 g/l BuOH	5.1	52864	13	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988152	PP_1419		outer membrane porin	1.4	8.08E-01	7,5 g/l BuOH	4.9	46644	4	Outer Membrane			
26988159	PP_1426	nadB	L-aspartate oxidase	1.7	7.81E-01	7,5 g/l BuOH	5.8	59215	2	Cytoplasmic	COG0029	Coenzyme metabolism	
26988164	PP_1431	lepA	GTP-binding protein LepA	1.1	7.58E-01	7,5 g/l BuOH	5.5	66116	4	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.2	6.97E-01	7,5 g/l BuOH	9.2	32060	3	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988169	PP_1436	pdxJ	pyridoxine 5'-phosphate synthase	1.1	9.06E-01	7,5 g/l BuOH	6.2	26737	2	Cytoplasmic	COG0854	Coenzyme metabolism	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.3	6.67E-01	7,5 g/l BuOH	6.0	86581	10	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.2	4.69E-01	0,75 g/l BuOH	5.7	42575	5	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	2.8	6.53E-02	7,5 g/l BuOH	9.0	45563	3	Cytoplasmic Membrane			
26988192	PP_1459		CBS domain-containing protein	2.0	2.12E-01	7,5 g/l BuOH	4.7	44174	2	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.5	9.27E-01	0,75 g/l BuOH	11.0	13012	4	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988203	PP_1470	hom	homoserine dehydrogenase	1.0	7.60E-01	0,75 g/l BuOH	5.1	46194	5	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.0	8.92E-01	7,5 g/l BuOH	6.2	51645	11	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.2	6.30E-01	0,75 g/l BuOH	5.8	40626	4	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.2	5.39E-01	0,75 g/l BuOH	5.7	50918	6	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.8	4.77E-01	7,5 g/l BuOH	4.7	58605	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.8	3.08E-01	7,5 g/l BuOH	6.6	96963	2	Cytoplasmic	COG2352	Energy production and conversion	
26988258	PP_1526		beta-(1-3)-glucosyl transferase	1.3	4.13E-01	7,5 g/l BuOH	8.1	97324	3	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism	
26988320	PP_1588		succinyldiaminopimelate transaminase	1.2	6.52E-01	0,75 g/l BuOH	5.4	43759	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.8	3.80E-01	0,75 g/l BuOH	9.3	27023	17	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.9	1.81E-01	0,75 g/l BuOH	4.9	30432	8	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988330	PP_1598		membrane-associated zinc metalloprotease	2.1	2.75E-01	7,5 g/l BuOH	9.3	48321	2	Cytoplasmic Membrane	COG0750	Cell envelope biogenesis, outer membrane	
26988331	PP_1599		surface antigen family outer membrane protein	1.0	7.93E-01	7,5 g/l BuOH	4.7	86513	11	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.2	5.63E-01	0,75 g/l BuOH	6.0	35135	5	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.5	4.34E-01	0,75 g/l BuOH	5.8	59474	13	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.9	1.17E-01	0,75 g/l BuOH	4.7	45490	6	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988361	PP_1629	recA	recombinase A	1.2	8.11E-01	7,5 g/l BuOH	5.3	37545	4	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988391	PP_1659		hypothetical protein	8.3	2.38E-03	0,75 g/l BuOH	5.9	48336	6	Periplasmic			
26988393	PP_1661		dehydrogenase subunit	2.6	4.56E-02	0,75 g/l BuOH	5.5	81020	9	Extracellular	COG2303	Amino acid transport and metabolism	
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	1.8	3.07E-01	0,75 g/l BuOH	4.6	36942	6	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.3	6.04E-01	7,5 g/l BuOH	5.4	45693	10	Outer Membrane	COG2067	Lipid metabolism	
26988452	PP_1720		alcohol dehydrogenase, zinc-containing	1.2	3.84E-01	0,75 g/l BuOH	4.7	33921	2	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26988468	PP_1737		VacJ family lipoprotein	2.1	3.02E-01	7,5 g/l BuOH	4.9	28084	2	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988474	PP_1743	actP	acetate permease	5.2	8.01E-02	7,5 g/l BuOH	9.6	58972	8	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	1.4	2.31E-01	7,5 g/l BuOH	8.2	57637	4	Cytoplasmic	COG2326	Function unknown	
26988486	PP_1755	fumC-2	fumarate hydratase	1.6	1.52E-01	0,75 g/l BuOH	6.4	49131	7	Cytoplasmic	COG0114	Energy production and conversion	
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.1	5.80E-01	7,5 g/l BuOH	4.7	102037	9	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988499	PP_1768	serC	phosphoserine aminotransferase	1.1	6.82E-01	0,75 g/l BuOH	5.1	39911	2	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
26988500	PP_1769	pheA	chorismate mutase	1.5	3.37E-01	0,75 g/l BuOH	6.4	40816	3	Cytoplasmic	COG0077	Amino acid transport and metabolism	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	1.0	7.18E-01	7,5 g/l BuOH	6.4	79133	7	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988511	PP_1780		mannosyltransferase	1.4	4.16E-01	7,5 g/l BuOH	5.8	180042	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	1.0	7.85E-01	7,5 g/l BuOH	6.1	40690	4	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	1.6	2.47E-01	7,5 g/l BuOH	6.4	128499	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	1.3	4.60E-01	0,75 g/l BuOH	5.9	58534	7	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.2	5.10E-01	7,5 g/l BuOH	6.4	40124	6	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988568	PP_1838		hypothetical protein	3.1	7.61E-02	7,5 g/l BuOH	6.8	76615	6	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.3	4.91E-01	7,5 g/l BuOH	9.2	60924	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988601	PP_1871	htpX	heat shock protein HtpX	2.5	5.08E-02	7,5 g/l BuOH	7.2	32199	3	Cytoplasmic Membrane	COG0501	Posttranslational modification, protein turnover, chaperones	
26988602	PP_1872		aminotransferase AlaT	1.2	8.52E-01	0,75 g/l BuOH	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.4	2.29E-01	7,5 g/l BuOH	6.9	89194	16	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.5	4.24E-01	7,5 g/l BuOH	4.7	120904	11	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP_1908		signal peptide peptidase SppA, 36K type	4.5	7.03E-02	7,5 g/l BuOH	6.4	36497	2	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.6	2.48E-01	0,75 g/l BuOH	4.7	32614	3	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.3	4.50E-01	7,5 g/l BuOH	6.0	25470	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.7	4.01E-03	7,5 g/l BuOH	5.9	43290	10	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.4	5.26E-01	7,5 g/l BuOH	5.6	56483	5	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	1.9	8.55E-01	7,5 g/l BuOH	5.6	51255	3	Cytoplasmic	COG0065	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.1	6.47E-01	0,75 g/l BuOH	5.3	40672	9	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.4	3.71E-01	7,5 g/l BuOH	3.9	96918	17	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.6	3.27E-01	0,75 g/l BuOH	7.8	32510	2	Cytoplasmic	COG0777	Lipid metabolism	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.2	5.91E-01	7,5 g/l BuOH	6.5	55400	9	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	1.4	2.88E-01	0,75 g/l BuOH	5.4	43284	3	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26988731	PP_2006		hypothetical protein	7.2	7.94E-03	0,75 g/l BuOH	5.1	63743	25	Unknown			
26988732	PP_2007		P-47-related protein	4.8	1.00E-01	0,75 g/l BuOH	5.8	44707	2	Unknown			
26988742	PP_2017	pepN	aminopeptidase N	1.1	8.64E-01	0,75 g/l BuOH	4.8	99573	13	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988744	PP_2019		hypothetical protein	1.6	3.23E-01	7,5 g/l BuOH	6.6	87732	3	Cytoplasmic Membrane	COG1033	General function prediction only	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.3	2.66E-01	7,5 g/l BuOH	5.8	187043	22	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.2	6.54E-01	7,5 g/l BuOH	4.8	86015	18	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	2.0	2.48E-01	7,5 g/l BuOH	5.8	29111	2	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.2	6.44E-01	0,75 g/l BuOH	4.5	37012	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	1.4	3.70E-01	0,75 g/l BuOH	6.0	57068	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms

26988836	PP_2112	acnA	aconitate hydratase	1.1	9.71E-01	0,75 g/l BuOH	5.7	99147	4	Cytoplasmic	COG1048	Energy production and conversion	
26988852	PP_2128	chev-2	chemotaxis protein CheV	2.7	9.21E-02	0,75 g/l BuOH	6.5	34556	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26988854	PP_2130		soluble lytic transglycosylase	2.6	2.83E-01	7,5 g/l BuOH	9.9	75337	6	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.0	9.58E-01	7,5 g/l BuOH	5.9	77449	3	Cytoplasmic	COG1250	Lipid metabolism	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.5	4.38E-01	7,5 g/l BuOH	7.7	53014	18	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	2.7	8.62E-03	7,5 g/l BuOH	7.7	50905	2	Cytoplasmic	COG1249	Energy production and conversion	
26988878	PP_2154	lolC	lipoprotein releasing system, transmembrane protein, LolC/E family	3.9	2.51E-01	7,5 g/l BuOH	9.6	45666	2	Cytoplasmic Membrane	COG4591	Cell envelope biogenesis, outer membrane	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.4	4.52E-01	7,5 g/l BuOH	5.3	26061	6	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988892	PP_2168	tal	transaldolase B	1.1	7.26E-01	0,75 g/l BuOH	5.0	33615	5	Unknown	COG0176	Carbohydrate transport and metabolism	
26988911	PP_2187		universal stress protein	3.2	9.83E-02	0,75 g/l BuOH	6.3	31384	2	Cytoplasmic	COG0589	Signal transduction mechanisms	
26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	1.1	9.02E-01	7,5 g/l BuOH	6.0	61223	6	Cytoplasmic	COG0365	Lipid metabolism	
26988939	PP_2215	fadAx	acetyl-CoA acetyltransferase	1.4	5.44E-01	0,75 g/l BuOH	6.9	41382	2	Cytoplasmic	COG0183	Lipid metabolism	
26988941	PP_2217	fadB1x	enoyl-CoA hydratase/isomerase	1.2	6.25E-01	0,75 g/l BuOH	5.2	27668	2	Cytoplasmic	COG1024	Lipid metabolism	
26988957	PP_2233		isochorismatase superfamily hydrolase	6.1	4.14E-03	7,5 g/l BuOH	6.0	19296	6	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988962	PP_2238		peptidase M24	1.1	6.54E-01	0,75 g/l BuOH	5.4	68915	2	Unknown	COG0006	Amino acid transport and metabolism	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.2	5.15E-01	0,75 g/l BuOH	5.1	68646	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.6	2.08E-01	0,75 g/l BuOH	4.8	48526	7	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
26989026	PP_2302	lon-2	ATP-dependent protease La	1.3	4.57E-01	7,5 g/l BuOH	5.9	88722	9	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.2	8.16E-01	0,75 g/l BuOH	9.3	9997	2	Unknown			
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	1.6	4.20E-01	7,5 g/l BuOH	8.5	8801	3	Outer Membrane			
26989048	PP_2324	aroF-1	phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	4.73E-01	0,75 g/l BuOH	6.4	40260	2	Cytoplasmic	COG0722	Amino acid transport and metabolism	
26989055	PP_2331		hypothetical protein	2.5	1.28E-01	7,5 g/l BuOH	7.9	57064	5	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	9.07E-01	7,5 g/l BuOH	5.0	93609	28	Cytoplasmic	COG1049	Energy production and conversion	
26989075	PP_2351		acetyl-CoA synthetase	1.8	3.58E-01	7,5 g/l BuOH	6.1	68868	6	Cytoplasmic	COG0365	Lipid metabolism	
26989088	PP_2364		hypothetical protein	1.6	3.11E-01	0,75 g/l BuOH	5.2	42461	4	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.1	6.16E-01	7,5 g/l BuOH	5.8	62191	11	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP_2375	metH	B12-dependent methionine synthase	1.0	8.94E-01	0,75 g/l BuOH	4.7	135408	8	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	1.2	4.97E-01	0,75 g/l BuOH	4.8	20507	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.1	9.37E-01	0,75 g/l BuOH	5.8	72697	9	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP_2466	infC	translation initiation factor IF-3	1.5	3.35E-01	0,75 g/l BuOH	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.1	8.13E-01	0,75 g/l BuOH	12.1	13280	5	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989193	PP_2470	pheT	phenylalanyl-tRNA synthetase subunit beta	1.3	7.56E-01	7,5 g/l BuOH	4.8	86617	3	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis	
26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	1.1	8.32E-01	7,5 g/l BuOH	6.5	45235	2	Cytoplasmic	COG2873	Amino acid transport and metabolism	
26989256	PP_2536		glutathione S-transferase family protein	1.7	1.19E-01	7,5 g/l BuOH	6.5	23574	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989289	PP_2569		major facilitator transporter	1.0	7.72E-01	0,75 g/l BuOH	9.0	60538	5	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989381	PP_2662		hypothetical protein	266.4	5.91E-03	7,5 g/l BuOH	4.3	42858	20	Outer Membrane			
26989382	PP_2663		hypothetical protein	15.0	1.56E-03	7,5 g/l BuOH	6.3	42469	4	Cytoplasmic	COG3287	Function unknown	
26989383	PP_2664		PAS/PAC sensor hybrid histidine kinase	9.7	1.66E-02	7,5 g/l BuOH	6.6	73094	9	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989387	PP_2668		efflux ABC transporter ATP-binding protein	8.7	2.16E-02	7,5 g/l BuOH	9.8	27178	6	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26989392	PP_2673		pentapeptide repeat-containing protein	13.7	2.03E-02	7,5 g/l BuOH	5.3	23569	1	Extracellular	COG1357	Function unknown	
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.0	6.64E-04	7,5 g/l BuOH	7.0	69173	32	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989395	PP_2676		periplasmic protein	23.8	9.44E-03	7,5 g/l BuOH	6.5	34540	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26989396	PP_2677		hypothetical protein	18.7	9.08E-03	7,5 g/l BuOH	5.3	28059	2	Unknown			
26989398	PP_2679		quinoprotein ethanol dehydrogenase	59.0	2.11E-03	7,5 g/l BuOH	9.1	64883	3	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	13.6	2.42E-05	7,5 g/l BuOH	5.5	54903	38	Cytoplasmic	COG1012	Energy production and conversion	
26989402	PP_2683		PAS/PAC sensor hybrid histidine kinase	5.7	6.64E-02	7,5 g/l BuOH	6.6	62695	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1.1	8.33E-01	7,5 g/l BuOH	6.3	38659	10	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26989546	PP_2827		alcohol dehydrogenase, zinc-containing	1.0	7.52E-01	0,75 g/l BuOH	5.4	36735	2	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26989572	PP_2853		hypothetical protein	1.2	9.51E-01	7,5 g/l BuOH	4.5	46020	4	Unknown			
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	1.0	8.64E-01	0,75 g/l BuOH	5.7	58659	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.2	6.77E-01	0,75 g/l BuOH	6.1	64654	6	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	1.2	8.56E-01	0,75 g/l BuOH	5.0	35225	2	Cytoplasmic	COG0113	Coenzyme metabolism	
26989647	PP_2928		saccharopine dehydrogenase	1.3	3.92E-01	0,75 g/l BuOH	5.0	45363	4	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989663	PP_2944		sensor histidine kinase	1.7	4.69E-01	7,5 g/l BuOH	6.1	67470	4	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989809	PP_3090		OmpA domain-containing protein	20.5	6.38E-02	7,5 g/l BuOH	9.0	93143	6	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	20.3	6.33E-02	7,5 g/l BuOH	6.8	138655	12	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	7.3	1.33E-01	7,5 g/l BuOH	5.7	26868	5	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989814	PP_3095		chaperone-associated ATPase	4.6	3.26E-02	7,5 g/l BuOH	6.1	96474	4	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26989818	PP_3099		hypothetical protein	16.1	6.71E-02	7,5 g/l BuOH	4.9	56072	20	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989824	PP_3105		hypothetical protein	14.3	4.05E-01	7,5 g/l BuOH	10.5	26470	2	Cytoplasmic Membrane			
26989825	PP_3106		hypothetical protein	1.3	8.11E-01	7,5 g/l BuOH	5.6	69529	13	Cytoplasmic	COG3501	Function unknown	
26989827	PP_3108		rhs-related protein	1.2	6.69E-01	7,5 g/l BuOH	6.0	155811	4	Unknown	COG3209	Cell envelope biogenesis, outer membrane	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.4	7.12E-01	7,5 g/l BuOH	9.0	57141	8	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989853	PP_3134		transferase hexapeptide repeat containing protein	1.9	2.13E-01	0,75 g/l BuOH	9.9	25699	3	Cytoplasmic	COG0110	General function prediction only	
26989854	PP_3135		glycosyl transferase	1.3	4.12E-01	7,5 g/l BuOH	8.6	35887	5	Cytoplasmic	COG1216	General function prediction only	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.4	5.87E-01	7,5 g/l BuOH	9.4	43092	3	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989860	PP_3141		Wec8/TagA/CpsF family glycosyl transferase	1.4	3.25E-01	7,5 g/l BuOH	10.2	27576	2	Unknown	COG1922	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	1.0	9.16E-01	7,5 g/l BuOH	9.7	29885	3	Unknown			
26990154	PP_3441		hypothetical protein	1.1	7.54E-01	7,5 g/l BuOH	9.3	43139	2	Cytoplasmic			
26990176	PP_3463		aldehyde dehydrogenase	1.1	3.73E-01	7,5 g/l BuOH	5.7	53383	2	Cytoplasmic	COG1012	Energy production and conversion	
26990220	PP_3508	cobW	cobalamin biosynthesis protein CobW	1.4	3.13E-01	0,75 g/l BuOH	4.6	38579	2	Cytoplasmic	COG0523	General function prediction only	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.4	3.43E-01	0,75 g/l BuOH	7.2	36863	13	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990265	PP_3553		acyl-CoA synthetase	5.2	9.94E-03	7,5 g/l BuOH	6.4	59576	12	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	3.1	2.51E-02	7,5 g/l BuOH	5.5	63339	4	Cytoplasmic	COG1960	Lipid metabolism	
26990269	PP_3557		methyl-accepting chemotaxis transducer	1.5	2.56E-01	7,5 g/l BuOH	4.7	76982	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	1.7	3.76E-01	7,5 g/l BuOH	6.9	85338	7	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990290	PP_3578		phosphoglucomutase	1.3	6.70E-01	7,5 g/l BuOH	5.6	58620	4	Unknown	COG0033	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	2.2	6.37E-02	7,5 g/l BuOH	5.2	53952	5	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.5	5.71E-01	7,5 g/l BuOH	5.9	43631	6	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990313	PP_3602		ketoglutarate semialdehyde dehydrogenase	1.3	7.71E-01	0,75 g/l BuOH	5.2	55538	3	Cytoplasmic	COG1012	Energy production and conversion	
26990349	PP_3638		acyl-CoA dehydrogenase	1.5	2.24E-01	0,75 g/l BuOH	6.1	38476	4	Cytoplasmic	COG1960	Lipid metabolism	
26990367	PP_3656		aromatic compound-specific porin	18.6	6.57E-02	7,5 g/l BuOH	5.3	46672	10	Outer Membrane			
26990369	PP_3658		aromatic compound MFS transporter	10.3	5.74E-01	7,5 g/l BuOH	9.5	48129	4	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26990373	PP_3662		decarboxylase family protein	1.8	6.73E-01	7,5 g/l BuOH	6.7	50729	3	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	1.3	6.89E-02	7,5 g/l BuOH	5.8	82061	13	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990399	PP_3691		DNA helicase-related protein	2.0	1.73E-01	7,5 g/l BuOH	5.0	245278	11	Unknown	COG1112	DNA replication, recombination, and repair	
26990459	PP_3754		beta-ketothiolase	2.9	7.42E-02	7,5 g/l BuOH	6.9	40988	6	Cytoplasmic	COG0183	Lipid metabolism	
26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	3.1	2.05E-02	7,5 g/l BuOH	6.3	30088	3	Cytoplasmic	COG1250	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.7	1.36E-01	7,5 g/l BuOH	4.9	129450	10	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	

26990480	PP_3775		sarcosine oxidase	1.9	4.28E-02	0,75 g/l BuOH	6.4	41164	12	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990481	PP_3776	rarD-3	rarD protein	2.1	1.78E-01	7,5 g/l BuOH	9.5	32267	2	Cytoplasmic Membrane	COG2962	General function prediction only	
26990482	PP_3777		hypothetical protein	1.7	2.02E-01	0,75 g/l BuOH	5.2	31324	4	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	2.0	4.11E-02	0,75 g/l BuOH	6.2	27714	6	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	2.0	2.63E-03	7,5 g/l BuOH	7.0	53071	6	Cytoplasmic	COG0635	Coenzyme metabolism	
26990489	PP_3784		hypothetical protein	1.5	8.23E-02	0,75 g/l BuOH	5.4	41070	5	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	1.2	7.72E-01	0,75 g/l BuOH	6.5	50495	4	Cytoplasmic			
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.5	2.32E-01	0,75 g/l BuOH	5.3	30957	7	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990544	PP_3839		alcohol dehydrogenase	2.4	1.16E-01	0,75 g/l BuOH	5.7	35397	9	Cytoplasmic	COG1064	General function prediction only	
26990662	PP_3957		choline/carnitine/betaine transporter family protein	1.6	2.92E-01	7,5 g/l BuOH	7.6	72789	3	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane	
26990695	PP_3990		hypothetical protein	1.1	6.70E-01	7,5 g/l BuOH	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990705	PP_4000	serS	seryl-tRNA synthetase	1.7	2.31E-01	0,75 g/l BuOH	5.1	46849	2	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	3.6	7.28E-02	7,5 g/l BuOH	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.3	8.72E-01	0,75 g/l BuOH	5.7	83310	4	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.6	2.42E-01	0,75 g/l BuOH	5.4	45695	9	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	2.8	1.09E-01	0,75 g/l BuOH	5.4	79899	17	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.1	9.04E-01	7,5 g/l BuOH	5.9	50555	7	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990737	PP_4034		allantoate amidohydrolase	2.6	4.58E-02	0,75 g/l BuOH	5.7	45010	19	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.1	6.87E-01	7,5 g/l BuOH	7.9	53519	5	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP_4037		oxidoreductase	1.9	1.59E-01	0,75 g/l BuOH	5.5	48815	20	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038		dihydropyrimidine dehydrogenase	1.6	2.34E-01	0,75 g/l BuOH	5.1	46093	18	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990753	PP_4052	malQ	4-alpha-glucanotransferase	1.5	2.87E-01	0,75 g/l BuOH	5.5	76475	6	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	1.1	9.55E-01	0,75 g/l BuOH	6.6	103167	2	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	1.6	4.01E-01	0,75 g/l BuOH	5.1	81044	6	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990759	PP_4058	glgB	glycogen branching enzyme	1.4	4.63E-01	0,75 g/l BuOH	5.9	82877	2	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990761	PP_4060		alpha-amylase family protein	1.8	2.67E-01	0,75 g/l BuOH	6.1	75542	2	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990806	PP_4111	fusA	elongation factor G	1.1	7.29E-01	0,75 g/l BuOH	5.0	77832	9	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990810	PP_4116	aceA	isocitrate lyase	27.4	8.34E-05	7,5 g/l BuOH	5.3	48633	16	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.0	7.68E-01	7,5 g/l BuOH	6.5	67609	9	Cytoplasmic	COG0649	Energy production and conversion	
26990817	PP_4123	nuoF	NADH dehydrogenase I subunit F	1.4	3.99E-01	0,75 g/l BuOH	7.1	49135	8	Cytoplasmic	COG1894	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.1	7.37E-01	0,75 g/l BuOH	5.9	97582	13	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	2.2	2.05E-01	7,5 g/l BuOH	6.1	37637	3	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.1	8.05E-01	0,75 g/l BuOH	8.7	20354	2	Cytoplasmic	COG0431	General function prediction only	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.9	1.35E-01	0,75 g/l BuOH	5.3	43264	8	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.4	9.15E-02	0,75 g/l BuOH	6.2	30111	13	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	2.0	1.09E-01	0,75 g/l BuOH	6.1	41239	20	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.8	3.20E-01	0,75 g/l BuOH	6.3	49912	12	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.0	8.28E-01	7,5 g/l BuOH	5.1	42434	5	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.1	7.63E-01	0,75 g/l BuOH	6.5	106521	21	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.1	5.92E-01	0,75 g/l BuOH	7.5	26000	6	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	5.74E-01	0,75 g/l BuOH	6.2	63448	21	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.2	2.83E-02	0,75 g/l BuOH	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.5	8.41E-02	7,5 g/l BuOH	7.0	47622	13	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.4	3.15E-01	7,5 g/l BuOH	9.7	26361	6	Unknown	COG2086	Energy production and conversion	
26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	1.8	2.37E-01	7,5 g/l BuOH	5.7	61082	8	Cytoplasmic	COG0644	Energy production and conversion	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	2.0	9.57E-02	7,5 g/l BuOH	9.6	53567	3	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.8	4.14E-01	7,5 g/l BuOH	9.0	22637	5	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	2.2	2.03E-01	7,5 g/l BuOH	5.2	35613	12	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	3.0	1.62E-01	7,5 g/l BuOH	8.5	53406	3	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990951	PP_4260		hypothetical protein	13.1	7.08E-02	7,5 g/l BuOH	4.9	19451	2	Unknown	COG3198	Function unknown	
26990966	PP_4275	zipA	cell division protein ZipA	1.9	2.51E-01	7,5 g/l BuOH	6.0	35312	9	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991011	PP_4321	dsbE	periplasmic protein thiol--disulphide oxidoreductase DsbE	18.8	1.72E-02	7,5 g/l BuOH	6.5	19892	3	Cytoplasmic Membrane	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26991012	PP_4322	ccmF	cytochrome c-type biogenesis protein CcmF	12.3	2.45E-02	7,5 g/l BuOH	9.7	72089	4	Cytoplasmic Membrane	COG1138	Posttranslational modification, protein turnover, chaperones	
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	1.6	2.83E-01	0,75 g/l BuOH	9.0	39451	5	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
26991028	PP_4338	cheA	chemotaxis protein CheA	1.1	8.32E-01	7,5 g/l BuOH	4.4	79674	5	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.1	9.94E-01	0,75 g/l BuOH	5.4	55551	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991082	PP_4393	cheV-3	chemotaxis protein CheV	1.5	3.75E-01	0,75 g/l BuOH	6.2	34498	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26991086	PP_4397		type IV pilus assembly PilZ	1.8	2.45E-01	0,75 g/l BuOH	6.7	28449	2	Cytoplasmic	COG5581	Signal transduction mechanisms	
26991088	PP_4399		glutamine synthetase	1.4	6.10E-01	0,75 g/l BuOH	6.2	45023	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991134	PP_4448		hypothetical protein	1.5	2.79E-01	0,75 g/l BuOH	6.0	66331	10	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991159	PP_4473		aspartate kinase	1.1	7.01E-01	7,5 g/l BuOH	5.0	44605	3	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.1	9.27E-01	0,75 g/l BuOH	5.1	94711	11	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991161	PP_4475	astE	succinylglutamate desuccinylase	3.4	3.87E-01	0,75 g/l BuOH	6.2	37580	2	Cytoplasmic	COG2988	Amino acid transport and metabolism	
26991163	PP_4477	astB	succinylarginine dihydrolase	1.8	2.44E-01	0,75 g/l BuOH	6.4	48862	2	Cytoplasmic	COG3724	Amino acid transport and metabolism	
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.2	5.78E-01	7,5 g/l BuOH	5.4	51330	2	Cytoplasmic	COG1012	Energy production and conversion	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.2	5.84E-01	0,75 g/l BuOH	6.5	43490	10	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	6.6	2.30E-04	7,5 g/l BuOH	6.4	71796	45	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.0	1.41E-01	0,75 g/l BuOH	5.4	50393	21	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	1.2	8.51E-01	7,5 g/l BuOH	6.4	56605	8	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.3	2.97E-01	0,75 g/l BuOH	5.7	42326	3	Cytoplasmic	COG0332	acyl-carrier-protein	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.3	4.02E-01	7,5 g/l BuOH	7.7	61812	4	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	1.6	3.88E-01	0,75 g/l BuOH	7.8	61658	5	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991254	PP_4570		hypothetical protein	2.8	1.11E-01	7,5 g/l BuOH	10.1	35846	4	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991255	PP_4571	cysK	cysteine synthase A	1.2	9.91E-01	0,75 g/l BuOH	5.5	34357	3	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991319	PP_4635		trans-2-enoyl-CoA reductase	2.2	9.11E-02	0,75 g/l BuOH	5.0	44265	3	Cytoplasmic	COG3007	Function unknown	
26991325	PP_4641	cstA	carbon starvation protein CstA	1.4	4.46E-01	7,5 g/l BuOH	9.0	73763	9	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.5	3.37E-01	7,5 g/l BuOH	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	1.9	2.81E-01	7,5 g/l BuOH	9.1	53016	3	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.6	5.36E-01	7,5 g/l BuOH	4.8	68764	4	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.3	3.56E-01	0,75 g/l BuOH	5.4	36370	17	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.7	2.16E-01	7,5 g/l BuOH	6.8	62781	9	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991368	PP_4684		hypothetical protein	1.3	6.81E-01	0,75 g/l BuOH	5.1	56095	5	Cytoplasmic	COG2187	Function unknown	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.0	8.33E-01	7,5 g/l BuOH	6.8	61455	6	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	1.5	2.87E-01	0,75 g/l BuOH	6.5	71251	5	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	4.1	3.83E-01	7,5 g/l BuOH	5.6	107252	3	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.1	6.54E-01	0,75 g/l BuOH	4.9	75010	24	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.1	9.33E-01	0,75 g/l BuOH	6.8	91460	12	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP_4713	nusA	transcription elongation factor NusA	1.2	9.39E-01	7,5 g/l BuOH	4.3	54673	6	Cytoplasmic	COG0195	Transcription	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	2.1	1.75E-01	7,5 g/l BuOH	5.4	69722	16	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	

26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	1.0	7.53E-01	0,75 g/l BuOH	5.8	40574	2	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.5	3.76E-01	0,75 g/l BuOH	4.6	68800	21	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991462	PP_4782	thiD	phosphomethylpyrimidine kinase	2.2	3.68E-01	0,75 g/l BuOH	5.1	28338	2	Cytoplasmic	COG0351	Coenzyme metabolism	
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.1	7.53E-01	0,75 g/l BuOH	5.7	45178	5	Cytoplasmic	COG0001	Coenzyme metabolism	
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	2.5	1.69E-01	7,5 g/l BuOH	8.5	56126	2	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.3	5.37E-01	7,5 g/l BuOH	5.6	96697	10	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	1.2	6.11E-01	7,5 g/l BuOH	6.1	22414	2	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991478	PP_4798		lytic murein transglycosylase	20.6	7.18E-02	7,5 g/l BuOH	7.7	48000	1	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.4	3.47E-01	0,75 g/l BuOH	6.1	45417	7	Cytoplasmic	COG0014	Amino acid transport and metabolism	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.5	3.73E-01	0,75 g/l BuOH	6.5	57695	2	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.8	1.88E-01	0,75 g/l BuOH	4.7	45837	5	Cytoplasmic	COG0151	Nucleotide transport and metabolism	
26991518	PP_4838	oprC	TonB-dependent copper receptor	41.9	2.09E-01	7,5 g/l BuOH	6.2	74540	5	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	1.0	9.00E-01	0,75 g/l BuOH	6.6	32427	2	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	4.0	3.19E-02	0,75 g/l BuOH	6.2	40270	8	Periplasmic	COG0683	Amino acid transport and metabolism	
26991550	PP_4870		azurin	15.9	1.51E-03	7,5 g/l BuOH	6.9	16028	5	Periplasmic	COG3241	Energy production and conversion	
26991556	PP_4876	rpsR	30S ribosomal protein S18	1.4	1.04E-02	7,5 g/l BuOH	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991557	PP_4877	rpsF	30S ribosomal protein S6	1.5	2.93E-01	0,75 g/l BuOH	4.7	16373	2	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.6	5.46E-03	0,75 g/l BuOH	7.9	96688	2	Cytoplasmic	COG0557	Transcription	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.4	5.29E-02	0,75 g/l BuOH	6.1	71958	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.3	4.29E-01	0,75 g/l BuOH	5.6	46833	13	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991568	PP_4890	hisZ	ATP phosphoribosyltransferase regulatory subunit	1.1	8.72E-01	7,5 g/l BuOH	4.7	42935	4	Cytoplasmic	COG3705	Amino acid transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.2	6.87E-01	7,5 g/l BuOH	9.8	33001	12	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.5	6.30E-01	7,5 g/l BuOH	5.1	44762	2	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991583	PP_4905		flagellar motor protein MotA	1.0	8.26E-01	7,5 g/l BuOH	6.2	30312	3	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.3	3.92E-01	7,5 g/l BuOH	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991588	PP_4910		hypothetical protein	1.7	2.10E-01	7,5 g/l BuOH	4.7	53632	7	Cytoplasmic	COG3726	General function prediction only	
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	1.3	6.20E-01	7,5 g/l BuOH	6.2	83181	2	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.1	8.08E-01	7,5 g/l BuOH	5.2	52637	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	2.0	6.82E-02	7,5 g/l BuOH	7.6	66279	10	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991622	PP_4944		carbamoyltransferase	1.1	6.22E-01	7,5 g/l BuOH	7.2	65646	9	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	1.0	8.52E-01	0,75 g/l BuOH	6.3	142580	9	Cytoplasmic	COG4230	Energy production and conversion	
26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	1.3	5.44E-01	0,75 g/l BuOH	4.8	78896	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.4	3.30E-01	0,75 g/l BuOH	5.6	38453	11	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991641	PP_4963	pgk	phosphoglycerate kinase	2.0	2.03E-01	0,75 g/l BuOH	4.9	40005	3	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
26991643	PP_4965	tktA	transketolase	1.1	7.41E-01	0,75 g/l BuOH	5.0	72463	15	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.9	5.35E-02	0,75 g/l BuOH	5.1	42779	17	Cytoplasmic	COG0192	Coenzyme metabolism	
26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	2.8	3.01E-02	0,75 g/l BuOH	6.2	32979	2	Cytoplasmic	COG0685	Amino acid transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.2	7.16E-01	0,75 g/l BuOH	5.7	49982	5	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	2.2	1.04E-01	0,75 g/l BuOH	7.4	62241	6	Cytoplasmic	COG3243	Lipid metabolism	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.7	8.23E-01	0,75 g/l BuOH	10.9	26214	7	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.1	7.65E-01	0,75 g/l BuOH	4.9	69017	24	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.8	3.27E-01	7,5 g/l BuOH	8.3	95875	4	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.1	5.91E-01	7,5 g/l BuOH	6.4	92004	5	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.1	7.25E-01	0,75 g/l BuOH	5.3	67157	4	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.5	3.53E-01	0,75 g/l BuOH	5.1	51740	13	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991732	PP_5056	pgm	phosphoglyceromutase	1.3	4.14E-01	0,75 g/l BuOH	4.9	55180	6	Cytoplasmic	COG0696	Carbohydrate transport and metabolism	
26991751	PP_5075	gltD	glutamate synthase subunit beta	1.3	6.15E-01	7,5 g/l BuOH	6.3	51819	2	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.5	1.84E-01	7,5 g/l BuOH	6.2	161772	17	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	2.1	9.94E-02	0,75 g/l BuOH	4.9	45127	18	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.3	7.25E-01	7,5 g/l BuOH	5.7	63668	8	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991766	PP_5090		sporulation domain protein	1.3	7.02E-01	7,5 g/l BuOH	10.6	24964	2	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	1.3	3.43E-01	7,5 g/l BuOH	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	1.7	3.02E-01	7,5 g/l BuOH	6.5	36984	3	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991796	PP_5120		conifer aldehyde dehydrogenase	2.0	1.95E-01	7,5 g/l BuOH	9.2	52453	3	Cytoplasmic	COG1012	Energy production and conversion	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.3	7.73E-01	0,75 g/l BuOH	5.8	65671	16	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.0	7.60E-01	0,75 g/l BuOH	6.3	44339	13	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	1.1	8.35E-01	7,5 g/l BuOH	5.4	112277	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	9.3	2.27E-01	7,5 g/l BuOH	6.5	42472	1	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	2.9	4.47E-02	0,75 g/l BuOH	6.4	40068	4	Periplasmic	COG0687	Amino acid transport and metabolism	
26991858	PP_5182		aminotransferase	1.3	5.50E-01	0,75 g/l BuOH	6.2	49871	4	Cytoplasmic	COG0161	Coenzyme metabolism	
26991859	PP_5183		glutamine synthetase	1.0	9.33E-01	7,5 g/l BuOH	4.8	50877	3	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991860	PP_5184		glutamine synthetase	1.2	6.02E-01	0,75 g/l BuOH	4.5	50974	3	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.2	9.03E-01	0,75 g/l BuOH	6.3	104037	4	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991890	PP_5214	rho	transcription termination factor Rho	1.1	5.70E-01	0,75 g/l BuOH	8.2	47041	5	Cytoplasmic	COG1158	Transcription	
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.1	6.71E-01	7,5 g/l BuOH	6.9	55958	3	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991893	PP_5217	ppk	polyphosphate kinase	2.4	6.27E-02	7,5 g/l BuOH	7.8	81732	7	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991934	PP_5258		aldehyde dehydrogenase family protein	1.4	4.55E-01	0,75 g/l BuOH	5.4	53106	2	Cytoplasmic	COG1012	Energy production and conversion	
26991954	PP_5278		aldehyde dehydrogenase family protein	1.6	3.35E-01	0,75 g/l BuOH	5.5	53053	6	Cytoplasmic	COG1012	Energy production and conversion	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.2	5.50E-01	7,5 g/l BuOH	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991964	PP_5288		phosphomannomutase	2.0	4.68E-02	7,5 g/l BuOH	5.0	50271	3	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	2.5	6.45E-02	7,5 g/l BuOH	9.2	78603	6	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991989	PP_5313	hupA	histone family protein DNA-binding protein	4.1	7.20E-01	0,75 g/l BuOH	11.0	10551	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.4	3.46E-01	0,75 g/l BuOH	5.2	38702	3	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.7	2.03E-01	0,75 g/l BuOH	5.3	65626	18	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.9	1.64E-01	0,75 g/l BuOH	6.5	51942	9	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.5	4.72E-01	7,5 g/l BuOH	7.2	30672	5	Cytoplasmic Membrane	COG4395	Function unknown	
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	1.1	9.11E-01	7,5 g/l BuOH	5.9	48114	2	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
26992055	PP_5379	copB	copper resistance B precursor	4.0	1.12E-01	0,75 g/l BuOH	5.0	40230	3	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992070	PP_5395		hypothetical protein	1.1	7.83E-01	7,5 g/l BuOH	5.6	31623	3	Cytoplasmic	COG1568	General function prediction only	
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.5	9.63E-01	7,5 g/l BuOH	6.0	66312	2	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	7.08E-01	0,75 g/l BuOH	4.6	49359	20	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.7	4.24E-01	0,75 g/l BuOH	9.2	31464	12	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.4	2.63E-01	0,75 g/l BuOH	5.2	55352	23	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.0	7.89E-01	7,5 g/l BuOH	5.3	16898	5	Cytoplasmic Membrane	COG0711	Energy production and conversion	
148550051				1.7	6.10E-02	0,75 g/l BuOH			20				
24982932				2.2	1.17E-01	0,75 g/l BuOH			2				
262377497				6.6	1.63E-01	0,75 g/l BuOH			2				
148545801				2.1	1.97E-01	0,75 g/l BuOH			2				
377579828				22.4	2.42E-01	0,75 g/l BuOH			9				

24983268	1.5	2.47E-01	0,75 g/l BuOH	19
261409533	3.5	2.54E-01	0,75 g/l BuOH	2
85060262	20.9	2.70E-01	0,75 g/l BuOH	2
313498081	1.4	2.88E-01	0,75 g/l BuOH	25
24982083	1.7	2.90E-01	0,75 g/l BuOH	5
308068146	3.7	3.38E-01	0,75 g/l BuOH	2
377579693	57.0	3.56E-01	0,75 g/l BuOH	14
24981833	1.3	3.59E-01	0,75 g/l BuOH	7
261409515	8.0	3.62E-01	0,75 g/l BuOH	2
377576772	31.2	3.63E-01	0,75 g/l BuOH	3
261409528	4.1	3.63E-01	0,75 g/l BuOH	5
377576450	17.0	3.97E-01	0,75 g/l BuOH	2
16760079	21.2	4.32E-01	0,75 g/l BuOH	7
354585424	4.8	4.82E-01	0,75 g/l BuOH	3
308069938	1.3	4.85E-01	0,75 g/l BuOH	5
377578772	68.9	5.03E-01	0,75 g/l BuOH	3
194367745	2.2	5.63E-01	0,75 g/l BuOH	5
148545524	1.2	5.68E-01	0,75 g/l BuOH	13
261408922	2.8	5.74E-01	0,75 g/l BuOH	3
377576294	23.8	5.91E-01	0,75 g/l BuOH	16
129138	14.8	6.64E-01	0,75 g/l BuOH	9
261341331	38.2	6.96E-01	0,75 g/l BuOH	2
261409526	2.9	7.18E-01	0,75 g/l BuOH	2
377578133	25.6	7.62E-01	0,75 g/l BuOH	2
261409489	2.2	8.25E-01	0,75 g/l BuOH	2
377577537	5.7	8.31E-01	0,75 g/l BuOH	5
377577725	7.3	8.34E-01	0,75 g/l BuOH	2
300718709	5.0	8.51E-01	0,75 g/l BuOH	2
24986054	2.7	9.10E-01	0,75 g/l BuOH	2
374606934	3.0	9.74E-01	0,75 g/l BuOH	4
298682197	8.1	3.72E-03	7,5 g/l BuOH	3
260609519	2.3	2.93E-02	7,5 g/l BuOH	5
194366647	43.4	3.02E-02	7,5 g/l BuOH	6
15599454	1.4	3.97E-02	7,5 g/l BuOH	5
194367479	29.3	4.98E-02	7,5 g/l BuOH	2
148546787	12.8	6.03E-02	7,5 g/l BuOH	3
344208989	24.6	7.00E-02	7,5 g/l BuOH	5
194364913	385.9	7.99E-02	7,5 g/l BuOH	2
194365395	11.7	9.40E-02	7,5 g/l BuOH	3
190573277	17.6	1.01E-01	7,5 g/l BuOH	2
24981839	1.7	1.07E-01	7,5 g/l BuOH	10
190572101	10.2	1.12E-01	7,5 g/l BuOH	7
194365946	17.6	1.22E-01	7,5 g/l BuOH	9
194364029	12.9	1.46E-01	7,5 g/l BuOH	2
222085864	45.5	2.04E-01	7,5 g/l BuOH	3
293604168	87.1	2.23E-01	7,5 g/l BuOH	3
190572496	2.5	2.41E-01	7,5 g/l BuOH	2
194364578	2.2	2.64E-01	7,5 g/l BuOH	11
254524919	2.9	2.66E-01	7,5 g/l BuOH	2
344205753	4.6	2.82E-01	7,5 g/l BuOH	3
190575561	2.8	2.84E-01	7,5 g/l BuOH	4
194367115	3.5	2.84E-01	7,5 g/l BuOH	2
254521740	3.2	3.43E-01	7,5 g/l BuOH	9
254521045	1.7	3.44E-01	7,5 g/l BuOH	10
190575345	1.6	3.90E-01	7,5 g/l BuOH	12
338780844	21.5	4.06E-01	7,5 g/l BuOH	12
222085378	104.3	4.16E-01	7,5 g/l BuOH	3
194364598	1.4	4.64E-01	7,5 g/l BuOH	2
24986476	1.2	4.85E-01	7,5 g/l BuOH	36
209548918	2.8	5.12E-01	7,5 g/l BuOH	2
24982353	1.1	5.53E-01	7,5 g/l BuOH	3
308070977	1.2	8.62E-01	7,5 g/l BuOH	2
313498866	1.2	8.66E-01	7,5 g/l BuOH	7
313496770	1.0	9.18E-01	7,5 g/l BuOH	12
251797465	1.5	9.85E-01	7,5 g/l BuOH	3

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.5	6.88E-01	0,75 g/l BuOH	9.1	61919	7	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.7	1.01E-01	0,75 g/l BuOH	4.9	40718	5	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	2.1	1.81E-01	0,75 g/l BuOH	5.8	90030	5	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.6	1.84E-01	0,75 g/l BuOH	6.1	31236	5	Cytoplasmic			
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.3	4.33E-01	0,75 g/l BuOH	4.9	75112	6	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.3	3.55E-01	0,75 g/l BuOH	8.1	34224	2	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986841	PP_0096	prlC	oligopeptidase A	1.2	5.96E-01	0,75 g/l BuOH	5.0	75721	8	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.2	4.64E-01	0,75 g/l BuOH	6.8	26001	6	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.2	4.82E-01	control	6.8	42059	7	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.5	2.87E-01	0,75 g/l BuOH	8.2	22960	2	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.1	7.81E-01	0,75 g/l BuOH	7.4	25597	2	Unknown			
26986909	PP_0165		GGDEF domain-containing protein	1.2	7.97E-01	0,75 g/l BuOH	6.3	71284	2	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986928	PP_0184	argH	argininosuccinate lyase	1.8	8.11E-02	0,75 g/l BuOH	5.4	52061	4	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.1	6.60E-01	0,75 g/l BuOH	9.6	46030	7	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	29.7	2.25E-02	0,75 g/l BuOH	11.3	32300	3	Cytoplasmic			
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.2	4.44E-01	0,75 g/l BuOH	5.2	51549	9	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.1	9.71E-01	control	6.1	44824	8	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.0	8.28E-01	control	5.4	48317	17	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.1	8.51E-01	0,75 g/l BuOH	5.2	15616	6	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.3	7.96E-01	control	6.1	47787	5	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.4	2.63E-01	0,75 g/l BuOH	6.0	80277	2	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987063	PP_0321		threonine aldolase	2.1	1.42E-01	0,75 g/l BuOH	5.4	38068	3	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	1.5	2.43E-01	0,75 g/l BuOH	4.7	24565	2	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.2	8.86E-01	0,75 g/l BuOH	5.3	55654	10	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.3	3.75E-01	0,75 g/l BuOH	5.6	99332	27	Cytoplasmic	COG2609	Energy production and conversion	
26987098	PP_0356	glcB	malate synthase G	1.7	1.87E-01	0,75 g/l BuOH	5.8	78346	2	Cytoplasmic	COG2225	Energy production and conversion	
26987108	PP_0366	bioD	dithiobiotin synthetase	1.1	9.33E-01	control	5.3	23871	2	Cytoplasmic	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	7.65E-01	0,75 g/l BuOH	5.8	65541	12	Cytoplasmic	COG1960	Lipid metabolism	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	48.0	1.73E-03	0,75 g/l BuOH	6.8	29075	2	Cytoplasmic	COG5424	Coenzyme metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.4	4.67E-01	control	4.6	69396	3	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.0	9.55E-01	0,75 g/l BuOH	11.4	8370	4	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987138	PP_0396		hypothetical protein	1.1	8.27E-01	control	7.0	50488	4	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.0	8.56E-01	0,75 g/l BuOH	5.8	73782	26	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987158	PP_0417	trpE	anthranilate synthase component I	2.1	2.47E-01	0,75 g/l BuOH	4.8	54406	2	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
26987159	PP_0418		GDSL family lipase	1.3	6.94E-01	0,75 g/l BuOH	4.4	67175	4	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.5	1.54E-01	0,75 g/l BuOH	6.8	36277	3	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987181	PP_0440	tuf	elongation factor Tu	1.4	3.72E-01	0,75 g/l BuOH	5.0	43495	2	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	1.5	2.99E-01	control	10.5	14866	5	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.3	6.94E-01	control	10.1	24251	7	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.3	2.82E-01	control	10.2	17686	5	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.1	8.19E-01	0,75 g/l BuOH	5.5	150992	45	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.0	9.54E-01	0,75 g/l BuOH	7.2	154797	38	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.0	9.33E-01	0,75 g/l BuOH	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.4	1.61E-01	control	10.8	17578	8	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.2	6.11E-01	0,75 g/l BuOH	4.9	78817	43	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.4	2.22E-01	0,75 g/l BuOH	5.0	43478	36	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.7	2.91E-01	control	10.3	21811	7	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	3.5	8.77E-02	0,75 g/l BuOH	11.7	29669	11	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	2.3	1.57E-01	0,75 g/l BuOH	11.9	15373	4	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.1	3.45E-01	control	11.6	13410	9	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.2	6.51E-01	control	10.3	20329	11	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.1	7.21E-01	control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.5	4.56E-01	control	10.2	13975	4	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.2	8.34E-01	0,75 g/l BuOH	10.4	19143	5	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.0	8.18E-01	control	10.9	12628	8	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.2	5.45E-01	control	10.6	17666	12	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.3	6.66E-01	control	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	2.5	1.23E-01	0,75 g/l BuOH	10.4	47853	3	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.3	4.15E-01	0,75 g/l BuOH	11.3	13256	6	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.1	5.55E-01	0,75 g/l BuOH	11.5	13660	4	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.0	9.26E-01	control	10.5	23056	11	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.1	6.69E-01	0,75 g/l BuOH	4.7	36629	8	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.4	2.81E-01	0,75 g/l BuOH	11.3	14363	4	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.5	3.83E-01	0,75 g/l BuOH	4.6	17972	12	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987282	PP_0544		ethanolamine transproter	1.1	8.07E-01	0,75 g/l BuOH	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	1.2	6.99E-01	control	5.9	55268	27	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.4	1.87E-01	0,75 g/l BuOH	6.5	49088	9	Cytoplasmic	COG0439	Lipid metabolism	
26987305	PP_0567	speA	arginine decarboxylase	2.4	1.73E-01	0,75 g/l BuOH	5.3	71043	2	Unknown	COG1166	Amino acid transport and metabolism	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.2	5.43E-01	0,75 g/l BuOH	5.0	69953	21	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.3	4.43E-01	0,75 g/l BuOH	5.9	53498	3	Cytoplasmic	COG1012	Energy production and conversion	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.2	5.71E-01	0,75 g/l BuOH	6.0	105800	7	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.4	4.38E-01	0,75 g/l BuOH	5.2	94861	6	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.1	6.91E-01	0,75 g/l BuOH	6.2	44897	11	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.3	5.07E-01	0,75 g/l BuOH	5.3	61860	10	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	2.5	2.00E-01	0,75 g/l BuOH	6.5	48871	2	Unknown	COG0334	Amino acid transport and metabolism	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.7	5.49E-01	control	7.8	39661	3	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	1.3	7.96E-01	0,75 g/l BuOH	9.9	92124	3	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	1.5	3.19E-01	control	5.3	23026	4	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.3	4.44E-01	0,75 g/l BuOH	8.4	54282	2	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.0	9.55E-01	control	9.5	20483	3	Unknown			
26987495	PP_0759		hypothetical protein	1.5	1.79E-01	control	7.0	29743	3	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.4	5.01E-01	0,75 g/l BuOH	5.5	62125	5	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.6	6.34E-01	control	5.0	67937	22	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.6	3.96E-01	control	9.6	50572	16	Unknown			
26987504	PP_0768		response regulator/hypothetical protein	1.1	8.56E-01	0,75 g/l BuOH	8.4	59272	2	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987509	PP_0773		OmpA/MotB domain protein	1.1	9.45E-01	0,75 g/l BuOH	9.5	24753	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	18.9	3.26E-02	0,75 g/l BuOH	6.7	34557	2	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.7	2.21E-01	0,75 g/l BuOH	9.6	66913	8	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	2.1	4.30E-01	0,75 g/l BuOH	4.8	32758	2	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.6	2.15E-01	0,75 g/l BuOH	6.6	29753	2	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.4	2.85E-01	0,75 g/l BuOH	6.2	44468	6	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	2.0	2.81E-01	0,75 g/l BuOH	7.1	60366	3	Periplasmic	COG0747	Amino acid transport and metabolism	
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.4	3.34E-01	0,75 g/l BuOH	4.9	54767	6	Cytoplasmic	COG1951	Energy production and conversion	
26987649	PP_0913		hypothetical protein	1.5	8.38E-01	0,75 g/l BuOH	4.4	47019	5	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.2	8.06E-01	0,75 g/l BuOH	5.8	78578	5	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987661	PP_0925		hypothetical protein	1.9	1.58E-01	0,75 g/l BuOH	5.8	31410	2	Unknown			
26987713	PP_0977	valS	valyl-tRNA synthetase	1.3	4.70E-01	0,75 g/l BuOH	5.1	107495	9	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.2	6.73E-01	0,75 g/l BuOH	7.4	52433	13	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	1.2	5.19E-01	0,75 g/l BuOH	6.4	40319	3	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	1.4	3.53E-02	control	5.5	33423	5	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	1.1	6.82E-01	control	6.3	37911	18	Cytoplasmic	COG0078	Amino acid transport and metabolism	

26987737	PP_1001	arcA	arginine deiminase	1.3	4.82E-01	control	5.7	46462	25	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.1	6.54E-01	control	9.1	51061	2	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.4	2.32E-01	control	7.0	36057	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.4	7.35E-02	0,75 g/l BuOH	6.4	65359	8	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	1.5	2.59E-01	0,75 g/l BuOH	6.5	33904	5	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987750	PP_1014		hypothetical protein	1.3	4.94E-01	0,75 g/l BuOH	6.4	45472	2	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.3	2.25E-01	0,75 g/l BuOH	6.2	45449	18	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	2.2	2.70E-01	0,75 g/l BuOH	10.1	33781	5	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.0	8.28E-01	0,75 g/l BuOH	6.7	41895	12	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.3	8.12E-01	control	5.9	49646	33	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.4	4.47E-01	control	6.8	55000	10	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.6	2.17E-01	control	6.7	25476	4	Unknown	COG0363	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.6	2.03E-01	0,75 g/l BuOH	5.1	61712	13	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.4	4.24E-01	0,75 g/l BuOH	7.0	51765	3	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.2	7.45E-01	0,75 g/l BuOH	5.2	58204	8	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.0	8.20E-01	0,75 g/l BuOH	4.7	140818	18	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.0	5.89E-01	control	8.2	27464	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.4	7.02E-01	0,75 g/l BuOH	8.9	33428	4	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987818	PP_1082	bfr	bacterioferritin	1.5	4.37E-01	0,75 g/l BuOH	4.4	17971	7	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.7	7.65E-02	0,75 g/l BuOH	4.9	21730	12	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.5	2.11E-01	0,75 g/l BuOH	5.1	45164	3	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.4	3.96E-01	0,75 g/l BuOH	5.5	75186	3	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987844	PP_1108		acylase	1.7	5.70E-02	control	8.7	88728	5	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.1	9.69E-01	control	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.8	8.03E-01	control	4.7	27345	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.4	3.86E-01	control	9.3	15682	5	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.8	4.27E-02	0,75 g/l BuOH	6.4	39402	6	Periplasmic	COG0683	Amino acid transport and metabolism	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.5	4.26E-01	0,75 g/l BuOH	4.5	46989	2	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.2	6.68E-01	0,75 g/l BuOH	5.7	106948	15	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.4	4.01E-01	0,75 g/l BuOH	5.0	63623	3	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.1	8.79E-01	control	4.6	46120	23	Outer Membrane			
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.3	5.29E-01	0,75 g/l BuOH	5.1	66568	12	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.3	8.93E-01	control	4.9	17833	12	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	1.4	5.08E-01	control	4.8	40784	2	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.6	1.32E-01	0,75 g/l BuOH	5.1	26916	2	Cytoplasmic	COG0152	Nucleotide transport and metabolism	
26987980	PP_1245		hypothetical protein	1.3	7.14E-01	0,75 g/l BuOH	9.4	31144	2	Unknown			
26988026	PP_1291		PhoH family protein	1.0	7.24E-01	control	5.7	51856	3	Cytoplasmic	COG1875	General function prediction only	
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	2.6	2.32E-05	0,75 g/l BuOH	5.6	36424	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988049	PP_1314		aldo/keto reductase family oxidoreductase	1.8	2.31E-01	0,75 g/l BuOH	6.5	38777	2	Cytoplasmic	COG0667	Energy production and conversion	
26988050	PP_1315	rplM	50S ribosomal protein L13	1.1	8.85E-01	0,75 g/l BuOH	10.3	15862	3	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.4	2.11E-01	control	11.7	14592	5	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.0	9.02E-01	control	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.1	8.88E-01	control	7.1	29032	6	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.4	1.67E-02	control	7.5	64637	6	Cytoplasmic Membrane	COG3107	General function prediction only	
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase	1.5	4.96E-01	control	9.9	38127	3	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	1.4	4.22E-01	0,75 g/l BuOH	4.9	47444	4	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988095	PP_1361	groEL	chaperonin GroEL	1.5	3.69E-01	control	4.7	56743	11	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	1.0	9.13E-01	control	6.7	52057	10	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.3	2.12E-01	0,75 g/l BuOH	4.8	67652	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	2.2	4.57E-01	0,75 g/l BuOH	9.6	52425	2	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.2	9.96E-01	control	5.1	52864	13	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988165	PP_1432	lepB	signal peptidase I	3.1	8.90E-02	0,75 g/l BuOH	9.2	32060	2	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.3	3.53E-01	control	6.0	86581	9	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.8	1.23E-01	0,75 g/l BuOH	5.7	42575	3	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.0	7.24E-01	control	11.0	13012	6	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988203	PP_1470	hom	homoserine dehydrogenase	1.6	2.62E-01	0,75 g/l BuOH	5.1	46194	3	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.3	5.07E-01	0,75 g/l BuOH	6.2	51645	9	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.2	6.26E-01	control	5.8	40626	5	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.3	4.98E-01	0,75 g/l BuOH	5.7	50918	5	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.3	2.38E-01	0,75 g/l BuOH	4.7	58605	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988323	PP_1591	rpsB	30S ribosomal protein S2	2.0	2.93E-01	control	9.3	27023	17	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.6	3.30E-01	0,75 g/l BuOH	4.9	30432	6	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.9	5.35E-01	0,75 g/l BuOH	4.7	86513	9	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.1	7.05E-01	0,75 g/l BuOH	6.0	35135	2	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.3	3.96E-01	0,75 g/l BuOH	5.8	59474	12	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.1	6.90E-01	0,75 g/l BuOH	4.7	45490	6	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.1	8.11E-01	0,75 g/l BuOH	11.0	27506	2	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988361	PP_1629	recA	recombinase A	1.2	5.48E-01	0,75 g/l BuOH	5.3	37545	4	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988391	PP_1659		hypothetical protein	2.0	4.37E-02	control	5.9	48336	6	Periplasmic			
26988393	PP_1661		dehydrogenase subunit	4.6	6.38E-03	control	5.5	81020	12	Extracellular	COG2303	Amino acid transport and metabolism	
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	1.3	5.44E-01	0,75 g/l BuOH	4.6	36942	3	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.4	8.00E-01	control	5.4	45693	8	Outer Membrane	COG2067	Lipid metabolism	
26988464	PP_1733	minD	septum site-determining protein MinD	1.7	2.72E-01	0,75 g/l BuOH	6.2	29650	2	Cytoplasmic	COG2894	Cell division and chromosome partitioning	
26988486	PP_1755	fumC-2	fumarate hydratase	1.2	5.82E-01	0,75 g/l BuOH	6.4	49131	6	Cytoplasmic	COG0114	Energy production and conversion	
26988498	PP_1767	gyrA	DNA gyrase subunit A	2.5	2.06E-01	0,75 g/l BuOH	4.7	102037	2	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	1.7	1.88E-01	0,75 g/l BuOH	6.4	79133	2	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1.3	5.12E-01	0,75 g/l BuOH	5.2	52989	3	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	1.1	9.76E-01	control	5.9	58534	7	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	2.1	1.45E-01	0,75 g/l BuOH	6.4	40124	5	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.1	8.77E-01	0,75 g/l BuOH	9.2	60924	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988602	PP_1872		aminotransferase AlaT	1.3	5.98E-01	0,75 g/l BuOH	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.0	9.48E-01	0,75 g/l BuOH	6.9	89194	10	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.2	6.87E-01	0,75 g/l BuOH	4.7	120904	4	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.7	1.54E-01	0,75 g/l BuOH	4.7	32614	3	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.3	4.75E-01	control	6.0	25470	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.1	6.00E-01	0,75 g/l BuOH	5.9	43290	9	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.1	6.36E-01	0,75 g/l BuOH	5.6	56483	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.1	6.75E-01	0,75 g/l BuOH	5.3	40672	10	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.3	3.31E-03	0,75 g/l BuOH	3.9	96918	12	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.5	4.50E-01	0,75 g/l BuOH	7.8	32510	2	Cytoplasmic	COG0777	Lipid metabolism	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.1	7.90E-01	0,75 g/l BuOH	6.5	55400	3	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988731	PP_2006		hypothetical protein	3.2	2.37E-02	control	5.1	63743	29	Unknown			
26988732	PP_2007		P-47-related protein	2.2	4.64E-02	control	5.8	44707	2	Unknown			
26988742	PP_2017	pepN	aminopeptidase N	1.3	5.11E-01	0,75 g/l BuOH	4.8	99573	9	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.2	5.76E-01	0,75 g/l BuOH	5.8	187043	13	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.4	4.26E-01	0,75 g/l BuOH	4.8	86015	12	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.6	3.69E-01	0,75 g/l BuOH	5.8	29111	2	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.3	8.68E-01	control	4.5	37012	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	1.6	4.90E-01	control	6.0	57068	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988836	PP_2112	acnA	aconitate hydratase	1.2	6.38E-01	0,75 g/l BuOH	5.7	99147	4	Cytoplasmic	COG1048	Energy production and conversion	
26988854	PP_2130		soluble lytic transglycosylase	5.0	8.19E-02	control	9.9	75337	6	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.1	6.88E-01	0,75 g/l BuOH	7.7	53014	12	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	

26988887	PP_2163		vacJ	VacJ family lipoprotein	1.1	5.73E-01	0,75 g/l BuOH	5.3	26061	4	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988892	PP_2168		tal	transaldolase B	3.5	2.03E-02	0,75 g/l BuOH	5.0	33615	2	Unknown	COG0176	Carbohydrate transport and metabolism	
26988937	PP_2213		fadDx	AMP-dependent synthetase and ligase	3.9	2.77E-02	0,75 g/l BuOH	6.0	61223	3	Cytoplasmic	COG0365	Lipid metabolism	
26988957	PP_2233			isochorismatase superfamily hydrolase	5.1	6.94E-03	0,75 g/l BuOH	6.0	19296	3	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988962	PP_2238			peptidase M24	2.1	2.08E-01	0,75 g/l BuOH	5.4	68915	2	Unknown	COG0006	Amino acid transport and metabolism	
26988973	PP_2249			methyl-accepting chemotaxis transducer	1.3	3.13E-01	0,75 g/l BuOH	5.1	68646	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989025	PP_2301		clpX	ATP-dependent protease ATP-binding subunit ClpX	1.7	1.42E-01	0,75 g/l BuOH	4.8	48526	6	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
26989026	PP_2302		lon-2	ATP-dependent protease La	1.1	6.45E-01	0,75 g/l BuOH	5.9	88722	6	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306			lipoprotein	1.5	4.77E-01	0,75 g/l BuOH	9.3	9997	3	Unknown			
26989046	PP_2322		oprI	outer membrane lipoprotein OprI	2.2	2.50E-01	0,75 g/l BuOH	8.5	8801	3	Outer Membrane			
26989048	PP_2324		aroF-1	phospho-2-dehydro-3-deoxyheptonate aldolase	1.3	4.43E-01	0,75 g/l BuOH	6.4	40260	2	Cytoplasmic	COG0722	Amino acid transport and metabolism	
26989055	PP_2331			hypothetical protein	1.4	7.42E-01	0,75 g/l BuOH	7.9	57064	3	Cytoplasmic Membrane			
26989063	PP_2339		acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	8.14E-01	0,75 g/l BuOH	5.0	93609	20	Cytoplasmic	COG1049	Energy production and conversion	
26989088	PP_2364			hypothetical protein	2.4	1.46E-01	0,75 g/l BuOH	5.2	42461	3	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP_2371		cysI	sulphite reductase hemoprotein, beta subunit	1.5	2.51E-01	0,75 g/l BuOH	5.8	62191	12	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP_2375		metH	B12-dependent methionine synthase	1.5	5.15E-01	0,75 g/l BuOH	4.7	135408	7	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989188	PP_2465		thrS	threonyl-tRNA synthetase	1.3	9.72E-01	control	5.8	72697	5	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP_2466		infC	translation initiation factor IF-3	1.3	5.94E-01	0,75 g/l BuOH	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468		rplT	50S ribosomal protein L20	5.4	1.23E-01	0,75 g/l BuOH	12.1	13280	5	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989193	PP_2470		pheT	phenylalanyl-tRNA synthetase subunit beta	1.2	4.74E-01	0,75 g/l BuOH	4.8	86617	2	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis	
26989289	PP_2569			major facilitator transporter	1.4	9.62E-01	0,75 g/l BuOH	9.0	60538	3	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989387	PP_2668			efflux ABC transporter ATP-binding protein	7.1	2.78E-01	0,75 g/l BuOH	9.8	27178	2	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26989393	PP_2674		qedH	quinoprotein ethanol dehydrogenase	39.3	3.58E-05	0,75 g/l BuOH	7.0	69173	9	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680			aldehyde dehydrogenase family protein	20.8	1.31E-03	0,75 g/l BuOH	5.5	54903	17	Cytoplasmic	COG1012	Energy production and conversion	
26989417	PP_2698		metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1.5	3.87E-01	control	6.3	38659	10	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26989572	PP_2853			hypothetical protein	1.4	9.33E-01	control	4.5	46020	4	Unknown			
26989580	PP_2861			methyl-accepting chemotaxis sensory transducer	1.3	3.30E-01	0,75 g/l BuOH	5.7	58659	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989623	PP_2904		glnS	glutaminyl-tRNA synthetase	1.9	2.61E-01	0,75 g/l BuOH	6.1	64654	3	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989647	PP_2928			saccharopine dehydrogenase	2.1	6.72E-02	0,75 g/l BuOH	5.0	45363	2	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989663	PP_2944			sensor histidine kinase	1.0	9.98E-01	0,75 g/l BuOH	6.1	67470	2	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989825	PP_3106			hypothetical protein	1.2	9.57E-01	0,75 g/l BuOH	5.6	69529	9	Cytoplasmic	COG3501	Function unknown	
26989827	PP_3108			rhs-related protein	1.3	6.22E-01	control	6.0	155811	3	Unknown	COG3209	Cell envelope biogenesis, outer membrane	
26989846	PP_3127			lipopolysaccharide biosynthesis protein	1.1	6.51E-01	control	9.0	57141	7	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989853	PP_3134			transferase hexapeptide repeat containing protein	1.8	3.19E-01	control	9.9	25699	4	Cytoplasmic	COG0110	General function prediction only	
26989854	PP_3135			glycosyl transferase	1.2	5.24E-01	control	8.6	35887	4	Cytoplasmic	COG1216	General function prediction only	
26989859	PP_3140			glycosyl transferase, group 2 family protein	1.3	4.48E-01	0,75 g/l BuOH	9.4	43092	3	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989860	PP_3141			WecB/TagA/CpsF family glycosyl transferase	1.8	2.59E-01	control	10.2	27576	3	Unknown	COG1922	Cell envelope biogenesis, outer membrane	
26989864	PP_3145			hypothetical protein	3.0	7.13E-02	control	9.7	29885	4	Unknown			
26990156	PP_3443			glyceraldehyde-3-phosphate dehydrogenase	1.1	8.16E-01	control	6.2	59980	3	Cytoplasmic	COG1012	Energy production and conversion	
26990223	PP_3511		ilvE	branched-chain amino acid aminotransferase	1.2	5.02E-01	0,75 g/l BuOH	7.2	36863	9	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990269	PP_3557			methyl-accepting chemotaxis transducer	1.1	4.73E-01	0,75 g/l BuOH	4.7	76982	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990281	PP_3569			quinate dehydrogenase (pyrroloquinoline-quinone)	1.2	4.26E-01	control	6.9	85338	3	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582			RND efflux transporter	1.3	7.75E-01	control	5.2	53952	2	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590		tyrB-2	aromatic amino acid aminotransferase	1.9	5.13E-01	0,75 g/l BuOH	5.9	43631	2	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990313	PP_3602			ketoglutarate semialdehyde dehydrogenase	1.2	6.52E-01	0,75 g/l BuOH	5.2	55538	5	Cytoplasmic	COG1012	Energy production and conversion	
26990349	PP_3638			acyl-CoA dehydrogenase	1.6	2.88E-01	0,75 g/l BuOH	6.1	38476	5	Cytoplasmic	COG1960	Lipid metabolism	
26990379	PP_3668			catalase/peroxidase HPI	1.3	2.37E-01	control	5.8	82061	12	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990399	PP_3691			DNA helicase-related protein	1.3	4.73E-01	0,75 g/l BuOH	5.0	245278	7	Unknown	COG1112	DNA replication, recombination, and repair	
26990466	PP_3761			multi-sensor hybrid histidine kinase	1.4	3.00E-01	0,75 g/l BuOH	4.9	129450	5	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775			sarcosine oxidase	1.5	3.06E-01	control	6.4	41164	13	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777			hypothetical protein	2.6	4.50E-02	control	5.2	31324	4	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778		proC-1	pyrroline-5-carboxylate reductase	1.4	1.30E-01	control	6.2	27714	10	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781			oxygen-independent coproporphyrinogen III oxidase family protein	1.3	4.51E-01	control	7.0	53071	4	Cytoplasmic	COG0635	Coenzyme metabolism	
26990489	PP_3784			hypothetical protein	1.7	1.30E-01	control	5.4	41070	3	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785			hypothetical protein	1.3	5.48E-01	control	6.5	50495	4	Cytoplasmic			
26990526	PP_3821		galU	UTP-glucose-1-phosphate uridylyltransferase	1.8	2.55E-02	0,75 g/l BuOH	5.3	30957	6	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990544	PP_3839			alcohol dehydrogenase	1.5	3.88E-01	0,75 g/l BuOH	5.7	35397	5	Cytoplasmic	COG1064	General function prediction only	
26990695	PP_3990			hypothetical protein	6.0	1.59E-01	0,75 g/l BuOH	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990716	PP_4011		icd	isocitrate dehydrogenase, NADP-dependent	1.0	8.86E-01	0,75 g/l BuOH	5.4	45695	9	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012			isocitrate dehydrogenase, NADP-dependent	1.6	2.38E-01	0,75 g/l BuOH	5.4	79899	16	Cytoplasmic	COG2838	Energy production and conversion	
26990737	PP_4034			allantoate amidohydrolase	1.6	6.19E-02	0,75 g/l BuOH	5.7	45010	19	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990738	PP_4035			NCS1 nucleoside transporter	1.1	6.68E-01	control	7.9	53519	5	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP_4037			oxidoreductase	1.1	7.32E-01	control	5.5	48815	21	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038			dihydropyrimidine dehydrogenase	1.1	6.30E-01	control	5.1	46093	16	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990753	PP_4052		malQ	4-alpha-glucanotransferase	1.7	3.30E-01	control	5.5	76475	6	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053			maltooligosyl trehalose synthase	2.5	2.08E-01	control	6.6	103167	3	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055		glgX	glycogen debranching protein GlgX	1.9	2.93E-01	control	5.1	81044	5	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990761	PP_4060			alpha-amylase family protein	1.2	5.38E-01	0,75 g/l BuOH	6.1	75542	3	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990806	PP_4111		fusA	elongation factor G	1.4	4.83E-01	0,75 g/l BuOH	5.0	77832	9	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990810	PP_4116		aceA	isocitrate lyase	3.7	1.23E-02	0,75 g/l BuOH	5.3	48633	3	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121		nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.4	3.28E-01	0,75 g/l BuOH	6.5	67609	6	Cytoplasmic	COG0649	Energy production and conversion	
26990817	PP_4123		nuoF	NADH dehydrogenase I subunit F	1.3	5.80E-01	0,75 g/l BuOH	7.1	49135	6	Cytoplasmic	COG1894	Energy production and conversion	
26990818	PP_4124		nuoG	NADH dehydrogenase subunit G	1.0	9.52E-01	0,75 g/l BuOH	5.9	97582	11	Unknown	COG1034	Energy production and conversion	
26990867	PP_4175		fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.4	3.44E-01	0,75 g/l BuOH	5.3	43264	8	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185		sucD	succinyl-CoA synthetase subunit alpha	1.0	8.64E-01	0,75 g/l BuOH	6.2	30111	14	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186		sucC	succinyl-CoA synthetase subunit beta	1.0	7.75E-01	0,75 g/l BuOH	6.1	41239	19	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187		lpdG	dihydrolipoamide dehydrogenase	1.2	7.92E-01	0,75 g/l BuOH	6.3	49912	10	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188		kgdB	dihydrolipoamide succinyltransferase	1.5	9.67E-01	control	5.1	42434	4	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189		sucA	2-oxoglutarate dehydrogenase E1 component	1.2	5.49E-01	0,75 g/l BuOH	6.5	106521	18	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190		sdhB	succinate dehydrogenase iron-sulfur subunit	1.4	2.23E-01	0,75 g/l BuOH	7.5	26000	5	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191		sdhA	succinate dehydrogenase flavoprotein subunit	1.2	6.71E-01	0,75 g/l BuOH	6.2	63448	16	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990886	PP_4194		gltA	type II citrate synthase	1.3	3.72E-01	0,75 g/l BuOH	7.0	47622	8	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202			electron transfer flavoprotein, beta subunit	1.1	9.47E-01	control	9.7	26361	4	Unknown	COG2086	Energy production and conversion	
26990895	PP_4203			electron-transferring-flavoprotein dehydrogenase	1.5	3.89E-01	0,75 g/l BuOH	5.7	61082	2	Cytoplasmic	COG0644	Energy production and conversion	
26990909	PP_4217		fpvA	outer membrane ferripyoverdine receptor	3.1	4.18E-01	0,75 g/l BuOH	5.5	89725	3	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990947	PP_4256		ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.4	4.09E-01	0,75 g/l BuOH	9.0	22637	2	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258		ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.0	8.31E-01	0,75 g/l BuOH	5.2	35613	9	Unknown	COG2010	Energy production and conversion	
26990966	PP_4275		zipA	cell division protein ZipA	1.1	7.48E-01	0,75 g/l BuOH	6.0	35312	7	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991027	PP_4337		cheB	chemotaxis-specific methylesterase	1.0	8.20E-01	0,75 g/l BuOH	9.0	39451	4	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
26991028	PP_4338		cheA	chemotaxis protein CheA	1.0	9.39E-01	0,75 g/l BuOH	4.4	79674	3	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991062	PP_4373		fleQ	sigma54 specific transcriptional regulator, Fis family	2.0	2.02E-01	0,75 g/l BuOH	5.4	55551	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991086	PP_4397			type IV pilus assembly PilZ	2.7	1.04E-01	0,75 g/l BuOH	6.7	28449	2	Cytoplasmic	COG5581	Signal transduction mechanisms	
26991088	PP_4399			glutamine synthetase	1.7	3.73E-01	0,75 g/l BuOH	6.2	45023	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991134	PP_4448			hypothetical protein	1.1	7.33E-01	0,75 g/l BuOH	6.0	66331	10	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991160	PP_4474		alaS	alanyl-tRNA synthetase	1.6	2.08E-01	0,75 g/l BuOH	5.1	94711	9	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991167	PP_4481		argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.6	2.22E-01	0,75 g/l BuOH	6.5	43490	9	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487		acsA	acetyl-CoA synthetase	17.6	4.48E-04	0,75 g/l BuOH	6.4	71796	18	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519		tolC	TolC family type I secretion outer membrane protein	1.1	7.90E-01	control	5.4	50393	23	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521			aerotaxis receptor	1.2	3.82E-01	control	6.4	56605	7	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991229	PP_4545			3-oxoacyl-[acyl carrier protein] synthase III	2.1	2.66E-02	0,75 g/l BuOH	5.7	42326	2	Cytoplasmic	COG0332	acyl-carrier-protein	
26991233	PP_4549		fadD	long-chain-fatty-acid--CoA ligase	1.0	6.66E-01	control	7.7	61812	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550		fadD2	long-chain-fatty-acid--CoA ligase	1.3	5.94E-01	0,75 g/l BuOH	7.8	61658	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism

26991255	PP_4571	cysK	cysteine synthase A	1.3	3.59E-01	control	5.5	34357	2	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991319	PP_4635		trans-2-enoyl-CoA reductase	1.6	3.66E-01	0,75 g/l BuOH	5.0	44265	2	Cytoplasmic	COG3007	Function unknown	
26991325	PP_4641	cstA	carbon starvation protein CstA	1.2	9.97E-01	0,75 g/l BuOH	9.0	73763	8	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.4	9.73E-01	0,75 g/l BuOH	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.6	4.03E-01	0,75 g/l BuOH	4.8	68764	2	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.3	2.97E-01	0,75 g/l BuOH	5.4	36370	14	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.0	8.26E-01	0,75 g/l BuOH	6.8	62781	4	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991368	PP_4684		hypothetical protein	2.3	2.74E-01	0,75 g/l BuOH	5.1	56095	3	Cytoplasmic	COG2187	Function unknown	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.4	3.86E-01	0,75 g/l BuOH	6.8	61455	5	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	1.0	9.94E-01	control	6.5	71251	5	Cytoplasmic	COG0365	Lipid metabolism	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.4	4.04E-01	0,75 g/l BuOH	4.9	75010	13	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.5	5.60E-01	0,75 g/l BuOH	6.8	91460	11	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.0	9.25E-01	0,75 g/l BuOH	5.4	69722	14	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	2.3	1.80E-01	0,75 g/l BuOH	5.8	40574	2	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.1	8.32E-01	0,75 g/l BuOH	4.6	68800	17	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991462	PP_4782	thiD	phosphomethylpyrimidine kinase	2.6	1.33E-01	0,75 g/l BuOH	5.1	28338	2	Cytoplasmic	COG0351	Coenzyme metabolism	
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.4	4.38E-01	0,75 g/l BuOH	5.7	45178	3	Cytoplasmic	COG0001	Coenzyme metabolism	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.7	2.32E-01	0,75 g/l BuOH	5.6	96697	6	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	1.0	9.77E-01	0,75 g/l BuOH	6.1	22414	2	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.6	2.44E-01	0,75 g/l BuOH	6.1	45417	6	Cytoplasmic	COG0014	Amino acid transport and metabolism	
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.5	2.78E-01	0,75 g/l BuOH	4.7	45837	3	Cytoplasmic	COG0151	Nucleotide transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	1.3	4.92E-01	0,75 g/l BuOH	6.2	40270	10	Periplasmic	COG0683	Amino acid transport and metabolism	
26991556	PP_4876	rpsR	30S ribosomal protein S18	1.3	7.62E-01	0,75 g/l BuOH	11.3	8927	1	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.6	1.35E-01	0,75 g/l BuOH	7.9	96688	3	Cytoplasmic	COG0557	Transcription	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.9	5.88E-03	0,75 g/l BuOH	6.1	71958	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.1	6.58E-01	0,75 g/l BuOH	5.6	46833	8	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.2	4.38E-01	0,75 g/l BuOH	9.8	33001	10	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991583	PP_4905		flagellar motor protein MotA	1.4	3.18E-01	0,75 g/l BuOH	6.2	30312	2	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.5	4.16E-01	0,75 g/l BuOH	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991588	PP_4910		hypothetical protein	1.6	3.05E-01	0,75 g/l BuOH	4.7	53632	5	Cytoplasmic	COG3726	General function prediction only	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.7	8.91E-01	control	5.2	52637	11	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.0	7.58E-01	0,75 g/l BuOH	7.6	66279	2	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991622	PP_4944		carbamoyltransferase	1.4	3.51E-01	0,75 g/l BuOH	7.2	65646	6	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	1.5	3.66E-01	0,75 g/l BuOH	6.3	142580	3	Cytoplasmic	COG4230	Energy production and conversion	
26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	1.0	9.90E-01	control	4.8	78896	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.2	4.76E-01	0,75 g/l BuOH	5.6	38453	7	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991641	PP_4963	pgk	phosphoglycerate kinase	1.6	2.60E-01	0,75 g/l BuOH	4.9	40005	4	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
26991643	PP_4965	tktA	transketolase	1.4	2.87E-01	0,75 g/l BuOH	5.0	72463	11	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.3	4.40E-01	control	5.1	42779	14	Cytoplasmic	COG0192	Coenzyme metabolism	
26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	1.3	2.82E-01	control	6.2	32979	3	Cytoplasmic	COG0685	Amino acid transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.5	5.00E-01	control	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	1.6	2.89E-01	0,75 g/l BuOH	7.4	62241	8	Cytoplasmic	COG3243	Lipid metabolism	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	3.5	4.85E-01	0,75 g/l BuOH	10.9	26214	7	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.1	6.25E-01	0,75 g/l BuOH	4.9	69017	23	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	3.9	4.19E-01	0,75 g/l BuOH	8.3	95875	2	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.2	7.41E-01	control	6.4	92004	3	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.5	3.83E-01	0,75 g/l BuOH	5.3	67157	2	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.0	8.77E-01	control	5.1	51740	12	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991732	PP_5056	pgm	phosphoglyceromutase	1.3	4.49E-01	0,75 g/l BuOH	4.9	55180	4	Cytoplasmic	COG0696	Carbohydrate transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.0	8.21E-01	0,75 g/l BuOH	6.2	161772	8	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991761	PP_5085	maeB	malic enzyme	1.5	2.05E-01	0,75 g/l BuOH	4.9	45127	15	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.9	1.97E-01	0,75 g/l BuOH	5.7	63668	5	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991785	PP_5109	ftsX	hypothetical protein	1.5	7.68E-01	0,75 g/l BuOH	6.5	36984	2	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991796	PP_5120		conifer aldehyde dehydrogenase	1.2	6.09E-01	control	9.2	52453	2	Cytoplasmic	COG1012	Energy production and conversion	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.4	2.17E-01	0,75 g/l BuOH	5.8	65671	14	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.3	4.23E-01	0,75 g/l BuOH	6.3	44339	15	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	1.3	3.94E-01	control	5.4	112277	4	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	1.1	9.77E-01	0,75 g/l BuOH	6.5	42472	1	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.2	5.03E-01	0,75 g/l BuOH	6.4	40068	5	Periplasmic	COG0687	Amino acid transport and metabolism	
26991859	PP_5183		glutamine synthetase	1.4	4.03E-01	0,75 g/l BuOH	4.8	50877	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.2	6.49E-01	control	6.3	104037	3	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991893	PP_5217	ppk	polyphosphate kinase	1.5	3.34E-01	control	7.8	81732	3	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991934	PP_5258		aldehyde dehydrogenase family protein	1.0	9.13E-01	control	5.4	53106	2	Cytoplasmic	COG1012	Energy production and conversion	
26991954	PP_5278		aldehyde dehydrogenase family protein	1.9	3.30E-01	0,75 g/l BuOH	5.5	53053	3	Cytoplasmic	COG1012	Energy production and conversion	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.2	4.01E-01	0,75 g/l BuOH	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991989	PP_5313	hupA	histone family protein DNA-binding protein	5.2	8.03E-01	0,75 g/l BuOH	11.0	10551	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.2	5.01E-01	0,75 g/l BuOH	5.3	65626	16	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.3	4.04E-01	0,75 g/l BuOH	6.5	51942	10	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	1.5	2.08E-02	0,75 g/l BuOH	7.2	30672	3	Cytoplasmic Membrane	COG4395	Function unknown	
26992055	PP_5379	copB	copper resistance B precursor	1.8	7.41E-01	control	5.0	40230	5	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992070	PP_5395		hypothetical protein	1.3	5.94E-01	0,75 g/l BuOH	5.6	31623	3	Cytoplasmic	COG1568	General function prediction only	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.5	2.70E-01	0,75 g/l BuOH	4.6	49359	15	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.1	6.04E-01	control	9.2	31464	12	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.5	1.54E-01	0,75 g/l BuOH	5.2	55352	19	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.8	3.58E-02	0,75 g/l BuOH	5.3	16898	4	Cytoplasmic Membrane	COG0711	Energy production and conversion	
262377497	Acinetobacter lwoffii SH145		outer membrane protein	2.3	2.04E-01	control			3				
206970188	Bacillus cereus AH1134		transporter, AcrB/AcrD/AcrF family	1.7	4.10E-01	0,75 g/l BuOH			3				
206977707	Bacillus cereus H3081.97		oligopeptide ABC transporter, permease protein	74.8	1.20E-01	control			2				
261341331	Enterobacter cancerogenus ATCC 35316		peptidoglycan-associated lipoprotein	30.8	4.79E-01	0,75 g/l BuOH			2				
300718709	Erwinia billingiae Eb661		elongation factor Tu 2	21.1	4.78E-01	0,75 g/l BuOH			3				
377576294	Escherichia hermannii NBRC 105704		hypothetical protein YedS	248.7	3.22E-01	0,75 g/l BuOH			16				
377579693	Escherichia hermannii NBRC 105704		maltoporin	56.3	3.20E-01	0,75 g/l BuOH			14				
377579828	Escherichia hermannii NBRC 105704		outer membrane pore protein E	10.8	5.14E-01	0,75 g/l BuOH			8				
377577602	Escherichia hermannii NBRC 105704		glucose-specific phosphotransferase system enzyme IICB component	32.2	3.89E-01	0,75 g/l BuOH			8				
377577537	Escherichia hermannii NBRC 105704		major curlin subunit	40.0	4.18E-01	0,75 g/l BuOH			5				
377578772	Escherichia hermannii NBRC 105704		preprotein translocase subunit SecD	188.5	1.75E-01	0,75 g/l BuOH			3				
377576772	Escherichia hermannii NBRC 105704		acriflavine resistance protein AcrB	45.3	2.11E-01	0,75 g/l BuOH			3				
377578133	Escherichia hermannii NBRC 105704		N-acetylglucosamine-specific phosphotransferase system enzyme II	29.1	6.31E-01	0,75 g/l BuOH			2				
377576450	Escherichia hermannii NBRC 105704		fructose-specific phosphotransferase system enzyme IIBC component	271.0	2.85E-01	0,75 g/l BuOH			2				
377577725	Escherichia hermannii NBRC 105704		mannitol-specific phosphotransferase system enzyme II	53.7	8.73E-01	0,75 g/l BuOH			2				
374606934	Paenibacillus dendritiformis C454		30S ribosomal protein S4	19.3	6.27E-01	0,75 g/l BuOH			4				
354585424	Paenibacillus lactis 154		ribosomal protein L2	23.4	1.23E-01	0,75 g/l BuOH			3				
308069938	Paenibacillus polymyxa E681		hypothetical protein PPE_03186	151.1	3.96E-03	0,75 g/l BuOH			5				
308068146	Paenibacillus polymyxa E681		ketol-acid reductoisomerase	59.1	1.82E-02	0,75 g/l BuOH			2				
251797465	Paenibacillus sp. JDR-2		50S ribosomal protein L19	263.1	4.15E-02	0,75 g/l BuOH			2				
261409528	Paenibacillus sp. Y412MC10		DNA-directed RNA polymerase subunit beta'	43.3	3.18E-02	0,75 g/l BuOH			5				
261408922	Paenibacillus sp. Y412MC10		50S ribosomal protein L20	9.8	5.19E-02	0,75 g/l BuOH			3				
261409526	Paenibacillus sp. Y412MC10		30S ribosomal protein S12	360.0	8.88E-02	0,75 g/l BuOH			2				
261409489	Paenibacillus sp. Y412MC10		30S ribosomal protein S9	297.0	1.56E-01	0,75 g/l BuOH			2				
261409504	Paenibacillus sp. Y412MC10		30S ribosomal protein S5	57.0	4.83E-02	0,75 g/l BuOH			2				
261409515	Paenibacillus sp. Y412MC10		30S ribosomal protein S3	4.9	3.42E-01	0,75 g/l BuOH			2				
15599454	Pseudomonas aeruginosa PAO1		50S ribosomal protein L22	1.0	9.95E-01	control			6				

260609519	Pseudomonas putida	coenzyme PQQ synthesis protein	4.7	3.09E-02	0,75 g/l BuOH	3
313496770	Pseudomonas putida BIRD-1	LPS-assembly protein lptD	1.1	6.40E-01	control	9
313498081	Pseudomonas putida BIRD-1	D-hydantoinase/dihydropyrimidinase	1.3	4.14E-01	0,75 g/l BuOH	22
269200090	Pseudomonas putida DOT-T1E	Ttg2C	1.3	4.05E-01	0,75 g/l BuOH	2
148550051	Pseudomonas putida F1	S-adenosyl-L-homocysteine hydrolase	1.2	6.05E-01	control	19
148545966	Pseudomonas putida F1	50S ribosomal protein L21	2.0	2.21E-01	control	5
148547806	Pseudomonas putida F1	hypothetical protein Pput_2589	1.1	8.59E-01	control	5
148545524	Pseudomonas putida F1	phosphoenolpyruvate carboxykinase	1.2	5.55E-01	0,75 g/l BuOH	11
24981839	Pseudomonas putida KT2440	ribosomal protein S3	1.3	1.84E-01	control	10
24981833	Pseudomonas putida KT2440	ribosomal protein L3	1.5	3.44E-01	control	8
24982932	Pseudomonas putida KT2440	ribosomal protein S16	1.1	8.69E-01	control	2
24986054	Pseudomonas putida KT2440	ParA family protein	2.4	2.78E-01	control	2
24986476	Pseudomonas putida KT2440	carbamoyl-phosphate synthase, large subunit	1.3	4.98E-01	0,75 g/l BuOH	30
24983268	Pseudomonas putida KT2440	ribosomal protein S1	1.2	5.40E-01	0,75 g/l BuOH	16
24982353	Pseudomonas putida KT2440	rod shape-determining protein MreB	1.8	3.05E-01	0,75 g/l BuOH	2
339485705	Pseudomonas putida S16	50S ribosomal protein L25/general stress protein Ctc	1.0	9.53E-01	control	5
85060262	Sodalis glossinidius str. 'morsitans'	elongation factor G	39.6	2.44E-01	0,75 g/l BuOH	2
190575345	Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	3.4	7.65E-01	control	11
190572988	Stenotrophomonas maltophilia K279a	outer membrane protein	1.4	9.65E-01	control	8
190575561	Stenotrophomonas maltophilia K279a	peptidoglycan-associated lipoprotein	1.3	8.89E-01	control	3
190572101	Stenotrophomonas maltophilia K279a	biopolymer transport exbB protein	1.1	8.67E-01	0,75 g/l BuOH	4
194367745	Stenotrophomonas maltophilia R551-3	hypothetical protein Smal_3973	6.1	8.67E-01	0,75 g/l BuOH	5
254521045	Stenotrophomonas sp. SKA14	TonB-dependent receptor domain protein	1.8	8.37E-01	control	9
254524919	Stenotrophomonas sp. SKA14	outer membrane protein	3.4	8.84E-01	control	2
254521740	Stenotrophomonas sp. SKA14	TonB-dependent outer membrane receptor	1.9	9.60E-01	control	2
254522278	Stenotrophomonas sp. SKA14	Oar protein	1.8	9.80E-01	control	2
14195580			1.1	6.56E-01	control	5
129138			163.5	4.01E-01	0,75 g/l BuOH	8

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.8	8.26E-02	7,5 g/l BuOH	9.1	61919	10	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.2	7.79E-01	7,5 g/l BuOH	4.9	40718	6	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.9	2.31E-01	7,5 g/l BuOH	5.8	90030	7	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.1	6.16E-01	7,5 g/l BuOH	6.1	31236	3	Cytoplasmic			
26986775	PP_0030		sensor histidine kinase	2.3	4.40E-02	7,5 g/l BuOH	6.4	52113	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986802	PP_0057		major facilitator family transporter	2.8	2.22E-04	7,5 g/l BuOH	9.3	58758	3	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.2	6.33E-01	7,5 g/l BuOH	4.9	75112	6	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.1	7.08E-01	control	6.4	44046	2	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986841	PP_0096	prlC	oligopeptidase A	1.3	5.39E-01	7,5 g/l BuOH	5.0	75721	12	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.7	1.46E-01	control	6.8	26001	3	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.2	4.03E-01	control	6.8	42059	7	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	3.1	1.09E-02	7,5 g/l BuOH	8.2	22960	3	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.3	9.10E-01	7,5 g/l BuOH	7.4	25597	4	Unknown			
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	3.1	4.92E-03	7,5 g/l BuOH	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.9	1.64E-01	7,5 g/l BuOH	6.3	71284	4	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	2.4	1.13E-01	7,5 g/l BuOH	7.7	78583	10	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986928	PP_0184	argH	argininosuccinate lyase	1.3	8.59E-01	7,5 g/l BuOH	5.4	52061	4	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.8	2.69E-01	7,5 g/l BuOH	9.6	46030	12	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.1	7.84E-01	control	5.2	51549	9	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.8	2.62E-01	control	6.1	44824	6	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	1.1	5.25E-01	7,5 g/l BuOH	5.4	48317	17	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	1.6	5.35E-01	control	5.2	15616	7	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.0	6.95E-01	control	6.1	47787	6	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.6	2.73E-01	7,5 g/l BuOH	6.0	80277	2	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	95.1	1.38E-03	7,5 g/l BuOH	8.5	58780	4	Cytoplasmic Membrane			
26987063	PP_0321		threonine aldolase	1.0	5.96E-01	control	5.4	38068	5	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.2	1.22E-01	control	5.3	55654	9	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.6	2.37E-01	control	5.6	99332	21	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	2.0	2.07E-01	7,5 g/l BuOH	5.3	109432	4	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987098	PP_0356	glcB	malate synthase G	6.7	1.52E-03	7,5 g/l BuOH	5.8	78346	8	Cytoplasmic	COG2225	Energy production and conversion	
26987108	PP_0366	bioD	dithiobiotin synthetase	2.1	1.44E-01	control	5.3	23871	2	Cytoplasmic	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	5.19E-01	7,5 g/l BuOH	5.8	65541	12	Cytoplasmic	COG1960	Lipid metabolism	
26987117	PP_0375		prolyl oligopeptidase family protein	20.1	4.54E-03	7,5 g/l BuOH	6.0	67549	3	Cytoplasmic	COG1506	Amino acid transport and metabolism	
26987118	PP_0376	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	4.4	4.93E-02	7,5 g/l BuOH	6.5	42507	2	Cytoplasmic	COG0535	General function prediction only	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	65.9	5.42E-04	7,5 g/l BuOH	6.8	29075	7	Cytoplasmic	COG5424	Coenzyme metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.3	4.22E-01	7,5 g/l BuOH	4.6	69396	9	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	2.0	8.00E-03	control	11.4	8370	5	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987138	PP_0396		hypothetical protein	1.0	7.51E-01	7,5 g/l BuOH	7.0	50488	3	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.2	6.98E-01	control	5.8	73782	26	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987158	PP_0417	trpE	anthranilate synthase component I	1.1	9.59E-01	7,5 g/l BuOH	4.8	54406	2	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
26987159	PP_0418		GDSL family lipase	1.1	5.82E-01	7,5 g/l BuOH	4.4	67175	4	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.0	7.12E-01	control	6.8	36277	4	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987181	PP_0440	tuf	elongation factor Tu	1.3	5.05E-01	control	5.0	43495	3	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	2.0	8.66E-02	control	10.5	14866	4	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	4.5	1.85E-01	control	10.1	24251	6	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.0	9.16E-01	control	10.2	17686	4	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.1	7.38E-01	7,5 g/l BuOH	5.5	150992	53	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.1	5.90E-01	7,5 g/l BuOH	7.2	154797	42	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.1	7.20E-01	7,5 g/l BuOH	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.0	7.74E-01	control	10.8	17578	8	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.0	9.46E-01	control	4.9	78817	43	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.2	5.46E-01	control	5.0	43478	34	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	3.3	2.89E-02	control	10.3	21811	5	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	5.2	2.06E-02	7,5 g/l BuOH	11.7	29669	12	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	3.4	8.66E-02	7,5 g/l BuOH	11.9	15373	4	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.0	9.69E-01	7,5 g/l BuOH	11.6	13410	9	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	2.9	1.47E-01	control	10.3	20329	6	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.2	4.46E-01	control	12.3	11403	2	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	2.1	2.72E-01	control	10.2	13975	3	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	2.5	5.93E-02	control	10.4	19143	3	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.4	2.07E-01	control	10.9	12628	5	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.4	2.77E-01	control	10.6	17666	9	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	2.7	2.57E-01	control	11.5	15189	5	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	3.0	4.69E-02	7,5 g/l BuOH	10.4	47853	7	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.1	5.55E-01	7,5 g/l BuOH	11.3	13256	5	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	1.4	2.63E-01	control	11.5	13660	3	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.0	6.49E-01	7,5 g/l BuOH	10.5	23056	11	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.0	9.49E-01	7,5 g/l BuOH	4.7	36629	9	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	1.5	3.63E-01	7,5 g/l BuOH	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	5.9	1.15E-01	7,5 g/l BuOH	4.6	17972	16	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987282	PP_0544		ethanolamine transproter	1.1	7.14E-01	control	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.2	1.28E-01	control	5.9	55268	18	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.2	4.94E-01	control	6.5	49088	9	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	3.4	9.54E-02	7,5 g/l BuOH	6.6	40223	3	Unknown	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	1.6	4.33E-01	7,5 g/l BuOH	5.3	71043	2	Unknown	COG1166	Amino acid transport and metabolism	
26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.9	2.56E-01	control	7.5	47782	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.1	4.47E-01	7,5 g/l BuOH	5.0	69953	20	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.4	4.76E-01	7,5 g/l BuOH	5.9	53498	4	Cytoplasmic	COG1012	Energy production and conversion	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.4	3.65E-01	7,5 g/l BuOH	6.0	105800	8	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.3	8.58E-01	7,5 g/l BuOH	5.2	94861	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987376	PP_0640		hypothetical protein	1.6	3.02E-01	7,5 g/l BuOH	6.6	44093	2	Cytoplasmic Membrane			
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.1	9.50E-01	7,5 g/l BuOH	6.2	44897	11	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.4	5.82E-01	7,5 g/l BuOH	5.3	61860	16	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.8	4.69E-01	7,5 g/l BuOH	6.5	48871	5	Unknown	COG0334	Amino acid transport and metabolism	
26987416	PP_0680		ATP-dependent protease	1.7	4.44E-01	7,5 g/l BuOH	4.5	89677	4	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987427	PP_0691	proB	gamma-glutamyl kinase	2.8	6.07E-01	control	7.8	39661	3	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	2.4	7.45E-02	7,5 g/l BuOH	9.9	92124	8	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	3.3	8.97E-02	control	5.3	23026	4	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	2.2	5.08E-01	7,5 g/l BuOH	10.5	31284	2	Cytoplasmic	COG2326	Function unknown	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.3	8.03E-01	control	6.4	23242	3	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	2.8	4.50E-01	7,5 g/l BuOH	5.9	34192	4	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	4.1	2.21E-02	7,5 g/l BuOH	8.4	54282	6	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.4	4.61E-01	control	9.5	20483	5	Unknown			
26987495	PP_0759		hypothetical protein	2.5	1.31E-02	control	7.0	29743	2	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.5	4.44E-01	7,5 g/l BuOH	5.5	62125	7	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.6	5.56E-01	control	5.0	67937	22	Outer Membrane			
26987502	PP_0766		hypothetical protein	2.2	1.80E-01	control	9.6	50572	9	Unknown			
26987504	PP_0768		response regulator/hypothetical protein	1.1	9.05E-01	7,5 g/l BuOH	8.4	59272	3	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987509	PP_0773		OmpA/MotB domain protein	4.1	2.39E-01	7,5 g/l BuOH	9.5	24753	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	

26987526	PP_0790		signaling modulator of AmpD, AmpE	6.3	1.87E-02	7,5 g/l BuOH	7.8	31007	2	Cytoplasmic Membrane	COG3725	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	25.4	7.06E-04	7,5 g/l BuOH	6.7	34557	5	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	192.6	2.08E-04	7,5 g/l BuOH	7.8	74391	3	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	1.6	2.16E-01	7,5 g/l BuOH	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	2.8	5.16E-02	7,5 g/l BuOH	9.6	66913	15	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	2.6	9.57E-02	7,5 g/l BuOH	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.3	5.84E-01	7,5 g/l BuOH	6.6	29753	2	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.1	8.95E-01	7,5 g/l BuOH	6.2	44468	9	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987617	PP_0881	dppB	alkaline phosphatase	1.2	5.38E-01	control	8.4	36980	2	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.2	8.20E-01	7,5 g/l BuOH	4.9	54767	6	Cytoplasmic	COG1951	Energy production and conversion	
26987649	PP_0913		hypothetical protein	1.9	4.00E-01	control	4.4	47019	6	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.5	2.21E-01	7,5 g/l BuOH	5.8	78578	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987661	PP_0925		hypothetical protein	1.3	4.46E-01	7,5 g/l BuOH	5.8	31410	2	Unknown			
26987666	PP_0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.7	9.12E-01	7,5 g/l BuOH	4.8	52678	2	Cytoplasmic	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.2	7.68E-01	7,5 g/l BuOH	6.2	51518	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987689	PP_0953		ABC transporter ATP-binding protein	1.3	6.81E-01	control	7.0	26579	2	Cytoplasmic	COG1137	General function prediction only	
26987695	PP_0959	ttg2B	hypothetical protein	7.1	8.40E-03	7,5 g/l BuOH	8.2	28489	3	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.5	1.08E-01	7,5 g/l BuOH	5.1	107495	9	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.0	9.37E-01	7,5 g/l BuOH	7.4	52433	14	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	4.0	1.12E-02	7,5 g/l BuOH	9.7	41323	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987719	PP_0983		permease YjgP/YjgQ family protein	5.4	1.10E-01	7,5 g/l BuOH	7.1	38733	2	Cytoplasmic Membrane	COG0795	General function prediction only	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	1.3	6.43E-01	control	6.4	40319	2	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	3.1	4.56E-03	control	5.5	33423	4	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	3.7	4.79E-02	control	6.3	37911	14	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	2.7	7.70E-02	control	5.7	46462	20	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.0	8.01E-01	control	9.1	51061	3	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	10.2	5.70E-03	control	7.0	36057	7	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	3.5	6.34E-02	control	6.4	65359	5	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	3.1	1.18E-01	control	6.5	33904	2	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987750	PP_1014		hypothetical protein	1.0	6.27E-01	7,5 g/l BuOH	6.4	45472	2	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.1	6.09E-01	7,5 g/l BuOH	6.2	45449	20	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.9	9.37E-02	7,5 g/l BuOH	10.1	33781	9	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.8	1.10E-01	7,5 g/l BuOH	9.9	30428	4	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.5	8.26E-01	7,5 g/l BuOH	6.7	41895	16	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.9	3.86E-01	control	5.9	49646	30	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.8	1.80E-01	control	6.8	55000	8	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	3.7	7.00E-02	control	6.7	25476	5	Unknown	COG0363	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.4	5.02E-01	7,5 g/l BuOH	5.1	61712	14	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.1	8.28E-01	7,5 g/l BuOH	7.0	51765	3	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.3	6.50E-01	control	5.2	58204	8	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.1	7.54E-01	7,5 g/l BuOH	4.7	140818	21	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987796	PP_1060		glutamate synthase, large subunit	15.5	7.09E-03	7,5 g/l BuOH	8.1	59136	2	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.3	5.11E-01	7,5 g/l BuOH	8.2	27464	4	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	7.4	9.99E-02	7,5 g/l BuOH	4.4	17971	9	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.4	3.76E-01	control	4.9	21730	12	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.4	8.15E-01	7,5 g/l BuOH	5.1	45164	3	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.6	2.04E-01	7,5 g/l BuOH	5.5	75186	4	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987844	PP_1108		acylase	1.7	1.68E-01	control	8.7	88728	4	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	1.4	6.74E-01	control	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	2.7	6.02E-01	control	4.7	27345	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	2.4	2.25E-01	7,5 g/l BuOH	9.3	15682	8	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	1.7	1.41E-02	7,5 g/l BuOH	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.4	3.73E-01	control	6.4	39402	4	Periplasmic	COG0683	Amino acid transport and metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.5	3.24E-01	7,5 g/l BuOH	4.8	105994	3	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987893	PP_1157		acetolactate synthase	1.5	2.28E-01	7,5 g/l BuOH	6.1	60059	2	Cytoplasmic	COG0028	Coenzyme metabolism	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.2	6.82E-01	7,5 g/l BuOH	4.5	46989	2	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.2	6.45E-01	7,5 g/l BuOH	5.7	106948	24	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987920	PP_1185	oprH	outer membrane protein H1	13.8	1.98E-01	7,5 g/l BuOH	6.8	21501	5	Outer Membrane			
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.6	5.23E-01	7,5 g/l BuOH	5.0	63623	5	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.1	5.84E-01	7,5 g/l BuOH	4.6	46120	21	Outer Membrane			
26987944	PP_1209		cold-shock domain-contain protein	2.2	3.18E-01	7,5 g/l BuOH	11.4	10246	2	Cytoplasmic	COG1278	Transcription	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.3	4.04E-01	7,5 g/l BuOH	5.1	66568	15	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987955	PP_1220	tolR	biopolymer transport protein TolR	12.6	2.36E-02	7,5 g/l BuOH	9.4	16247	3	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.0	5.27E-01	control	9.8	47431	5	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.2	9.76E-01	control	4.9	17833	11	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988026	PP_1291		PhoH family protein	2.1	4.25E-01	control	5.7	51856	3	Cytoplasmic	COG1875	General function prediction only	
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.9	4.79E-01	7,5 g/l BuOH	5.6	69049	4	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.0	8.05E-01	control	11.7	14592	5	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.8	1.70E-01	7,5 g/l BuOH	8.4	45901	7	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.4	6.13E-01	7,5 g/l BuOH	7.1	29032	7	Unknown	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.2	3.09E-01	control	7.5	64637	10	Cytoplasmic Membrane	COG3107	General function prediction only	
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.0	8.80E-01	control	5.3	53602	2	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	1.3	6.14E-01	control	4.9	47444	5	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988095	PP_1361	groEL	chaperonin GroEL	1.6	3.84E-01	control	4.7	56743	12	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	1.4	5.32E-01	control	6.7	52057	11	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.3	7.67E-02	7,5 g/l BuOH	4.8	67652	8	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988117	PP_1383		BenF-like porin	1.5	8.10E-01	control	6.8	46022	3	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.0	7.86E-01	7,5 g/l BuOH	5.1	52864	13	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988152	PP_1419		outer membrane porin	2.6	4.62E-01	7,5 g/l BuOH	4.9	46644	3	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	3.1	3.88E-02	7,5 g/l BuOH	9.2	32060	3	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.0	8.13E-01	control	6.0	86581	9	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.3	3.55E-01	7,5 g/l BuOH	5.7	42575	5	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	8.7	3.60E-03	7,5 g/l BuOH	9.0	45563	3	Cytoplasmic Membrane			
26988198	PP_1465	rplS	50S ribosomal protein L19	1.7	5.07E-01	control	11.0	13012	6	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988203	PP_1470	hom	homoserine dehydrogenase	1.7	5.45E-01	7,5 g/l BuOH	5.1	46194	5	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.3	4.33E-01	7,5 g/l BuOH	6.2	51645	11	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.3	5.47E-01	control	5.8	40626	3	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.1	7.48E-01	control	5.7	50918	6	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	2.1	2.37E-01	7,5 g/l BuOH	4.7	58605	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	2.3	2.33E-01	7,5 g/l BuOH	6.6	96963	2	Cytoplasmic	COG2352	Energy production and conversion	
26988258	PP_1526		beta-(1-3)-glucosyl transferase	2.0	4.01E-02	7,5 g/l BuOH	8.1	97324	3	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism	
26988320	PP_1588		succinyldiaminopimelate transaminase	1.0	9.37E-01	7,5 g/l BuOH	5.4	43759	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988323	PP_1591	rpsB	30S ribosomal protein S2	3.0	5.73E-02	control	9.3	27023	15	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.3	4.69E-01	control	4.9	30432	6	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.7	3.30E-01	7,5 g/l BuOH	4.7	86513	7	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.4	6.50E-01	7,5 g/l BuOH	6.0	35135	5	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.2	8.31E-01	control	5.8	59474	12	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.8	2.65E-01	control	4.7	45490	7	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988361	PP_1629	recA	recombinase A	1.4	5.19E-01	7,5 g/l BuOH	5.3	37545	3	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988391	PP_1659		hypothetical protein	18.1	8.93E-04	control	5.9	48336	3	Periplasmic			

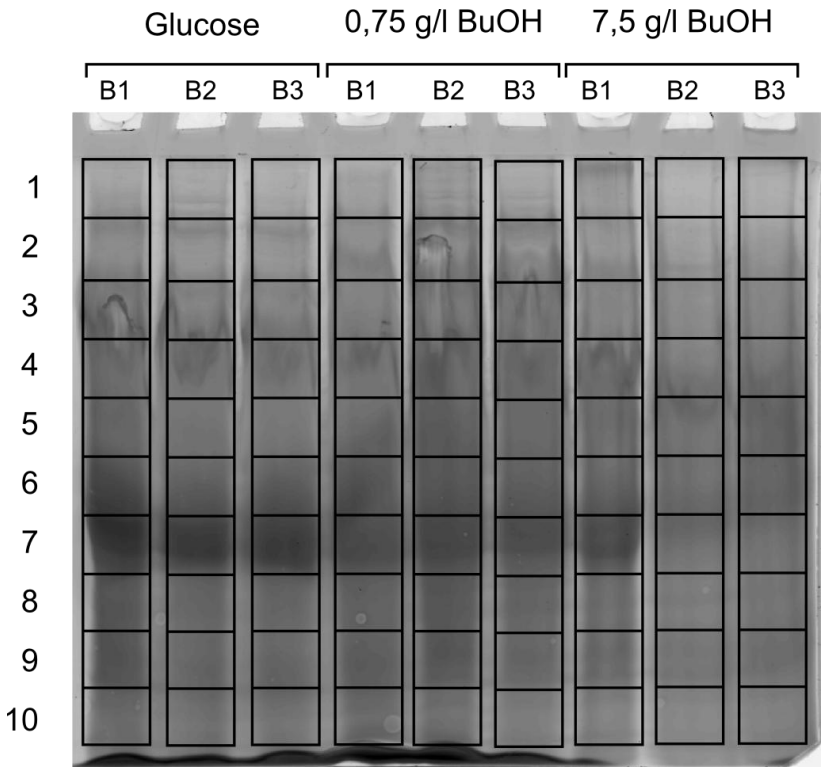
26988393	PP_1661		dehydrogenase subunit	12.3	1.43E-03	control	5.5	81020	12	Extracellular	COG2303	Amino acid transport and metabolism		
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	1.5	7.48E-01	control	4.6	36942	5	Cytoplasmic	COG0150	Nucleotide transport and metabolism		
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.1	7.56E-01	7,5 g/l BuOH	5.4	45693	9	Outer Membrane	COG2067	Lipid metabolism		
26988452	PP_1720		alcohol dehydrogenase, zinc-containing	1.8	9.66E-01	7,5 g/l BuOH	4.7	33921	2	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only	
26988474	PP_1743	actP	acetate permease	29.3	5.49E-03	7,5 g/l BuOH	9.6	58972	6	Cytoplasmic Membrane	COG4147	General function prediction only		
26988483	PP_1752		hypothetical protein	1.1	8.90E-01	control	8.2	57637	4	Cytoplasmic	COG2326	Function unknown		
26988486	PP_1755	fumC-2	fumarate hydratase	1.0	8.68E-01	control	6.4	49131	5	Cytoplasmic	COG0114	Energy production and conversion		
26988492	PP_1761		sensory box protein/GGDEF family protein	2.3	2.93E-01	7,5 g/l BuOH	6.8	108193	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms		
26988498	PP_1767	gyrA	DNA gyrase subunit A	2.9	1.02E-01	7,5 g/l BuOH	4.7	102037	8	Cytoplasmic	COG0188	DNA replication, recombination, and repair		
26988500	PP_1769	pheA	chorismate mutase	1.8	7.97E-01	7,5 g/l BuOH	6.4	40816	3	Cytoplasmic	COG0077	Amino acid transport and metabolism		
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	1.6	7.25E-01	7,5 g/l BuOH	6.4	79133	5	Cytoplasmic	COG0128	Amino acid transport and metabolism		
26988511	PP_1780		mannosyltransferase	1.1	8.16E-01	control	5.8	180042	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane		
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	1.8	5.78E-01	7,5 g/l BuOH	6.1	40690	4	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane		
26988517	PP_1786		glycosyl transferase	2.2	1.73E-01	7,5 g/l BuOH	6.4	128499	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane		
26988522	PP_1791		aldolase/synthase	1.3	6.05E-01	control	5.9	58534	7	Cytoplasmic	COG0119	Amino acid transport and metabolism		
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	2.2	1.94E-01	7,5 g/l BuOH	6.4	40124	5	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane		
26988568	PP_1838		hypothetical protein	6.8	4.07E-02	7,5 g/l BuOH	6.8	76615	5	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane		
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.2	5.87E-01	7,5 g/l BuOH	9.2	60924	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription	Translation, ribosomal structure and biogenesis
26988601	PP_1871	htpX	heat shock protein HtpX	4.3	1.92E-03	7,5 g/l BuOH	7.2	32199	3	Cytoplasmic Membrane	COG0501	Posttranslational modification, protein turnover, chaperones		
26988602	PP_1872		aminotransferase AlaT	1.0	9.19E-01	7,5 g/l BuOH	5.8	44705	2	Cytoplasmic	COG0436	Amino acid transport and metabolism		
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.4	2.19E-01	7,5 g/l BuOH	6.9	89194	15	Cytoplasmic Membrane	COG1960	Lipid metabolism		
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	2.0	1.81E-01	7,5 g/l BuOH	4.7	120904	12	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis		
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.1	7.90E-01	control	4.7	32614	3	Cytoplasmic	COG0331	Lipid metabolism		
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.0	9.02E-01	control	6.0	25470	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.9	2.96E-02	7,5 g/l BuOH	5.9	43290	10	Cytoplasmic	COG1448	Amino acid transport and metabolism		
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.5	3.85E-01	7,5 g/l BuOH	5.6	56483	6	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	1.8	9.43E-01	7,5 g/l BuOH	5.6	51255	2	Cytoplasmic	COG0065	Amino acid transport and metabolism		
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.2	7.99E-01	7,5 g/l BuOH	5.3	40672	6	Cytoplasmic	COG0136	Amino acid transport and metabolism		
26988719	PP_1993		peptidoglycan-binding LysM	1.8	8.96E-02	7,5 g/l BuOH	3.9	96918	17	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.5	3.91E-01	7,5 g/l BuOH	6.5	55400	7	Cytoplasmic	COG0034	Nucleotide transport and metabolism		
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	1.1	8.50E-01	7,5 g/l BuOH	5.4	43284	2	Cytoplasmic	COG0626	Amino acid transport and metabolism		
26988731	PP_2006		hypothetical protein	19.5	1.21E-03	control	5.1	63743	17	Unknown				
26988742	PP_2017	pepN	aminopeptidase N	1.2	6.05E-01	7,5 g/l BuOH	4.8	99573	11	Cytoplasmic	COG0308	Amino acid transport and metabolism		
26988744	PP_2019		hypothetical protein	1.7	1.54E-01	7,5 g/l BuOH	6.6	87732	2	Cytoplasmic Membrane	COG1033	General function prediction only		
26988805	PP_2080		NAD-glutamate dehydrogenase	1.5	2.95E-01	7,5 g/l BuOH	5.8	187043	16	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism		
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.7	2.45E-01	7,5 g/l BuOH	4.8	86015	19	Cytoplasmic	COG0574	Carbohydrate transport and metabolism		
26988812	PP_2087	cmpX	TM helix repeat-containing protein	3.0	5.16E-02	7,5 g/l BuOH	5.8	29111	2	Cytoplasmic Membrane				
26988814	PP_2089	oprF	OmpF family protein	1.4	6.60E-01	control	4.5	37012	31	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane		
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	2.3	1.12E-01	control	6.0	57068	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26988836	PP_2112	acnA	aconitate hydratase	1.0	7.37E-01	control	5.7	99147	4	Cytoplasmic	COG1048	Energy production and conversion		
26988854	PP_2130		soluble lytic transglycosylase	2.2	2.43E-01	control	9.9	75337	7	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane		
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.8	7.39E-01	7,5 g/l BuOH	5.9	77449	4	Cytoplasmic	COG1250	Lipid metabolism		
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.6	4.32E-01	7,5 g/l BuOH	7.7	53014	18	Cytoplasmic	COG0057	Carbohydrate transport and metabolism		
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	5.2	5.49E-03	7,5 g/l BuOH	7.7	50905	3	Cytoplasmic	COG1249	Energy production and conversion		
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.4	3.25E-01	7,5 g/l BuOH	5.3	26061	6	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane		
26988892	PP_2168	tal	transaldolase B	2.9	2.08E-01	7,5 g/l BuOH	5.0	33615	3	Unknown	COG0176	Carbohydrate transport and metabolism		
26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	3.7	1.72E-01	7,5 g/l BuOH	6.0	61223	5	Cytoplasmic	COG0365	Lipid metabolism		
26988957	PP_2233		isochorismatase superfamily hydrolase	20.4	4.36E-03	7,5 g/l BuOH	6.0	19296	6	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
26988962	PP_2238		peptidase M24	2.6	2.10E-01	7,5 g/l BuOH	5.4	68915	2	Unknown	COG0006	Amino acid transport and metabolism		
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.0	9.53E-01	7,5 g/l BuOH	5.1	68646	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.1	8.75E-01	7,5 g/l BuOH	4.8	48526	7	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones		
26989026	PP_2302	lon-2	ATP-dependent protease La	1.8	3.15E-01	7,5 g/l BuOH	5.9	88722	9	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones		
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	3.9	1.21E-01	7,5 g/l BuOH	8.5	8801	2	Outer Membrane				
26989055	PP_2331		hypothetical protein	3.6	2.71E-02	7,5 g/l BuOH	7.9	57064	3	Cytoplasmic Membrane				
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.2	8.16E-01	7,5 g/l BuOH	5.0	93609	28	Cytoplasmic	COG1049	Energy production and conversion		
26989075	PP_2351		acetyl-CoA synthetase	7.5	3.95E-02	7,5 g/l BuOH	6.1	68868	6	Cytoplasmic	COG0365	Lipid metabolism		
26989088	PP_2364		hypothetical protein	1.6	8.96E-01	7,5 g/l BuOH	5.2	42461	4	Unknown	COG2866	Amino acid transport and metabolism		
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.6	2.86E-01	7,5 g/l BuOH	5.8	62191	9	Cytoplasmic	COG0155	Inorganic ion transport and metabolism		
26989099	PP_2375	metH	B12-dependent methionine synthase	1.7	2.39E-01	7,5 g/l BuOH	4.7	135408	8	Cytoplasmic	COG1410	Amino acid transport and metabolism		
26989144	PP_2421		acetyltransferase	27.7	3.22E-04	7,5 g/l BuOH	8.3	20697	2	Cytoplasmic	COG0456	General function prediction only		
26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	4.4	1.71E-01	7,5 g/l BuOH	4.8	20507	2	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones		
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.3	9.63E-01	control	5.8	72697	9	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis		
26989189	PP_2466	infC	translation initiation factor IF-3	1.8	3.16E-01	control	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis		
26989191	PP_2468	rplT	50S ribosomal protein L20	4.2	4.69E-02	7,5 g/l BuOH	12.1	13280	4	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis		
26989193	PP_2470	pheT	phenylalanyl-tRNA synthetase subunit beta	1.5	6.29E-01	7,5 g/l BuOH	4.8	86617	3	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis		
26989289	PP_2569		major facilitator transporter	1.0	8.22E-01	control	9.0	60538	5	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism		
26989381	PP_2662		hypothetical protein	199.6	6.83E-03	7,5 g/l BuOH	4.3	42858	20	Outer Membrane				
26989382	PP_2663		hypothetical protein	11.6	1.92E-02	7,5 g/l BuOH	6.3	42469	4	Cytoplasmic	COG3287	Function unknown		
26989383	PP_2664		PAS/PAC sensor hybrid histidine kinase	22.0	4.12E-04	7,5 g/l BuOH	6.6	73094	9	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms		
26989387	PP_2668		efflux ABC transporter ATP-binding protein	17.8	1.30E-02	7,5 g/l BuOH	9.8	27178	6	Cytoplasmic Membrane	COG1131	Defense mechanisms		
26989392	PP_2673		pentapeptide repeat-containing protein	25.8	4.11E-03	7,5 g/l BuOH	5.3	23569	2	Extracellular	COG1357	Function unknown		
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	24.6	2.70E-06	7,5 g/l BuOH	7.0	69173	33	Periplasmic	COG4993	Carbohydrate transport and metabolism		
26989394	PP_2675		cytochrome c-type protein	42.5	5.14E-03	7,5 g/l BuOH	4.9	16280	2	Unknown	COG2010	Energy production and conversion		
26989395	PP_2676		periplasmic protein	37.0	9.02E-03	7,5 g/l BuOH	6.5	34540	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
26989396	PP_2677		hypothetical protein	44.1	2.31E-04	7,5 g/l BuOH	5.3	28059	2	Unknown				
26989398	PP_2679		quinoprotein ethanol dehydrogenase	251.8	2.84E-04	7,5 g/l BuOH	9.1	64883	2	Periplasmic	COG4993	Carbohydrate transport and metabolism		
26989399	PP_2680		aldehyde dehydrogenase family protein	73.4	6.91E-07	7,5 g/l BuOH	5.5	54903	37	Cytoplasmic	COG1012	Energy production and conversion		
26989402	PP_2683		PAS/PAC sensor hybrid histidine kinase	19.2	1.27E-03	7,5 g/l BuOH	6.6	62695	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms		
26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1.5	3.56E-01	control	6.3	38659	8	Cytoplasmic	COG0620	Amino acid transport and metabolism		
26989546	PP_2827		alcohol dehydrogenase, zinc-containing	2.2	3.25E-01	7,5 g/l BuOH	5.4	36735	2	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only	
26989572	PP_2853		hypothetical protein	1.2	9.32E-01	control	4.5	46020	6	Unknown				
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	1.0	9.93E-01	7,5 g/l BuOH	5.7	58659	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.7	3.58E-01	7,5 g/l BuOH	6.1	64654	5	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
26989647	PP_2928		saccharopine dehydrogenase	1.7	6.86E-01	7,5 g/l BuOH	5.0	45363	5	Cytoplasmic	COG1748	Amino acid transport and metabolism		
26989663	PP_2944		sensor histidine kinase	2.0	2.49E-01	7,5 g/l BuOH	6.1	67470	4	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms		
26989809	PP_3090		OmpA domain-containing protein	47.7	2.26E-02	7,5 g/l BuOH	9.0	93143	7	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989810	PP_3091		hypothetical protein	18.6	6.49E-02	7,5 g/l BuOH	6.8	138655	12	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989811	PP_3092		hypothetical protein	5.4	2.53E-01	7,5 g/l BuOH	5.7	26868	4	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport		
26989814	PP_3095		chaperone-associated ATPase	4.8	2.95E-02	7,5 g/l BuOH	6.1	96474	4	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones		
26989818	PP_3099		hypothetical protein	10.1	1.03E-01	7,5 g/l BuOH	4.9	56072	19	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport		
26989824	PP_3105		hypothetical protein	14.8	3.68E-01	7,5 g/l BuOH	10.5	26470	2	Cytoplasmic Membrane				
26989825	PP_3106		hypothetical protein	1.4	7.59E-01	7,5 g/l BuOH	5.6	69529	10	Cytoplasmic	COG3501	Function unknown		
26989827	PP_3108		rhs-related protein	1.0	7.63E-01	control	6.0	155811	2	Unknown	COG3209	Cell envelope biogenesis, outer membrane		
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.2	8.95E-01	7,5 g/l BuOH	9.0	57141	9	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane		
26989854	PP_3135		glycosyl transferase	1.2	3.56E-01	7,5 g/l BuOH	8.6	35887	5	Cytoplasmic	COG1216	General function prediction only		
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.9	1.43E-01	7,5 g/l BuOH	9.4	43092	3	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane		
26989860	PP_3141		WecB/TagA/CpsF family glycosyl transferase	1.9	1.25E-01	control	10.2	27576	3	Unknown	COG1922	Cell envelope biogenesis, outer membrane		
26989864	PP_3145		hypothetical protein	2.8	8.36E-02	control	9.7	29885	4	Unknown				
26990154	PP_3441		hypothetical protein	1.3	7.06E-01	control	9.3	43139	2	Cytoplasmic				
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	2.1	1.69E-01	control	6.2	59980	3	Cytoplasmic	COG1012	Energy production and conversion		

26990176	PP_3463		aldehyde dehydrogenase	56.9	1.63E-01	7,5 g/l BuOH	5.7	53383	3	Cytoplasmic	COG1012	Energy production and conversion	
26990203	PP_3491		enoly-coenzyme A hydratase/isomerase family protein	1.0	7.28E-01	7,5 g/l BuOH	4.9	39382	2	Cytoplasmic	COG1024	Lipid metabolism	
26990220	PP_3508	cobW	cobalamin biosynthesis protein CobW	1.4	7.99E-01	7,5 g/l BuOH	4.6	38579	3	Cytoplasmic	COG0523	General function prediction only	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.1	6.51E-01	control	7.2	36863	11	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990265	PP_3553		acyl-CoA synthetase	25.0	8.49E-04	7,5 g/l BuOH	6.4	59576	11	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	13.4	6.17E-03	7,5 g/l BuOH	5.5	63339	5	Cytoplasmic	COG1960	Lipid metabolism	
26990269	PP_3557		methyl-accepting chemotaxis transducer	1.4	2.66E-01	7,5 g/l BuOH	4.7	76982	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	2.1	1.08E-01	7,5 g/l BuOH	6.9	85338	7	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990290	PP_3578		phosphoglucomutase	2.5	1.80E-01	7,5 g/l BuOH	5.6	58620	3	Unknown	COG0033	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	2.3	8.51E-02	7,5 g/l BuOH	5.2	53952	5	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	2.5	1.17E-01	7,5 g/l BuOH	5.9	43631	8	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990313	PP_3602		ketoglutarate semialdehyde dehydrogenase	1.2	6.94E-01	control	5.2	55538	6	Cytoplasmic	COG1012	Energy production and conversion	
26990349	PP_3638		acyl-CoA dehydrogenase	1.3	8.16E-01	control	6.1	38476	2	Cytoplasmic	COG1960	Lipid metabolism	
26990367	PP_3656		aromatic compound-specific porin	18.1	5.46E-02	7,5 g/l BuOH	5.3	46672	12	Outer Membrane			
26990369	PP_3658		aromatic compound MFS transporter	108.9	7.20E-02	7,5 g/l BuOH	9.5	48129	4	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26990373	PP_3662		decarboxylase family protein	3.5	3.06E-01	7,5 g/l BuOH	6.7	50729	4	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	1.1	7.47E-01	control	5.8	82061	11	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990399	PP_3691		DNA helicase-related protein	2.1	1.16E-01	7,5 g/l BuOH	5.0	245278	10	Unknown	COG1112	DNA replication, recombination, and repair	
26990429	PP_3721	aspC	aspartate aminotransferase	1.2	5.92E-01	control	5.1	42461	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990459	PP_3754		beta-ketothiolase	4.4	5.53E-02	7,5 g/l BuOH	6.9	40988	7	Cytoplasmic	COG0183	Lipid metabolism	
26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	3.5	1.04E-02	7,5 g/l BuOH	6.3	30088	3	Cytoplasmic	COG1250	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.9	6.01E-02	7,5 g/l BuOH	4.9	129450	9	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	2.7	4.87E-02	control	6.4	41164	11	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777		hypothetical protein	4.1	2.27E-02	control	5.2	31324	4	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	3.0	1.32E-02	control	6.2	27714	6	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	1.6	7.44E-02	7,5 g/l BuOH	7.0	53071	6	Cytoplasmic	COG0635	Coenzyme metabolism	
26990489	PP_3784		hypothetical protein	1.9	1.33E-01	control	5.4	41070	4	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	1.5	4.19E-01	control	6.5	50495	5	Cytoplasmic			
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.2	9.75E-01	7,5 g/l BuOH	5.3	30957	7	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990544	PP_3839		alcohol dehydrogenase	1.8	2.39E-01	control	5.7	35397	4	Cytoplasmic	COG1064	General function prediction only	
26990627	PP_3922		periplasmic protease	14.8	4.38E-05	7,5 g/l BuOH	9.8	37502	3	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990662	PP_3957		choline/carnitine/betaine transporter family protein	2.0	6.52E-02	7,5 g/l BuOH	7.6	72789	3	Cytoplasmic Membrane	COG1292	Cell envelope biogenesis, outer membrane	
26990695	PP_3990		hypothetical protein	1.7	5.07E-01	7,5 g/l BuOH	8.4	24356	2	Cytoplasmic Membrane	COG0670	General function prediction only	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	4.6	2.72E-02	7,5 g/l BuOH	6.4	91296	2	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.3	7.13E-01	7,5 g/l BuOH	5.7	83310	3	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.6	3.20E-01	control	5.4	45695	10	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.7	2.50E-01	control	5.4	79899	11	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.8	3.08E-01	7,5 g/l BuOH	5.9	50555	7	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990737	PP_4034		allantoate amidohydrolase	1.7	2.20E-01	control	5.7	45010	18	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.0	8.57E-01	control	7.9	53519	3	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP_4037		oxidoreductase	2.0	1.76E-01	control	5.5	48815	18	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038		dihydropyrimidine dehydrogenase	1.9	1.47E-01	control	5.1	46093	18	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990753	PP_4052	malQ	4-alpha-glucanotransferase	2.6	8.56E-02	control	5.5	76475	4	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	3.2	1.03E-01	control	6.6	103167	7	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	2.0	2.40E-01	control	5.1	81044	5	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990759	PP_4058	glgB	glycogen branching enzyme	1.2	4.51E-01	7,5 g/l BuOH	5.9	82877	2	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990806	PP_4111	fusA	elongation factor G	1.1	9.70E-01	7,5 g/l BuOH	5.0	77832	7	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990810	PP_4116	aceA	isocitrate lyase	21.8	9.57E-04	7,5 g/l BuOH	5.3	48633	17	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.7	1.62E-01	7,5 g/l BuOH	6.5	67609	9	Cytoplasmic	COG0649	Energy production and conversion	
26990817	PP_4123	nuoF	NADH dehydrogenase I subunit F	1.2	6.94E-01	control	7.1	49135	6	Cytoplasmic	COG1894	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.0	8.46E-01	7,5 g/l BuOH	5.9	97582	13	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	2.9	3.25E-02	7,5 g/l BuOH	6.1	37637	4	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.0	9.04E-01	control	8.7	20354	2	Cytoplasmic	COG0431	General function prediction only	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.4	4.76E-01	control	5.3	43264	5	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.2	1.35E-01	control	6.2	30111	7	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.8	1.91E-01	control	6.1	41239	19	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.2	5.73E-01	control	6.3	49912	11	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.7	9.56E-01	control	5.1	42434	3	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.1	6.91E-01	7,5 g/l BuOH	6.5	106521	22	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.2	6.83E-01	7,5 g/l BuOH	7.5	26000	4	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.0	9.84E-01	control	6.2	63448	19	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.6	2.33E-01	7,5 g/l BuOH	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.8	7.66E-02	7,5 g/l BuOH	7.0	47622	13	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.1	6.85E-01	7,5 g/l BuOH	9.7	26361	6	Unknown	COG2086	Energy production and conversion	
26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	3.4	8.91E-02	7,5 g/l BuOH	5.7	61082	9	Cytoplasmic	COG0644	Energy production and conversion	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	2.2	5.33E-02	7,5 g/l BuOH	9.6	53567	3	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	2.6	1.48E-01	7,5 g/l BuOH	9.0	22637	5	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	2.0	1.43E-01	7,5 g/l BuOH	5.2	35613	11	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	2.5	1.27E-01	7,5 g/l BuOH	8.5	53406	4	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	2.2	1.52E-01	7,5 g/l BuOH	6.0	35312	8	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991011	PP_4321	dsbE	periplasmic protein thiol--disulphide oxidoreductase DsbE	60.8	2.56E-03	7,5 g/l BuOH	6.5	19892	3	Cytoplasmic Membrane	COG0526	Posttranslational modification, protein turnover, chaperones	Energy production and conversion
26991012	PP_4322	ccmF	cytochrome c-type biogenesis protein CcmF	45.2	1.48E-02	7,5 g/l BuOH	9.7	72089	4	Cytoplasmic Membrane	COG1138	Posttranslational modification, protein turnover, chaperones	
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	2.0	3.08E-01	control	9.0	39451	3	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
26991028	PP_4338	cheA	chemotaxis protein CheA	1.1	6.60E-01	control	4.4	79674	3	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.3	6.03E-01	7,5 g/l BuOH	5.4	55551	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991134	PP_4448		hypothetical protein	1.6	4.33E-01	control	6.0	66331	10	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991159	PP_4473		aspartate kinase	2.1	7.95E-02	7,5 g/l BuOH	5.0	44605	2	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.6	2.96E-01	7,5 g/l BuOH	5.1	94711	11	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.3	9.12E-01	7,5 g/l BuOH	6.5	43490	7	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	39.8	2.57E-05	7,5 g/l BuOH	6.4	71796	41	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.1	4.05E-01	control	5.4	50393	22	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	1.0	9.18E-01	7,5 g/l BuOH	6.4	56605	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	2.6	1.31E-01	7,5 g/l BuOH	5.7	42326	4	Cytoplasmic	COG0332	acyl-carrier-protein	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.1	6.81E-01	7,5 g/l BuOH	7.7	61812	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	1.1	9.40E-01	control	7.8	61658	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991254	PP_4570		hypothetical protein	4.2	1.71E-02	7,5 g/l BuOH	10.1	35846	3	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991255	PP_4571	cysK	cysteine synthase A	1.5	7.48E-02	control	5.5	34357	2	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991325	PP_4641	cstA	carbon starvation protein CstA	2.7	1.12E-01	7,5 g/l BuOH	9.0	73763	10	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	2.0	1.66E-01	7,5 g/l BuOH	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	2.3	1.96E-01	7,5 g/l BuOH	9.1	53016	2	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	2.1	2.53E-01	7,5 g/l BuOH	4.8	68764	2	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	7.33E-01	7,5 g/l BuOH	5.4	36370	18	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	2.1	2.04E-01	7,5 g/l BuOH	6.8	62781	9	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991368	PP_4684		hypothetical protein	2.3	2.28E-01	7,5 g/l BuOH	5.1	56095	3	Cytoplasmic	COG2187	Function unknown	
26991381	PP_4697	pcnB	poly(A) polymerase	2.5	7.79E-02	7,5 g/l BuOH	9.6	52721	2	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.5	3.29E-01	7,5 g/l BuOH	6.8	61455	5	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	1.5	5.47E-01	control	6.5	71251	5	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	3.0	2.86E-01	7,5 g/l BuOH	5.6	107252	3	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.2	7.52E-01	7,5 g/l BuOH	4.9	75010	22	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.3	5.42E-01	7,5 g/l BuOH	6.8	91460	9	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	

26991396	PP_4713	nusA	transcription elongation factor NusA	2.1	3.81E-01	7,5 g/l BuOH	4.3	54673	6	Cytoplasmic	COG0195	Transcription		
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.9	1.10E-01	7,5 g/l BuOH	5.4	69722	16	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones		
26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	3.1	2.91E-01	7,5 g/l BuOH	5.8	40574	2	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.3	5.04E-01	control	4.6	68800	20	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones		
26991423	PP_4740	hsdR	type I restriction-modification system, R subunit	1.1	7.52E-01	7,5 g/l BuOH	5.2	89615	2	Cytoplasmic	COG4096	Defense mechanisms		
26991434	PP_4753		N-methylproline demethylase	1.9	1.24E-01	7,5 g/l BuOH	6.5	75215	2	Cytoplasmic	COG1902	Energy production and conversion		
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.1	6.87E-01	control	5.7	45178	5	Cytoplasmic	COG0001	Coenzyme metabolism		
26991474	PP_4794	leuS	leucyl-tRNA synthetase	2.5	1.42E-01	7,5 g/l BuOH	5.6	96697	9	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis		
26991475	PP_4795		rare lipoprotein B	1.1	9.11E-01	control	6.1	22414	2	Unknown	COG2980	Cell envelope biogenesis, outer membrane		
26991478	PP_4798		lytic murein transglycosylase	4.2	7.57E-02	7,5 g/l BuOH	7.7	48000	2	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane		
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.1	9.85E-01	7,5 g/l BuOH	6.1	45417	7	Cytoplasmic	COG0014	Amino acid transport and metabolism		
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.0	7.75E-01	control	4.7	45837	3	Cytoplasmic	COG0151	Nucleotide transport and metabolism		
26991518	PP_4838	oprC	TonB-dependent copper receptor	56.0	7.58E-01	7,5 g/l BuOH	6.2	74540	4	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
26991547	PP_4867		extracellular ligand-binding receptor	2.0	2.13E-01	control	6.2	40270	5	Periplasmic	COG0683	Amino acid transport and metabolism		
26991550	PP_4870		azurin	24.6	1.37E-03	7,5 g/l BuOH	6.9	16028	5	Periplasmic	COG3241	Energy production and conversion		
26991556	PP_4876	rpsR	30S ribosomal protein S18	1.3	1.85E-01	7,5 g/l BuOH	11.3	8927	3	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis		
26991559	PP_4880	vacB	ribonuclease R	1.0	8.54E-01	control	7.9	96688	2	Cytoplasmic	COG0557	Transcription		
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.1	4.79E-01	7,5 g/l BuOH	6.1	71958	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26991567	PP_4889	purA	adenylosuccinate synthetase	1.2	6.70E-01	control	5.6	46833	9	Cytoplasmic	COG0104	Nucleotide transport and metabolism		
26991568	PP_4890	hisZ	ATP phosphoribosyltransferase regulatory subunit	2.3	3.39E-01	7,5 g/l BuOH	4.7	42935	2	Cytoplasmic	COG3705	Amino acid transport and metabolism		
26991569	PP_4891	hflC	HflC protein	1.6	1.85E-01	7,5 g/l BuOH	9.8	33001	13	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones		
26991583	PP_4905		flagellar motor protein MotA	1.6	1.45E-02	7,5 g/l BuOH	6.2	30312	4	Cytoplasmic Membrane	COG1291	Cell motility and secretion		
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.6	2.07E-01	7,5 g/l BuOH	8.6	31547	2	Cytoplasmic Membrane	COG0688	Lipid metabolism		
26991588	PP_4910		hypothetical protein	2.8	1.77E-02	7,5 g/l BuOH	4.7	53632	7	Cytoplasmic	COG3726	General function prediction only		
26991600	PP_4922	thiC	thiamine biosynthesis protein ThiC	1.3	5.50E-01	7,5 g/l BuOH	5.7	69727	2	Cytoplasmic	COG0422	Coenzyme metabolism		
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.6	8.06E-01	control	5.2	52637	9	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	2.5	1.08E-01	7,5 g/l BuOH	7.6	66279	8	Cytoplasmic Membrane	COG1132	Defense mechanisms		
26991622	PP_4944		carbamoyltransferase	1.3	5.26E-01	7,5 g/l BuOH	7.2	65646	8	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones		
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	1.4	4.14E-01	7,5 g/l BuOH	6.3	142580	12	Cytoplasmic	COG4230	Energy production and conversion		
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.1	6.37E-01	control	5.6	38453	9	Cytoplasmic	COG0191	Carbohydrate transport and metabolism		
26991641	PP_4963	pgk	phosphoglycerate kinase	1.0	7.22E-01	control	4.9	40005	2	Cytoplasmic	COG0126	Carbohydrate transport and metabolism		
26991643	PP_4965	tktA	transketolase	1.3	4.84E-01	7,5 g/l BuOH	5.0	72463	10	Cytoplasmic	COG0021	Carbohydrate transport and metabolism		
26991645	PP_4967	metK	S-adenosylmethionine synthetase	2.4	5.33E-02	control	5.1	42779	14	Cytoplasmic	COG0192	Coenzyme metabolism		
26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	3.7	2.12E-02	control	6.2	32979	3	Cytoplasmic	COG0685	Amino acid transport and metabolism		
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.3	5.93E-01	control	5.7	49982	4	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones		
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	1.5	5.61E-01	control	7.4	62241	2	Cytoplasmic	COG3243	Lipid metabolism		
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	2.2	4.12E-01	7,5 g/l BuOH	10.9	26214	4	Cytoplasmic	COG3937	Function unknown		
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.0	9.88E-01	7,5 g/l BuOH	4.9	69017	23	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26991701	PP_5025	mdoH	glucosyltransferase MdoH	5.2	2.16E-02	7,5 g/l BuOH	8.3	95875	4	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane		
26991716	PP_5040	fbp	fructose-1,6-bisphosphatase	1.6	5.09E-01	7,5 g/l BuOH	5.9	37246	2	Cytoplasmic	COG0158	Carbohydrate transport and metabolism		
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.0	7.53E-01	7,5 g/l BuOH	6.4	92004	4	Cytoplasmic	COG0058	Carbohydrate transport and metabolism		
26991720	PP_5044		GTP-binding protein TypA	1.4	6.64E-01	7,5 g/l BuOH	5.3	67157	3	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms		
26991722	PP_5046	glnA	glutamine synthetase, type I	1.5	3.70E-01	control	5.1	51740	13	Cytoplasmic	COG0174	Amino acid transport and metabolism		
26991732	PP_5056	pgm	phosphoglyceromutase	1.2	8.72E-01	7,5 g/l BuOH	4.9	55180	5	Cytoplasmic	COG0696	Carbohydrate transport and metabolism		
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.8	2.32E-01	7,5 g/l BuOH	6.2	161772	15	Cytoplasmic	COG0069	Amino acid transport and metabolism		
26991761	PP_5085	maeB	malic enzyme	1.4	3.80E-01	control	4.9	45127	14	Cytoplasmic	COG0281	Energy production and conversion		
26991765	PP_5089	argS	arginyl-tRNA synthetase	2.2	2.31E-01	7,5 g/l BuOH	5.7	63668	6	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis		
26991772	PP_5096		hypothetical protein	3.4	1.34E-02	7,5 g/l BuOH	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown		
26991785	PP_5109	ftsX	hypothetical protein	2.3	6.65E-02	7,5 g/l BuOH	6.5	36984	3	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning		
26991796	PP_5120		conifer aldehyde dehydrogenase	1.0	7.53E-01	control	9.2	52453	3	Cytoplasmic	COG1012	Energy production and conversion		
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.7	1.76E-01	7,5 g/l BuOH	5.8	65671	15	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism	
26991821	PP_5145	ptsP	PTSINtr with GAF domain, PtsP	2.6	2.80E-01	7,5 g/l BuOH	5.3	83337	3	Cytoplasmic	COG3605	Signal transduction mechanisms		
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.2	9.02E-01	7,5 g/l BuOH	6.3	44339	13	Cytoplasmic	COG0111	Amino acid transport and metabolism		
26991849	PP_5173		acriflavin resistance protein	1.1	9.16E-01	7,5 g/l BuOH	5.4	112277	6	Cytoplasmic Membrane	COG0841	Defense mechanisms		
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	1.2	8.81E-01	7,5 g/l BuOH	6.5	42472	2	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism		
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	2.2	1.59E-01	control	6.4	40068	2	Periplasmic	COG0687	Amino acid transport and metabolism		
26991858	PP_5182		aminotransferase	1.5	4.59E-01	7,5 g/l BuOH	6.2	49871	2	Cytoplasmic	COG0161	Coenzyme metabolism		
26991859	PP_5183		glutamine synthetase	1.3	5.65E-01	7,5 g/l BuOH	4.8	50877	3	Cytoplasmic	COG0174	Amino acid transport and metabolism		
26991860	PP_5184		glutamine synthetase	1.1	1.00E+00	control	4.5	50974	2	Cytoplasmic	COG0174	Amino acid transport and metabolism		
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.9	2.30E-01	control	6.3	104037	3	Cytoplasmic	COG1003	Amino acid transport and metabolism		
26991890	PP_5214	rho	transcription termination factor Rho	1.2	8.10E-01	7,5 g/l BuOH	8.2	47041	5	Cytoplasmic	COG1158	Transcription		
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.3	3.02E-01	7,5 g/l BuOH	6.9	55958	2	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism	
26991893	PP_5217	ppk	polyphosphate kinase	1.6	2.49E-01	7,5 g/l BuOH	7.8	81732	6	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism		
26991954	PP_5278		aldehyde dehydrogenase family protein	1.2	9.54E-01	7,5 g/l BuOH	5.5	53053	4	Cytoplasmic	COG1012	Energy production and conversion		
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.8	5.04E-02	7,5 g/l BuOH	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis		
26991964	PP_5288		phosphomannomutase	4.6	4.98E-02	7,5 g/l BuOH	5.0	50271	3	Cytoplasmic	COG1109	Carbohydrate transport and metabolism		
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	3.3	4.97E-02	7,5 g/l BuOH	9.2	78603	6	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.3	5.04E-01	control	5.3	65626	14	Cytoplasmic	COG5016	Energy production and conversion		
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.4	3.69E-01	control	6.5	51942	10	Cytoplasmic	COG0439	Lipid metabolism		
26992029	PP_5353		hypothetical protein	2.2	8.28E-02	7,5 g/l BuOH	7.2	30672	4	Cytoplasmic Membrane	COG4395	Function unknown		
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	1.6	4.61E-01	7,5 g/l BuOH	5.9	48114	2	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane		
26992055	PP_5379	copB	copper resistance B precursor	10.5	6.34E-02	control	5.0	40230	4	Outer Membrane	COG3667	Inorganic ion transport and metabolism		
26992070	PP_5395		hypothetical protein	1.2	6.04E-01	7,5 g/l BuOH	5.6	31623	2	Cytoplasmic	COG1568	General function prediction only		
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	2.1	5.05E-01	7,5 g/l BuOH	6.0	66312	2	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane		
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.4	6.20E-01	7,5 g/l BuOH	4.6	49359	19	Cytoplasmic	COG0055	Energy production and conversion		
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.9	1.82E-01	control	9.2	31464	7	Cytoplasmic	COG0224	Energy production and conversion		
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.0	7.91E-01	7,5 g/l BuOH	5.2	55352	20	Cytoplasmic	COG0056	Energy production and conversion		
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.6	1.11E-01	7,5 g/l BuOH	5.3	16898	5	Cytoplasmic Membrane	COG0711	Energy production and conversion		
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	4.3	4.18E-02	7,5 g/l BuOH	6.7	31712	3	Cytoplasmic Membrane	COG0356	Energy production and conversion		
313498081				1.1	6.82E-01	control			22					
148550051				2.0	9.30E-02	control			17					
148549148				1.3	4.95E-01	control			17					
254521045				1.0	4.76E-01	control			12					
190575345				1.9	8.54E-01	control			12					
313496770				1.1	6.37E-01	control			10					
24981833				2.0	1.71E-01	control			7					
24982083				3.5	5.02E-02	control			4					
14195580				2.5	9.76E-02	control			4					
194367115				1.1	5.65E-01	control			4					
206970188				38.8	9.39E-01	control			3					
24982932				2.7	8.20E-02	control			2					
262377497				16.2	2.68E-02	control			2					
206977707				59.9	1.22E-01	control			2					
24986054				7.2	8.57E-02	control			2					
254522278				2.1	4.25E-01	control			2					
24986476				1.4	3.89E-01	7,5 g/l BuOH			32					
338780844				12.7	6.11E-01	7,5 g/l BuOH			14					
377576294				21.5	5.29E-01	7,5 g/l BuOH			13					
24981839				1.3	2.15E-01	7,5 g/l BuOH			11					
148545524				1.2	8.93E-01	7,5 g/l BuOH			10					

194364578	1.6	3.27E-01	7,5 g/l BuOH	10
148547806	1.1	7.29E-01	7,5 g/l BuOH	9
254521740	1.9	3.66E-01	7,5 g/l BuOH	9
194365946	19.2	1.14E-01	7,5 g/l BuOH	9
190572101	10.7	9.72E-02	7,5 g/l BuOH	7
194366647	32.2	3.15E-02	7,5 g/l BuOH	6
15599454	1.5	1.25E-01	7,5 g/l BuOH	5
129138	18.1	6.21E-01	7,5 g/l BuOH	5
344208989	4.5	3.59E-01	7,5 g/l BuOH	5
194367745	3.3	1.45E-01	7,5 g/l BuOH	5
260609519	8.0	7.78E-03	7,5 g/l BuOH	5
190575561	2.1	2.81E-01	7,5 g/l BuOH	4
308069938	147.4	7.59E-01	7,5 g/l BuOH	4
222085378	66.6	5.55E-01	7,5 g/l BuOH	3
194365395	15.9	2.84E-01	7,5 g/l BuOH	2
298682197	55.9	4.95E-04	7,5 g/l BuOH	3
148546787	5.6	1.05E-01	7,5 g/l BuOH	3
194364913	5.9	4.21E-01	7,5 g/l BuOH	3
293604168	36.9	4.97E-01	7,5 g/l BuOH	3
222085864	28.8	2.15E-01	7,5 g/l BuOH	3
344205753	2.0	4.23E-01	7,5 g/l BuOH	3
254524919	1.4	3.63E-01	7,5 g/l BuOH	2
377577537	65.8	5.05E-01	7,5 g/l BuOH	2
269200090	3.1	3.50E-02	7,5 g/l BuOH	2
190572491	1.2	7.88E-01	7,5 g/l BuOH	2
308070977	883.5	1.55E-01	7,5 g/l BuOH	2
24982353	1.7	4.96E-01	7,5 g/l BuOH	2
194364029	2.4	3.95E-01	7,5 g/l BuOH	2
194364598	1.5	3.28E-01	7,5 g/l BuOH	2
194367479	5.3	2.57E-01	7,5 g/l BuOH	2
190572433	54.5	1.16E-01	7,5 g/l BuOH	2

5.2.3.3 GeLCMSMS



Gelbild der GeLCMSMS-Analyse von mit 0,75 g/l bzw. 7,5 g/l Butanol behandelten sowie unbehandelten Zellen von *P. putida* KT2440 aus dem Bioreaktor. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Front den unteren Rand des Gels erreicht hatte, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Jede Spur wurde in 10 Fraktionen unterteilt und die markierten Bereiche aus dem Gel ausgeschnitten und mit Trypsin verdaut.

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986746	PP_0001	parB	parB-like partition protein	1.6	2.50E-01	7,5g BuOH	6.5	32390	10	Cytoplasmic	COG1475	Transcription	
26986747	PP_0002		ParA family protein	1.3	4.02E-01	0,75g BuOH	6.7	28919	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
26986748	PP_0003	gidB	16S rRNA methyltransferase GidB	1.3	3.93E-01	0,75g BuOH	7.1	24063	2	Unknown	COG0357	Cell envelope biogenesis, outer membrane	
26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	1.5	2.86E-01	0,75g BuOH	6.4	69567	2	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
26986750	PP_0005	trmE	tRNA modification GTPase TrmE	1.1	6.07E-01	7,5g BuOH	5.0	48963	3	Cytoplasmic	COG0486	General function prediction only	
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	3.0	6.30E-02	0,75g BuOH	9.1	61919	11	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.6	2.02E-02	0,75g BuOH	4.9	40718	15	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.4	4.29E-02	7,5g BuOH	5.8	90030	22	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.1	5.79E-01	0,75g BuOH	6.1	31236	14	Cytoplasmic			
26986764	PP_0019		hypothetical protein	1.4	2.11E-01	0,75g BuOH	4.8	24854	3	Unknown			
26986765	PP_0020		hypothetical protein	1.1	4.96E-01	0,75g BuOH	4.9	33146	4	Cytoplasmic			
26986774	PP_0029	czrR-1	DNA-binding response regulator CzrR	1.2	3.78E-01	0,75g BuOH	6.1	25537	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26986802	PP_0057		major facilitator family transporter	1.7	5.72E-01	7,5g BuOH	9.3	58758	2	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.8	2.17E-01	7,5g BuOH	4.9	75112	21	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.7	2.88E-01	7,5g BuOH	4.8	36024	2	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986808	PP_0063		lipid A biosynthesis lauroyl acyltransferase	1.3	3.93E-01	0,75g BuOH	10.1	32840	2	Cytoplasmic Membrane	COG1560	Cell envelope biogenesis, outer membrane	
26986813	PP_0068	def	peptide deformylase	1.2	5.26E-01	0,75g BuOH	5.1	19410	3	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
26986815	PP_0070		SuaS/YciO/YrdC/YwlC family protein	1.6	1.83E-01	0,75g BuOH	6.1	20493	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.6	2.13E-01	0,75g BuOH	8.1	34224	14	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986818	PP_0073	hemF	coproporphyrinogen III oxidase	1.3	4.00E-01	0,75g BuOH	5.6	34393	3	Cytoplasmic	COG0408	Coenzyme metabolism	
26986819	PP_0074	aroE	shikimate 5-dehydrogenase	1.2	5.79E-01	7,5g BuOH	5.0	29289	5	Cytoplasmic	COG0169	Amino acid transport and metabolism	
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1.1	6.56E-01	0,75g BuOH	5.0	28482	8	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.6	3.41E-02	7,5g BuOH	6.4	44046	5	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986831	PP_0086		hypothetical protein	3.4	9.76E-02	7,5g BuOH	7.9	7959	4	Unknown	COG3360	Function unknown	
26986839	PP_0094		HAD superfamily hydrolase	1.6	3.77E-01	7,5g BuOH	5.1	24540	4	Cytoplasmic	COG0546	General function prediction only	
26986841	PP_0096	prlC	oligopeptidase A	1.2	2.16E-01	7,5g BuOH	5.0	75721	23	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.5	4.49E-02	0,75g BuOH	6.8	26001	18	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.8	1.29E-01	0,75g BuOH	6.8	42059	6	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986851	PP_0106		cytochrome c oxidase, subunit III	3.1	9.91E-02	0,75g BuOH	8.7	33623	3	Cytoplasmic Membrane	COG1845	Energy production and conversion	
26986857	PP_0112		metal ABC transporter periplasmic protein	1.1	6.43E-01	7,5g BuOH	7.8	27711	16	Cytoplasmic Membrane	COG1464	Inorganic ion transport and metabolism	
26986861	PP_0116		lipoprotein	1.2	3.96E-01	7,5g BuOH	7.4	25597	5	Unknown			
26986868	PP_0123	polA	DNA polymerase I	1.2	4.33E-01	0,75g BuOH	5.1	99607	11	Cytoplasmic	COG0749	DNA replication, recombination, and repair	
26986869	PP_0124	engB	ribosome biogenesis GTP-binding protein YsxC	1.5	4.28E-02	0,75g BuOH	9.6	23440	11	Cytoplasmic	COG0218	General function prediction only	
26986871	PP_0126		cytochrome c4	2.5	1.22E-01	0,75g BuOH	8.0	21260	3	Periplasmic	COG2863	Energy production and conversion	
26986872	PP_0127		DsbA family thiol:disulfide interchange protein	1.3	6.04E-01	0,75g BuOH	7.1	23073	5	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.3	4.08E-01	0,75g BuOH	9.6	29387	3	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986884	PP_0139		lipoprotein	2.4	2.17E-02	0,75g BuOH	9.5	23212	3	Unknown	COG3218	General function prediction only	
26986885	PP_0140		hypothetical protein	2.1	9.67E-02	7,5g BuOH	5.4	33062	3	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26986886	PP_0141		ABC transporter ATP-binding protein	2.1	2.49E-02	0,75g BuOH	6.7	28270	3	Cytoplasmic Membrane	COG1127	Secondary metabolites biosynthesis, transport, and catabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.4	2.81E-01	0,75g BuOH	7.3	50185	2	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986907	PP_0163		GntR family transcriptional regulator	1.5	8.43E-01	7,5g BuOH	7.3	25518	4	Cytoplasmic	COG1802	Transcription	
26986909	PP_0165		GGDEF domain-containing protein	6.0	1.13E-02	0,75g BuOH	6.3	71284	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.6	1.87E-01	0,75g BuOH	7.8	51116	5	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.1	5.12E-01	0,75g BuOH	7.7	78583	14	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986912	PP_0168		surface adhesion protein	3.3	4.02E-02	0,75g BuOH	3.9	888214	6	Extracellular	COG2931	Secondary metabolites biosynthesis, transport, and catabolism	
26986917	PP_0173		transcriptional factor-related protein	1.1	8.18E-01	7,5g BuOH	10.1	23493	5	Unknown			
26986927	PP_0183		glutathione S-transferase family protein	1.2	3.99E-01	0,75g BuOH	5.4	24438	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26986928	PP_0184	argH	argininosuccinate lyase	1.6	1.23E-01	0,75g BuOH	5.4	52061	14	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	1.1	6.46E-01	0,75g BuOH	6.5	27422	11	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
26986931	PP_0187	hemD	uroporphyrinogen-III synthase	1.3	2.57E-01	0,75g BuOH	6.8	27045	2	Unknown	COG1587	Coenzyme metabolism	
26986932	PP_0188		uroporphyrin-III C-methyltransferase	1.3	8.09E-01	7,5g BuOH	4.8	40556	12	Cytoplasmic Membrane	COG2959	Coenzyme metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.2	3.68E-01	0,75g BuOH	9.6	46030	7	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	2.7	4.56E-01	0,75g BuOH	11.3	32300	6	Cytoplasmic			
26986940	PP_0196		ABC transporter ATP-binding protein	1.5	3.10E-01	0,75g BuOH	5.7	70615	5	Cytoplasmic	COG0488	General function prediction only	
26986947	PP_0203		hypothetical protein	1.3	7.32E-01	7,5g BuOH	5.9	62682	15	Unknown	COG0624	Amino acid transport and metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.0	9.53E-01	7,5g BuOH	5.2	51549	25	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.8	3.50E-02	0,75g BuOH	6.1	44824	13	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986958	PP_0215		signal transduction protein	1.7	1.60E-01	7,5g BuOH	7.0	45294	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
26986968	PP_0225		amino-acid ABC transporter ATP-binding protein YecC	1.3	4.32E-01	0,75g BuOH	10.2	27596	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26986970	PP_0227		cystine transporter subunit	1.3	1.55E-01	7,5g BuOH	8.7	28756	24	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26986977	PP_0234	oprE	outer membrane porin	1.2	4.58E-01	0,75g BuOH	5.4	48317	16	Outer Membrane			
26986978	PP_0235	lsfA	peroxidase	1.1	7.84E-01	7,5g BuOH	6.0	23948	10	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26986986	PP_0243	gshA	glutamate--cysteine ligase	2.2	4.49E-02	0,75g BuOH	4.8	59067	6	Cytoplasmic	COG2918	Coenzyme metabolism	
26986988	PP_0245		S1 RNA-binding domain-containing protein	1.2	7.11E-01	0,75g BuOH	8.7	94304	2	Cytoplasmic	COG2183	Transcription	
26986989	PP_0246	ompR	osmolarity response regulator	1.2	3.60E-01	7,5g BuOH	5.9	27492	10	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26986990	PP_0247	envZ	integral membrane sensor signal transduction histidine kinase	1.1	6.62E-01	7,5g BuOH	6.1	48808	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986995	PP_0252	hslO	Hsp33-like chaperonin	1.6	1.11E-01	0,75g BuOH	4.4	33472	9	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
26987002	PP_0260	nudE	ADP-ribose diphosphatase NudE	2.8	6.67E-02	0,75g BuOH	4.5	20947	2	Cytoplasmic			
26987005	PP_0263		two component, sigma54 specific, transcriptional regulator, Fis family	5.6	1.87E-02	7,5g BuOH	5.9	50990	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
26987010	PP_0268	oprQ	outer membrane porin	2.6	1.70E-02	0,75g BuOH	6.1	47787	11	Outer Membrane			
26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding protein	1.0	8.05E-01	0,75g BuOH	5.2	27869	23	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987025	PP_0283		amino acid ABC transporter ATP-binding protein	1.4	2.44E-01	0,75g BuOH	7.7	28381	5	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism	
26987029	PP_0287		AsmA family protein	1.0	9.78E-01	7,5g BuOH	6.0	80277	5	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	1.8	5.49E-01	7,5g BuOH	8.5	50780	3	Cytoplasmic Membrane			
26987031	PP_0289	hisB	imidazoleglycerol-phosphate dehydratase	1.0	7.16E-01	0,75g BuOH	6.4	23420	5	Cytoplasmic	COG0131	Amino acid transport and metabolism	
26987032	PP_0290	hisH	imidazole glycerol phosphate synthase subunit HisH	1.0	6.91E-01	0,75g BuOH	6.4	23535	9	Cytoplasmic	COG0118	Amino acid transport and metabolism	
26987034	PP_0292	hisA	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	1.7	8.98E-02	7,5g BuOH	4.9	25907	7	Cytoplasmic	COG0106	Amino acid transport and metabolism	
26987035	PP_0293	hisF	imidazole glycerol phosphate synthase subunit HisF	1.3	5.80E-02	0,75g BuOH	5.0	27131	5	Cytoplasmic	COG0107	Amino acid transport and metabolism	
26987036	PP_0294		glycine betaine/L-proline ABC transporter ATP-binding subunit	8.6	1.32E-03	0,75g BuOH	7.9	43724	3	Cytoplasmic Membrane	COG4175	Amino acid transport and metabolism	
26987038	PP_0296		glycine betaine/L-proline ABC transporter periplasmic protein	2.0	2.62E-02	0,75g BuOH	6.6	34568	13	Unknown	COG2113	Amino acid transport and metabolism	
26987050	PP_0308		membrane dipeptidase	1.1	9.51E-01	0,75g BuOH	5.4	35978	3	Cytoplasmic	COG2355	Amino acid transport and metabolism	
26987063	PP_0321		threonine aldolase	1.2	3.35E-01	7,5g BuOH	5.4	38068	7	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987068	PP_0326	soxG	sarcosine oxidase, gamma subunit family	2.6	1.26E-01	0,75g BuOH	7.3	22961	3	Cytoplasmic	COG4583	Amino acid transport and metabolism	
26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	5.7	7.61E-02	0,75g BuOH	6.6	42328	3	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
26987077	PP_0335		glutathione S-transferase family protein	1.5	1.22E-01	7,5g BuOH	6.4	23174	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	3.2	4.93E-02	0,75g BuOH	4.7	24565	6	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.3	1.32E-01	0,75g BuOH	5.3	55654	20	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.8	4.81E-02	0,75g BuOH	5.6	99332	60	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.1	5.56E-01	0,75g BuOH	5.3	109432	20	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987083	PP_0341	waaF	lipopolysaccharide heptosyltransferase II	1.2	6.26E-01	7,5g BuOH	6.7	38423	3	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane	
26987089	PP_0347		hypothetical protein	1.5	2.27E-01	0,75g BuOH	7.4	53779	2	Cytoplasmic			
26987098	PP_0356	glcB	malate synthase G	5.1	5.25E-03	7,5g BuOH	5.8	78346	26	Cytoplasmic	COG2225	Energy production and conversion	
26987104	PP_0362	bioB	biotin synthase	1.9	3.28E-02	7,5g BuOH	5.6	38950	4	Cytoplasmic	COG0502	Coenzyme metabolism	
26987106	PP_0364	bioH	carboxylesterase	1.0	7.58E-01	0,75g BuOH	4.8	26344	2	Cytoplasmic	COG0596	General function prediction only	
26987108	PP_0366	bioD	dithiobiotin synthetase	2.4	8.73E-02	0,75g BuOH	5.3	23871	12	Cytoplasmic	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	2.5	5.07E-03	0,75g BuOH	5.8	65541	25	Cytoplasmic	COG1960	Lipid metabolism	
26987112	PP_0370		acyl-CoA dehydrogenase domain-containing protein	3.9	1.55E-02	0,75g BuOH	4.9	63592	6	Cytoplasmic	COG1960	Lipid metabolism	
26987117	PP_0375		prolyl oligopeptidase family protein	1.3	6.74E-01	7,5g BuOH	6.0	67549	5	Cytoplasmic	COG1506	Amino acid transport and metabolism	
26987118	PP_0376	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	2.3	4.99E-04	7,5g BuOH	6.5	42507	5	Cytoplasmic	COG0535	General function prediction only	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	4.0	1.83E-03	7,5g BuOH	6.8	29075	20	Cytoplasmic	COG5424	Coenzyme metabolism	
26987121	PP_0379	pqqB	pyrroloquinoline quinone biosynthesis protein PqqB	3.8	2.15E-03	7,5g BuOH	5.5	33331	14	Cytoplasmic	COG1235	General function prediction only	
26987124	PP_0382		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2.9	9.36E-02	0,75g BuOH	4.9	29311	3	Cytoplasmic	COG0388	General function prediction only	
26987128	PP_0386		sensory box protein	3.1	1.17E-02	0,75g BuOH	5.6	139392	7	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.8	2.10E-01	7,5g BuOH	4.6	69396	21	Cytoplasmic	COG0568	Transcription	
26987130	PP_0388	dnaG	DNA primase	3.3	8.60E-01	7,5g BuOH	6.8	73829	1	Cytoplasmic	COG0358	DNA replication, recombination, and repair	
26987137	PP_0395		SpoVR family protein	4.2	2.10E-02	0,75g BuOH	5.4	61330	10	Cytoplasmic	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	2.5	1.76E-02	0,75g BuOH	7.0	50488	6	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.4	2.00E-02	7,5g BuOH	5.8	73782	49	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987143	PP_0401	ksgA	dimethyladenosine transferase	1.2	4.06E-01	0,75g BuOH	8.5	29666	3	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
26987145	PP_0403	surA	survival protein SurA	1.7	2.80E-01	7,5g BuOH	5.2	49082	14	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
26987146	PP_0405		aminoglycoside phosphotransferase	2.8	1.80E-02	7,5g BuOH	4.8	38238	4	Cytoplasmic	COG3178	General function prediction only	
26987147	PP_0406		nucleotidyl transferase	1.3	3.24E-01	0,75g BuOH	6.0	23814	3	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
26987151	PP_0410	uhpA	LuxR family two component transcriptional regulator	1.4	8.83E-02	7,5g BuOH	7.2	22750	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26987153	PP_0412		polyamine ABC transporter periplasmic protein	2.2	7.14E-02	0,75g BuOH	5.3	37801	10	Periplasmic	COG0687	Amino acid transport and metabolism	
26987156	PP_0415	rpe	ribulose-phosphate 3-epimerase	1.9	8.15E-02	7,5g BuOH	5.6	27672	5	Cytoplasmic	COG0036	Carbohydrate transport and metabolism	
26987158	PP_0417	trpE	anthranilate synthase component I	2.2	7.05E-02	0,75g BuOH	4.8	54406	10	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism

26987159	PP 0418		GDSL family lipase	1.6	2.78E-01	0,75g BuOH	4.4	67175	2	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987162	PP 0421	trpD	anthranilate phosphoribosyltransferase	2.0	2.40E-01	0,75g BuOH	5.6	37245	3	Cytoplasmic	COG0547	Amino acid transport and metabolism	
26987163	PP 0422	trpC	indole-3-glycerol-phosphate synthase	1.1	5.90E-01	0,75g BuOH	4.7	30433	10	Cytoplasmic	COG0134	Amino acid transport and metabolism	
26987171	PP 0430		hypothetical protein	2.1	2.99E-02	0,75g BuOH	6.7	33680	4	Unknown	COG2070	General function prediction only	
26987173	PP 0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.1	6.59E-01	0,75g BuOH	6.8	36277	12	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987175	PP 0434	anmK	anhydro-N-acetylmuramic acid kinase	1.4	1.11E-01	0,75g BuOH	5.8	38235	3	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
26987177	PP 0436	tyrS	tyrosyl-tRNA synthetase	1.3	2.97E-01	7,5g BuOH	5.5	44287	13	Cytoplasmic	COG0162	Translation, ribosomal structure and biogenesis	
26987181	PP 0440	tuf	elongation factor Tu	1.3	4.28E-01	7,5g BuOH	5.0	43495	34	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987183	PP 0442	nusG	transcription antitermination protein NusG	3.6	2.85E-01	0,75g BuOH	6.3	20048	3	Cytoplasmic	COG0250	Transcription	
26987185	PP 0444	rplA	50S ribosomal protein L1	1.4	2.19E-01	0,75g BuOH	10.1	24251	20	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP 0445	rplJ	50S ribosomal protein L10	5.0	3.03E-01	7,5g BuOH	10.2	17686	5	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP 0447	rpoB	DNA-directed RNA polymerase subunit beta	1.9	1.04E-01	0,75g BuOH	5.5	150992	84	Cytoplasmic	COG0085	Transcription	
26987189	PP 0448	rpoC	DNA-directed RNA polymerase subunit beta'	2.2	1.34E-01	0,75g BuOH	7.2	154797	75	Cytoplasmic	COG0086	Transcription	
26987190	PP 0449	rpsL	30S ribosomal protein S12	1.5	6.92E-01	7,5g BuOH	11.7	13727	2	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP 0450	rpsG	30S ribosomal protein S7	11.1	9.95E-02	7,5g BuOH	10.8	17578	3	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP 0451	fusA	elongation factor G	1.2	5.62E-01	0,75g BuOH	4.9	78817	57	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP 0452	tuf	elongation factor Tu	1.3	2.29E-01	0,75g BuOH	5.0	43478	47	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP 0455	rplD	50S ribosomal protein L4	1.3	2.73E-01	0,75g BuOH	10.3	21811	8	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP 0457	rplB	50S ribosomal protein L2	2.0	6.88E-02	0,75g BuOH	11.7	29669	15	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP 0461	rplP	50S ribosomal protein L16	5.8	3.74E-02	7,5g BuOH	11.9	15373	2	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP 0464	rplN	50S ribosomal protein L14	3.0	5.33E-01	7,5g BuOH	11.6	13410	2	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987206	PP 0465	rplX	50S ribosomal protein L24	79.2	2.13E-01	7,5g BuOH	10.8	11329	2	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis	
26987207	PP 0466	rplE	50S ribosomal protein L5	1.2	6.24E-01	7,5g BuOH	10.3	20329	12	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987209	PP 0468	rpsH	30S ribosomal protein S8	6.8	6.31E-02	7,5g BuOH	10.2	13975	3	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP 0469	rplF	50S ribosomal protein L6	1.7	1.97E-01	0,75g BuOH	10.4	19143	9	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP 0470	rplR	50S ribosomal protein L18	1.8	8.79E-01	7,5g BuOH	10.9	12628	4	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP 0471	rpsE	30S ribosomal protein S5	3.1	2.59E-01	7,5g BuOH	10.6	17666	6	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP 0473	rplO	50S ribosomal protein L15	79.3	3.08E-02	7,5g BuOH	11.5	15189	4	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP 0474	secY	preprotein translocase subunit SecY	1.2	9.17E-01	7,5g BuOH	10.4	47853	3	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP 0476	rpsM	30S ribosomal protein S13	2.9	2.39E-01	7,5g BuOH	11.3	13256	3	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP 0477	rpsK	30S ribosomal protein S11	2.0	9.22E-01	7,5g BuOH	11.5	13660	2	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP 0478	rpsD	30S ribosomal protein S4	1.6	2.93E-02	0,75g BuOH	10.5	23056	15	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP 0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.1	5.06E-01	0,75g BuOH	4.7	36629	21	Cytoplasmic	COG0202	Transcription	
26987221	PP 0480	rplQ	50S ribosomal protein L17	8.0	8.08E-02	7,5g BuOH	11.3	14363	3	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP 0482		bacterioferritin	6.1	4.70E-01	0,75g BuOH	4.6	17972	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987224	PP 0483	uvrA	excinuclease ABC subunit A	1.4	2.95E-01	7,5g BuOH	7.0	104378	13	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
26987226	PP 0485	ssb	single-stranded DNA-binding protein	2.0	4.03E-01	0,75g BuOH	6.0	20059	5	Cytoplasmic	COG0629	DNA replication, recombination, and repair	
26987233	PP 0493	selA	selenocysteine synthase	1.2	1.44E-01	0,75g BuOH	7.7	51723	3	Cytoplasmic	COG1921	seryl-tRNASer selenium transferase	
26987239	PP 0500		dTDP-4-dehydrorhamnose reductase	1.4	4.10E-01	7,5g BuOH	6.6	32700	2	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26987240	PP 0501		NAD-dependent epimerase/dehydratase	1.0	9.33E-01	7,5g BuOH	5.2	33325	4	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987249	PP 0510	trx-1	thioredoxin	1.4	7.18E-02	7,5g BuOH	4.6	31822	7	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
26987253	PP 0515	ribE-1	riboflavin synthase subunit alpha	1.9	1.62E-01	0,75g BuOH	6.5	23597	3	Cytoplasmic	COG0307	Coenzyme metabolism	
26987259	PP 0521		hypothetical protein	1.2	9.80E-01	7,5g BuOH	6.4	28523	3	Unknown			
26987260	PP 0522	ribA	GTP cyclohydrolase II	1.2	4.62E-01	0,75g BuOH	7.0	22350	4	Cytoplasmic	COG0807	Coenzyme metabolism	
26987266	PP 0528	ispA	polyprenyl synthetase	34.9	1.20E-01	7,5g BuOH	4.9	31352	3	Cytoplasmic	COG0142	Coenzyme metabolism	
26987276	PP 0538	ppa	inorganic pyrophosphatase	1.2	5.17E-01	0,75g BuOH	4.6	19189	7	Cytoplasmic	COG0221	Energy production and conversion	
26987280	PP 0542		ethanolamine ammonia-lyase small subunit	1.4	3.51E-01	0,75g BuOH	6.9	29573	4	Cytoplasmic	COG4302	Amino acid transport and metabolism	
26987281	PP 0543	eutB	ethanolamine ammonia lyase large subunit	1.1	9.28E-01	0,75g BuOH	5.0	49939	2	Cytoplasmic	COG4303	Amino acid transport and metabolism	
26987282	PP 0544		ethanolamine transproter	1.8	2.96E-01	0,75g BuOH	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP 0545		aldehyde dehydrogenase family protein	1.2	3.59E-01	7,5g BuOH	5.9	55268	31	Cytoplasmic	COG1012	Energy production and conversion	
26987285	PP 0547	mpl	UDP-N-acetylmuramate	1.6	6.13E-02	0,75g BuOH	6.1	48202	5	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
26987288	PP 0550		hypothetical protein	1.9	8.16E-02	0,75g BuOH	7.6	23787	8	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987296	PP 0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.5	1.19E-01	0,75g BuOH	6.5	49088	22	Cytoplasmic	COG0439	Lipid metabolism	
26987297	PP 0559	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	1.9	5.20E-01	0,75g BuOH	4.7	16186	5	Unknown	COG0511	Lipid metabolism	
26987298	PP 0560	aroQ-1	3-dehydroquinate dehydratase	541.5	3.59E-02	7,5g BuOH	6.9	16491	2	Cytoplasmic	COG0757	Amino acid transport and metabolism	
26987302	PP 0564		hypothetical protein	1.1	6.69E-01	7,5g BuOH	6.6	40223	11	Unknown	COG5345	Function unknown	
26987305	PP 0567	speA	arginine decarboxylase	1.2	9.94E-01	7,5g BuOH	5.3	71043	8	Unknown	COG1166	Amino acid transport and metabolism	
26987308	PP 0570		alpha-2-macroglobulin domain protein	1.4	9.76E-02	0,75g BuOH	5.2	178472	25	Unknown	COG2373	General function prediction only	
26987319	PP 0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.6	4.90E-01	7,5g BuOH	7.5	47782	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987322	PP 0584		methyl-accepting chemotaxis transducer	1.3	3.66E-01	7,5g BuOH	5.0	69953	26	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987329	PP 0591	add	adenosine deaminase	1.0	8.87E-01	7,5g BuOH	4.8	35845	4	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
26987330	PP 0592		short chain dehydrogenase	1.1	4.99E-01	0,75g BuOH	6.0	24627	3	Extracellular	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987334	PP 0596		beta alanine--pyruvate transaminase	1.7	1.90E-01	7,5g BuOH	6.8	48529	9	Cytoplasmic	COG0161	Coenzyme metabolism	
26987335	PP 0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.1	4.91E-01	0,75g BuOH	5.9	53498	11	Cytoplasmic	COG1012	Energy production and conversion	
26987336	PP 0599		hypothetical protein	1.2	8.18E-01	7,5g BuOH	9.6	83247	2	Unknown	COG3008	General function prediction only	
26987339	PP 0602	ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	1.3	3.68E-01	0,75g BuOH	9.7	34827	5	Cytoplasmic	COG0196	Coenzyme metabolism	
26987340	PP 0603	ileS	isoleucyl-tRNA synthetase	1.1	5.82E-01	0,75g BuOH	6.0	105800	38	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP 0622		competence lipoprotein ComL	3.0	1.93E-01	7,5g BuOH	4.8	38410	11	Unknown	COG4105	General function prediction only	
26987360	PP 0624		hypothetical protein	1.3	3.27E-01	7,5g BuOH	6.1	26401	3	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
26987361	PP 0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	2.2	7.68E-02	7,5g BuOH	5.2	94861	49	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987364	PP 0628		hypothetical protein	2.2	1.26E-01	0,75g BuOH	9.1	24364	2	Cytoplasmic			
26987367	PP 0631	coaE	dephospho-CoA kinase	1.8	2.83E-02	7,5g BuOH	6.6	22652	4	Cytoplasmic	COG0237	Coenzyme metabolism	
26987376	PP 0640		hypothetical protein	1.7	2.87E-01	0,75g BuOH	6.6	44093	4	Cytoplasmic Membrane			
26987390	PP 0654	mdh	malate dehydrogenase	1.2	7.61E-01	0,75g BuOH	5.1	29434	3	Cytoplasmic	COG0039	Energy production and conversion	
26987407	PP 0671	glyA	serine hydroxymethyltransferase	1.6	1.39E-01	0,75g BuOH	6.2	44897	22	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987408	PP 0672		sensory box protein	6.2	1.59E-02	0,75g BuOH	5.7	144317	2	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987410	PP 0674		ABC transporter ATP-binding protein	1.4	2.67E-01	7,5g BuOH	5.3	61860	30	Cytoplasmic	COG0488	General function prediction only	
26987411	PP 0675	gdhA	glutamate dehydrogenase	1.0	9.56E-01	0,75g BuOH	6.5	48871	11	Unknown	COG0334	Amino acid transport and metabolism	
26987415	PP 0679		hypothetical protein	1.4	1.46E-02	7,5g BuOH	7.6	18133	2	Cytoplasmic Membrane			
26987416	PP 0680		ATP-dependent protease	1.5	5.10E-02	7,5g BuOH	4.5	89677	11	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987420	PP 0684	fklB-1	peptidyl-prolyl cis-trans isomerase, FKBP-type	2.4	3.33E-01	0,75g BuOH	4.4	21678	4	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26987423	PP 0687	ispB	polyprenyl synthetase	2.1	2.78E-02	0,75g BuOH	4.8	35269	8	Cytoplasmic	COG0142	Coenzyme metabolism	
26987426	PP 0690	obgE	GTPase ObgE	1.7	1.63E-01	7,5g BuOH	4.5	44825	8	Cytoplasmic	COG0536	General function prediction only	
26987427	PP 0691	proB	gamma-glutamyl kinase	1.7	3.94E-02	0,75g BuOH	7.8	39661	2	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987429	PP 0693		hypothetical protein	1.1	6.11E-01	7,5g BuOH	5.1	106556	9	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26987441	PP 0705		DNA-3-methyladenine glycosylase II	1.1	6.83E-01	0,75g BuOH	6.4	22893	2	Unknown	COG0122	DNA replication, recombination, and repair	
26987443	PP 0707		MscS mechanosensitive ion channel	1.4	3.54E-01	0,75g BuOH	9.9	92124	5	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP 0711		isochorismatase superfamily hydrolase	2.0	1.50E-02	0,75g BuOH	5.3	23026	11	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP 0712		hypothetical protein	2.2	9.39E-02	0,75g BuOH	10.5	31284	4	Cytoplasmic	COG2326	Function unknown	
26987455	PP 0719		GTP-dependent nucleic acid-binding protein EngD	1.6	3.34E-01	0,75g BuOH	4.7	39962	5	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
26987456	PP 0720	pth	peptidyl-tRNA hydrolase	1.5	1.42E-01	0,75g BuOH	10.1	20949	5	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis	
26987457	PP 0721		50S ribosomal protein L25/general stress protein Ctc	1.1	4.13E-01	7,5g BuOH	6.4	23242	12	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP 0722	prsA	ribose-phosphate pyrophosphokinase	1.5	2.71E-01	0,75g BuOH	5.9	34192	8	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987460	PP 0724	lolB	outer membrane lipoprotein LolB	1.2	2.59E-01	7,5g BuOH	8.2	22895	4	Unknown	COG3017	Cell envelope biogenesis, outer membrane	
26987461	PP 0725		hypothetical protein	4.3	5.82E-02	7,5g BuOH	4.6	63994	13	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987468	PP 0732	hemA	glutamyl-tRNA reductase	1.5	1.59E-01	7,5g BuOH	5.5	46305	2	Cytoplasmic	COG0373	Coenzyme metabolism	
26987471	PP 0735		molybdopterin biosynthesis protein MoeB	2.7	2.20E-01	0,75g BuOH	5.1	26584	2	Cytoplasmic	COG0476	Coenzyme metabolism	
26987478	PP 0742		hypothetical protein	1.2	4.96E-01	7,5g BuOH	6.2	36114	3	Unknown	COG3380	General function prediction only	
26987479	PP 0743		NAD-dependent epimerase/dehydratase	2.0	1.61E-01	0,75g BuOH	9.7	33119	3	Cytoplasmic Membrane	COG1090	General function prediction only	
26987482	PP 0746	upp	uracil phosphoribosyltransferase	1.4	2.28E-01	0,75g BuOH	7.1	23000	5	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
26987487	PP 0751	mqo-1	malate:quinone oxidoreductase	1.3	9.80E-02	7,5g BuOH	8.4	54282	12	Cytoplasmic	COG0579	General function prediction only	
26987492	PP 0756		phospholipid/glycerol acyltransferase	1.3	4.61E-02	7,5g BuOH	8.3	47784	4	Cytoplasmic			
26987495	PP 0759		hypothetical protein	1.1	9.78E-01	7,5g BuOH	7.0	29743	9	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987498	PP 0762	hprA	glycerate dehydrogenase	1.2	4.15E-01	7,5g BuOH	6.1	34094	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26987499	PP 0763		long-chain-fatty-acid--CoA ligase	2.3	1.30E-01	0,75g BuOH	5.5	62125	8	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP 0765		hypothetical protein	1.2	1.80E-01	0,75g BuOH	5.0	67937	22	Outer Membrane			
26987502	PP 0766		hypothetical protein	1.5	2.54E-02	0,75g BuOH	9.6	50572	33	Unknown			
26987504	PP 0768		response regulator/hypothetical protein	2.7	4.28E-02	0,75g BuOH	8.4	59272	14	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987505	PP 0769		histidine kinase	1.2	2.29E-01	7,5g BuOH	4.6	25229	10	Cytoplasmic	COG0642	Signal transduction mechanisms	
26987509	PP 0773		OmpA/MotB domain protein	2.7	1.10E-01	7,5g BuOH	9.5	24753	13	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987510	PP 0774	pta	phosphate acetyltransferase	23.5	1.54E-01	0,75g BuOH	5.2	74642	3	Cytoplasmic Membrane	COG0280	Energy production and conversion	
26987515	PP 0779		methyl-accepting chemotaxis transducer/sensory box protein	1.3	3.67E-01	0,75g BuOH	6.2	49856	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987522	PP 0786	trxB	thioredoxin reductase	1.2	1.92E-01	0,75g BuOH	5.1	33841	9	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
26987523	PP 0787	nadC	nicotinate-nucleotide pyrophosphorylase	1.1	5.80E-01	0,75g BuOH	5.2	30163	8	Cytoplasmic	COG0157	Coenzyme metabolism	
26987525	PP 0789	ampD	N-acetyl-anhydromuranmyl-L-alanine amidase	3.1	5.71E-02	0,75g BuOH	5.9	21294	2	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26987528	PP 0792	fruR	DNA-binding transcriptional regulator FruR	2.6	2.69E-01	7,5g BuOH	6.7	36210	5	Cytoplasmic	COG1609	Transcription	
26987529	PP 0793	fruB	phosphoenolpyruvate-protein phosphotransferase	2.2	6.72E-02	0,75g BuOH	4.8	101497	11	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	

26987542	PP_0806		surface adhesion protein	6.0	2.06E-01	0,75g BuOH	3.5	615675	5	Extracellular			
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	2.3	2.19E-01	7,5g BuOH	6.7	34557	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	5.4	2.64E-01	7,5g BuOH	7.8	74391	2	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987553	PP_0817		aminotransferase	1.9	3.48E-01	7,5g BuOH	8.1	44996	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26987559	PP_0823	selD	selenophosphate synthetase	1.7	1.86E-01	0,75g BuOH	5.4	36245	2	Unknown	COG0709	Amino acid transport and metabolism	
26987560	PP_0824		phosphonate ABC transporter periplasmic phosphonate-binding protein	1.1	5.23E-01	0,75g BuOH	8.6	31104	15	Periplasmic	COG3221	Inorganic ion transport and metabolism	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.8	2.00E-01	0,75g BuOH	9.6	66913	13	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	3.9	6.99E-02	0,75g BuOH	4.8	32758	2	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.3	2.20E-01	0,75g BuOH	6.6	29753	7	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987576	PP_0840	cysE	serine O-acetyltransferase	1.4	5.42E-01	7,5g BuOH	6.7	28206	4	Cytoplasmic	COG1045	Amino acid transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.7	1.79E-01	0,75g BuOH	6.2	44468	12	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987582	PP_0846	hscA	chaperone protein HscA	5.4	1.38E-02	0,75g BuOH	4.7	65888	3	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26987588	PP_0852		Cro/CI family transcriptional regulator	20.8	1.19E-01	7,5g BuOH	5.6	34931	2	Unknown	COG1426	Function unknown	
26987589	PP_0853	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.1	6.61E-01	0,75g BuOH	6.2	39687	10	Cytoplasmic	COG0821	Lipid metabolism	
26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.3	1.74E-01	7,5g BuOH	5.1	47738	17	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
26987591	PP_0855		hypothetical protein	1.4	3.79E-01	7,5g BuOH	4.6	22514	5	Unknown	COG2976	Function unknown	
26987592	PP_0856		hypothetical protein	3.2	1.82E-02	0,75g BuOH	4.7	40737	6	Outer Membrane	COG1520	Function unknown	
26987593	PP_0857	engA	GTP-binding protein EngA	1.9	1.15E-01	0,75g BuOH	9.2	54154	10	Cytoplasmic Membrane	COG1160	General function prediction only	
26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2.2	1.14E-01	0,75g BuOH	6.5	29780	2	Cytoplasmic	COG0388	General function prediction only	
26987617	PP_0881	dppB	alkaline phosphatase	8.2	2.36E-02	0,75g BuOH	8.4	36980	4	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	1.5	3.86E-02	0,75g BuOH	7.1	60366	28	Periplasmic	COG0747	Amino acid transport and metabolism	
26987622	PP_0886		hypothetical protein	2.4	1.14E-01	7,5g BuOH	8.4	25634	7	Periplasmic	COG3471	Function unknown	
26987624	PP_0888		two component transcriptional regulator, Fis family	2.0	1.14E-01	0,75g BuOH	5.0	20775	4	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription
26987629	PP_0893		intracellular protease, PfpI family	1.8	2.16E-01	7,5g BuOH	5.5	21071	5	Cytoplasmic	COG0693	General function prediction only	
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.2	5.75E-01	7,5g BuOH	4.9	54767	22	Cytoplasmic	COG1951	Energy production and conversion	
26987637	PP_0901	colR	winged helix family two component transcriptional regulator	1.1	6.53E-01	7,5g BuOH	6.2	25489	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987640	PP_0904		lipopolysaccharide kinase	2.2	2.45E-01	0,75g BuOH	8.6	26976	3	Cytoplasmic			
26987645	PP_0909		hypothetical protein	1.9	7.72E-02	7,5g BuOH	6.4	38380	5	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.6	5.87E-01	0,75g BuOH	4.4	47019	18	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.0	9.86E-01	7,5g BuOH	5.8	78578	4	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987651	PP_0915	sodB	superoxide dismutase	1.9	5.48E-02	7,5g BuOH	5.8	21938	8	Periplasmic	COG0605	Inorganic ion transport and metabolism	
26987655	PP_0919		hypothetical protein	2.1	1.40E-01	7,5g BuOH	10.2	18933	4	Unknown			
26987661	PP_0925		hypothetical protein	1.7	1.96E-01	0,75g BuOH	5.8	31410	5	Unknown			
26987663	PP_0927	aroP	amino acid ABC transporter permease	2.5	2.68E-01	0,75g BuOH	9.4	49167	2	Cytoplasmic Membrane	COG1113	Amino acid transport and metabolism	
26987666	PP_0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.9	1.25E-01	0,75g BuOH	4.8	52678	11	Cytoplasmic	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.6	8.77E-02	0,75g BuOH	6.2	51518	17	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987670	PP_0934	mreC	rod shape-determining protein MreC	1.2	9.55E-01	0,75g BuOH	7.8	35514	2	Unknown	COG1792	Cell envelope biogenesis, outer membrane	
26987673	PP_0937	cafA	ribonuclease, Rne/Rng family	1.5	8.37E-01	0,75g BuOH	5.2	54840	2	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26987674	PP_0938		hypothetical protein	9.9	1.78E-02	0,75g BuOH	6.2	138482	4	Outer Membrane	COG3164	Function unknown	
26987676	PP_0940	tldD	tldD protein	1.5	3.79E-01	7,5g BuOH	4.9	50161	10	Cytoplasmic	COG0312	General function prediction only	
26987678	PP_0942	pmbA	pmbA protein	3.8	2.69E-02	0,75g BuOH	5.0	48296	7	Cytoplasmic	COG0312	General function prediction only	
26987685	PP_0949		hypothetical protein	1.2	6.08E-01	0,75g BuOH	6.2	32097	3	Cytoplasmic	COG1660	General function prediction only	
26987688	PP_0952	rpoN	RNA polymerase factor sigma-54	1.4	7.59E-01	7,5g BuOH	4.4	56215	6	Cytoplasmic	COG1508	Transcription	
26987689	PP_0953		ABC transporter ATP-binding protein	1.5	2.06E-01	0,75g BuOH	7.0	26579	6	Cytoplasmic	COG1137	General function prediction only	
26987691	PP_0955		hypothetical protein	8.2	4.54E-01	0,75g BuOH	6.5	21349	2	Cytoplasmic	COG3117	Function unknown	
26987695	PP_0959	ttg2B	hypothetical protein	2.7	1.05E-01	0,75g BuOH	8.2	28489	5	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987697	PP_0961	ttg2D	toluene tolerance family protein	1.2	5.41E-01	7,5g BuOH	9.7	23751	9	Unknown	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.6	2.13E-01	0,75g BuOH	5.2	44973	12	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.2	2.27E-01	7,5g BuOH	8.4	22938	11	Cytoplasmic	COG0040	Amino acid transport and metabolism	
26987702	PP_0966	hisD	histidinol dehydrogenase	2.3	1.28E-01	0,75g BuOH	5.1	47605	5	Cytoplasmic	COG0141	Amino acid transport and metabolism	
26987703	PP_0967	hisC	histidinol-phosphate aminotransferase	1.7	1.16E-01	0,75g BuOH	4.9	38768	6	Cytoplasmic	COG0079	Amino acid transport and metabolism	
26987709	PP_0973	ndpA	nucleoid-associated protein NdpA	1.4	7.56E-01	7,5g BuOH	5.6	37617	2	Cytoplasmic	COG3081	General function prediction only	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.6	9.24E-02	7,5g BuOH	5.1	107495	37	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.6	1.83E-01	0,75g BuOH	7.4	52433	28	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	3.1	6.03E-02	0,75g BuOH	6.4	40319	4	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	2.4	1.26E-02	0,75g BuOH	5.5	33423	9	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	2.8	1.48E-02	0,75g BuOH	6.3	37911	29	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	2.0	7.09E-03	0,75g BuOH	5.7	46462	38	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.5	2.83E-01	0,75g BuOH	9.1	51061	2	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	6.7	7.07E-03	0,75g BuOH	7.0	36057	18	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	5.0	4.94E-03	0,75g BuOH	6.4	65359	23	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	5.2	3.19E-02	0,75g BuOH	6.5	33904	8	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987748	PP_1012	gltR-2	winged helix family two component transcriptional regulator	2.7	1.95E-01	0,75g BuOH	6.4	27124	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987750	PP_1014		hypothetical protein	1.9	1.69E-01	0,75g BuOH	6.4	45472	12	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.1	8.01E-01	7,5g BuOH	6.2	45449	63	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.4	3.30E-01	0,75g BuOH	10.1	33781	9	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.8	8.64E-01	7,5g BuOH	9.9	30428	3	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.5	2.79E-01	0,75g BuOH	6.7	41895	19	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.3	3.65E-01	0,75g BuOH	5.9	49646	37	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.7	9.68E-02	0,75g BuOH	6.8	55000	19	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.4	2.51E-01	0,75g BuOH	6.7	25476	11	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	2.2	2.61E-02	0,75g BuOH	5.4	25004	8	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.0	7.07E-01	0,75g BuOH	5.1	61712	28	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.5	8.82E-02	0,75g BuOH	7.0	51765	25	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	2.7	2.60E-02	0,75g BuOH	5.2	58204	18	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	2.0	1.13E-01	0,75g BuOH	4.7	140818	45	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987792	PP_1056		iron-chelator utilization protein	1.1	6.50E-01	0,75g BuOH	5.2	28123	2	Cytoplasmic	COG2375	Inorganic ion transport and metabolism	
26987794	PP_1058		hypothetical protein	1.2	5.09E-01	7,5g BuOH	9.5	117041	6	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987804	PP_1068		amino acid ABC transporter ATP-binding protein	3.6	2.85E-02	0,75g BuOH	8.2	28149	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.1	4.63E-01	0,75g BuOH	8.9	33428	34	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987810	PP_1074	glpR	DeoR family transcriptional regulator	1.9	2.16E-01	0,75g BuOH	5.7	27749	2	Cytoplasmic	COG1349	Transcription	Carbohydrate transport and metabolism
26987811	PP_1075	glpK	glycerol kinase	1.8	2.75E-01	0,75g BuOH	4.9	55282	2	Cytoplasmic	COG0554	Energy production and conversion	
26987818	PP_1082	bfr	bacterioferritin	2.2	8.86E-01	0,75g BuOH	4.4	17971	6	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpC/TSA family protein	2.7	3.52E-02	0,75g BuOH	4.9	21730	19	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987822	PP_1086	pyrC	dihydroorotase	1.4	5.72E-01	7,5g BuOH	6.9	38414	6	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
26987823	PP_1087		OmpA family outer membrane protein	1.1	6.95E-01	7,5g BuOH	10.0	34341	14	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987824	PP_1088	argG	argininosuccinate synthase	1.1	6.96E-01	0,75g BuOH	5.1	45164	19	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.0	9.31E-01	0,75g BuOH	5.5	75186	20	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987834	PP_1098		ATP-binding Mrp/Nbp35 family protein	1.8	2.13E-01	0,75g BuOH	4.8	38207	4	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
26987840	PP_1104		succinylglutamate desuccinylase/aspartoacylase	3.2	1.66E-01	0,75g BuOH	6.3	40904	2	Cytoplasmic	COG3608	General function prediction only	
26987844	PP_1108		acylase	1.2	5.77E-01	0,75g BuOH	8.7	88728	11	Periplasmic	COG2366	General function prediction only	
26987847	PP_1111		synthetase	11.5	2.94E-03	0,75g BuOH	6.0	29406	3	Cytoplasmic	COG2872	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	5.6	1.70E-02	0,75g BuOH	7.6	32597	11	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	1.8	9.84E-02	0,75g BuOH	5.0	24084	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.2	4.57E-01	0,75g BuOH	4.7	27345	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987862	PP_1126		Beta-agarase	5.2	1.84E-02	0,75g BuOH	6.6	86407	2	Periplasmic			
26987865	PP_1129	pdxH	pyridoxamine 5'-phosphate oxidase	1.3	2.04E-01	0,75g BuOH	6.4	24581	6	Cytoplasmic	COG0259	Coenzyme metabolism	
26987867	PP_1131		17 kDa surface antigen	1.1	7.21E-01	0,75g BuOH	9.3	15682	2	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987873	PP_1137	braG	branched chain amino acid ABC transporter ATP-binding protein	2.2	1.17E-01	0,75g BuOH	7.6	25545	6	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
26987874	PP_1138	livG	leucine/isoleucine/valine transporter ATP-binding subunit	3.0	8.70E-02	0,75g BuOH	9.7	28280	7	Cytoplasmic	COG0411	Amino acid transport and metabolism	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	1.2	2.57E-01	0,75g BuOH	10.0	46299	2	Cytoplasmic Membrane	COG4177	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.1	4.65E-01	7,5g BuOH	6.4	39402	34	Periplasmic	COG0683	Amino acid transport and metabolism	
26987879	PP_1143		3-hydroxyisobutyrate dehydrogenase	1.5	3.81E-01	0,75g BuOH	5.8	30664	2	Unknown	COG2084	Lipid metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.2	5.41E-01	0,75g BuOH	4.8	105994	12	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987893	PP_1157		acetolactate synthase	2.2	3.66E-02	0,75g BuOH	6.1	60059	9	Cytoplasmic	COG0028		
26987897	PP_1162		glutathione S-transferase family protein	1.5	1.44E-02	7,5g BuOH	6.8	22677	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.2	7.41E-01	0,75g BuOH	4.5	40989	9	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.2	3.10E-01	0,75g BuOH	5.7	106948	33	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987919	PP_1184		dienelactone hydrolase	1.3	2.73E-01	0,75g BuOH	6.8	28722	14	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26987920	PP_1185	oprH	outer membrane protein H1	12.7	1.91E-01	7,5g BuOH	6.8	21501	2	Outer Membrane			
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.3	5.43E-01	0,75g BuOH	5.0	63623	20	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	2.3	1.03E-01	0,75g BuOH	4.6	46120	24	Outer Membrane			
26987945	PP_1210		DNA-binding stress protein	5.9	3.21E-01	7,5g BuOH	5.0	17861	4	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.4	1.76E-01	7,5g BuOH	5.1	66568	30	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987949	PP_1214		hypothetical protein	1.0	9.88E-01	7,5g BuOH	4.4	26842	2	Cytoplasmic	COG0217	Function unknown	
26987951	PP_1216	ruvA	Holliday junction DNA helicase RuvA	1.9	7.50E-02	0,75g BuOH	8.5	22384	2	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.2	6.59E-01	7,5g BuOH	6.3	25310	7	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	

26987957	PP_1222	tolB	translocation protein TolB	2.2	2.15E-02	0,75g BuOH	9.8	47431	14	Unknown	COG0823	Intracellular trafficking and secretion			
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	4.4	2.93E-01	7,5g BuOH	4.9	17833	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane			
26987960	PP_1225		radical SAM domain protein	1.2	9.45E-01	7,5g BuOH	4.9	24096	3	Cytoplasmic	COG0602	Posttranslational modification, protein turnover, chaperones			
26987961	PP_1226	exsB	exsB protein	2.5	1.07E-01	0,75g BuOH	4.7	23961	4	Cytoplasmic	COG0603	General function prediction only			
26987965	PP_1230		hypothetical protein	2.1	1.57E-01	0,75g BuOH	5.1	53328	2	Cytoplasmic Membrane	COG5339	Function unknown			
26987967	PP_1232		hypothetical protein	2.3	6.52E-02	0,75g BuOH	6.9	53219	4	Unknown	COG4783	General function prediction only			
26987971	PP_1236		glycine cleavage system transcriptional repressor	1.1	5.64E-01	0,75g BuOH	4.8	20529	2	Cytoplasmic	COG2716	Amino acid transport and metabolism			
26987972	PP_1237	dapA	dihydrodipicolinate synthase	1.2	2.92E-01	7,5g BuOH	6.0	31654	12	Cytoplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane		
26987973	PP_1238		lipoprotein	1.7	3.67E-01	7,5g BuOH	4.8	40784	17	Unknown	COG3317	Cell envelope biogenesis, outer membrane			
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.5	1.47E-01	0,75g BuOH	5.1	26916	17	Cytoplasmic	COG0152	Nucleotide transport and metabolism			
26987981	PP_1246		hypothetical protein	2.3	3.23E-01	7,5g BuOH	6.0	65952	2	Unknown	COG5373	Function unknown			
26988009	PP_1274		short chain dehydrogenase	1.8	2.14E-01	0,75g BuOH	10.2	28618	8	Cytoplasmic	COG0300	General function prediction only			
26988026	PP_1291		PhoH family protein	2.5	5.22E-02	0,75g BuOH	5.7	51856	12	Cytoplasmic	COG1875	General function prediction only			
26988031	PP_1296	estB	carboxylesterase	5.7	1.18E-02	0,75g BuOH	4.9	24402	3	Cytoplasmic Membrane	COG0400	General function prediction only			
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	2.6	3.26E-03	0,75g BuOH	5.6	36424	24	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms		
26988033	PP_1298	aapQ	polar amino acid ABC transporter inner membrane subunit	5.4	9.57E-02	0,75g BuOH	10.2	43229	3	Cytoplasmic Membrane	COG4597	Amino acid transport and metabolism			
26988035	PP_1300	aapP	general amino acid ABC transporter ATP-binding protein	3.8	2.32E-02	0,75g BuOH	7.6	28879	7	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism			
26988037	PP_1302		hypothetical protein	1.4	1.18E-01	7,5g BuOH	5.8	27492	3	Cytoplasmic	COG0327	Function unknown			
26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2	1.4	1.91E-01	0,75g BuOH	6.8	35284	9	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism		
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.6	2.58E-01	0,75g BuOH	5.6	69049	19	Cytoplasmic	COG2895	Inorganic ion transport and metabolism			
26988046	PP_1311		tryptophanyl-tRNA synthetase	1.0	8.55E-01	0,75g BuOH	5.4	49297	5	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis			
26988049	PP_1314		aldo/keto reductase family oxidoreductase	1.0	8.34E-01	7,5g BuOH	6.5	38777	13	Cytoplasmic	COG0667	Energy production and conversion			
26988050	PP_1315	rplM	50S ribosomal protein L13	13.3	4.15E-01	7,5g BuOH	10.3	15862	4	Unknown	COG0102	Translation, ribosomal structure and biogenesis			
26988051	PP_1316	rpsI	30S ribosomal protein S9	4.0	5.67E-02	7,5g BuOH	11.7	14592	3	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis			
26988052	PP_1317	petA	ubiquinol-cytochrome c reductase, iron-sulfur subunit	1.4	7.13E-02	0,75g BuOH	7.5	20855	12	Cytoplasmic Membrane	COG0723	Energy production and conversion			
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	4.7	4.83E-03	0,75g BuOH	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion			
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.1	6.90E-01	0,75g BuOH	7.1	29032	10	Unknown	COG2857	Energy production and conversion			
26988055	PP_1320	sspA	stringent starvation protein A	1.5	2.30E-01	0,75g BuOH	6.4	23566	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones			
26988060	PP_1325		LppC family lipoprotein	1.2	7.43E-01	7,5g BuOH	7.5	64637	26	Cytoplasmic Membrane	COG3107	General function prediction only			
26988061	PP_1326		uroporphyrin-III C/tetrapyrrole methyltransferase	1.7	7.71E-02	7,5g BuOH	5.4	31389	5	Cytoplasmic	COG0313	General function prediction only			
26988063	PP_1329	mraW	S-adenosyl-methyltransferase MraW	1.2	4.17E-01	0,75g BuOH	7.2	34314	3	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane			
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.8	3.62E-03	0,75g BuOH	5.3	53602	23	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane			
26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.8	1.16E-01	0,75g BuOH	6.6	46750	11	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane			
26988069	PP_1335	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	2.6	6.44E-02	0,75g BuOH	5.7	48300	3	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane			
26988072	PP_1338	murC	UDP-N-acetylmuramate--L-alanine ligase	2.8	3.09E-02	0,75g BuOH	6.3	52166	3	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane			
26988073	PP_1339	ddl	D-alanine--D-alanine ligase	1.7	1.74E-01	0,75g BuOH	4.7	34131	2	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane			
26988075	PP_1341	ftsA	cell division protein FtsA	2.1	8.17E-02	0,75g BuOH	4.9	47444	9	Cytoplasmic	COG0849	Cell division and chromosome partitioning			
26988076	PP_1342	ftsZ	cell division protein FtsZ	1.5	9.23E-02	7,5g BuOH	4.7	41830	13	Cytoplasmic	COG0206	Cell division and chromosome partitioning			
26988077	PP_1343	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	1.0	9.38E-01	0,75g BuOH	4.8	33269	8	Cytoplasmic	COG0774	Cell envelope biogenesis, outer membrane			
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	1.2	6.25E-01	0,75g BuOH	5.0	42236	5	Cytoplasmic	COG1364	Amino acid transport and metabolism			
26988081	PP_1347		glutathione S-transferase family protein	1.2	3.44E-01	0,75g BuOH	5.3	23247	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones			
26988086	PP_1352		nucleotide-binding protein	1.3	2.64E-01	7,5g BuOH	7.4	18561	6	Cytoplasmic	COG1666	Function unknown			
26988092	PP_1358		hypothetical protein	1.2	2.01E-01	0,75g BuOH	7.8	32006	9	Unknown	COG0748	Inorganic ion transport and metabolism			
26988095	PP_1361	groEL	chaperonin GroEL	1.6	1.23E-01	7,5g BuOH	4.7	56743	54	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones			
26988096	PP_1362	pykA	pyruvate kinase	3.3	2.26E-02	0,75g BuOH	6.7	52057	20	Cytoplasmic	COG0469	Carbohydrate transport and metabolism			
26988100	PP_1366		transcriptional regulator MvaT, P16 subunit	13.7	1.35E-01	7,5g BuOH	10.1	14184	4	Cytoplasmic					
26988101	PP_1367	purU	formyltetrahydrofolate deformylase	1.2	4.00E-01	0,75g BuOH	6.6	32376	4	Cytoplasmic	COG0788	Nucleotide transport and metabolism			
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.2	5.73E-01	0,75g BuOH	4.8	67652	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26988106	PP_1372		hypothetical protein	2.0	1.05E-01	7,5g BuOH	6.5	52321	16	Unknown	COG0433	Replication, recombination, and repair			
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	1.9	1.86E-01	7,5g BuOH	6.5	48194	8	Cytoplasmic	COG0015	Nucleotide transport and metabolism			
26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase	1.2	8.57E-01	7,5g BuOH	5.1	28656	8	Unknown	COG0596	General function prediction only			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.1	7.57E-01	0,75g BuOH	5.1	52864	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion		
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.4	3.03E-01	0,75g BuOH	5.3	112835	4	Cytoplasmic Membrane	COG0841	Defense mechanisms			
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	5.5	2.74E-02	0,75g BuOH	4.9	31783	3	Cytoplasmic	COG2513	Carbohydrate transport and metabolism			
26988126	PP_1392		NAD-dependent epimerase/dehydratase	1.1	5.15E-01	0,75g BuOH	8.0	21985	6	Unknown	COG2910	General function prediction only			
26988129	PP_1395		AraC family transcriptional regulator	1.1	4.60E-01	0,75g BuOH	7.6	34370	2	Cytoplasmic	COG4977	Transcription			
26988137	PP_1403	bglX	periplasmic beta-glucosidase	37.3	5.98E-01	7,5g BuOH	6.1	83414	2	Periplasmic	COG1472	Carbohydrate transport and metabolism			
26988145	PP_1412		enoyl-CoA hydratase/isomerase	4.2	8.38E-02	0,75g BuOH	6.5	40490	5	Cytoplasmic	COG1024	Lipid metabolism			
26988151	PP_1418		tricarboxylate transport protein TctC	1.3	4.31E-01	0,75g BuOH	6.6	34981	6	Periplasmic	COG3181	Function unknown			
26988156	PP_1423		hypothetical protein	1.5	3.06E-01	0,75g BuOH	6.0	33350	4	Unknown	COG0354	General function prediction only			
26988159	PP_1426	nadB	L-aspartate oxidase	2.3	1.18E-01	0,75g BuOH	5.8	59215	2	Cytoplasmic	COG0029	Coenzyme metabolism			
26988160	PP_1427	algU	RNA polymerase sigma factor AlgU	1.2	4.26E-01	7,5g BuOH	5.2	22282	9	Cytoplasmic	COG1595	Transcription			
26988161	PP_1428	mucA	anti sigma-E protein, RseA	1.3	9.98E-01	7,5g BuOH	4.9	20944	2	Cytoplasmic Membrane	COG3073	Signal transduction mechanisms			
26988162	PP_1429	algN	sigma E regulatory protein, MucB/RseB	1.5	1.65E-01	7,5g BuOH	6.6	34982	4	Periplasmic	COG3026	Signal transduction mechanisms			
26988163	PP_1430	algY	protease Do	1.1	6.68E-01	7,5g BuOH	6.6	52617	11	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones			
26988164	PP_1431	lepA	GTP-binding protein LepA	2.8	2.39E-01	0,75g BuOH	5.5	66116	4	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane			
26988165	PP_1432	lepB	signal peptidase I	1.1	5.90E-01	7,5g BuOH	9.2	32060	5	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion			
26988167	PP_1434	era	GTP-binding protein Era	1.8	2.95E-01	0,75g BuOH	6.9	34243	2	Cytoplasmic Membrane	COG1159	General function prediction only			
26988169	PP_1436	pdxJ	pyridoxine 5'-phosphate synthase	1.0	9.39E-01	7,5g BuOH	6.2	26737	9	Cytoplasmic	COG0854	Coenzyme metabolism			
26988176	PP_1443	lon-1	ATP-dependent protease La	1.0	9.80E-01	7,5g BuOH	6.4	89794	7	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones			
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	2.4	5.67E-02	0,75g BuOH	6.0	86581	11	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism			
26988187	PP_1454		anhydrase family 3 protein	1.1	8.19E-01	7,5g BuOH	6.5	18548	2	Cytoplasmic	COG0663	General function prediction only			
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	2.8	6.87E-02	0,75g BuOH	5.7	42575	16	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism			
26988191	PP_1458		metabolite-proton symporter	1.5	4.32E-01	7,5g BuOH	9.0	45563	4	Cytoplasmic Membrane					
26988194	PP_1461	ffh	signal recognition particle protein	1.0	7.97E-01	0,75g BuOH	10.7	58232	6	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion			
26988198	PP_1465	rplS	50S ribosomal protein L19	27.3	2.28E-01	7,5g BuOH	11.0	13012	3	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis			
26988202	PP_1469	dsbC	thiol:disulfide interchange protein DsbC	1.2	5.02E-01	0,75g BuOH	7.9	27601	3	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones			
26988203	PP_1470	hom	homoserine dehydrogenase	1.7	5.86E-02	7,5g BuOH	5.1	46194	12	Cytoplasmic	COG0460	Amino acid transport and metabolism			
26988204	PP_1471	thrC	threonine synthase	1.6	9.81E-02	7,5g BuOH	6.2	51645	26	Cytoplasmic	COG0498	Amino acid transport and metabolism			
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	2.0	3.20E-02	0,75g BuOH	5.8	40626	14	Cytoplasmic	COG1902	Energy production and conversion			
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.1	6.29E-01	0,75g BuOH	5.7	50918	11	Unknown	COG1012	Energy production and conversion			
26988219	PP_1486		polyamine ABC transporter periplasmic polyamine-binding protein	1.6	1.34E-01	0,75g BuOH	6.4	41728	16	Periplasmic	COG0687	Amino acid transport and metabolism			
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.1	6.79E-01	0,75g BuOH	4.7	58605	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26988227	PP_1494		response regulator/GGDEF domain-containing protein	1.2	7.91E-01	0,75g BuOH	5.7	37046	2	Cytoplasmic	COG3706	Signal transduction mechanisms			
26988228	PP_1496	lysS	lysyl-tRNA synthetase	1.2	1.74E-01	0,75g BuOH	5.0	57137	22	Cytoplasmic	COG1190	Translation, ribosomal structure and biogenesis			
26988231	PP_1499		hypothetical protein	1.4	4.38E-01	7,5g BuOH	6.3	49645	4	Cytoplasmic	COG3930	Function unknown			
26988234	PP_1502		OmpA/MotB domain protein	3.4	1.39E-01	7,5g BuOH	9.5	28964	10	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane			
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.2	5.31E-01	0,75g BuOH	6.6	96963	16	Cytoplasmic	COG2352	Energy production and conversion			
26988238	PP_1506	adk	adenylate kinase	1.9	1.11E-01	7,5g BuOH	5.7	23222	16	Cytoplasmic	COG0563	Nucleotide transport and metabolism			
26988239	PP_1507		hypothetical protein	2.4	9.14E-02	0,75g BuOH	6.0	23544	2	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones			
26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	1.1	6.81E-01	0,75g BuOH	4.2	29130	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism			
26988245	PP_1513		hypothetical protein	1.9	2.27E-01	7,5g BuOH	9.0	27864	3	Cytoplasmic					
26988258	PP_1526		beta-(1-3)-glucosyltransferase	1.8	2.71E-01	0,75g BuOH	8.1	97324	4	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism			
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.2	9.83E-01	0,75g BuOH	5.6	35858	8	Unknown	COG2171	Amino acid transport and metabolism			
26988320	PP_1588		succinyldiaminopimelate transaminase	1.1	6.50E-01	7,5g BuOH	5.4	43759	7	Cytoplasmic	COG0436	Amino acid transport and metabolism			
26988321	PP_1589	glnD	PII uridylyl-transferase	1.9	1.31E-01	0,75g BuOH	5.9	102620	8	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones			
26988322	PP_1590	map	methionine aminopeptidase	1.3	8.59E-02	7,5g BuOH	6.6	28956	9	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis			
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	7.83E-01	0,75g BuOH	9.3	27023	20	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis			
26988324	PP_1592	tsf	elongation factor Ts	1.2	3.92E-01	7,5g BuOH	4.9	30432	28	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis			
26988325	PP_1593	pyrH	uridylate kinase	1.4	3.95E-01	0,75g BuOH	6.2	26484	8	Cytoplasmic	COG0528	Nucleotide transport and metabolism			
26988326	PP_1594	frr	ribosome recycling factor	1.2	6.45E-01	0,75g BuOH	8.9	20152	11	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis			
26988327	PP_1595	uppS	undecaprenyl diphosphate synthase	1.7	1.20E-01	7,5g BuOH	8.5	27951	4	Cytoplasmic	COG0020	Lipid metabolism			
26988331	PP_1599		surface antigen family outer membrane protein	1.6	1.26E-01	7,5g BuOH	4.7	86513	14	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane			
26988335	PP_1603	lpxA	UDP-N-acetylglucosamine acyltransferase	1.3	6.58E-01	7,5g BuOH	6.9	28107	3	Cytoplasmic	COG1043	acyl carrier protein			
26988338	PP_1606	dnaE	DNA polymerase III subunit alpha	6.7	4.06E-02	0,75g BuOH	5.3	130923	6	Cytoplasmic	COG0587	DNA replication, recombination, and repair			
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.6	4.56E-03	7,5g BuOH	6.0	35135	21	Cytoplasmic	COG0825	Lipid metabolism			
26988342	PP_1610	pyrG	CTP synthetase	2.0	6.80E-02	0,75g BuOH	5.8	59474	25	Cytoplasmic	COG0504	Nucleotide transport and metabolism			
26988343	PP_1611	kdsA-1	2-dehydro-3-deoxyphosphooctonate aldolase	1.6	1.69E-01	0,75g BuOH	5.8	31034	8	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane			
26988344	PP_1612	eno	phosphopyruvate hydratase	1.8	1.31E-01	7,5g BuOH	4.7	45490	21	Cytoplasmic	COG0148	Carbohydrate transport and metabolism			
26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	2.1	1.60E-01	0,75g BuOH	6.3	39364	5	Cytoplasmic	COG1062	Energy production and conversion			
26988353	PP_1621	pcm	protein-L-isoaspartate O-methyltransferase	1.3	9.39E-02	0,75g BuOH	7.1	25497	2	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones			
26988354	PP_1622	nlpD	peptidase M23B	2.0	2.82E-01	0,75g BuOH	11.0	27506	5	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane			
26988355	PP_1623	rpoS	RNA polymerase sigma factor RpoS	2.0	1.10E-01	7,5g BuOH	4.9	38175	11	Cytoplasmic	COG0568	Transcription			
26988358	PP_1626	mutS	DNA mismatch repair protein MutS	2.0	1.60E-01	0,75g BuOH	6.3	95111	2	Cytoplasmic	COG0249	DNA replication, recombination, and repair			
26988361	PP_1629	recA	recombinase A	2.1	2.48E-01	0,75g BuOH	5.3	37545	9	Cytoplasmic	COG0468	DNA replication, recombination, and repair			
26988367	PP_1635		LuxR family two component transcriptional regulator	1.8	2.34E-01	0,75g BuOH	4.8	23481	4	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription		
26988370	PP_1638	fpr	oxidoreductase FAD/NAD(P)-binding domain protein	1.1	6.65E-01	0,75g BuOH	5.1	29710	8	Cytoplasmic	COG1018	Energy production and conversion			

26988373	PP	1641		C32 tRNA thiolase		1.1	8.64E-01	7,5g BuOH	6.8	31043	2	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
26988374	PP	1642		hypothetical protein		2.2	5.53E-02	7,5g BuOH	9.1	25287	2	Unknown	COG2818	DNA replication, recombination, and repair	
26988381	PP	1649	ldhA	D-lactate dehydrogenase		1.5	3.57E-01	0,75g BuOH	6.6	37126	5	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26988382	PP	1650	gacS	multi-sensor hybrid histidine kinase		1.2	2.94E-03	7,5g BuOH	5.4	100653	6	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26988386	PP	1654	cysM	cysteine synthase B		1.1	9.34E-01	0,75g BuOH	4.9	32305	2	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26988388	PP	1656	relA	(p)ppGpp synthetase I, SpoT/RelA		1.2	3.26E-01	0,75g BuOH	7.9	83609	9	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26988390	PP	1658		hypothetical protein		1.1	9.02E-01	0,75g BuOH	9.6	20470	2	Cytoplasmic	COG3122	Function unknown	
26988391	PP	1659		hypothetical protein		2.0	1.25E-01	0,75g BuOH	5.9	48336	19	Periplasmic			
26988393	PP	1661		dehydrogenase subunit		1.7	1.40E-01	0,75g BuOH	5.5	81020	33	Extracellular	COG2303	Amino acid transport and metabolism	
26988395	PP	1663		hypothetical protein		1.4	2.68E-01	0,75g BuOH	9.2	26313	10	Periplasmic			
26988397	PP	1665	purM	phosphoribosylaminoimidazole synthetase		1.6	4.98E-01	0,75g BuOH	4.6	36942	9	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
26988398	PP	1666		hypothetical protein		1.2	7.97E-01	7,5g BuOH	5.5	37790	3	Unknown	COG3249	Function unknown	
26988400	PP	1668		DNA replication initiation factor		1.3	5.55E-01	7,5g BuOH	8.7	26586	9	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
26988404	PP	1672	cobO	cob(I)yrinic acid a,c-diamide adenosyltransferase		1.4	1.12E-01	0,75g BuOH	7.7	22602	7	Cytoplasmic	COG2109	Coenzyme metabolism	
26988418	PP	1686		glutathione peroxidase		1.3	7.48E-01	0,75g BuOH	8.9	22309	2	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
26988429	PP	1697		GntR family transcriptional regulator		2.9	9.14E-01	7,5g BuOH	8.7	34197	2	Cytoplasmic	COG2188	Transcription	
26988434	PP	1702	rdgC	recombination associated protein		1.2	5.17E-01	0,75g BuOH	4.6	34283	4	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
26988446	PP	1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type		1.7	9.85E-03	7,5g BuOH	4.8	26520	14	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988451	PP	1719	prc	carboxyl-terminal protease		1.1	7.40E-01	0,75g BuOH	7.1	79096	27	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26988452	PP	1720		alcohol dehydrogenase, zinc-containing		1.4	3.61E-01	0,75g BuOH	4.7	33921	7	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26988453	PP	1721		HAD superfamily hydrolase		2.2	5.59E-02	0,75g BuOH	4.5	24571	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26988454	PP	1722		ABC transporter ATP-binding protein		2.4	1.99E-01	0,75g BuOH	8.0	36445	2	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26988457	PP	1725		type I phosphodiesterase/nucleotide pyrophosphatase		2.5	1.08E-01	0,75g BuOH	6.4	31520	3	Cytoplasmic	COG1524	General function prediction only	
26988458	PP	1726		ABC transporter periplasmic protein		1.0	9.14E-01	7,5g BuOH	6.0	38636	23	Unknown	COG1840	Inorganic ion transport and metabolism	
26988464	PP	1733	minD	septum site-determining protein MinD		1.7	1.77E-01	0,75g BuOH	6.2	29650	17	Cytoplasmic	COG2894	Cell division and chromosome partitioning	
26988465	PP	1734	minC	septum formation inhibitor		25.2	1.08E-01	0,75g BuOH	8.9	29680	2	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
26988472	PP	1741		substrate-binding region of ABC-type glycine betaine transport system		2.7	8.00E-02	0,75g BuOH	9.6	31215	4	Periplasmic	COG2113	Amino acid transport and metabolism	
26988474	PP	1743	actP	acetate permease		2.8	1.21E-01	7,5g BuOH	9.6	58972	5	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP	1752		hypothetical protein		2.7	2.56E-02	0,75g BuOH	8.2	57637	9	Cytoplasmic	COG2326	Function unknown	
26988486	PP	1755	fumC-2	fumarate hydratase		1.6	1.68E-01	7,5g BuOH	6.4	49131	22	Cytoplasmic	COG0114	Energy production and conversion	
26988490	PP	1759		DSBA oxidoreductase		1.1	8.64E-01	7,5g BuOH	4.7	21492	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
26988492	PP	1761		sensory box protein/GGDEF family protein		1.2	6.78E-01	0,75g BuOH	6.8	108193	4	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26988494	PP	1763		short chain dehydrogenase		1.9	1.74E-01	0,75g BuOH	4.7	26253	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988495	PP	1764		phosphoglycolate phosphatase		1.2	2.87E-01	0,75g BuOH	4.5	24373	6	Cytoplasmic	COG0546	General function prediction only	
26988496	PP	1765	ubiG	3-demethylubiquinone-9 3-methyltransferase		1.1	6.10E-01	0,75g BuOH	5.7	26084	4	Cytoplasmic	COG2227	Coenzyme metabolism	
26988498	PP	1767	gyrA	DNA gyrase subunit A		1.2	1.85E-01	7,5g BuOH	4.7	102037	23	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988499	PP	1768	serC	phosphoserine aminotransferase		1.4	2.21E-01	0,75g BuOH	5.1	39911	11	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
26988500	PP	1769	pheA	chorismate mutase		2.0	1.15E-02	0,75g BuOH	6.4	40816	11	Cytoplasmic	COG0077	Amino acid transport and metabolism	
26988501	PP	1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase		1.6	2.58E-01	0,75g BuOH	6.4	79133	9	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988502	PP	1771	cmk	cytidylate kinase		1.4	1.83E-01	7,5g BuOH	4.9	24691	9	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
26988506	PP	1775		beta-lactamase domain protein	Infinity		3.54E-08	0,75g BuOH	6.5	52195	2	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
26988507	PP	1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase		2.1	2.04E-02	0,75g BuOH	5.2	52989	7	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP	1780		mannosyltransferase		1.6	1.16E-01	0,75g BuOH	5.8	180042	18	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988514	PP	1783	rmlA	glucose-1-phosphate thymidylyltransferase		2.5	9.08E-02	0,75g BuOH	4.9	32517	8	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
26988515	PP	1784	rmlD	dTDP-4-dehydrorhamnose reductase		3.3	8.94E-02	0,75g BuOH	6.7	32131	3	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26988516	PP	1785	rmlB	dTDP-glucose 4,6-dehydratase		1.6	1.34E-01	0,75g BuOH	6.1	40690	6	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP	1786		glycosyl transferase		2.1	2.40E-02	0,75g BuOH	6.4	128499	15	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988518	PP	1787		hypothetical protein		2.1	1.06E-01	0,75g BuOH	5.3	37903	7	Unknown			
26988521	PP	1790		acylneuraminate cytidylyltransferase		1.1	4.28E-01	7,5g BuOH	6.4	26350	3	Cytoplasmic	COG1083	Cell envelope biogenesis, outer membrane	
26988522	PP	1791		aldolase/synthase		1.1	6.94E-01	7,5g BuOH	5.9	58534	9	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988529	PP	1799	gmd	GDP-mannose 4,6 dehydratase		1.4	2.44E-01	0,75g BuOH	6.4	40124	19	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988530	PP	1800	rmd	oxidoreductase Rmd		1.6	1.97E-01	0,75g BuOH	7.2	32310	5	Unknown	COG1089	Cell envelope biogenesis, outer membrane	
26988536	PP	1806		KpsF/GutQ family protein		1.3	4.01E-01	7,5g BuOH	6.1	33741	2	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
26988537	PP	1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase		1.0	8.99E-01	7,5g BuOH	6.0	30469	6	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
26988545	PP	1815	pyrF	orotidine 5'-phosphate decarboxylase		2.0	1.01E-01	0,75g BuOH	4.9	24551	4	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
26988546	PP	1816		alcohol dehydrogenase, zinc-containing		2.4	9.76E-02	0,75g BuOH	7.4	35802	4	Cytoplasmic	COG2130	General function prediction only	
26988549	PP	1819		methyl-accepting chemotaxis sensory transducer		1.2	7.62E-01	0,75g BuOH	4.7	68069	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988551	PP	1821		glutathione S-transferase family protein		1.1	8.13E-01	0,75g BuOH	5.6	23207	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988558	PP	1828		hypothetical protein		1.1	5.89E-01	7,5g BuOH	7.7	29758	2	Cytoplasmic			
26988560	PP	1830	aroC	chorismate synthase		1.7	1.62E-01	7,5g BuOH	6.5	38987	6	Cytoplasmic	COG0082	Amino acid transport and metabolism	
26988562	PP	1832		oxidase		2.1	1.14E-01	7,5g BuOH	4.8	19469	6	Cytoplasmic	COG1791	Function unknown	
26988568	PP	1838		hypothetical protein		2.4	5.37E-03	7,5g BuOH	6.8	76615	7	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988572	PP	1842		amidotransferase		1.1	5.74E-01	0,75g BuOH	4.9	27317	5	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
26988575	PP	1845		enoyl-CoA hydratase		1.9	2.06E-01	0,75g BuOH	7.7	24641	10	Cytoplasmic	COG1024	Lipid metabolism	
26988588	PP	1858	efp	elongation factor P		2.6	2.84E-01	0,75g BuOH	4.5	21303	6	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988589	PP	1859	ohr	OsmC family protein		2.9	3.22E-01	7,5g BuOH	6.8	14665	3	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
26988596	PP	1866		phospho-2-dehydro-3-deoxyheptonate aldolase		1.1	9.08E-01	0,75g BuOH	6.4	49706	3	Cytoplasmic	COG3200	Amino acid transport and metabolism	
26988598	PP	1868		DEAD-box ATP dependent DNA helicase		1.6	6.78E-02	0,75g BuOH	9.2	60924	17	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988600	PP	1870	tpm	thiopurine S-methyltransferase		3.0	4.41E-02	0,75g BuOH	4.7	24365	5	Cytoplasmic			
26988601	PP	1871	htpX	heat shock protein HtpX		1.6	1.27E-01	7,5g BuOH	7.2	32199	7	Cytoplasmic Membrane	COG0501	Posttranslational modification, protein turnover, chaperones	
26988602	PP	1872		aminotransferase AlaT		1.5	2.49E-01	7,5g BuOH	5.8	44705	10	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988606	PP	1876		hypothetical protein		3.9	5.43E-02	0,75g BuOH	8.8	38962	3	Cytoplasmic	COG2607	General function prediction only	
26988608	PP	1878		hypothetical protein		1.7	1.33E-01	7,5g BuOH	7.3	29093	4	Cytoplasmic			
26988623	PP	1893	fadE	acyl-CoA dehydrogenase		1.8	2.49E-02	0,75g BuOH	6.9	89194	22	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988624	PP	1894		glutathione S-transferase family protein		2.6	1.98E-02	0,75g BuOH	5.0	23668	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988625	PP	1895		ABC transporter ATP-binding protein		1.1	8.34E-01	7,5g BuOH	7.1	34488	3	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26988628	PP	1898		MotA/TolQ/ExbB proton channel		1.2	8.23E-01	0,75g BuOH	7.0	24408	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26988632	PP	1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase		1.0	9.96E-01	7,5g BuOH	5.2	27809	5	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
26988635	PP	1905	rne	ribonuclease, Rne/Rng family		1.3	5.32E-01	0,75g BuOH	4.7	120904	33	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP	1908		signal peptide peptidase SppA, 36K type		1.3	6.16E-01	7,5g BuOH	6.4	36497	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988638	PP	1909	maf	Maf-like protein		1.2	5.41E-01	7,5g BuOH	4.9	22268	2	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
26988639	PP	1910		hypothetical protein		1.6	9.44E-01	7,5g BuOH	4.2	19332	1	Cytoplasmic	COG1399	General function prediction only	
26988642	PP	1913	fabD	malonyl CoA-acyl carrier protein transacylase		1.1	9.43E-01	7,5g BuOH	4.7	32614	8	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP	1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase		1.0	9.46E-01	0,75g BuOH	6.0	25470	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988644	PP	1915	acpP	acyl carrier protein		4.2	3.67E-01	0,75g BuOH	3.8	8712	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26988646	PP	1917	pabC	4-amino-4-deoxychorismate lyase		1.5	8.95E-03	0,75g BuOH	7.2	29486	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26988668	PP	1941		hypothetical protein		1.0	7.03E-01	0,75g BuOH	7.8	23098	2	Unknown	COG1309	Transcription	
26988673	PP	1946		short chain dehydrogenase/reductase family oxidoreductase		1.9	1.67E-01	0,75g BuOH	5.3	27212	4	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988691	PP	1964		deoxynucleotide monophosphate kinase		2.0	1.31E-01	0,75g BuOH	5.9	30146	2	Unknown			
26988696	PP	1970		lipoprotein		1.5	6.17E-01	0,75g BuOH	4.9	22337	6	Unknown			
26988697	PP	1971		hypothetical protein		1.1	9.69E-01	0,75g BuOH	4.5	21577	4	Cytoplasmic	COG3816	Function unknown	
26988698	PP	1972	tyrB-1	aromatic amino acid aminotransferase		1.2	4.06E-01	0,75g BuOH	5.9	43290	19	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP	1977	gltX	glutamyl-tRNA synthetase		1.6	1.50E-01	7,5g BuOH	5.6	56483	17	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988709	PP	1983		sensory box protein		1.7	6.39E-03	0,75g BuOH	5.7	128000	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26988711	PP	1985	leuC	isopropylmalate isomerase large subunit		1.2	2.79E-01	0,75g BuOH	5.6	51255	6	Cytoplasmic	COG0065	Amino acid transport and metabolism	
26988712	PP	1986	leuD	isopropylmalate isomerase small subunit		1.2	4.44E-01	0,75g BuOH	5.3	24284	11	Cytoplasmic	COG0066	Amino acid transport and metabolism	
26988713	PP	1987		UbiE/COQ5 family methlytransferase		2.8	2.01E-01	0,75g BuOH	5.8	28181	2	Cytoplasmic	COG2226	Coenzyme metabolism	
26988714	PP	1988	leuB	3-isopropylmalate dehydrogenase		1.3	2.43E-01	0,75g BuOH	4.8	38824	6	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988715	PP	1989	asd	aspartate-semialdehyde dehydrogenase		1.2	6.06E-01	0,75g BuOH	5.3	40672	16	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP	1993		peptidoglycan-binding LysM		1.4	6.75E-01	0,75g BuOH	3.9	96918	23	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988720	PP	1995	trpF	N-(5'-phosphoribosyl)anthranilate isomerase		2.1	3.23E-01	0,75g BuOH	5.3	21886	2	Cytoplasmic	COG0135	Amino acid transport and metabolism	
26988721	PP	1996	accD	acetyl-CoA carboxylase subunit beta		1.1	6.17E-01	0,75g BuOH	7.8	32510	5	Cytoplasmic	COG0777	Lipid metabolism	
26988722	PP	1997	folC	FolC bifunctional protein		5.5	2.30E-01	0,75g BuOH	4.8	46895	2	Cytoplasmic	COG0285	Coenzyme metabolism	
26988725	PP	2000	purF	amidophosphoribosyltransferase		1.4	2.62E-01	0,75g BuOH	6.5	55400	9	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988726	PP	2001	metZ	O-succinylhomoserine sulfhydrylase		1.9	4.65E-02	0,75g BuOH	5.4	43284	3	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26988727	PP	2002		oxidoreductase		1.5	4.14E-03	0,75g BuOH	6.6	27212	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988731	PP	2006		hypothetical protein		6.5	4.13E-03	0,75g BuOH	5.1	63743	31	Unknown			
26988732	PP	2007		P-47-related protein		6.7	1.23E-03	0,75g BuOH	5.8	44707	7	Unknown			
26988742	PP	2017	pepN	aminopeptidase N		1.4	3.21E-01	0,75g BuOH	4.8	99573	25	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988743	PP	2018		BNR domain-containing protein		1.2	2.81E-01	0,75g BuOH	4.5	33691	6	Unknown	COG4447	General function prediction only	
26988744	PP	2019		hypothetical protein		1.4	2.55E-01	0,75g BuOH	6.6	87732	6	Cytoplasmic Membrane	COG1033	General function prediction only	
26988746	PP	2021		hypothetical protein		4.2	1.29E-01	0,75g BuOH	7.2	40684	2	Periplasmic	COG2706	Carbohydrate transport and metabolism	
26988749	PP	2024	sbcC	SMC domain protein		2.2	1.09E-01	0,75g BuOH	5.5	136091	7	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26988757	PP	2032		ATPase		1.4	3.21E-01	0,75g BuOH	5.0	35347	2	Cytoplasmic	COG0714	General function prediction only	
26988805	PP	2080		NAD-glutamate dehydrogenase		1.5	1.58E-01	0,75g BuOH	5.8	187043	56	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988806	PP	2081		hypothetical protein		2.9	6.29E-02	0,75g BuOH	6.6	30824	4	Cytoplasmic	COG1806	Function unknown	
26988807	PP	2082	ppsA	phosphoenolpyruvate synthase		1.5	6.87E-02	7,5g BuOH	4.8	86015	41	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	

26988809	PP 2084	menG	ribonuclease activity regulator protein RraA	4.4	6.15E-02	7,5g BuOH	4.6	17646	2	Cytoplasmic	COG0684	Coenzyme metabolism	
26988812	PP 2087	cmpX	TM helix repeat-containing protein	1.0	8.71E-01	0,75g BuOH	5.8	29111	7	Cytoplasmic Membrane			
26988814	PP 2089	oprF	OmpF family protein	1.9	1.44E-03	0,75g BuOH	4.5	37012	24	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988820	PP 2095	pyrD	dihydroorotate dehydrogenase 2	1.3	5.98E-01	0,75g BuOH	8.2	35545	4	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism	
26988823	PP 2098	dacB	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	1.2	4.36E-01	0,75g BuOH	9.9	50799	2	Periplasmic	COG2027	Cell envelope biogenesis, outer membrane	
26988835	PP 2111	aer-2	aerotaxis receptor Aer-2	2.5	2.16E-02	0,75g BuOH	6.0	57068	20	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988836	PP 2112	acnA	aconitate hydratase	1.2	5.36E-01	7,5g BuOH	5.7	99147	20	Cytoplasmic	COG1048	Energy production and conversion	
26988841	PP 2117	pdxB	erythronate-4-phosphate dehydrogenase	1.5	1.62E-01	0,75g BuOH	5.1	41614	3	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26988852	PP 2128	chev-2	chemotaxis protein CheV	2.9	6.29E-02	0,75g BuOH	6.5	34556	5	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26988853	PP 2129		MOSC domain containing protein	1.3	1.73E-01	7,5g BuOH	5.5	29621	9	Cytoplasmic	COG3217	General function prediction only	
26988854	PP 2130		soluble lytic transglycosylase	3.0	1.61E-01	0,75g BuOH	9.9	75337	9	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988855	PP 2131		ABC transporter ATP-binding protein	1.2	6.29E-01	7,5g BuOH	5.1	71398	8	Cytoplasmic	COG0488	General function prediction only	
26988860	PP 2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.2	4.50E-01	0,75g BuOH	5.9	77449	11	Cytoplasmic	COG1250	Lipid metabolism	
26988863	PP 2139	topA	DNA topoisomerase I	1.3	3.93E-01	0,75g BuOH	8.0	97239	25	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
26988867	PP 2143	lexA-1	LexA repressor	3.6	6.75E-02	0,75g BuOH	6.7	22147	4	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
26988868	PP 2144		TetR family transcriptional regulator	1.1	6.09E-01	0,75g BuOH	9.8	26183	3	Cytoplasmic	COG1309	Transcription	
26988869	PP 2145	nagZ	beta-hexosaminidase	1.0	8.98E-01	0,75g BuOH	6.3	36513	4	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
26988872	PP 2148	mfd	transcription-repair coupling factor	1.8	1.02E-02	0,75g BuOH	5.7	128301	10	Unknown	COG1197	DNA replication, recombination, and repair	Transcription
26988875	PP 2151	sthA	soluble pyridine nucleotide transhydrogenase	2.2	1.52E-01	7,5g BuOH	7.7	50905	9	Cytoplasmic	COG1249	Energy production and conversion	
26988876	PP 2152		glycerophosphoryl diester phosphodiesterase	2.0	9.67E-02	0,75g BuOH	7.5	26252	8	Cytoplasmic	COG0584	Energy production and conversion	
26988877	PP 2153		type IV pilus assembly PilZ	1.5	2.09E-01	0,75g BuOH	5.0	21858	3	Cytoplasmic			
26988879	PP 2155	lolD	lipoprotein releasing system, ATP-binding protein	1.4	2.73E-01	7,5g BuOH	7.3	25304	4	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26988882	PP 2158		two component heavy metal response transcriptional regulator	1.3	5.33E-01	0,75g BuOH	5.0	25354	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26988884	PP 2160	queF	7-cyano-7-deazaguanine reductase	1.0	8.38E-01	7,5g BuOH	6.5	30686	3	Cytoplasmic	COG2904	Function unknown	
26988887	PP 2163	vacJ	VacJ family lipoprotein	1.6	6.66E-02	7,5g BuOH	5.3	26061	10	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988892	PP 2168	tal	transaldolase B	1.9	3.79E-02	7,5g BuOH	5.0	33615	16	Unknown	COG0176	Carbohydrate transport and metabolism	
26988899	PP 2175		short-chain dehydrogenase/reductase SDR	1.2	5.91E-01	0,75g BuOH	6.6	24818	2	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988911	PP 2187		universal stress protein	1.5	4.11E-02	0,75g BuOH	6.3	31384	4	Cytoplasmic	COG0589	Signal transduction mechanisms	
26988919	PP 2195		periplasmic polyamine-binding protein	1.4	2.99E-01	7,5g BuOH	5.5	39788	5	Periplasmic	COG0687	Amino acid transport and metabolism	
26988937	PP 2213	fadDx	AMP-dependent synthetase and ligase	1.5	1.33E-01	0,75g BuOH	6.0	61223	12	Cytoplasmic	COG0365	Lipid metabolism	
26988938	PP 2214	fadB2x	short-chain dehydrogenase/reductase SDR	1.6	2.38E-01	0,75g BuOH	6.7	26030	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988939	PP 2215	fadAx	acetyl-CoA acetyltransferase	1.3	3.24E-01	0,75g BuOH	6.9	41382	9	Cytoplasmic	COG0183	Lipid metabolism	
26988941	PP 2217	fadB1x	enoyl-CoA hydratase/isomerase	2.0	6.76E-02	0,75g BuOH	5.2	27668	9	Cytoplasmic	COG1024	Lipid metabolism	
26988957	PP 2233		isochorismatase superfamily hydrolase	13.0	2.21E-03	7,5g BuOH	6.0	19296	16	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988962	PP 2238		peptidase M24	1.4	2.49E-02	0,75g BuOH	5.4	68915	8	Unknown	COG0006	Amino acid transport and metabolism	
26988973	PP 2249		methyl-accepting chemotaxis transducer	1.3	2.92E-01	0,75g BuOH	5.1	68646	20	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988988	PP 2264		extracellular solute-binding protein, family 1	1.6	1.26E-01	0,75g BuOH	5.6	65243	27	Unknown	COG1653	Carbohydrate transport and metabolism	
26988989	PP 2265	folD-2	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	2.0	2.10E-01	0,75g BuOH	6.4	30623	5	Cytoplasmic	COG0190	Coenzyme metabolism	
26989016	PP 2292		hypothetical protein	1.1	5.08E-01	0,75g BuOH	5.8	28522	12	Cytoplasmic			
26989023	PP 2299	tig	trigger factor	1.2	7.56E-01	7,5g BuOH	4.5	49190	24	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
26989024	PP 2300	clpP	ATP-dependent Clp protease proteolytic subunit	1.8	1.56E-01	0,75g BuOH	5.6	23515	8	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26989025	PP 2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.4	5.10E-01	7,5g BuOH	4.8	48526	19	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
26989026	PP 2302	lon-2	ATP-dependent protease La	1.2	3.02E-01	7,5g BuOH	5.9	88722	23	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989027	PP 2303	hupB	histone family protein DNA-binding protein	30.6	1.57E-01	7,5g BuOH	10.2	9250	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26989028	PP 2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.2	5.50E-01	7,5g BuOH	4.8	68580	12	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
26989031	PP 2307		CHAD domain containing protein	1.5	1.22E-01	7,5g BuOH	10.8	29498	9	Cytoplasmic	COG5607	Function unknown	
26989032	PP 2308		acyl-CoA thioesterase II	1.5	4.22E-02	0,75g BuOH	6.1	28745	4	Unknown	COG1946	Lipid metabolism	
26989044	PP 2320		ErfK/YbiS/YcfS/YnhG family protein	1.4	2.23E-01	7,5g BuOH	5.4	35051	10	Unknown	COG1376	Function unknown	
26989046	PP 2322	oprI	outer membrane lipoprotein OprI	39.4	1.02E-01	7,5g BuOH	8.5	8801	3	Outer Membrane			
26989048	PP 2324	aroF-1	phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	4.34E-01	7,5g BuOH	6.4	40260	9	Cytoplasmic	COG0722	Amino acid transport and metabolism	
26989051	PP 2327	cysB	transcriptional regulator CysB	2.0	9.40E-02	0,75g BuOH	6.7	35955	7	Cytoplasmic	COG0583	Transcription	
26989052	PP 2328	cysH	phosphoadenosine phosphosulfate reductase	1.1	5.58E-01	7,5g BuOH	6.5	27896	7	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26989054	PP 2330		alpha-L-glutamate ligase-like protein	3.8	9.94E-02	0,75g BuOH	6.8	35904	2	Cytoplasmic			
26989055	PP 2331		hypothetical protein	2.9	5.69E-02	0,75g BuOH	7.9	57064	4	Cytoplasmic Membrane			
26989058	PP 2334	prpB	2-methylisocitrate lyase	1.2	1.63E-01	0,75g BuOH	5.4	31811	7	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26989059	PP 2335		methylcitrate synthase	3.1	9.08E-02	0,75g BuOH	6.7	41995	12	Cytoplasmic	COG0372	Energy production and conversion	
26989060	PP 2336		aconitate hydratase	1.6	3.62E-01	0,75g BuOH	5.3	93961	5	Cytoplasmic	COG1048	Energy production and conversion	
26989061	PP 2337		hypothetical protein	72.0	8.07E-02	0,75g BuOH	5.2	41312	2	Cytoplasmic	COG2828	Function unknown	
26989062	PP 2338	prpD	2-methylcitrate dehydratase	1.9	4.27E-02	0,75g BuOH	7.1	54860	11	Cytoplasmic	COG2079	General function prediction only	
26989063	PP 2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.6	1.47E-02	7,5g BuOH	5.0	93609	50	Cytoplasmic	COG1049	Energy production and conversion	
26989075	PP 2351		acetyl-CoA synthetase	1.2	4.89E-01	0,75g BuOH	6.1	68868	5	Cytoplasmic	COG0365	Lipid metabolism	
26989078	PP 2354		multi-sensor hybrid histidine kinase	1.4	5.63E-01	0,75g BuOH	5.0	88511	3	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989080	PP 2356		phytochrome family protein	1.1	6.50E-01	7,5g BuOH	6.2	83859	3	Cytoplasmic Membrane	COG4251	Signal transduction mechanisms	
26989085	PP 2361	csuC	type 1 pili usher pathway chaperone CsuC	3.1	1.30E-02	0,75g BuOH	10.3	28448	6	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
26989088	PP 2364		hypothetical protein	2.0	8.82E-02	0,75g BuOH	5.2	42461	7	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP 2371	cysI	sulphite reductase hemoprotein, beta subunit	1.2	3.02E-01	0,75g BuOH	5.8	62191	27	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP 2375	metH	B12-dependent methionine synthase	1.3	3.44E-01	0,75g BuOH	4.7	135408	32	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989119	PP 2396		hypothetical protein	1.2	7.57E-01	0,75g BuOH	8.9	20592	12	Periplasmic			
26989144	PP 2421		acetyltransferase	1.7	1.01E-01	7,5g BuOH	8.3	20697	4	Cytoplasmic	COG0456	General function prediction only	
26989145	PP 2422		alkylhydroperoxidase-like protein	50.5	6.91E-01	7,5g BuOH	7.4	12135	2	Unknown	COG0599	Function unknown	
26989159	PP 2436		LysR family transcriptional regulator	1.9	2.41E-01	0,75g BuOH	9.4	35025	4	Cytoplasmic	COG0583	Transcription	
26989162	PP 2439	ahpC	alkyl hydroperoxide reductase, C subunit	1.2	3.55E-01	0,75g BuOH	4.8	20507	10	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26989165	PP 2442		hypothetical protein	1.2	7.68E-01	7,5g BuOH	5.2	23851	9	Cytoplasmic	COG3132	Function unknown	
26989170	PP 2447		hypothetical protein	2.5	2.75E-01	0,75g BuOH	10.2	26784	2	Unknown			
26989176	PP 2453	ansA	L-asparaginase, type II	1.2	6.08E-01	0,75g BuOH	7.9	38608	7	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
26989177	PP 2454	rbsB	monosaccharide-transporting ATPase	1.4	4.13E-01	7,5g BuOH	5.9	33763	14	Periplasmic	COG1879	Carbohydrate transport and metabolism	
26989183	PP 2460		inosine/uridine-preferring nucleoside hydrolase	1.8	2.37E-01	0,75g BuOH	6.2	34388	2	Unknown	COG1957	Nucleotide transport and metabolism	
26989188	PP 2465	thrS	threonyl-tRNA synthetase	1.3	2.62E-01	7,5g BuOH	5.8	72697	14	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP 2466	infC	translation initiation factor IF-3	1.2	3.51E-01	7,5g BuOH	10.0	20120	12	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP 2468	rplT	50S ribosomal protein L20	1.5	9.55E-01	7,5g BuOH	12.1	13280	3	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989192	PP 2469	pheS	phenylalanyl-tRNA synthetase subunit alpha	1.1	4.16E-01	0,75g BuOH	5.2	38082	6	Cytoplasmic	COG0016	Translation, ribosomal structure and biogenesis	
26989193	PP 2470	pheT	phenylalanyl-tRNA synthetase subunit beta	1.2	3.78E-01	0,75g BuOH	4.8	86617	17	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis	
26989197	PP 2474		glutathione S-transferase family protein	1.6	7.83E-02	0,75g BuOH	6.1	23793	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989198	PP 2475		TetR family transcriptional regulator	2.3	1.49E-01	0,75g BuOH	6.4	22413	3	Cytoplasmic	COG1309	Transcription	
26989211	PP 2488		succinic-semialdehyde dehydrogenase	1.2	8.63E-01	7,5g BuOH	5.1	50254	2	Cytoplasmic	COG1012	Energy production and conversion	
26989244	PP 2524		HD domain-containing protein	1.7	2.40E-01	0,75g BuOH	6.5	24016	3	Cytoplasmic	COG1418	General function prediction only	
26989248	PP 2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	1.3	3.91E-01	7,5g BuOH	6.5	45235	9	Cytoplasmic	COG2873	Amino acid transport and metabolism	
26989256	PP 2536		glutathione S-transferase family protein	2.3	1.28E-01	0,75g BuOH	6.5	23574	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989258	PP 2538		hypothetical protein	1.8	6.84E-02	0,75g BuOH	8.2	26353	3	Unknown			
26989260	PP 2540		short chain dehydrogenase/reductase family oxidoreductase	1.6	3.16E-01	0,75g BuOH	7.7	26775	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989265	PP 2545		trans-aconitate 2-methyltransferase	1.4	5.78E-01	7,5g BuOH	6.8	30767	4	Cytoplasmic	COG4106	General function prediction only	
26989270	PP 2550		hypothetical protein	2.7	3.93E-01	0,75g BuOH	4.6	25315	2	Cytoplasmic	COG0217	Function unknown	
26989381	PP 2662		hypothetical protein	22.1	6.21E-03	7,5g BuOH	4.3	42858	20	Outer Membrane			
26989382	PP 2663		hypothetical protein	10.7	1.68E-04	7,5g BuOH	6.3	42469	13	Cytoplasmic	COG3287	Function unknown	
26989383	PP 2664		PAS/PAC sensor hybrid histidine kinase	39.7	7.10E-06	7,5g BuOH	6.6	73094	19	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989384	PP 2665	agmR	LuxR family two component transcriptional regulator	1.3	8.20E-01	7,5g BuOH	5.9	24536	9	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26989387	PP 2668		efflux ABC transporter ATP-binding protein	3.2	1.35E-03	7,5g BuOH	9.8	27178	10	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26989388	PP 2669		YVTN family beta-propeller repeat-containing protein	2.1	3.88E-01	7,5g BuOH	6.2	36051	12	Unknown	COG3391	Function unknown	
26989391	PP 2672		LuxR family DNA-binding response regulator	1.2	7.83E-01	7,5g BuOH	8.3	23226	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26989392	PP 2673		pentapeptide repeat-containing protein	4.9	4.54E-02	7,5g BuOH	5.3	23569	16	Extracellular	COG1357	Function unknown	
26989393	PP 2674	qedH	quinoprotein ethanol dehydrogenase	5.5	6.30E-03	7,5g BuOH	7.0	69173	71	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989394	PP 2675		cytochrome c-type protein	21.0	3.08E-03	7,5g BuOH	4.9	16280	7	Unknown	COG2010	Energy production and conversion	
26989395	PP 2676		periplasmic protein	6.1	1.29E-02	7,5g BuOH	6.5	34540	18	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26989396	PP 2677		hypothetical protein	6.2	5.74E-04	7,5g BuOH	5.3	28059	12	Unknown			
26989397	PP 2678		beta-lactamase domain protein	4.7	3.00E-05	7,5g BuOH	6.4	33711	18	Unknown	COG0491	General function prediction only	
26989398	PP 2679		quinoprotein ethanol dehydrogenase	6.0	2.01E-03	7,5g BuOH	9.1	64883	26	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP 2680		aldehyde dehydrogenase family protein	15.7	1.76E-03	7,5g BuOH	5.5	54903	45	Cytoplasmic	COG1012	Energy production and conversion	
26989402	PP 2683		PAS/PAC sensor hybrid histidine kinase	2.1	7.72E-02	7,5g BuOH	6.6	62695	14	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989417	PP 2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1.4	2.90E-01	7,5g BuOH	6.3	38659	25	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26989418	PP 2699		hypothetical protein	1.5	4.51E-01	7,5g BuOH	6.5	40451	4	Cytoplasmic			
26989432	PP 2713		DNA-binding response regulator	1.7	5.87E-01	7,5g BuOH	5.2	24701	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26989525	PP 2806		TetR family transcriptional regulator	9.7	5.15E-02	0,75g BuOH	5.3	21294	5	Unknown	COG3226	Function unknown	
26989545	PP 2826	mexT	transcriptional regulator MexT	1.5	8.17E-01	7,5g BuOH	6.7	33299	3	Cytoplasmic Membrane	COG0583	Transcription	
26989572	PP 2853		hypothetical protein	2.3	8.52E-02	0,75g BuOH	4.5	46020	3	Unknown			
26989580	PP 2861		methyl-accepting chemotaxis sensory transducer	1.7	7.16E-02	0,75g BuOH	5.7	58659	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989596	PP 2877		bile acid/Na+ symporter family protein	1.3	3.43E-01	0,75g BuOH	9.3	35469	2	Cytoplasmic Membrane	COG0385	General function prediction only	
26989603	PP 2884		XRE family transcriptional regulator	6.5	1.04E-01	0,75g BuOH	4.9	19995	2	Cytoplasmic	COG1396	Transcription	

26989609	PP_2890	xthA	exonuclease III	1.0	9.57E-01	7,5g BuOH	6.7	30951	5	Cytoplasmic	COG0708	DNA replication, recombination, and repair		
26989610	PP_2891		acetyltransferase	1.8	9.62E-02	0,75g BuOH	7.6	25615	4	Cytoplasmic Membrane				
26989621	PP_2902		UDP-2,3-diacylglucosamine hydrolase	1.0	5.63E-01	0,75g BuOH	8.7	27325	2	Cytoplasmic	COG2908	Function unknown		
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.0	6.94E-01	0,75g BuOH	6.1	64654	9	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	2.4	1.85E-02	0,75g BuOH	5.8	51676	4	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis		
26989627	PP_2908		DNA-binding transcriptional regulator CsiR	1.1	6.41E-01	7,5g BuOH	7.9	25953	2	Cytoplasmic	COG1802	Transcription		
26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	1.5	1.65E-01	7,5g BuOH	5.0	35225	10	Cytoplasmic	COG0113	Coenzyme metabolism		
26989635	PP_2916	ribE-2	riboflavin synthase subunit alpha	7.0	2.72E-02	0,75g BuOH	4.9	22902	2	Cytoplasmic	COG0307	Coenzyme metabolism		
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase	1.4	1.03E-01	0,75g BuOH	8.0	59671	9	Unknown	COG0579	General function prediction only		
26989647	PP_2928		saccharopine dehydrogenase	1.8	2.03E-01	0,75g BuOH	5.0	45363	6	Cytoplasmic	COG1748	Amino acid transport and metabolism		
26989648	PP_2929	nspC	carboxynorspermidine decarboxylase	1.3	5.23E-01	7,5g BuOH	4.9	41026	2	Cytoplasmic	COG0019	Amino acid transport and metabolism		
26989651	PP_2932		amidase	2.0	2.37E-03	7,5g BuOH	4.5	60346	6	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis		
26989652	PP_2933		glutathione S-transferase YghU	1.0	9.57E-01	0,75g BuOH	6.0	31202	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
26989661	PP_2942		response regulator	1.1	5.91E-01	0,75g BuOH	5.6	51291	4	Cytoplasmic	COG3437	Transcription		Signal transduction mechanisms
26989738	PP_3019		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2.8	5.32E-02	0,75g BuOH	5.1	26214	6	Cytoplasmic	COG0388	General function prediction only		
26989790	PP_3071		acetoacetyl-CoA synthetase	6.3	2.24E-01	0,75g BuOH	6.4	72303	2	Cytoplasmic	COG0365	Lipid metabolism		
26989807	PP_3088		hypothetical protein	24.8	7.19E-02	7,5g BuOH	4.4	39853	3	Unknown	COG3515	Intracellular trafficking, secretion, and vesicular transport		
26989808	PP_3089		hypothetical protein	2.7	3.38E-02	0,75g BuOH	5.3	19453	5	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport		
26989809	PP_3090		OmpA domain-containing protein	1.8	9.40E-01	0,75g BuOH	9.0	93143	5	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989810	PP_3091		hypothetical protein	2.1	4.14E-01	7,5g BuOH	6.8	138655	17	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989811	PP_3092		hypothetical protein	7.5	3.76E-02	0,75g BuOH	5.7	26868	4	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport		
26989813	PP_3094		hypothetical protein	9.6	2.43E-01	7,5g BuOH	4.7	25945	6	Unknown	COG3521	Intracellular trafficking, secretion, and vesicular transport		
26989814	PP_3095		chaperone-associated ATPase	7.9	2.40E-02	7,5g BuOH	6.1	96474	23	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones		
26989818	PP_3099		hypothetical protein	5.4	5.62E-02	7,5g BuOH	4.9	56072	26	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport		
26989819	PP_3100		hypothetical protein	4.0	2.67E-01	7,5g BuOH	7.7	21741	3	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport		
26989825	PP_3106		hypothetical protein	1.8	2.61E-01	0,75g BuOH	5.6	69529	7	Cytoplasmic	COG3501	Function unknown		
26989827	PP_3108		rhs-related protein	1.2	6.84E-01	0,75g BuOH	6.0	155811	17	Unknown	COG3209	Cell envelope biogenesis, outer membrane		
26989841	PP_3122		3-oxoacid CoA-transferase subunit A	4.7	1.44E-02	7,5g BuOH	5.2	25125	2	Cytoplasmic	COG1788	Lipid metabolism		
26989845	PP_3126		polysaccharide export protein	14.3	2.52E-01	0,75g BuOH	4.9	19528	2	Unknown	COG1596	Cell wall		membrane
26989846	PP_3127		lipopolysaccharide biosynthesis protein	3.4	1.10E-02	0,75g BuOH	9.0	57141	18	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane		
26989847	PP_3128		protein-tyrosine kinase	2.9	3.51E-02	0,75g BuOH	7.1	29623	6	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning		
26989848	PP_3129	galE	UDP-glucose 4-epimerase	3.4	9.70E-02	0,75g BuOH	6.3	34967	2	Cytoplasmic	COG1087	Cell envelope biogenesis, outer membrane		
26989849	PP_3130		hypothetical protein	4.2	6.49E-02	0,75g BuOH	6.4	96618	2	Unknown				
26989853	PP_3134		transferase hexapeptide repeat containing protein	4.9	5.09E-02	0,75g BuOH	9.9	25699	4	Cytoplasmic	COG0110	General function prediction only		
26989854	PP_3135		glycosyl transferase	3.0	4.79E-02	0,75g BuOH	8.6	35887	9	Cytoplasmic	COG1216	General function prediction only		
26989858	PP_3139		glycosyl transferase, group 1 family protein	3.5	1.05E-01	0,75g BuOH	7.9	44606	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane		
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.6	2.26E-01	0,75g BuOH	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane		
26989860	PP_3141		WecB/TagA/CpsF family glycosyl transferase	2.0	1.04E-01	0,75g BuOH	10.2	27576	5	Unknown	COG1922	Cell envelope biogenesis, outer membrane		
26989864	PP_3145		hypothetical protein	1.1	8.18E-01	7,5g BuOH	9.7	29885	16	Unknown				
26989876	PP_3157		inositol monophosphatase family protein	3.2	6.64E-02	0,75g BuOH	4.3	27793	6	Cytoplasmic	COG0483	Carbohydrate transport and metabolism		
26989904	PP_3185	pet18	transcriptional activator, TenA family	1.3	3.18E-01	0,75g BuOH	4.9	23859	2	Unknown	COG0819	Transcription		
26989905	PP_3186		transcriptional activator, TenA family	1.8	8.50E-02	0,75g BuOH	4.8	24300	5	Cytoplasmic	COG0819	Transcription		
26989966	PP_3248		Dyp-type peroxidase family	1.2	6.05E-01	7,5g BuOH	4.6	31295	6	Unknown	COG2837	Inorganic ion transport and metabolism		
26989967	PP_3249		aldo/keto reductase	1.1	9.89E-01	7,5g BuOH	8.2	39057	3	Cytoplasmic	COG0656	General function prediction only		
26990018	PP_3300		TetR family transcriptional regulator	1.5	1.80E-01	7,5g BuOH	7.8	22603	2	Unknown	COG1309	Transcription		
26990076	PP_3361		hypothetical protein	1.3	7.38E-01	7,5g BuOH	6.3	110896	3	Cytoplasmic	COG0160	Amino acid transport and metabolism		
26990079	PP_3364		response regulator	1.2	7.00E-01	0,75g BuOH	6.4	91750	3	Cytoplasmic	COG4251	Signal transduction mechanisms		
26990095	PP_3380	ptxS	PtxS family transcriptional regulator	3.5	9.95E-02	0,75g BuOH	6.9	36789	2	Cytoplasmic	COG1609	Transcription		
26990144	PP_3431		Thi/PfpI domain protein	1.5	6.31E-02	0,75g BuOH	6.5	25246	15	Unknown	COG0693	General function prediction only		
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	3.1	2.56E-03	0,75g BuOH	6.2	59980	16	Cytoplasmic	COG1012	Energy production and conversion		
26990161	PP_3448	nfrB	bacteriophage N4 adsorption protein B	1.7	5.37E-01	0,75g BuOH	7.4	82370	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane		
26990172	PP_3459		hypothetical protein	1.8	2.15E-01	0,75g BuOH	9.0	42365	10	Periplasmic				
26990203	PP_3491		enoyl-coenzyme A hydratase/isomerase family protein	1.2	7.81E-01	7,5g BuOH	4.9	39382	6	Cytoplasmic	COG1024	Lipid metabolism		
26990204	PP_3492	acdA	acyl-CoA dehydrogenase domain-containing protein	1.7	3.65E-02	0,75g BuOH	5.7	41553	7	Cytoplasmic	COG1960	Lipid metabolism		
26990219	PP_3507	cobN	cobaltochelatase subunit CobN	1.2	9.88E-01	7,5g BuOH	5.4	138545	6	Cytoplasmic	COG1429	Coenzyme metabolism		
26990220	PP_3508	cobW	cobalamin biosynthesis protein CobW	1.1	7.45E-01	0,75g BuOH	4.6	38579	8	Cytoplasmic	COG0523	General function prediction only		
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.0	7.86E-01	0,75g BuOH	7.2	36863	20	Cytoplasmic	COG0115	Amino acid transport and metabolism		Coenzyme metabolism
26990239	PP_3527		TetR family transcriptional regulator	3.8	7.44E-01	0,75g BuOH	6.5	26116	2	Cytoplasmic	COG1309	Transcription		
26990242	PP_3530		hypothetical protein	1.1	6.42E-01	0,75g BuOH	6.2	31546	5	Cytoplasmic	COG3257	General function prediction only		
26990252	PP_3540	mvaB	hydroxymethylglutaryl-CoA lyase	1.7	7.64E-02	7,5g BuOH	5.4	31341	8	Cytoplasmic	COG0119	Amino acid transport and metabolism		
26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	1.2	4.15E-01	0,75g BuOH	6.0	26030	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism		General function prediction only
26990263	PP_3551		LuxR family DNA-binding response regulator	1.4	1.97E-01	7,5g BuOH	5.0	22465	2	Cytoplasmic	COG4566	Signal transduction mechanisms		
26990265	PP_3553		acyl-CoA synthetase	2.3	1.37E-01	7,5g BuOH	6.4	59576	16	Cytoplasmic	COG0318	Lipid metabolism		Secondary metabolites biosynthesis, transport, and catabolism
26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	2.1	1.32E-01	7,5g BuOH	5.5	63339	20	Cytoplasmic	COG1960	Lipid metabolism		
26990269	PP_3557		methyl-accepting chemotaxis transducer	1.6	2.83E-01	7,5g BuOH	4.7	76982	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion		Signal transduction mechanisms
26990270	PP_3558		substrate binding region of ABC-type glycine betaine transport system	2.1	2.15E-01	7,5g BuOH	5.5	36928	6	Periplasmic	COG2113	Amino acid transport and metabolism		
26990275	PP_3563		hypothetical protein	1.6	4.30E-01	7,5g BuOH	5.1	30285	3	Unknown	COG2340	Function unknown		
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	2.8	1.19E-01	0,75g BuOH	6.9	85338	3	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism		
26990290	PP_3578		phosphoglucomutase	1.5	1.97E-01	0,75g BuOH	5.6	58620	13	Unknown	COG0033	Carbohydrate transport and metabolism		
26990294	PP_3582		RND efflux transporter	2.0	2.96E-01	7,5g BuOH	5.2	53952	4	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane		Intracellular trafficking and secretion
26990298	PP_3587	tpx	redoxin domain protein	4.2	1.69E-01	7,5g BuOH	4.7	17409	4	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones		
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	2.4	8.23E-03	7,5g BuOH	5.9	43631	16	Cytoplasmic	COG1448	Amino acid transport and metabolism		
26990313	PP_3602		ketoglutarate semialdehyde dehydrogenase	1.2	6.16E-01	0,75g BuOH	5.2	55538	10	Cytoplasmic	COG1012	Energy production and conversion		
26990314	PP_3603		GntR family transcriptional regulator	1.3	3.45E-01	7,5g BuOH	9.0	28149	4	Cytoplasmic	COG2186	Transcription		
26990322	PP_3611		hypothetical protein	4.3	3.11E-02	0,75g BuOH	9.7	20824	8	Unknown				
26990331	PP_3620		hypothetical protein	1.2	5.56E-01	7,5g BuOH	4.3	81519	2	Cytoplasmic	COG1944	Function unknown		
26990333	PP_3622		isoquinoline 1-oxidoreductase, beta subunit	1.1	8.16E-01	0,75g BuOH	7.0	80889	18	Cytoplasmic Membrane	COG1529	Energy production and conversion		
26990334	PP_3623		gluconate 2-dehydrogenase acceptor subunit	1.0	6.25E-01	7,5g BuOH	7.2	47849	3	Cytoplasmic Membrane	COG2010	Energy production and conversion		
26990342	PP_3631		hypothetical protein	118.1	1.32E-01	7,5g BuOH	7.7	23586	2	Unknown	COG3103	Signal transduction mechanisms		
26990347	PP_3636		sulfonate ABC transporter periplasmic sulfonate-binding protein	1.3	4.85E-01	0,75g BuOH	7.3	43742	9	Cytoplasmic Membrane	COG0715	Inorganic ion transport and metabolism		
26990348	PP_3637		sulfonate ABC transporter ATP-binding protein	1.0	9.45E-01	0,75g BuOH	7.1	29618	3	Cytoplasmic Membrane	COG1116	Inorganic ion transport and metabolism		
26990349	PP_3638		acyl-CoA dehydrogenase	1.6	1.13E-01	0,75g BuOH	6.1	38476	8	Cytoplasmic	COG1960	Lipid metabolism		
26990355	PP_3644		luciferase family protein	1.4	4.30E-01	0,75g BuOH	5.4	38951	2	Cytoplasmic	COG2141	Energy production and conversion		
26990360	PP_3649		GntR family transcriptional regulator	1.9	6.39E-02	7,5g BuOH	7.0	28178	5	Cytoplasmic	COG1802	Transcription		
26990362	PP_3651		GAF sensor hybrid histidine kinase	1.3	8.96E-01	0,75g BuOH	4.9	79274	2	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms		
26990367	PP_3656		aromatic compound-specific porin	52.5	4.04E-01	7,5g BuOH	5.3	46672	5	Outer Membrane				
26990373	PP_3662		decarboxylase family protein	1.3	2.99E-01	7,5g BuOH	6.7	50729	11	Cytoplasmic	COG1611	General function prediction only		
26990379	PP_3668		catalase/peroxidase HPI	1.9	1.92E-02	7,5g BuOH	5.8	82061	48	Cytoplasmic	COG0376	Inorganic ion transport and metabolism		
26990389	PP_3680		hypothetical protein	1.6	2.74E-01	0,75g BuOH	6.3	75093	7	Unknown	COG3593	DNA replication, recombination, and repair		
26990399	PP_3691		DNA helicase-related protein	1.1	8.40E-01	0,75g BuOH	5.0	245278	53	Unknown	COG1112	DNA replication, recombination, and repair		
26990415	PP_3707		hypothetical protein	1.1	6.23E-01	0,75g BuOH	5.4	52925	2	Cytoplasmic				
26990421	PP_3713	catA	catechol 1,2-dioxygenase	1.5	5.19E-01	7,5g BuOH	5.1	34249	9	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism		
26990448	PP_3742		glutathione S-transferase family protein	2.8	8.38E-02	0,75g BuOH	6.4	24042	6	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
26990459	PP_3754		beta-ketothiolase	2.2	2.13E-02	7,5g BuOH	6.9	40988	19	Cytoplasmic	COG0183	Lipid metabolism		
26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	2.3	4.13E-01	7,5g BuOH	6.3	30088	9	Cytoplasmic	COG1250	Lipid metabolism		
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.9	1.97E-01	0,75g BuOH	4.9	129450	23	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms		
26990480	PP_3775		sarcosine oxidase	2.1	6.74E-03	0,75g BuOH	6.4	41164	20	Cytoplasmic	COG0665	Amino acid transport and metabolism		
26990482	PP_3777		hypothetical protein	3.1	4.62E-02	0,75g BuOH	5.2	31324	11	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis		
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	1.8	1.33E-01	0,75g BuOH	6.2	27714	17	Cytoplasmic	COG0345	Amino acid transport and metabolism		
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	1.1	7.43E-01	0,75g BuOH	7.0	53071	8	Cytoplasmic	COG0635	Coenzyme metabolism		
26990488	PP_3783		hypothetical protein	1.5	1.31E-01	0,75g BuOH	5.8	34938	11	Cytoplasmic				
26990489	PP_3784		hypothetical protein	1.8	1.06E-01	0,75g BuOH	5.4	41070	11	Unknown	COG0251	Translation, ribosomal structure and biogenesis		
26990490	PP_3785		hypothetical protein	2.7	1.22E-01	0,75g BuOH	6.5	50495	9	Cytoplasmic				
26990491	PP_3786		aminotransferase	1.1	6.58E-01	0,75g BuOH	6.4	44067	2	Cytoplasmic	COG0436	Amino acid transport and metabolism		
26990492	PP_3787		hypothetical protein	2.4	9.12E-02	0,75g BuOH	6.8	33215	3	Unknown	COG0332	acyl-carrier-protein		
26990495	PP_3790	dapF	diaminopimelate epimerase	2.7	1.52E-01	0,75g BuOH	6.0	29286	3	Cytoplasmic	COG0253	Amino acid transport and metabolism		
26990519	PP_3814		polyamine ABC transporter periplasmic polyamine-binding protein	1.9	7.25E-03	0,75g BuOH	5.2	37113	5	Periplasmic	COG0687	Amino acid transport and metabolism		
26990524	PP_3819	gor	glutathione reductase	1.8	1.70E-01	0,75g BuOH	5.2	49180	6	Cytoplasmic	COG1249	Energy production and conversion		
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.6	4.87E-02	7,5g BuOH	5.3	30957	12	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane		
26990537	PP_3832		carbon storage regulator	1.6	2.82E-01	0,75g BuOH	7.8	7271	3	Unknown	COG1551	Signal transduction mechanisms		
26990544	PP_3839		alcohol dehydrogenase	1.0	7.85E-01	7,5g BuOH	5.7	35397	10	Cytoplasmic	COG1064	General function prediction only		
26990627	PP_3922		periplasmic protease	1.4	3.49E-01	7,5g BuOH	9.8	37502	5	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones		Intracellular trafficking and secretion
26990631	PP_3926		short chain dehydrogenase	1.2	4.64E-01	0,75g BuOH	7.4	26721	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism		General function prediction only
26990659	PP_3954		periplasmic protein	1.4	9.15E-02	0,75g BuOH	9.3	33239	12	Unknown	COG2358	General function prediction only		
26990693	PP_3988		hypothetical protein	1.3	3.41E-01	0,75g BuOH	6.3	76259	13	Cytoplasmic	COG0323	DNA replication, recombination, and repair		
26990704	PP_3999	cobA-2	uroporphyrin-III C-methyltransferase	1.9	1.02E-01	0,75g BuOH	6.8	49494	4	Cytoplasmic	COG0007	Coenzyme metabolism		
26990705	PP_4000	serS	seryl-tRNA synthetase	1.3	1.75E-01	0,75g BuOH	5.1	46849	12	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis		

26990707	PP_4002		recombination factor protein RarA	2.9	1.67E-02	7,5g BuOH	6.1	49147	2	Cytoplasmic	COG2256	DNA replication, recombination, and repair			
26990708	PP_4003	lolA	outer-membrane lipoprotein carrier protein	1.3	3.76E-01	0,75g BuOH	9.5	25146	7	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane			
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	2.0	1.31E-01	0,75g BuOH	6.4	91296	3	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning			
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.0	8.25E-01	7,5g BuOH	5.7	83310	19	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones			
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.0	6.49E-02	0,75g BuOH	5.4	45695	31	Unknown	COG0538	Energy production and conversion			
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	4.1	6.79E-02	0,75g BuOH	5.4	79899	33	Cytoplasmic	COG2838	Energy production and conversion			
26990721	PP_4016	purB	adenylosuccinate lyase	1.2	7.02E-01	0,75g BuOH	5.9	50555	17	Cytoplasmic	COG0015	Nucleotide transport and metabolism			
26990726	PP_4021	est	alpha/beta hydrolase fold	1.0	7.92E-01	0,75g BuOH	6.1	30206	9	Cytoplasmic	COG0596	General function prediction only			
26990732	PP_4029	nudC	NADH pyrophosphatase	2.4	3.72E-02	0,75g BuOH	5.0	30868	3	Cytoplasmic	COG2816	DNA replication, recombination, and repair			
26990733	PP_4030		enoyl-CoA hydratase	1.9	9.35E-02	0,75g BuOH	5.2	30613	4	Cytoplasmic	COG1024	Lipid metabolism			
26990737	PP_4034		allantoate amidohydrolase	2.1	2.65E-02	0,75g BuOH	5.7	45010	23	Cytoplasmic	COG0624	Amino acid transport and metabolism			
26990738	PP_4035		NCS1 purine-cytosine transporter	2.2	1.46E-01	0,75g BuOH	7.9	53519	4	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism		
26990739	PP_4037		oxidoreductase	1.7	8.91E-02	0,75g BuOH	5.5	48815	29	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only		
26990740	PP_4038		dihydropyrimidine dehydrogenase	2.0	5.31E-02	0,75g BuOH	5.1	46093	22	Cytoplasmic	COG0167	Nucleotide transport and metabolism			
26990742	PP_4041		glycoside hydrolase 15-related	2.9	1.49E-01	0,75g BuOH	6.4	69769	2	Cytoplasmic	COG3387	Carbohydrate transport and metabolism			
26990744	PP_4043	gnd	6-phosphogluconate dehydrogenase	1.9	3.32E-01	7,5g BuOH	6.4	35366	8	Cytoplasmic	COG1023	Carbohydrate transport and metabolism			
26990752	PP_4051		maltooligosyltrehalose trehalohydrolase	2.5	6.62E-02	0,75g BuOH	6.0	64544	9	Cytoplasmic	COG0296	Carbohydrate transport and metabolism			
26990753	PP_4052	malQ	4-alpha-glucanotransferase	1.1	7.59E-01	0,75g BuOH	5.5	76475	17	Cytoplasmic	COG1640	Carbohydrate transport and metabolism			
26990754	PP_4053		maltooligosyl trehalose synthase	1.2	4.06E-01	0,75g BuOH	6.6	103167	22	Cytoplasmic	COG3280	Carbohydrate transport and metabolism			
26990756	PP_4055	glgX	glycogen debranching protein GlgX	2.7	1.80E-02	0,75g BuOH	5.1	81044	15	Cytoplasmic	COG1523	Carbohydrate transport and metabolism			
26990759	PP_4058	glgB	glycogen branching enzyme	2.1	9.68E-02	0,75g BuOH	5.9	82877	7	Cytoplasmic	COG0296	Carbohydrate transport and metabolism			
26990760	PP_4059		trehalose synthase	3.0	3.32E-01	0,75g BuOH	5.4	125589	4	Cytoplasmic	COG0366	Carbohydrate transport and metabolism			
26990761	PP_4060		alpha-amylase family protein	1.6	2.16E-01	0,75g BuOH	6.1	75542	8	Cytoplasmic	COG0366	Carbohydrate transport and metabolism			
26990765	PP_4064	ivd	acyl-CoA dehydrogenase domain-containing protein	1.8	4.09E-02	0,75g BuOH	7.2	46572	10	Cytoplasmic	COG1960	Lipid metabolism			
26990766	PP_4065		propionyl-CoA carboxylase	6.6	2.21E-02	0,75g BuOH	6.9	57504	5	Cytoplasmic	COG4799	Lipid metabolism			
26990767	PP_4066		gamma-carboxygeranoyl-CoA hydratase	1.6	1.96E-01	0,75g BuOH	5.5	30015	5	Cytoplasmic	COG1024	Lipid metabolism			
26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	3.9	6.61E-02	0,75g BuOH	5.8	69729	4	Cytoplasmic	COG4770	Lipid metabolism			
26990769	PP_4068		Cro/CI family transcriptional regulator	1.2	5.71E-01	0,75g BuOH	4.9	26361	2	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms		
26990794	PP_4099	gacA	DNA-binding response regulator GacA	2.7	8.56E-02	0,75g BuOH	6.3	23138	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription		
26990799	PP_4104		glutathione S-transferase family protein	1.0	8.85E-01	7,5g BuOH	7.8	26354	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones			
26990806	PP_4111	fusA	elongation factor G	1.5	3.53E-01	0,75g BuOH	5.0	77832	19	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis			
26990809	PP_4115		NoIW domain protein	2.6	1.06E-01	0,75g BuOH	6.7	29306	6	Unknown					
26990810	PP_4116	aceA	isocitrate lyase	37.7	2.87E-03	7,5g BuOH	5.3	48633	42	Cytoplasmic	COG2224	Energy production and conversion			
26990814	PP_4120	nuoB	NADH dehydrogenase subunit B	1.8	7.95E-02	0,75g BuOH	4.9	25523	6	Cytoplasmic Membrane	COG0377	Energy production and conversion			
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	2.0	9.35E-02	0,75g BuOH	6.5	67609	25	Cytoplasmic	COG0649	Energy production and conversion			
26990817	PP_4123	nuoF	NADH dehydrogenase I subunit F	1.3	1.54E-01	0,75g BuOH	7.1	49135	17	Cytoplasmic	COG1894	Energy production and conversion			
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.6	1.28E-01	0,75g BuOH	5.9	97582	29	Unknown	COG1034	Energy production and conversion			
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	1.3	8.70E-01	0,75g BuOH	6.1	37637	2	Cytoplasmic Membrane	COG1005	Energy production and conversion			
26990820	PP_4126	nuoI	NADH dehydrogenase subunit I	2.1	3.88E-01	0,75g BuOH	6.0	20517	2	Cytoplasmic	COG1143	Energy production and conversion			
26990824	PP_4130	nuoM	NADH dehydrogenase subunit M	3.3	9.59E-02	0,75g BuOH	8.2	55614	2	Cytoplasmic Membrane	COG1008	Energy production and conversion			
26990832	PP_4138		NADPH-dependent FMN reductase	1.3	7.30E-01	0,75g BuOH	8.7	20354	10	Cytoplasmic	COG0431	General function prediction only			
26990837	PP_4144	gloB	hydroxyacylglutathione hydrolase	1.3	2.11E-01	0,75g BuOH	6.3	28767	4	Cytoplasmic	COG0491	General function prediction only			
26990847	PP_4154		hypothetical protein	1.5	2.43E-01	7,5g BuOH	5.1	99530	2	Cytoplasmic	COG0160	Amino acid transport and metabolism			
26990855	PP_4163		hypothetical protein	1.1	7.99E-01	0,75g BuOH	5.5	88880	2	Unknown					
26990861	PP_4169	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1.0	8.47E-01	0,75g BuOH	6.6	36520	9	Cytoplasmic	COG0240	Energy production and conversion			
26990867	PP_4175	fabB	3-oxoacyl-[acyl carrier protein] synthase I	1.5	2.76E-01	0,75g BuOH	5.3	43264	15	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism		
26990870	PP_4178		dienelactone hydrolase	1.3	2.64E-01	0,75g BuOH	7.1	26269	13	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism			
26990871	PP_4179	htpG	heat shock protein 90	2.1	1.37E-02	7,5g BuOH	5.0	71610	41	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones			
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.6	1.05E-01	0,75g BuOH	6.2	30111	20	Cytoplasmic	COG0074	Energy production and conversion			
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.7	3.29E-02	0,75g BuOH	6.1	41239	28	Cytoplasmic	COG0045	Energy production and conversion			
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.6	2.34E-01	0,75g BuOH	6.3	49912	22	Cytoplasmic	COG1249	Energy production and conversion			
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.1	4.08E-01	7,5g BuOH	5.1	42434	20	Cytoplasmic	COG0508	Energy production and conversion			
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.3	1.84E-01	0,75g BuOH	6.5	106521	47	Cytoplasmic	COG0567	Energy production and conversion			
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.1	3.38E-01	0,75g BuOH	7.5	26000	18	Cytoplasmic Membrane	COG0479	Energy production and conversion			
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	3.89E-01	0,75g BuOH	6.2	63448	25	Cytoplasmic Membrane	COG1053	Energy production and conversion			
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.3	3.92E-01	0,75g BuOH	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion			
26990886	PP_4194	gltA	type II citrate synthase	1.9	6.54E-02	7,5g BuOH	7.0	47622	30	Cytoplasmic	COG0372	Energy production and conversion			
26990890	PP_4198		OmpA/MotB domain protein	1.4	5.19E-01	7,5g BuOH	8.9	29694	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane			
26990892	PP_4200		hypothetical protein	1.1	4.54E-01	7,5g BuOH	8.1	29611	2	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms		
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.4	1.59E-01	7,5g BuOH	4.9	31237	17	Unknown	COG2025	Energy production and conversion			
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.1	8.26E-01	7,5g BuOH	9.7	26361	18	Unknown	COG2086	Energy production and conversion			
26990895	PP_4203		electron transferring-flavoprotein dehydrogenase	1.9	1.24E-02	7,5g BuOH	5.7	61082	22	Cytoplasmic	COG0644	Energy production and conversion			
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	7.5	9.94E-01	0,75g BuOH	5.5	89725	8	Outer Membrane	COG4773	Inorganic ion transport and metabolism			
26990928	PP_4237	dsbG	disulfide isomerase/thiol-disulfide oxidase	1.5	2.80E-01	0,75g BuOH	8.6	27578	3	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones			
26990940	PP_4249		hypothetical protein	4.4	7.35E-02	0,75g BuOH	7.0	24715	2	Cytoplasmic	COG3571	General function prediction only			
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	3.5	2.02E-02	0,75g BuOH	9.6	53567	2	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones			
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.3	6.07E-02	7,5g BuOH	9.0	22637	8	Cytoplasmic	COG2993	Energy production and conversion			
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.8	5.28E-02	7,5g BuOH	5.2	35613	15	Unknown	COG2010	Energy production and conversion			
26990956	PP_4265	anr	transcriptional regulator Anr	1.0	9.73E-01	7,5g BuOH	6.5	27221	2	Cytoplasmic	COG0664	Signal transduction mechanisms			
26990957	PP_4266	apt	adenine phosphoribosyltransferase	1.6	1.26E-01	0,75g BuOH	4.6	20018	4	Cytoplasmic	COG0503	Nucleotide transport and metabolism			
26990965	PP_4274	ligA	NAD-dependent DNA ligase LigA	1.0	3.52E-01	0,75g BuOH	5.3	84112	2	Cytoplasmic	COG0272	DNA replication, recombination, and repair			
26990966	PP_4275	zipA	cell division protein ZipA	1.5	6.34E-01	7,5g BuOH	6.0	35312	8	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning			
26990967	PP_4276		chromosome segregation protein SMC	3.6	6.43E-02	0,75g BuOH	4.7	131729	7	Cytoplasmic	COG1196	Cell division and chromosome partitioning			
26990968	PP_4277		GntR family transcriptional regulator	1.4	2.70E-01	0,75g BuOH	7.5	24972	10	Cytoplasmic	COG1802	Transcription			
26990970	PP_4279	xdhB	xanthine dehydrogenase, XdhB subunit	3.2	8.32E-02	0,75g BuOH	6.4	88031	2	Cytoplasmic	COG4631	Nucleotide transport and metabolism			
26990972	PP_4281	gad	guanine deaminase	1.4	6.42E-02	0,75g BuOH	5.3	48084	2	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only		
26990974	PP_4283		GntR family transcriptional regulator	1.0	7.06E-01	0,75g BuOH	6.8	27912	8	Cytoplasmic	COG1802	Transcription			
26990978	PP_4287		hypothetical protein	1.3	4.71E-01	7,5g BuOH	4.9	19028	2	Cytoplasmic	COG3195	Function unknown			
26990985	PP_4294		hypothetical protein	1.2	2.20E-01	7,5g BuOH	7.2	31614	2	Cytoplasmic Membrane	COG2354	Function unknown			
26990986	PP_4295		TetR family transcriptional regulator	1.0	9.61E-01	0,75g BuOH	6.6	22721	5	Cytoplasmic	COG1309	Transcription			
26990989	PP_4298	hyi	hydroxypyruvate isomerase	1.4	4.73E-02	7,5g BuOH	5.0	29057	9	Cytoplasmic	COG3622	Carbohydrate transport and metabolism			
26990990	PP_4299	glxR	2-hydroxy-3-oxopropionate reductase	1.2	4.98E-01	0,75g BuOH	6.6	30864	4	Cytoplasmic	COG2084	Lipid metabolism			
26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	1.4	2.75E-01	7,5g BuOH	6.3	36692	5	Periplasmic	COG1613	Inorganic ion transport and metabolism			
26991006	PP_4315		PhzF family phenazine biosynthesis protein	2.8	1.77E-01	0,75g BuOH	4.5	28437	4	Cytoplasmic	COG0384	General function prediction only			
26991018	PP_4328		hypothetical protein	2.2	2.16E-01	0,75g BuOH	7.1	55477	2	Unknown					
26991022	PP_4332	cheW	purine-binding chemotaxis protein CheW	3.2	9.70E-01	7,5g BuOH	4.1	17784	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms		
26991026	PP_4336	motC	flagellar motor protein	2.9	5.37E-02	0,75g BuOH	4.9	25930	6	Cytoplasmic Membrane	COG1291	Cell motility and secretion			
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	1.1	7.31E-01	7,5g BuOH	9.0	39451	7	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms		
26991028	PP_4338	cheA	chemotaxis protein CheA	3.7	1.07E-01	0,75g BuOH	4.4	79674	20	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms		
26991029	PP_4339	cheZ	chemotaxis phosphatase, CheZ	1.2	4.34E-01	7,5g BuOH	4.8	29533	17	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms		
26991032	PP_4342	fleN	flagellar number regulator FleN	2.1	8.91E-02	0,75g BuOH	8.0	29670	7	Cytoplasmic Membrane	COG0455	Cell motility			
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.2	3.99E-01	7,5g BuOH	5.4	55551	10	Cytoplasmic	COG2204	Signal transduction mechanisms			
26991067	PP_4378	fliC	flagellin FliC	15.1	4.71E-02	0,75g BuOH	4.2	67846	29	Extracellular	COG1344	Cell motility and secretion			
26991068	PP_4379		beta-ketoacyl-acyl-carrier-protein synthase I	1.1	9.37E-01	0,75g BuOH	4.8	33207	5	Cytoplasmic	COG0332	acyl-carrier-protein			
26991069	PP_4380	flgL	flagellar hook-associated protein FlgL	121.7	3.01E-02	0,75g BuOH	4.3	54938	3	Extracellular	COG1344	Cell motility and secretion			
26991077	PP_4388	flgE	flagellar hook protein FlgE	2.1	2.37E-01	0,75g BuOH	4.3	45796	2	Extracellular	COG1749	Cell motility and secretion			
26991081	PP_4392	cheR	chemotaxis protein methyltransferase CheR	2.3	1.28E-01	0,75g BuOH	9.3	31084	2	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms		
26991082	PP_4393	cheV-3	chemotaxis protein CheV	2.6	1.09E-01	0,75g BuOH	6.2	34498	12	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms		
26991086	PP_4397		type IV pilus assembly PilZ	1.6	1.01E-01	0,75g BuOH	6.7	28449	19	Cytoplasmic	COG5581	Signal transduction mechanisms			
26991088	PP_4399		glutamine synthetase	1.6	3.41E-01	7,5g BuOH	6.2	45023	2	Cytoplasmic	COG0174	Amino acid transport and metabolism			
26991116	PP_4428		amino acid ABC transporter periplasmic amino acid-binding protein	1.4	3.49E-01	0,75g BuOH	5.8	30355	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms		
26991134	PP_4448		hypothetical protein	1.3	1.28E-01	0,75g BuOH	6.0	56331	27	Cytoplasmic	COG0433	Replication, recombination, and repair			
26991155	PP_4469	gmk-1	phosphonate metabolism protein/1,5-bisphosphokinase (PRPP-forming) PhnN	1.3	8.98E-01	7,5g BuOH	9.7	21513	3	Cytoplasmic	COG3709	Inorganic ion transport and metabolism			
26991159	PP_4473		aspartate kinase	1.7	1.77E-01	0,75g BuOH	5.0	44605	12	Cytoplasmic	COG0527	Amino acid transport and metabolism			
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.3	1.63E-01	7,5g BuOH	5.1	94711	33	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis			
26991161	PP_4475	astE	succinylglutamate desuccinylase	2.0	1.08E-01	0,75g BuOH	6.2	37580	3	Cytoplasmic	COG2988	Amino acid transport and metabolism			
26991163	PP_4477	astB	succinylarginine dihydrolase	1.8	9.75E-02	0,75g BuOH	6.4	48862	7	Cytoplasmic	COG3724	Amino acid transport and metabolism			
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.9	1.71E-02	0,75g BuOH	5.4	51330	4	Cytoplasmic	COG1012	Energy production and conversion			
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.0	9.00E-01	7,5g BuOH	6.5	43490	16	Cytoplasmic	COG4992	Amino acid transport and metabolism			
26991169	PP_4483		basic amino acid ABC transporter ATP-binding protein	1.1	6.07E-01	7,5g BuOH	7.8	28000	5	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism			
26991172	PP_4486		cationic amino acid ABC transporter periplasmic protein	1.2	5.22E-01	0,75g BuOH	8.1	28302	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms		
26991173	PP_4487	acsA	acetyl-CoA synthetase	6.9	2.08E-03	7,5g BuOH	6.4	71796	48	Cytoplasmic	COG0365	Lipid metabolism			
26991191	PP_4506		nitroreductase	1.2	9.15E-01	0,75g BuOH	6.6	19994	8	Unknown	COG0778	Energy production and conversion			
26991202	PP_4517		hypothetical protein	1.4	2.36E-01	7,5g BuOH	3.8	21967	4	Cytoplasmic	COG3318	General function prediction only			
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.4	4.70E-01	7,5g BuOH	5.4	50393	27	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion		
26991206	PP_4521		aerotaxis receptor	1.8	5.38E-03	0,75g BuOH	6.4	56605	18	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	2.0	1.40E-01	0,75g BuOH	10.3	48478	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription		

26991224	PP_4540		alpha/beta fold family hydrolase	1.9	1.08E-01	0,75g BuOH	7.4	30640	2	Cytoplasmic	COG0596	General function prediction only			
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.9	4.73E-02	0,75g BuOH	5.7	42326	14	Cytoplasmic	COG0332	acyl-carrier-protein			
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	3.5	1.22E-01	0,75g BuOH	8.3	140950	10	Cytoplasmic	COG1643	DNA replication, recombination, and repair			
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	3.0	7.54E-02	0,75g BuOH	7.7	61812	4	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism		
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	1.1	5.46E-01	0,75g BuOH	7.8	61658	9	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism		
26991235	PP_4551		alpha/beta fold family hydrolase	1.2	7.18E-01	7,5g BuOH	7.3	34587	2	Cytoplasmic	COG2267	Lipid metabolism			
26991255	PP_4571	cysK	cysteine synthase A	1.2	3.09E-01	0,75g BuOH	5.5	34357	8	Cytoplasmic	COG0031	Amino acid transport and metabolism			
26991257	PP_4573		ATPase AAA	1.0	8.33E-01	0,75g BuOH	5.8	32146	15	Cytoplasmic	COG0714	General function prediction only			
26991261	PP_4577		LamB/YcsF family protein	1.2	5.40E-01	0,75g BuOH	5.8	27871	4	Cytoplasmic	COG1540	General function prediction only			
26991265	PP_4581		hypothetical protein	1.4	3.48E-01	0,75g BuOH	6.2	28647	3	Cytoplasmic	COG0121	General function prediction only			
26991267	PP_4583		oligopeptidase B	1.4	8.38E-01	7,5g BuOH	4.7	75818	2	Unknown	COG1770	Amino acid transport and metabolism			
26991272	PP_4588		nitronate monooxygenase	1.3	3.96E-01	0,75g BuOH	6.0	21997	9	Unknown	COG0778	Energy production and conversion			
26991275	PP_4591	rnd	ribonuclease D	1.7	2.95E-02	7,5g BuOH	5.5	42668	4	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis			
26991286	PP_4602		AraC family transcriptional regulator	1.1	4.84E-01	0,75g BuOH	8.9	31224	4	Cytoplasmic	COG2207	Transcription			
26991303	PP_4619		maleylacetoacetate isomerase	4.0	2.32E-02	0,75g BuOH	6.2	22876	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones			
26991316	PP_4632		short chain dehydrogenase	2.0	4.38E-02	7,5g BuOH	7.8	26619	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only		
26991319	PP_4635		trans-2-enoyl-CoA reductase	1.2	3.43E-01	0,75g BuOH	5.0	44265	19	Cytoplasmic	COG3007	Function unknown			
26991325	PP_4641	cstA	carbon starvation protein CstA	1.4	3.06E-01	0,75g BuOH	9.0	73763	8	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms			
26991330	PP_4646		oxidoreductase FAD/NAD(P)-binding domain protein	1.6	1.76E-01	0,75g BuOH	5.2	28960	8	Cytoplasmic	COG1018	Energy production and conversion			
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	6.0	5.37E-02	0,75g BuOH	9.1	53016	5	Cytoplasmic Membrane	COG1271	Energy production and conversion			
26991338	PP_4654	trmA	tRNA (uracil-5-)-methyltransferase	1.2	4.57E-01	0,75g BuOH	5.7	40878	2	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis			
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	2.2	1.08E-01	0,75g BuOH	9.4	26835	2	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism			
26991341	PP_4657		metallopeptidase, zinc binding	1.2	3.75E-01	0,75g BuOH	6.7	34400	3	Unknown	COG2321	General function prediction only			
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.5	2.22E-01	0,75g BuOH	4.8	68764	14	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26991343	PP_4659	ggt-2	gamma-glutamyltransferase	1.6	1.94E-01	7,5g BuOH	6.0	59835	14	Periplasmic	COG0405	Amino acid transport and metabolism			
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	1.1	4.72E-01	7,5g BuOH	6.1	30321	9	Cytoplasmic	COG2084	Lipid metabolism			
26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.7	6.67E-02	0,75g BuOH	6.0	54367	10	Cytoplasmic	COG1012	Energy production and conversion			
26991361	PP_4677	pssA-2	CDP-diacylglycerol--serine O-phosphatidyltransferase	2.0	1.85E-01	0,75g BuOH	9.2	30359	2	Cytoplasmic Membrane	COG1183	Lipid metabolism			
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	9.66E-01	7,5g BuOH	5.4	36370	25	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism		
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.1	6.15E-01	0,75g BuOH	6.8	62781	26	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome)			
26991366	PP_4682		hypothetical protein	2.8	2.50E-01	0,75g BuOH	8.2	27215	3	Unknown	COG4783	General function prediction only			
26991367	PP_4683	mrcB	penicillin-binding protein 1B	1.3	4.66E-01	7,5g BuOH	9.5	85156	3	Cytoplasmic Membrane	COG0744	Cell envelope biogenesis, outer membrane			
26991368	PP_4684		hypothetical protein	2.5	6.07E-02	0,75g BuOH	5.1	56095	8	Cytoplasmic	COG2187	Function unknown			
26991373	PP_4689		periplasmic protein	1.1	6.67E-01	0,75g BuOH	7.1	30685	6	Periplasmic	COG4558	Inorganic ion transport and metabolism			
26991379	PP_4695		multi-sensor signal transduction histidine kinase	1.8	2.01E-01	0,75g BuOH	6.2	109316	2	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism	General function prediction only		
26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	12.8	2.66E-02	0,75g BuOH	5.3	52585	3	Cytoplasmic	COG2204	Signal transduction mechanisms			
26991381	PP_4697	pcnB	poly(A) polymerase	2.2	2.05E-01	0,75g BuOH	9.6	52721	3	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis			
26991383	PP_4699	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.3	9.39E-02	0,75g BuOH	5.8	27762	4	Unknown	COG0413	Coenzyme metabolism			
26991384	PP_4700	panC	pantoate--beta-alanine ligase	1.5	2.63E-01	0,75g BuOH	7.7	31189	4	Cytoplasmic	COG0414	Coenzyme metabolism			
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.7	7.92E-02	0,75g BuOH	6.8	61455	18	Cytoplasmic	COG0166	Carbohydrate transport and metabolism			
26991386	PP_4702	acsB	acetyl-CoA synthetase	2.6	1.19E-01	0,75g BuOH	6.5	71251	11	Cytoplasmic	COG0365	Lipid metabolism			
26991388	PP_4704		hypothetical protein	1.2	2.06E-01	0,75g BuOH	5.6	107252	12	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane			
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.1	7.00E-01	0,75g BuOH	4.9	75010	34	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis			
26991395	PP_4712	infB	translation initiation factor IF-2	1.4	1.07E-01	0,75g BuOH	6.8	91460	30	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis			
26991396	PP_4713	nusA	transcription elongation factor NusA	1.4	2.01E-01	7,5g BuOH	4.3	54673	22	Cytoplasmic	COG0195	Transcription			
26991398	PP_4715	tpiA	triosephosphate isomerase	1.2	4.96E-01	7,5g BuOH	4.7	25991	10	Cytoplasmic	COG0149	Carbohydrate transport and metabolism			
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.0	7.93E-01	0,75g BuOH	5.4	69722	17	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones			
26991402	PP_4719	rrmJ	ribosomal RNA methyltransferase RrmJ/FtsJ	1.9	5.14E-01	7,5g BuOH	8.5	23164	3	Cytoplasmic	COG0293	Translation, ribosomal structure and biogenesis			
26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	1.2	3.23E-01	0,75g BuOH	5.8	40574	7	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism		
26991408	PP_4725	dapB	dihydrodipicolinate reductase	1.3	4.07E-01	0,75g BuOH	5.9	28423	5	Cytoplasmic	COG0289	Amino acid transport and metabolism			
26991409	PP_4726	dnaJ	chaperone protein DnaJ	2.8	2.42E-03	0,75g BuOH	6.7	40181	5	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones			
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.4	5.98E-01	7,5g BuOH	4.6	68800	53	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones			
26991411	PP_4728	grpE	heat shock protein GrpE	1.6	3.04E-01	0,75g BuOH	4.7	20531	5	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones			
26991414	PP_4731	omlA	SmpA/OmlA domain protein	3.0	4.07E-01	7,5g BuOH	4.4	19586	7	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane			
26991423	PP_4740	hsdR	type I restriction-modification system, R subunit	1.4	1.09E-01	0,75g BuOH	5.2	89615	6	Cytoplasmic	COG4096	Defense mechanisms			
26991429	PP_4748		amino acid ABC transporter periplasmic amino acid-binding protein	1.1	6.38E-01	0,75g BuOH	5.4	28338	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms		
26991434	PP_4753		N-methylproline demethylase	1.1	9.77E-01	7,5g BuOH	6.5	75215	9	Cytoplasmic	COG1902	Energy production and conversion			
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	2.2	2.35E-01	0,75g BuOH	6.2	35615	7	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only		
26991443	PP_4762	tesB	acyl-CoA thioesterase II	1.1	8.84E-01	0,75g BuOH	6.1	32319	5	Cytoplasmic	COG1946	Lipid metabolism			
161378119	PP_4779		AMP nucleosidase	4.1	1.31E-02	0,75g BuOH	6.8	54498	9	Cytoplasmic	COG0775	Nucleotide transport and metabolism			
26991460	PP_4780		acyl-CoA dehydrogenase domain-containing protein	2.2	7.97E-02	0,75g BuOH	6.6	59803	3	Cytoplasmic	COG1960	Lipid metabolism			
26991462	PP_4782	thiD	phosphomethylpyrimidine kinase	1.7	1.83E-01	7,5g BuOH	5.1	28338	5	Cytoplasmic	COG0351	Coenzyme metabolism			
26991463	PP_4783	thiE	thiamine-phosphate pyrophosphorylase	1.2	4.09E-01	7,5g BuOH	7.6	21702	3	Unknown	COG0352	Coenzyme metabolism			
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	2.5	3.69E-02	0,75g BuOH	5.7	45178	10	Cytoplasmic	COG0001	Coenzyme metabolism			
26991469	PP_4789		CBS domain containing protein	1.6	2.21E-01	7,5g BuOH	4.7	31393	7	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism			
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.3	2.84E-01	7,5g BuOH	5.6	96097	29	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis			
26991475	PP_4795		rare lipoprotein B	1.5	2.32E-01	7,5g BuOH	6.1	22414	12	Unknown	COG2980	Cell envelope biogenesis, outer membrane			
26991478	PP_4798		lytic murein transglycosylase	2.2	3.64E-02	7,5g BuOH	7.7	48000	11	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane			
26991481	PP_4801	lipB	lipoate-protein ligase B	1.3	8.63E-01	7,5g BuOH	6.0	23689	3	Cytoplasmic	COG0321	Coenzyme metabolism			
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.1	3.42E-01	0,75g BuOH	6.6	42288	7	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane			
26991490	PP_4810	nadD	nicotinic acid mononucleotide adenylyltransferase	1.2	4.93E-01	0,75g BuOH	5.6	25291	2	Cytoplasmic	COG1057	Coenzyme metabolism			
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.2	2.65E-01	0,75g BuOH	6.1	45417	11	Cytoplasmic	COG0014	Amino acid transport and metabolism			
26991494	PP_4814		ATP-dependent protease La	1.4	2.52E-01	0,75g BuOH	4.1	21846	5	Cytoplasmic	COG2802	General function prediction only			
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	2.8	8.39E-02	0,75g BuOH	6.5	57695	21	Cytoplasmic	COG0138	Nucleotide transport and metabolism			
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.3	1.82E-01	7,5g BuOH	4.7	45837	7	Cytoplasmic	COG0151	Nucleotide transport and metabolism			
26991504	PP_4824		integral membrane sensor hybrid histidine kinase	1.4	4.02E-01	0,75g BuOH	6.6	101587	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms			
26991518	PP_4838	oprC	TonB-dependent copper receptor	13.7	3.87E-01	7,5g BuOH	6.2	74540	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism			
26991528	PP_4848		DnaJ family curved-DNA-binding protein	1.3	1.64E-01	0,75g BuOH	9.8	34808	13	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones			
26991536	PP_4856		bacterioferritin	17.4	1.19E-01	7,5g BuOH	4.7	19202	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism			
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	1.8	1.33E-01	0,75g BuOH	6.3	27400	5	Cytoplasmic	COG4221	General function prediction only			
26991543	PP_4863		branched chain amino acid ABC transporter ATP-binding protein	2.1	7.10E-02	0,75g BuOH	9.3	26312	8	Unknown	COG0410	Amino acid transport and metabolism			
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	5.0	6.08E-02	0,75g BuOH	6.6	32427	2	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism			
26991547	PP_4867		extracellular ligand-binding receptor	1.4	4.80E-02	0,75g BuOH	6.2	40270	26	Periplasmic	COG0683	Amino acid transport and metabolism			
26991549	PP_4869	nadE	NAD synthetase	1.2	1.75E-01	0,75g BuOH	5.6	29273	10	Cytoplasmic	COG0171	Coenzyme metabolism			
26991550	PP_4870		azurin	24.7	2.79E-03	7,5g BuOH	6.9	16028	6	Periplasmic	COG3241	Energy production and conversion			
26991554	PP_4874	rplI	50S ribosomal protein L9	1.4	9.51E-01	7,5g BuOH	5.3	15466	2	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis			
26991557	PP_4877	rpsF	30S ribosomal protein S6	2.4	4.13E-01	7,5g BuOH	4.7	16373	2	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis			
26991558	PP_4879		RNA methyltransferase	1.2	4.33E-01	0,75g BuOH	6.8	27014	8	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis			
26991559	PP_4880	vacB	ribonuclease R	1.8	6.84E-02	0,75g BuOH	7.9	96688	21	Cytoplasmic	COG0557	Transcription			
26991560	PP_4881		iron ABC transporter periplasmic iron-binding protein	1.7	2.14E-01	0,75g BuOH	5.0	36800	5	Periplasmic	COG1840	Inorganic ion transport and metabolism			
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	2.6	4.11E-02	0,75g BuOH	6.1	71958	18	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms		
26991567	PP_4889	purA	adenylosuccinate synthetase	1.0	8.79E-01	7,5g BuOH	5.6	46833	18	Cytoplasmic	COG0104	Nucleotide transport and metabolism			
26991568	PP_4890	hisZ	ATP phosphoribosyltransferase regulatory subunit	1.5	3.30E-01	0,75g BuOH	4.7	42935	4	Cytoplasmic	COG3705	Amino acid transport and metabolism			
26991569	PP_4891	hflC	HflC protein	1.7	8.65E-02	0,75g BuOH	9.8	33001	16	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones			
26991572	PP_4894	hfq	RNA-binding protein Hfq	192.1	3.16E-02	7,5g BuOH	9.0	9462	3	Cytoplasmic	COG1923	General function prediction only			
26991580	PP_4902	orn	oligoribonuclease	2.3	5.57E-02	0,75g BuOH	5.8	20787	6	Cytoplasmic	COG1949	RNA processing and modification			
26991582	PP_4904	motB	flagellar motor protein MotB	1.2	4.91E-01	0,75g BuOH	4.8	37802	6	Cytoplasmic Membrane	COG1360	Cell motility and secretion			
26991583	PP_4905		flagellar motor protein MotA	1.3	4.50E-01	0,75g BuOH	6.2	30312	2	Cytoplasmic Membrane	COG1291	Cell motility and secretion			
26991584	PP_4906		metal-dependent hydrolase HDOD	3.3	3.58E-02	0,75g BuOH	7.7	57677	2	Unknown					
26991585	PP_4907	rhdA-2	rhodanese domain protein	1.2	7.03E-01	7,5g BuOH	6.1	29517	12	Cytoplasmic	COG2897	Inorganic ion transport and metabolism			
26991586	PP_4908	psd	phosphatidylserine decarboxylase	2.1	1.49E-01	0,75g BuOH	8.6	31547	5	Cytoplasmic Membrane	COG0688	Lipid metabolism			
26991587	PP_4909	serB	phosphoserine phosphatase SerB	1.6	1.28E-01	0,75g BuOH	5.1	45033	3	Cytoplasmic	COG0560	Amino acid transport and metabolism			
26991588	PP_4910		hypothetical protein	2.3	2.97E-01	0,75g BuOH	4.7	53632	4	Cytoplasmic	COG3726	General function prediction only			
26991589	PP_4911		hypothetical protein	1.4	1.09E-01	7,5g BuOH	8.5	27337	5	Periplasmic	COG3009	Function unknown			
26991593	PP_4915	parE	DNA topoisomerase IV subunit B	3.9	5.65E-02	0,75g BuOH	6.2	69556	2	Cytoplasmic	COG0187	DNA replication, recombination, and repair			
26991597	PP_4919		NUDIX hydrolase	1.2	3.00E-01	0,75g BuOH	4.7	23607	7	Cytoplasmic					
26991600	PP_4922	thiC	thiamine biosynthesis protein ThiC	1.2	5.29E-01	7,5g BuOH	5.7	69727	12	Cytoplasmic	COG0422	Coenzyme metabolism			
26991601	PP_4923		TolC family type I secretion outer membrane protein	4.1	5.71E-02	0,75g BuOH	5.2	52637	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion		
26991609	PP_4931		FAD dependent oxidoreductase	1.6	1.89E-01	0,75g BuOH	7.2	42015	6	Cytoplasmic	COG0578	Energy production and conversion			
26991610	PP_4932		aldo/keto reductase	1.7	1.31E-01	0,75g BuOH	6.4	29123	2	Cytoplasmic	COG0667	Energy production and conversion			
26991611	PP_4933		hypothetical protein	2.5	1.90E-01	0,75g BuOH	10.0	37000	2	Unknown					
26991612	PP_4934		bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase	1.3	3.01E-01	0,75g BuOH	5.8	49970	9	Cytoplasmic	COG2870	Cell envelope biogenesis, outer membrane			
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	3.3	5.68E-02	0,75g BuOH	7.6	66279	7	Cytoplasmic Membrane	COG1132	Defense mechanisms			
26991615	PP_4937		toluene tolerance protein	1.6	3.12E-01	0,75g BuOH	10.4	25956	4	Cytoplasmic					
26991617	PP_4939		hypothetical protein	1.2	4.02E-01	0,75g BuOH	7.1	28978	4	Cytoplasmic					
26991622	PP_4944		carbamoyltransferase	1.1	7.64E-01	0,75g BuOH	7.2	65646	9	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones			
26991624	PP_4946	putP	sodium/proline symporter	2.1	1.80E-01	0,75g BuOH	7.0	52422	2	Cytoplasmic Membrane	COG0591	Amino acid transport and metabolism	General function prediction only		

26991625	PP 4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	2.3	3.75E-02	0,75g BuOH	6.3	142580	34	Cytoplasmic	COG4230	Energy production and conversion	
26991627	PP 4949		TldD/PmbA family protein	1.2	3.98E-01	0,75g BuOH	6.6	55611	3	Unknown	COG0312	General function prediction only	
26991628	PP 4950		hypothetical protein	1.5	4.74E-01	7,5g BuOH	4.9	47741	2	Unknown	COG0312	General function prediction only	
26991637	PP 4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	5.4	6.39E-02	0,75g BuOH	4.8	78896	16	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26991638	PP 4960	fda	fructose-1,6-bisphosphate aldolase	1.4	3.03E-01	7,5g BuOH	5.6	38453	22	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991641	PP 4963	pgk	phosphoglycerate kinase	1.7	3.87E-02	7,5g BuOH	4.9	40005	18	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
26991643	PP 4965	tktA	transketolase	1.1	6.90E-01	0,75g BuOH	5.0	72463	32	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991644	PP 4966		ArsR family transcriptional regulator	1.7	1.99E-01	7,5g BuOH	6.4	36148	3	Cytoplasmic	COG2226	Coenzyme metabolism	
26991645	PP 4967	metK	S-adenosylmethionine synthetase	1.8	2.29E-01	0,75g BuOH	5.1	42779	20	Cytoplasmic	COG0192	Coenzyme metabolism	
26991654	PP 4977	metF	5,10-methylenetetrahydrofolate reductase	1.2	8.52E-01	7,5g BuOH	6.2	32979	11	Cytoplasmic	COG0685	Amino acid transport and metabolism	
26991657	PP 4980		DEAD-box ATP dependent DNA helicase	1.5	3.07E-01	0,75g BuOH	10.7	68073	9	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991658	PP 4981		hypothetical protein	1.3	9.63E-01	0,75g BuOH	8.8	22129	8	Unknown	COG2353	Function unknown	
26991665	PP 4988		chemotaxis protein CheA	1.7	6.58E-02	0,75g BuOH	4.7	180005	5	Unknown	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991666	PP 4989	pilJ	methyl-accepting chemotaxis sensory transducer	2.1	3.45E-01	7,5g BuOH	4.6	73623	2	Outer Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991670	PP 4993	gshB	glutathione synthetase	1.3	3.86E-01	0,75g BuOH	5.1	35254	6	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26991675	PP 4998	pyrB	aspartate carbamoyltransferase catalytic subunit	2.1	1.96E-01	0,75g BuOH	7.1	36344	6	Cytoplasmic	COG0540	Nucleotide transport and metabolism	
26991676	PP 4999	pyrC	dihydroorotase	1.1	8.72E-01	7,5g BuOH	5.4	44116	7	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
26991678	PP 5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.3	7.52E-01	7,5g BuOH	5.7	49982	17	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP 5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	6.4	2.74E-03	0,75g BuOH	7.4	62241	20	Cytoplasmic	COG3243	Lipid metabolism	
26991682	PP 5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	2.1	9.76E-02	0,75g BuOH	9.6	62722	9	Cytoplasmic	COG3243	Lipid metabolism	
26991683	PP 5006		TetR family transcriptional regulator	1.2	7.33E-01	0,75g BuOH	5.3	23055	2	Cytoplasmic	COG1309	Transcription	
26991684	PP 5007		poly(hydroxyalkanoate) granule-associated protein	2.1	2.28E-02	0,75g BuOH	10.9	26214	17	Cytoplasmic	COG3937	Function unknown	
26991688	PP 5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.5	4.78E-02	0,75g BuOH	9.5	28397	10	Cytoplasmic	COG2226	Coenzyme metabolism	
26991689	PP 5012		hypothetical protein	1.6	2.63E-01	0,75g BuOH	5.4	22983	2	Unknown	COG3165	Function unknown	
26991696	PP 5020		methyl-accepting chemotaxis sensory transducer	1.1	9.46E-01	0,75g BuOH	4.9	69017	34	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991698	PP 5022		amino acid ABC transporter ATP-binding protein	2.4	7.37E-02	0,75g BuOH	7.6	27004	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26991700	PP 5024		amino acid ABC transporter periplasmic amino acid-binding protein	1.1	8.92E-01	0,75g BuOH	8.6	29848	17	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991701	PP 5025	mdoH	glucosyltransferase MdoH	1.2	4.23E-01	0,75g BuOH	8.3	95875	5	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991702	PP 5026	mdoG	glucan biosynthesis protein G	1.1	6.48E-01	0,75g BuOH	6.5	62340	11	Periplasmic	COG3131	Inorganic ion transport and metabolism	
26991704	PP 5028	pip	proline iminopeptidase	1.3	3.74E-01	0,75g BuOH	6.2	36589	14	Cytoplasmic	COG0596	General function prediction only	
26991711	PP 5035	hutC	histidine utilization repressor	1.9	2.83E-01	0,75g BuOH	6.6	27624	2	Cytoplasmic	COG2188	Transcription	
26991715	PP 5039		hypothetical protein	2.7	3.93E-01	0,75g BuOH	4.8	23220	4	Unknown	COG3803	Function unknown	
26991716	PP 5040	fbp	fructose-1,6-bisphosphatase	1.2	5.68E-01	7,5g BuOH	5.9	37246	11	Cytoplasmic	COG0158	Carbohydrate transport and metabolism	
26991717	PP 5041	glgP	glycogen/starch/alpha-glucan phosphorylase	2.1	1.98E-02	0,75g BuOH	6.4	92004	19	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP 5044		GTP-binding protein TypA	1.5	7.89E-01	0,75g BuOH	5.3	67157	16	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP 5046	glnA	glutamine synthetase, type I	1.2	1.96E-01	0,75g BuOH	5.1	51740	21	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991732	PP 5056	pgm	phosphoglyceromutase	1.4	1.92E-02	0,75g BuOH	4.9	55180	12	Cytoplasmic	COG0696	Carbohydrate transport and metabolism	
26991734	PP 5058		carboxyl-terminal protease	2.2	1.07E-01	0,75g BuOH	5.6	46333	8	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26991739	PP 5063	betB	betaine aldehyde dehydrogenase	1.3	4.25E-01	7,5g BuOH	4.8	52986	5	Cytoplasmic	COG1012	Energy production and conversion	
26991740	PP 5064	betA	choline dehydrogenase	6.7	4.19E-02	0,75g BuOH	6.8	62544	2	Cytoplasmic Membrane	COG2303	Amino acid transport and metabolism	
26991750	PP 5074	hemE	uroporphyrinogen decarboxylase	2.1	8.29E-02	7,5g BuOH	6.7	38883	4	Cytoplasmic	COG0407	Coenzyme metabolism	
26991751	PP 5075	gltD	glutamate synthase subunit beta	1.6	4.25E-01	7,5g BuOH	6.3	51819	6	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26991752	PP 5076	gltB	glutamate synthase subunit alpha	1.3	2.46E-01	0,75g BuOH	6.2	161772	40	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP 5077		sporulation domain protein	1.2	5.63E-01	7,5g BuOH	7.1	55434	9	Unknown	COG3267	Intracellular trafficking and secretion	
26991754	PP 5078	aroB	3-dehydroquinate synthase	1.1	9.64E-01	7,5g BuOH	6.0	39485	5	Cytoplasmic	COG0337	Amino acid transport and metabolism	
26991760	PP 5084		penicillin-binding protein, 1A family	1.2	6.43E-01	0,75g BuOH	7.2	89193	2	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP 5085	maeB	malic enzyme	1.0	8.36E-01	7,5g BuOH	4.9	45127	32	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP 5089	argS	arginyl-tRNA synthetase	1.4	1.57E-03	0,75g BuOH	5.7	63668	18	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991770	PP 5094		alanine racemase domain protein	1.0	7.90E-01	7,5g BuOH	6.8	24192	6	Cytoplasmic	COG0325	General function prediction only	
26991771	PP 5095	proC-2	pyrroline-5-carboxylate reductase	1.5	9.96E-02	0,75g BuOH	4.7	28258	9	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26991774	PP 5098	metW	methionine biosynthesis protein MetW	1.0	7.07E-01	0,75g BuOH	5.6	24002	2	Cytoplasmic	COG2226	Coenzyme metabolism	
26991779	PP 5103	trmB	tRNA (guanine-N(7)-)-methyltransferase	1.6	6.13E-01	7,5g BuOH	7.3	27203	3	Cytoplasmic	COG0220	General function prediction only	
26991780	PP 5104	thiG	thiazole synthase	1.5	3.02E-01	7,5g BuOH	5.8	28917	9	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
26991786	PP 5110	ftsE	cell division ATP-binding protein FtsE	1.4	6.78E-01	7,5g BuOH	11.0	24830	4	Cytoplasmic Membrane	COG2884	Cell division and chromosome partitioning	
26991787	PP 5111	ftsY	signal recognition particle-docking protein FtsY	1.1	7.97E-01	0,75g BuOH	4.9	51680	6	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
26991788	PP 5112		peptidase M16 domain protein	2.4	5.50E-02	7,5g BuOH	5.9	50095	3	Periplasmic	COG0612	General function prediction only	
26991789	PP 5113		peptidase M16 domain protein	1.4	1.06E-01	0,75g BuOH	8.0	52389	3	Unknown	COG0612	General function prediction only	
26991790	PP 5114		hypothetical protein	1.2	4.90E-01	7,5g BuOH	8.2	22311	4	Unknown	COG0742	DNA replication, recombination, and repair	
26991794	PP 5118		rhodanese domain protein	1.4	8.06E-02	7,5g BuOH	5.6	30750	12	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991796	PP 5120		conifer aldehyde dehydrogenase	1.6	3.62E-01	0,75g BuOH	9.2	52453	3	Cytoplasmic	COG1012	Energy production and conversion	
26991802	PP 5126		signal transduction protein	3.4	9.84E-02	7,5g BuOH	5.6	28452	3	Unknown	COG1639	Signal transduction mechanisms	
26991803	PP 5127		hypothetical protein	1.1	9.57E-01	7,5g BuOH	6.9	44126	2	Cytoplasmic	COG1092	General function prediction only	
26991804	PP 5128	ilvD	dihydroxy-acid dehydratase	1.5	3.10E-02	7,5g BuOH	5.8	65671	30	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991820	PP 5144		hypothetical protein	1.0	8.65E-01	0,75g BuOH	5.3	26452	3	Unknown	COG3332	Function unknown	
26991821	PP 5145	ptsP	PTSINtr with GAF domain, PtsP	1.0	9.95E-01	7,5g BuOH	5.3	83337	17	Cytoplasmic	COG3605	Signal transduction mechanisms	
26991823	PP 5147		HAD superfamily hydrolase	1.5	2.31E-01	0,75g BuOH	4.7	24940	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991826	PP 5150	rpiA	ribose-5-phosphate isomerase A	1.3	1.45E-01	7,5g BuOH	4.9	23496	7	Unknown	COG0120	Carbohydrate transport and metabolism	
26991829	PP 5153		fumarylacetoacetate (FAA) hydrolase	1.2	7.61E-01	0,75g BuOH	4.7	23906	3	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
26991830	PP 5154		FAD linked oxidase domain protein	2.0	2.13E-01	0,75g BuOH	5.2	49990	2	Cytoplasmic	COG0277	Energy production and conversion	
26991831	PP 5155	serA	D-3-phosphoglycerate dehydrogenase	1.1	8.00E-01	0,75g BuOH	6.3	44339	19	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991836	PP 5160		hypothetical protein	1.4	4.28E-01	7,5g BuOH	8.9	27008	5	Cytoplasmic Membrane			
26991841	PP 5165		NLPA lipoprotein	1.2	9.66E-01	7,5g BuOH	8.7	28159	3	Unknown	COG1464	Inorganic ion transport and metabolism	
26991849	PP 5173		acriflavin resistance protein	1.2	4.72E-01	7,5g BuOH	5.4	112277	9	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991850	PP 5174		RND efflux transporter	2.8	1.26E-01	0,75g BuOH	5.5	38032	4	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991851	PP 5175		efflux transporter RND family, MFP subunit	3.4	1.53E-02	0,75g BuOH	6.5	38304	6	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991855	PP 5179	potG	spermidine/putrescine ABC transporter ATPase	2.5	5.00E-02	0,75g BuOH	6.5	42472	7	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26991856	PP 5180	potF-1	putrescine ABC transporter periplasmic putrescine-binding protein	1.4	3.92E-01	7,5g BuOH	8.0	39788	11	Periplasmic	COG0687	Amino acid transport and metabolism	
26991857	PP 5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.3	3.47E-01	7,5g BuOH	6.4	40068	23	Periplasmic	COG0687	Amino acid transport and metabolism	
26991858	PP 5182		aminotransferase	1.3	1.48E-01	7,5g BuOH	6.2	49871	11	Cytoplasmic	COG0161	Coenzyme metabolism	
26991859	PP 5183		glutamine synthetase	1.0	9.91E-01	0,75g BuOH	4.8	50877	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991860	PP 5184		glutamine synthetase	1.7	1.36E-01	0,75g BuOH	4.5	50974	7	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991861	PP 5185	argA	N-acetylglutamate synthase	1.7	1.48E-01	0,75g BuOH	5.9	47440	3	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991862	PP 5186	argE	acetylornithine deacetylase	1.4	5.39E-01	7,5g BuOH	4.9	41425	3	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26991863	PP 5187		adenylate cyclase	1.2	3.49E-01	7,5g BuOH	5.6	52133	7	Cytoplasmic	COG3025	Function unknown	
26991868	PP 5192	gcvP-2	glycine dehydrogenase	1.3	4.55E-01	0,75g BuOH	6.3	104037	12	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991870	PP 5194	gcvT	glycine cleavage system aminomethyltransferase T	1.8	1.14E-01	0,75g BuOH	5.3	39379	7	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26991877	PP 5201		hypothetical protein	1.3	4.87E-01	7,5g BuOH	3.9	19468	3	Unknown	COG3079	Function unknown	
26991882	PP 5206		secretion protein HlyD family protein	1.4	1.09E-01	0,75g BuOH	9.6	34522	8	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26991883	PP 5207		ABC transporter ATP-binding protein/permease	1.4	3.84E-01	0,75g BuOH	7.8	98772	2	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26991886	PP 5210		alcohol dehydrogenase, zinc-containing	3.5	1.08E-01	0,75g BuOH	7.6	33856	5	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26991890	PP 5214	rho	transcription termination factor Rho	1.1	5.18E-01	0,75g BuOH	8.2	47041	30	Cytoplasmic	COG1158	Transcription	
26991892	PP 5216	ppx	Ppx/GppA phosphatase	2.0	7.33E-02	0,75g BuOH	6.9	55958	10	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991893	PP 5217	ppk	polyphosphate kinase	1.1	6.05E-01	0,75g BuOH	7.8	81732	15	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991896	PP 5220	elbB	isoprenoid biosynthesis protein with amidotransferase-like domain	1.1	6.99E-01	0,75g BuOH	5.0	23391	4	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
26991903	PP 5227	lysA-2	diaminopimelate decarboxylase	5.7	8.30E-03	0,75g BuOH	4.9	45213	2	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26991905	PP 5229		hypothetical protein	1.4	7.62E-02	7,5g BuOH	6.1	26395	4	Cytoplasmic	COG3159	Function unknown	
26991907	PP 5231		HAD superfamily hydrolase	1.2	4.65E-01	7,5g BuOH	5.1	25611	7	Cytoplasmic	COG1011	General function prediction only	
26991928	PP 5252		amidohydrolase 3	1.2	1.02E-01	0,75g BuOH	6.4	72743	14	Unknown	COG1574	General function prediction only	
26991934	PP 5258		aldehyde dehydrogenase family protein	1.9	1.06E-02	0,75g BuOH	5.4	53106	10	Cytoplasmic	COG1012	Energy production and conversion	
26991941	PP 5265	xpt	xanthine phosphoribosyltransferase	1.3	5.26E-01	7,5g BuOH	6.1	20386	5	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
26991954	PP 5278		aldehyde dehydrogenase family protein	1.7	1.03E-01	0,75g BuOH	5.5	53053	11	Cytoplasmic	COG1012	Energy production and conversion	
26991958	PP 5282	rpmB	50S ribosomal protein L28	1.1	7.07E-01	0,75g BuOH	12.3	8922	2	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991959	PP 5283		periplasmic dipeptide-binding protein	3.7	2.98E-02	0,75g BuOH	8.5	57512	5	Periplasmic	COG0747	Amino acid transport and metabolism	
26991961	PP 5285	coaBC	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase	1.7	2.11E-01	0,75g BuOH	7.0	43126	2	Cytoplasmic	COG0452	Coenzyme metabolism	
26991964	PP 5288		phosphomannomutase	2.8	9.74E-02	7,5g BuOH	5.0	50271	14	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991965	PP 5289	argB	acetylglutamate kinase	2.4	8.63E-02	7,5g BuOH	5.7	31953	14	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991967	PP 5291	pyrE	orotate phosphoribosyltransferase	1.1	9.76E-01	7,5g BuOH	4.9	23079	5	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
26991968	PP 5292	crc	exodeoxyribonuclease III Xth	1.8	1.31E-01	0,75g BuOH	4.9	29786	3	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
26991972	PP 5296	gmk	guanylate kinase	1.7	1.56E-01	0,75g BuOH	6.4	23184	3	Cytoplasmic	COG0194	Nucleotide transport and metabolism	
26991978	PP 5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	1.5	3.52E-01	0,75g BuOH	9.2	78603	11	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991979	PP 5303		endoribonuclease	7.6	1.08E-01	7,5g BuOH	4.8	13508	10	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
26991980	PP 5304		lipoprotein	1.7	2.59E-01	7,5g BuOH	5.1	26284	3	Unknown			
26991985	PP 5309		LysR family transcriptional regulator	1.1	4.40E-01	0,75g BuOH	7.0	33763	5	Cytoplasmic	COG0583	Transcription	
26991987	PP 5311		signal transduction protein	38.4	9.32E-02	0,75g BuOH	5.9	51775	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
26991989	PP 5313	hupA	histone family protein DNA-binding protein	12.1	7.59E-01	7,5g BuOH	11.0	10551	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
26991996	PP 5320	phoB	transcriptional regulator	1.0	6.55E-01	7,5g BuOH	5.2	27080	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26992000	PP 5324		response regulator receiver protein	1.1	5.74E-01	7,5g BuOH	8.9	31770	7	Cytoplasmic	COG2204	Signal transduction mechanisms	

26992001	PP_5325	phoU	phosphate transporter PhoU	1.3	1.86E-01	0,75g BuOH	5.0	28893	5	Cytoplasmic	COG0704	Inorganic ion transport and metabolism			
26992005	PP_5329	pstS	phosphate ABC transporter phosphate-binding protein	1.5	1.09E-01	7,5g BuOH	9.4	34955	7	Cytoplasmic Membrane	COG0226	Inorganic ion transport and metabolism			
26992008	PP_5332		aldose 1-epimerase	1.1	6.37E-01	0,75g BuOH	4.7	33226	5	Cytoplasmic	COG0676	Carbohydrate transport and metabolism			
26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.0	8.34E-01	7,5g BuOH	5.2	38702	4	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism			
26992014	PP_5338	aspA	aspartate ammonia-lyase	1.6	7.24E-01	0,75g BuOH	5.9	51562	5	Cytoplasmic	COG1027	Amino acid transport and metabolism			
26992017	PP_5341		ABC transporter periplasmic polyamine-binding protein	1.0	7.54E-01	7,5g BuOH	8.8	40667	5	Periplasmic	COG0687	Amino acid transport and metabolism			
26992021	PP_5345		acetyltransferase	1.5	1.77E-01	0,75g BuOH	6.0	25042	6	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.3	6.94E-02	0,75g BuOH	5.3	65626	32	Cytoplasmic	COG5016	Energy production and conversion			
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	2.9	4.16E-02	0,75g BuOH	6.5	51942	23	Cytoplasmic	COG0439	Lipid metabolism			
26992028	PP_5352	uvrD	DNA-dependent helicase II	2.2	2.91E-01	0,75g BuOH	6.2	81692	4	Cytoplasmic	COG0210	DNA replication, recombination, and repair			
26992029	PP_5353		hypothetical protein	1.4	2.40E-01	0,75g BuOH	7.2	30672	4	Cytoplasmic Membrane	COG4395	Function unknown			
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	2.2	2.97E-02	0,75g BuOH	5.9	48114	2	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane			
26992070	PP_5395		hypothetical protein	1.0	9.42E-01	0,75g BuOH	5.6	31623	13	Cytoplasmic	COG1568	General function prediction only			
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	2.0	5.60E-01	0,75g BuOH	6.0	66312	4	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane			
26992086	PP_5411	glmU	UDP-N-acetylglucosamine pyrophosphorylase	2.1	1.19E-01	0,75g BuOH	6.7	48471	8	Cytoplasmic	COG1207	Cell envelope biogenesis, outer membrane			
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.3	2.09E-01	7,5g BuOH	4.6	49359	52	Cytoplasmic	COG0055	Energy production and conversion			
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.6	7.67E-02	7,5g BuOH	9.2	31464	16	Cytoplasmic	COG0224	Energy production and conversion			
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.3	2.44E-01	0,75g BuOH	5.2	55352	39	Cytoplasmic	COG0056	Energy production and conversion			
26992091	PP_5416	atpH	F0F1 ATP synthase subunit delta	1.7	9.12E-02	7,5g BuOH	5.7	19197	5	Cytoplasmic	COG0712	Energy production and conversion			
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.6	1.57E-01	7,5g BuOH	5.3	16898	4	Cytoplasmic Membrane	COG0711	Energy production and conversion			
148545375	Pput_0118		hypothetical protein	1.1	5.65E-01	0,75g BuOH	4.7	23815	2	Cytoplasmic					
148545499	Pput_0243		Serine O-acetyltransferase	1.2	4.88E-01	0,75g BuOH	6.8	33529	3	Cytoplasmic	COG1045	Amino acid transport and metabolism			
148545524	Pput_0268		phosphoenolpyruvate carboxykinase	1.3	2.85E-01	0,75g BuOH	5.0	55582	20	Cytoplasmic	COG1866	Energy production and conversion			
148545739	Pput_0487	rplC	50S ribosomal protein L3	2.4	7.99E-02	0,75g BuOH	10.7	22603	9	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis			
148545811	Pput_0561		1-deoxy-D-xylulose-5-phosphate synthase	2.4	7.53E-02	0,75g BuOH	5.9	68154	5	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism		
148546138	Pput_0894		ornithine decarboxylase	2.0	1.42E-02	7,5g BuOH	4.7	43509	8	Cytoplasmic	COG0019	Amino acid transport and metabolism			
148546274	Pput_1031		RNA polymerase sigma factor	1.5	4.75E-01	7,5g BuOH	9.0	21796	2	Cytoplasmic	COG1595	Transcription			
148546787	Pput_1548		TPR repeat-containing protein	13.7	2.17E-02	7,5g BuOH	4.8	43184	9	Cytoplasmic Membrane	COG4235	Posttranslational modification, protein turnover, chaperones			
148547528	Pput_2307		hypothetical protein	1.4	3.63E-01	0,75g BuOH	7.4	58966	7	Periplasmic					
148547837	Pput_2621		hypothetical protein	12.0	8.88E-02	7,5g BuOH	5.2	28589	2	Cytoplasmic					
148548678	Pput_3470	tig	trigger factor	1.4	1.09E-01	7,5g BuOH	4.5	48459	26	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones			
148549194	Pput_3988		pseudouridine synthase	2.8	1.12E-01	0,75g BuOH	7.0	23909	2	Cytoplasmic	COG0564	Translation, ribosomal structure and biogenesis			
148549226	Pput_4020		phospholipid/glycerol acyltransferase	19.1	8.29E-01	7,5g BuOH	9.4	68479	1	Cytoplasmic Membrane	COG0204	Lipid metabolism			
148549381	Pput_4175	fabZ	(3R)-hydroxymyristoyl-ACP dehydratase	1.0	8.84E-01	0,75g BuOH	6.8	16583	5	Cytoplasmic	COG0764	Lipid metabolism			
148549632	Pput_4430		ATP-dependent RNA helicase RhlB	4.2	5.52E-02	0,75g BuOH	8.4	53170	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription		
148549970	Pput_4768		HflK protein	1.1	7.35E-01	7,5g BuOH	5.2	43479	18	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones			
148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	1.3	7.16E-01	7,5g BuOH	5.4	51447	31	Cytoplasmic	COG0499	Coenzyme metabolism			
24986476		Pseudomonas putida KT2440	carbamoyl-phosphate synthase, large subunit	1.4	7.04E-01	7,5g BuOH			48						
24983268		Pseudomonas putida KT2440	ribosomal protein S1	1.0	9.67E-01	7,5g BuOH			36						
313499732		Pseudomonas putida BIRD-1	Gap 2	1.3	5.34E-02	7,5g BuOH			29						
314498081		Pseudomonas putida BIRD-1	D-hydantoinase/dihydropyrimidinase	1.1	7.41E-01	0,75g BuOH			31						
24982804		Pseudomonas putida KT2440	preprotein translocase, SecA subunit	1.1	5.98E-01	0,75g BuOH			22						
313496770		Pseudomonas putida BIRD-1	LPS-assembly protein lptD	1.8	2.60E-01	7,5g BuOH			19						
315649711		Paenibacillus vortex V453	DNA-directed RNA polymerase subunit beta	8.0	2.34E-01	0,75g BuOH			14						
152973457		Klebsiella pneumoniae subsp. pneumoniae MGH 78578	ATPase with chaperone activity, ATP-binding subunit	3.2	8.32E-01	0,75g BuOH			13						
254522278		Stenotrophomonas sp. SKA14	Oar protein	1.7	3.28E-01	7,5g BuOH			13						
377576294		Escherichia hermannii NBRC 105704	hypothetical protein YedS	4.8	6.00E-01	0,75g BuOH			13						
24981839		Pseudomonas putida KT2440	ribosomal protein S3	1.7	8.91E-02	0,75g BuOH			13						
24987101		Pseudomonas putida KT2440	conserved hypothetical protein TIGR00255	2.6	5.67E-02	7,5g BuOH			14						
354585434		Paenibacillus lactis 154	DNA-directed RNA polymerase, beta' subunit	7.7	1.64E-01	0,75g BuOH			11						
254521045		Stenotrophomonas sp. SKA14	TonB-dependent receptor domain protein	4.1	1.85E-01	7,5g BuOH			12						
190575345		Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	2.3	4.70E-01	7,5g BuOH			12						
377579435		Escherichia hermannii NBRC 105704	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	69.6	6.36E-01	0,75g BuOH			10						
261409071		Paenibacillus sp. Y412MC10	chaperonin GroEL	1.1	9.48E-01	7,5g BuOH			10						
190572930		Stenotrophomonas maltophilia K279a	elongation factor Tu	6.9	3.16E-02	7,5g BuOH			10						
377576439		Escherichia hermannii NBRC 105704	galactose/methyl-galactoside ABC transporter substrate binding periplasmic protein	2.5	9.01E-01	0,75g BuOH			10						
377579124		Escherichia hermannii NBRC 105704	malate dehydrogenase	2.4	9.66E-01	0,75g BuOH			10						
377576277		Escherichia hermannii NBRC 105704	outer membrane protein A	3.1	8.07E-01	0,75g BuOH			10						
354585430		Paenibacillus lactis 154	translation elongation factor G	2.2	7.88E-01	0,75g BuOH			9						
190574492		Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	1.1	4.90E-01	7,5g BuOH			9						
261406039		Paenibacillus sp. Y412MC10	stage IV sporulation protein A	2.9	6.64E-01	0,75g BuOH			9						
308070977		Paenibacillus polymyxa E681	Elongation factor Tu (EF-Tu)	1.7	5.13E-01	0,75g BuOH			10						
313498324		Pseudomonas putida BIRD-1	Ribosyldihydronicotinamide dehydrogenase (quinone)	1.7	1.83E-01	0,75g BuOH			9						
24981833		Pseudomonas putida KT2440	ribosomal protein L3	1.2	6.05E-01	0,75g BuOH			8						
254521740		Stenotrophomonas sp. SKA14	TonB-dependent outer membrane receptor	6.1	7.46E-02	7,5g BuOH			8						
261409551		Paenibacillus sp. Y412MC10	ATPase AAA-2 domain-containing protein	2.5	9.76E-01	7,5g BuOH			8						
190572988		Stenotrophomonas maltophilia K279a	outer membrane protein	2.5	2.50E-01	7,5g BuOH			8						
156935823		Cronobacter sakazakii ATCC BAA-894	elongation factor Tu	1.8	4.07E-01	0,75g BuOH			8						
24982353		Pseudomonas putida KT2440	rod shape-determining protein MreB	1.0	8.58E-01	0,75g BuOH			8						
16801615		Listeria innocua Clip11262	glyceraldehyde-3-phosphate dehydrogenase	1.3	7.19E-01	0,75g BuOH			7						
298682197		Pseudomonas putida DOT-T1E	hypothetical protein	3.0	2.64E-02	7,5g BuOH			7						
24981896		Pseudomonas putida KT2440	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	2.5	5.16E-02	0,75g BuOH			7						
377579693		Escherichia hermannii NBRC 105704	maltoporin	276.5	1.81E-01	0,75g BuOH			7						
377578292		Escherichia hermannii NBRC 105704	elongation factor G	4.2	5.21E-01	0,75g BuOH			6						
377578621		Escherichia hermannii NBRC 105704	phosphoenolpyruvate carboxylase	46.1	3.73E-01	0,75g BuOH			6						
334137473		Paenibacillus sp. HGF7	chaperonin GroL	2.7	5.14E-01	0,75g BuOH			6						
344209060		Stenotrophomonas maltophilia JV3	60 kDa chaperonin	10.7	3.05E-02	7,5g BuOH			7						
190572101		Stenotrophomonas maltophilia K279a	biopolymer transport exbB protein	1.9	1.97E-01	7,5g BuOH			7						
377578145		Escherichia hermannii NBRC 105704	glutamate/aspartate ABC transporter substrate binding periplasmic protein	2.5	8.45E-01	0,75g BuOH			6						
296102816		Enterobacter cloacae subsp. cloacae ATCC 13047	glyceraldehyde-3-phosphate dehydrogenase	10.3	1.79E-01	0,75g BuOH			6						
344206052		Stenotrophomonas maltophilia JV3	alpha/beta hydrolase fold domain-containing protein	37.7	2.76E-01	7,5g BuOH			6						
261407950		Paenibacillus sp. Y412MC10	30S ribosomal protein S2	1.1	7.71E-01	0,75g BuOH			6						
377576845		Escherichia hermannii NBRC 105704	ribose ABC transporter substrate binding periplasmic protein	1.8	9.63E-01	0,75g BuOH			6						
377576355		Escherichia hermannii NBRC 105704	arginine ABC transporter substrate binding protein ArtJ	6.9	4.42E-01	0,75g BuOH			6						
315649653		Paenibacillus vortex V453	Phosphoenolpyruvate carboxylase	1.3	5.84E-01	0,75g BuOH			5						
377578099		Escherichia hermannii NBRC 105704	2-oxoglutarate dehydrogenase E1 component	12.0	3.49E-01	0,75g BuOH			5						
315646628		Paenibacillus vortex V453	catalytic domain of components of various dehydrogenase complexes	3.0	4.36E-01	0,75g BuOH			5						
377576497		Escherichia hermannii NBRC 105704	hypothetical protein EH105704_01_06580	311.8	1.09E-01	0,75g BuOH			5						
16804497		Listeria monocytogenes EGD-e	glyceraldehyde-3-phosphate dehydrogenase	2.0	9.74E-01	7,5g BuOH			5						
104780459		Pseudomonas entomophila L48	peptide chain release factor 2	3.3	4.66E-02	0,75g BuOH			5						
260597147		Cronobacter turicensis z3032	phosphoglyceromutase	3.0	7.24E-01	0,75g BuOH			5						
377577374		Escherichia hermannii NBRC 105704	glutamine ABC transporter substrate binding periplasmic protein	1.9	6.50E-01	0,75g BuOH			5						
377579911		Escherichia hermannii NBRC 105704	30S ribosomal protein S4	6.7	5.88E-01	0,75g BuOH			5						
377579920		Escherichia hermannii NBRC 105704	50S ribosomal protein L6	8.2	4.79E-01	0,75g BuOH			5						
259906930		Erwinia pyrifoliae Ep1/96	DNA-directed RNA polymerase subunit beta'	1.1	6.77E-01	0,75g BuOH			4						
344208107		Stenotrophomonas maltophilia JV3	TonB-dependent receptor	3.8	2.02E-01	7,5g BuOH			4						
261409528		Paenibacillus sp. Y412MC10	DNA-directed RNA polymerase subunit beta'	1.5	6.47E-01	0,75g BuOH			4						
24983623		Pseudomonas putida KT2440	conserved hypothetical protein	3.4	5.09E-02	0,75g BuOH			4						
194366647		Stenotrophomonas maltophilia R551-3	endothelin-converting enzyme 1	371.8	3.63E-02	7,5g BuOH			4						
354582092		Paenibacillus lactis 154	dihydroxy-acid dehydratase	1.5	5.32E-01	0,75g BuOH			4						
261405767		Paenibacillus sp. Y412MC10	acetyl-CoA synthetase	1.5	4.78E-01	0,75g BuOH			4						
251794236		Escherichia hermannii sp. JDR-2	extracellular solute-binding protein	3.1	1.80E-01	0,75g BuOH			4						
377577662		Escherichia hermannii NBRC 105704	dipeptide ABC transporter substrate binding periplasmic protein	3.2	8.54E-01	0,75g BuOH			4						
308071147		Paenibacillus polymyxa E681	ATP synthase subunit beta	2.3	6.62E-01	0,75g BuOH			4						
283787348		Citrobacter rodentium ICC168	elongation factor Tu	11.6	9.59E-01	0,75g BuOH			4						
354586098		Paenibacillus lactis 154	enolase	1.1	9.04E-01	0,75g BuOH			4						
261406245		Paenibacillus sp. Y412MC10	pyruvate dehydrogenase E1 component subunit alpha	6.7	2.33E-01	0,75g BuOH			4						
377577317		Escherichia hermannii NBRC 105704	enolase	3.4	7.75E-01	0,75g BuOH			4						
377578097		Escherichia hermannii NBRC 105704	succinyl-CoA ligase subunit beta	15.7	1.42E-01	0,75g BuOH			4						
308068146		Paenibacillus polymyxa E681	ketol-acid reductoisomerase	3.2	5.96E-01	0,75g BuOH			4						
253576477		Paenibacillus sp. oral taxon 786 str. D14	periplasmic binding protein/LacI transcriptional regulator	1.6	5.79E-01	7,5g BuOH			4						
354581590		Paenibacillus lactis 154	succinyl-CoA synthetase, beta subunit	8.8	2.09E-01	0,75g BuOH			4						
377576216		Escherichia hermannii NBRC 105704	putative ABC transporter substrate binding periplasmic protein	6.6	5.95E-01	0,75g BuOH			5						
261823229		Pectobacterium wasabiae WPP163	50S ribosomal protein L2	58.4	4.07E-01	0,75g BuOH			4						
377576662		Escherichia hermannii NBRC 105704	cysteine synthase A	3.6	6.94E-01	0,75g BuOH			4						
377578749		Escherichia hermannii NBRC 105704	D-methionine ABC transporter substrate binding periplasmic protein	7.2	8.85E-01	0,75g BuOH			4						
24982449		Pseudomonas putida KT2440	transcriptional regulator HexR	5.5	7.67E-04	0,75g BuOH			4						

269200099	Pseudomonas putida DOT-T1E	hypothetical protein		1.2	5.67E-01	0,75g BuOH	4
377578821	Escherichia hermannii NBRC 105704	putative tellurium resistance protein		3.6	4.82E-01	0,75g BuOH	4
338780844	Achromobacter xylosoxidans AXX-A	outer membrane porin protein 1		8.1	4.15E-01	7,5g BuOH	4
377577075	Escherichia hermannii NBRC 105704	aspartokinase/homoserine dehydrogenase ThrA		37.2	7.92E-01	0,75g BuOH	3
190575057	Stenotrophomonas maltophilia K279a	NAD-dependent glutamate dehydrogenase		9.6	2.12E-01	7,5g BuOH	3
253575833	Paenibacillus sp. oral taxon 786 str. D14	iron-containing alcohol dehydrogenase		7.6	3.26E-01	0,75g BuOH	3
365846643	Yokenella regensburgei ATCC 43003	pyruvate dehydrogenase (acetyl-transferring), homodimeric type		3.5	5.88E-01	0,75g BuOH	3
377577022	Escherichia hermannii NBRC 105704	translation initiation factor IF-2		19.6	5.70E-01	0,75g BuOH	3
261408990	Paenibacillus sp. Y412MC10	transketolase		6.1	9.92E-02	0,75g BuOH	3
253573723	Paenibacillus sp. oral taxon 786 str. D14	butyryl-CoA dehydrogenase		3.6	4.42E-01	0,75g BuOH	3
260599976	Cronobacter turicensis z3032	glutamine synthetase		4.6	2.35E-01	0,75g BuOH	3
251796218	Paenibacillus sp. JDR-2	chaperone protein DnaK		2.1	2.74E-01	7,5g BuOH	3
374322939	Paenibacillus terrae HPL-003	acetolactate synthase large subunit		17.4	5.71E-02	0,75g BuOH	3
261406205	Paenibacillus sp. Y412MC10	glutamine synthetase		1.6	2.67E-01	0,75g BuOH	3
308069292	Paenibacillus polymyxa E681	dihydrolipoyl dehydrogenase (E3 component of pyruvate complex)		8.1	6.82E-02	0,75g BuOH	3
357011295	Paenibacillus elgii B69	family 1 extracellular solute-binding protein		1.1	6.85E-01	7,5g BuOH	3
320539767	Serratia symbiotica str. Tucson	F1 sector of membrane-bound ATP synthase, alpha subunit		5.1	6.46E-01	0,75g BuOH	2
375309808	Paenibacillus sp. Aloe-11	flotillin		1.7	5.46E-01	0,75g BuOH	3
190573698	Stenotrophomonas maltophilia K279a	phosphopyruvate hydratase		19.4	1.35E-01	7,5g BuOH	2
261409493	Paenibacillus sp. Y412MC10	DNA-directed RNA polymerase subunit alpha		3.6	2.91E-01	0,75g BuOH	3
152971407	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	serine hydroxymethyltransferase		22.7	7.29E-01	0,75g BuOH	4
261407994	Paenibacillus sp. Y412MC10	succinyl-CoA synthetase subunit beta		1.3	4.99E-01	0,75g BuOH	2
190575684	Stenotrophomonas maltophilia K279a	type II citrate synthase		15.0	3.68E-02	7,5g BuOH	3
377578400	Escherichia hermannii NBRC 105704	branched-chain amino acid ABC transporter substrate binding periplasmic protein		5.5	5.24E-01	0,75g BuOH	3
350548353				5.8	7.14E-01	0,75g BuOH	3
253576842	Paenibacillus sp. oral taxon 786 str. D14	cysteine synthase A		1.0	6.94E-01	7,5g BuOH	4
24985446	Pseudomonas putida KT2440	shikimate 5-dehydrogenase/quinate 5-dehydrogenase family protein		3.0	1.44E-02	0,75g BuOH	3
308070978	Paenibacillus polymyxa E681	elongation factor G		10.0	4.23E-01	7,5g BuOH	3
317046845	Pantoea sp. At-9b	transaldolase		5.0	6.62E-01	0,75g BuOH	3
354723915	Enterobacter mori LMG 25706	ATP phosphoribosyltransferase		9.7	2.13E-01	0,75g BuOH	3
15599454	Pseudomonas aeruginosa PAO1	50S ribosomal protein L22		3.8	2.28E-01	7,5g BuOH	3
156935819	Cronobacter sakazakii ATCC BAA-894	50S ribosomal protein L1		10.2	1.38E-01	0,75g BuOH	3
354581545	Paenibacillus lactis 154	translation elongation factor Ts		1.7	9.68E-01	7,5g BuOH	3
24986054	Pseudomonas putida KT2440	ParA family protein		3.0	1.44E-01	0,75g BuOH	3
304404108	Paenibacillus curdlanolyticus YK9	ribosomal protein S4		4.1	3.75E-01	0,75g BuOH	3
354582719	Paenibacillus lactis 154	3-isopropylmalate dehydratase, small subunit		3.2	2.87E-01	0,75g BuOH	3
260595953	Cronobacter turicensis z3032	superoxide dismutase		4.6	3.82E-01	0,75g BuOH	3
313497709	Pseudomonas putida BIRD-1	SuaS/YciO/YrdC/YwlC family protein		3.1	9.05E-02	0,75g BuOH	3
377576376	Escherichia hermannii NBRC 105704	putative glutathione S-transferase YliJ		3.1	3.20E-01	0,75g BuOH	3
123440765	Yersinia enterocolitica subsp. enterocolitica 8081	adenylosuccinate synthetase		1.4	3.62E-01	7,5g BuOH	3
293604168	Achromobacter piechaudii ATCC 43553	outer membrane protein A		29.9	7.96E-01	7,5g BuOH	2
285017314	Xanthomonas albilineans GPE PC73	DNA-directed RNA polymerase, subunit Beta-prime protein		9.4	5.35E-02	7,5g BuOH	2
377577602	Escherichia hermannii NBRC 105704	glucose-specific phosphotransferase system enzyme IICB component		79.6	4.68E-01	0,75g BuOH	2
308067011	Paenibacillus polymyxa E681	glyceraldehyde-3-phosphate dehydrogenase		9.3	2.79E-01	7,5g BuOH	2
226944437	Azotobacter vinelandii DJ	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase		3.2	6.42E-01	0,75g BuOH	1
192360633	Cellvibrio japonicus Ueda107	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase		165.9	9.09E-03	7,5g BuOH	1
331702721	Pseudomonas avellanae	aconitase		2.7	2.50E-01	0,75g BuOH	1
190572528	Stenotrophomonas maltophilia K279a	TonB outer membrane protein oar family		4.8	2.93E-01	7,5g BuOH	2
374605319	Paenibacillus dendritiformis C454	aconitate hydratase 1		11.4	9.42E-01	0,75g BuOH	2
260451185	Escherichia coli DH1	DNA-directed RNA polymerase, beta' subunit		32.7	6.63E-01	0,75g BuOH	2
167465045				3.4	8.68E-01	0,75g BuOH	2
330501406	Pseudomonas mendocina NK-01	transketolase		1.0	8.93E-01	7,5g BuOH	2
375307378	Paenibacillus sp. Aloe-11	peptide ABC transporter		2.7	9.83E-01	7,5g BuOH	2
354580128	Paenibacillus lactis 154	putative serine protein kinase, PrkA		1.4	5.90E-01	0,75g BuOH	2
190572301	Stenotrophomonas maltophilia K279a	peptidyl-dipeptidase Dcp		16.7	1.42E-01	7,5g BuOH	2
377577192	Escherichia hermannii NBRC 105704	transketolase TktA		5.1	5.24E-01	0,75g BuOH	2
251797391	Paenibacillus sp. JDR-2	polyribonucleotide nucleotidyltransferase		9.1	8.73E-01	0,75g BuOH	2
293604988	Achromobacter piechaudii ATCC 43553	methyl-accepting chemotaxis protein I		1.4	6.35E-01	7,5g BuOH	2
317054845	Ruminococcus albus 7	chaperonin GroEL		1.0		-	0
261409679	Paenibacillus sp. Y412MC10	ATP synthase F1 subunit alpha		5.9	8.00E-01	0,75g BuOH	1
261407922	Paenibacillus sp. Y412MC10	beta-lactamase domain-containing protein		11.8	2.71E-01	0,75g BuOH	2
222106811	Agrobacterium vitis S4	chaperonin GroEL	Infinity		1.36E-01	7,5g BuOH	2
168335361	Epulopiscium sp. 'N.t. morphotype B'	ABC transporter related protein		5.5	3.11E-01	0,75g BuOH	2
317405440	Achromobacter xylosoxidans C54	chaperonin		18.4	8.78E-01	7,5g BuOH	1
302870826	Caldicellulosiruptor obsidiansis OB47	ABC transporter-like protein		1.3	6.74E-01	0,75g BuOH	2
197285722	Proteus mirabilis HI4320	serine hydroxymethyltransferase	Infinity		3.74E-01	7,5g BuOH	1
359781137	Pseudomonas psychrotolerans L19	F0F1 ATP synthase subunit alpha		5.4	9.20E-01	0,75g BuOH	1
251797795	Paenibacillus sp. JDR-2	6-phosphogluconate dehydrogenase		2.5	1.07E-01	0,75g BuOH	2
251796396	Paenibacillus sp. JDR-2	RNA binding S1 domain-containing protein		1.7	6.87E-01	0,75g BuOH	2
337750195	Paenibacillus mucilaginosus KNP414	ABC transporter substrate-binding protein		1.9	6.58E-01	7,5g BuOH	2
119944441	Psychromonas ingrahamii 37	phosphopyruvate hydratase		9.3	7.40E-01	0,75g BuOH	1
261342208	Enterobacter cancerogenus ATCC 35316	phosphopyruvate hydratase		8.6	8.85E-01	0,75g BuOH	1
260597119	Cronobacter turicensis z3032	type II citrate synthase		2.2	8.72E-01	7,5g BuOH	2
261409688	Paenibacillus sp. Y412MC10	glycine hydroxymethyltransferase		2.8	3.73E-01	0,75g BuOH	2
261409360	Paenibacillus sp. Y412MC10	O-acetylhomoserine aminocarboxypropyltransferase		2.0	4.93E-01	0,75g BuOH	2
308068359	Paenibacillus polymyxa E681	isocitrate dehydrogenase		1.7	8.73E-01	0,75g BuOH	2
37526691	Photorhabdus luminescens subsp. laumondii TTO1	isocitrate dehydrogenase		4.3	3.04E-02	0,75g BuOH	2
212640607	Anoxybacillus flavithermus WK1	L-alanine dehydrogenase		65.6	1.06E-01	0,75g BuOH	2
261404073	Paenibacillus sp. Y412MC10	phosphoglycerate kinase		2.3	5.32E-01	0,75g BuOH	2
377578625	Escherichia hermannii NBRC 105704	argininosuccinate synthase		48.8	4.47E-01	0,75g BuOH	2
261821375	Pectobacterium wasabiae WPP163	aspartyl-tRNA synthetase		5.4	3.21E-01	7,5g BuOH	2
190572099	Stenotrophomonas maltophilia K279a	hypothetical protein Smlt0008		25.1	2.69E-01	7,5g BuOH	2
261404510	Paenibacillus sp. Y412MC10	sulfate ABC transporter periplasmic sulfate-binding protein		2.9	3.44E-01	0,75g BuOH	2
190572978	Stenotrophomonas maltophilia K279a	malate dehydrogenase		30.2	4.01E-02	7,5g BuOH	2
308067147	Paenibacillus polymyxa E681	manganese-dependent inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase)		1.1	6.20E-01	0,75g BuOH	2
374323041	Paenibacillus terrae HPL-003	Vegetative protein 296 (VEG296)		1.6	4.83E-01	0,75g BuOH	2
269200087	Pseudomonas putida DOT-T1E	putative KspF/GutQ family protein		2.6	3.18E-02	0,75g BuOH	2
261409518	Paenibacillus sp. Y412MC10	50S ribosomal protein L2		1.4	6.58E-01	0,75g BuOH	2
253577368	Paenibacillus sp. oral taxon 786 str. D14	fructose-1,6-bisphosphate aldolase, class II		1.2	6.67E-01	7,5g BuOH	2
377579828	Escherichia hermannii NBRC 105704	outer membrane pore protein E		14.7	2.19E-01	0,75g BuOH	2
24986578	Pseudomonas putida KT2440	ribosomal protein L11 methyltransferase		1.1	6.52E-01	0,75g BuOH	2
190576298	Stenotrophomonas maltophilia K279a	TonB dependent receptor protein		2.4	1.76E-01	7,5g BuOH	1
113460341	Haemophilus somnus 129PT	elongation factor Tu		5.4	7.47E-01	0,75g BuOH	2
194366390	Stenotrophomonas maltophilia R551-3	FKBP-type peptidylprolyl isomerase		23.9	1.69E-02	7,5g BuOH	2
260551344	Acinetobacter sp. RUH2624	membrane-bound ATP synthase F1 sector		5.1	1.83E-01	7,5g BuOH	2
354585439	Paenibacillus lactis 154	ribosomal protein L1		1.5	7.90E-01	0,75g BuOH	2
116667412		Chain C, Structure Of The 30s Subunit Of A Pre-Translocational E. Coli Ribosome Obtained By Fitting Atomic Models For Rna And Protein Components Into Cryo-Em Map Emd-1056		353.7	5.69E-02	0,75g BuOH	2
190575561	Stenotrophomonas maltophilia K279a	peptidoglycan-associated lipoprotein		2.9	1.76E-01	7,5g BuOH	2
261338832	Enterobacter cancerogenus ATCC 35316	hypothetical protein ENTCAN_05027		1.8	8.02E-01	0,75g BuOH	2
377576592	Escherichia hermannii NBRC 105704	histidine ABC transporter substrate binding periplasmic protein		5.7	4.86E-01	0,75g BuOH	2
15836991	Xylella fastidiosa 9a5c	two-component system, regulatory protein		2.8	3.04E-01	7,5g BuOH	2
260770896	Vibrio furnissii CIP 102972	cyclic AMP receptor protein		4.0	2.03E-01	0,75g BuOH	2
261407949	Paenibacillus sp. Y412MC10	translation elongation factor Ts		1.1	8.05E-01	0,75g BuOH	2
167464877				1.6	6.59E-01	0,75g BuOH	2
24982083	Pseudomonas putida KT2440	ribosomal protein L21		1.2	3.32E-01	0,75g BuOH	2
135596		RecName: Full=Tellurium resistance protein TerD		5.5	1.63E-01	0,75g BuOH	2
190575124	Stenotrophomonas maltophilia K279a	superoxide dismutase		4.7	6.70E-02	7,5g BuOH	2
323357360	Microbacterium testaceum StLB037	50S ribosomal protein L5		1.6	2.10E-01	0,75g BuOH	2
152973456	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	molecular chaperone (small heat shock protein)		1.7	4.95E-01	0,75g BuOH	2
194364650	Stenotrophomonas maltophilia R551-3	3-ketoacyl-ACP reductase		3.9	1.05E-01	7,5g BuOH	2
261341225	Enterobacter cancerogenus ATCC 35316	peroxiredoxin		4.6	4.08E-01	0,75g BuOH	2
190574022	Stenotrophomonas maltophilia K279a	transmembrane protein		249.1	6.80E-02	7,5g BuOH	2
190573688	Stenotrophomonas maltophilia K279a	pit accessory protein		67.4	1.65E-01	7,5g BuOH	2
190575505	Stenotrophomonas maltophilia K279a	TetR family transcriptional regulator		7.0	1.19E-01	7,5g BuOH	2

5.2.3.3 GeLCMSMS_P_putida_KT2440_0.75g_BuOH_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986746	PP_0001	parB	parB-like partition protein	1.1	6.07E-01	0,75 g/l BuOH	6.5	32390	9	Cytoplasmic	COG1475	Transcription	
26986747	PP_0002		ParA family protein	1.1	9.61E-01	0,75 g/l BuOH	6.7	28919	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
26986748	PP_0003	gidB	16S rRNA methyltransferase GidB	1.4	1.71E-01	0,75 g/l BuOH	7.1	24063	2	Unknown	COG0357	Cell envelope biogenesis, outer membrane	
26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	1.5	9.83E-02	0,75 g/l BuOH	6.4	69567	3	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.4	1.16E-01	0,75 g/l BuOH	9.1	61919	10	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986755	PP_0010	dnaA	chromosomal replication initiation protein	1.6	4.43E-01	Control	8.3	56473	2	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.2	2.38E-01	0,75 g/l BuOH	4.9	40718	13	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.0	9.98E-01	0,75 g/l BuOH	5.8	90030	22	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.4	3.14E-01	0,75 g/l BuOH	6.1	31236	13	Cytoplasmic			
26986764	PP_0019		hypothetical protein	1.8	1.84E-01	0,75 g/l BuOH	4.8	24854	3	Unknown			
26986765	PP_0020		hypothetical protein	1.2	1.27E-01	0,75 g/l BuOH	4.9	33146	5	Cytoplasmic			
26986774	PP_0029	czrR-1	DNA-binding response regulator CzrR	1.1	9.41E-01	Control	6.1	25537	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.1	6.84E-01	Control	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.2	6.88E-01	0,75 g/l BuOH	4.9	75112	16	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.0	7.21E-01	0,75 g/l BuOH	4.8	36024	4	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986808	PP_0063		lipid A biosynthesis lauroyl acyltransferase	1.2	5.33E-01	Control	10.1	32840	2	Cytoplasmic Membrane	COG1560	Cell envelope biogenesis, outer membrane	
26986813	PP_0068	def	peptide deformylase	1.3	4.64E-01	0,75 g/l BuOH	5.1	19410	3	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
26986815	PP_0070		Sua5/YciO/YrdC/YwlC family protein	1.0	7.35E-01	0,75 g/l BuOH	6.1	20493	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.5	6.82E-02	0,75 g/l BuOH	8.1	34224	14	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986819	PP_0074	aroE	shikimate 5-dehydrogenase	1.2	1.79E-01	0,75 g/l BuOH	5.0	29289	4	Cytoplasmic	COG0169	Amino acid transport and metabolism	
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1.3	3.76E-01	Control	5.0	28482	8	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.3	1.81E-01	Control	6.4	44046	5	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986831	PP_0086		hypothetical protein	1.7	7.91E-02	0,75 g/l BuOH	7.9	7959	3	Unknown	COG3360	Function unknown	
26986839	PP_0094		HAD superfamily hydrolase	1.1	8.22E-01	0,75 g/l BuOH	5.1	24540	4	Cytoplasmic	COG0546	General function prediction only	
26986841	PP_0096	prlC	oligopeptidase A	1.1	6.28E-01	0,75 g/l BuOH	5.0	75721	21	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.0	9.83E-01	0,75 g/l BuOH	6.8	26001	18	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	1.1	7.31E-01	0,75 g/l BuOH	6.8	42059	9	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986851	PP_0106		cytochrome c oxidase, subunit III	1.1	8.09E-01	0,75 g/l BuOH	8.7	33623	3	Cytoplasmic Membrane	COG1845	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	1.3	4.49E-01	0,75 g/l BuOH	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986857	PP_0112		metal ABC transporter periplasmic protein	1.4	2.52E-01	0,75 g/l BuOH	7.8	27711	14	Cytoplasmic Membrane	COG1464	Inorganic ion transport and metabolism	
26986861	PP_0116		lipoprotein	1.2	5.16E-01	0,75 g/l BuOH	7.4	25597	6	Unknown			
26986868	PP_0123	polA	DNA polymerase I	1.6	7.47E-02	Control	5.1	99607	20	Cytoplasmic	COG0749	DNA replication, recombination, and repair	
26986869	PP_0124	engB	ribosome biogenesis GTP-binding protein YsxC	1.3	1.88E-01	0,75 g/l BuOH	9.6	23440	9	Cytoplasmic	COG0218	General function prediction only	
26986871	PP_0126		cytochrome c4	1.7	7.65E-01	Control	8.0	21260	3	Periplasmic	COG2863	Energy production and conversion	
26986872	PP_0127		DsbA family thiol:disulfide interchange protein	1.5	4.44E-01	0,75 g/l BuOH	7.1	23073	5	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
26986878	PP_0133	algB	two component, sigma54 specific, transcriptional regulator, Fis family	1.3	3.66E-01	0,75 g/l BuOH	5.4	49604	2	Cytoplasmic	COG2204	Signal transduction mechanisms	
26986884	PP_0139		lipoprotein	1.0	9.62E-01	0,75 g/l BuOH	9.5	23212	3	Unknown	COG3218	General function prediction only	
26986885	PP_0140		hypothetical protein	1.0	9.08E-01	Control	5.4	33062	4	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26986886	PP_0141		ABC transporter ATP-binding protein	1.1	9.06E-01	0,75 g/l BuOH	6.7	28270	3	Cytoplasmic Membrane	COG1127	Secondary metabolites biosynthesis, transport, and catabolism	
26986887	PP_0142		hypothetical protein	1.3	2.50E-01	Control	5.3	40379	2	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	2.0	1.04E-01	0,75 g/l BuOH	7.3	50185	2	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986902	PP_0158	gcdH	acyl-CoA dehydrogenase domain-containing protein	1.3	1.50E-01	Control	6.2	43242	4	Cytoplasmic	COG1960	Lipid metabolism	
26986909	PP_0165		GGDEF domain-containing protein	1.0	2.40E-01	0,75 g/l BuOH	6.3	71284	13	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.1	6.36E-01	0,75 g/l BuOH	7.8	51116	4	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.0	4.94E-01	Control	7.7	78583	13	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986912	PP_0168		surface adhesion protein	6.1	8.54E-03	Control	3.9	888214	21	Extracellular	COG2931	Secondary metabolites biosynthesis, transport, and catabolism	
26986917	PP_0173		transcriptional factor-related protein	1.5	4.37E-01	0,75 g/l BuOH	10.1	23493	3	Unknown			
26986927	PP_0183		glutathione S-transferase family protein	1.3	2.16E-01	0,75 g/l BuOH	5.4	24438	11	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26986928	PP_0184	argH	argininosuccinate lyase	1.2	1.12E-02	0,75 g/l BuOH	5.4	52061	15	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	1.0	8.14E-01	Control	6.5	27422	8	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
26986931	PP_0187	hemD	uroporphyrinogen-III synthase	1.3	4.42E-01	0,75 g/l BuOH	6.8	27045	2	Unknown	COG1587	Coenzyme metabolism	
26986932	PP_0188		uroporphyrin-III C-methyltransferase	1.1	4.33E-02	0,75 g/l BuOH	4.8	40556	11	Cytoplasmic Membrane	COG2959	Coenzyme metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.0	8.65E-01	0,75 g/l BuOH	9.6	46030	7	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	1.9	8.87E-01	0,75 g/l BuOH	11.3	32300	6	Cytoplasmic			
26986940	PP_0196		ABC transporter ATP-binding protein	2.9	4.59E-02	0,75 g/l BuOH	5.7	70615	6	Cytoplasmic	COG0488	General function prediction only	
26986947	PP_0203		hypothetical protein	1.1	5.68E-01	Control	5.9	62682	14	Unknown	COG0624	Amino acid transport and metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.2	1.42E-01	0,75 g/l BuOH	5.2	51549	21	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.0	9.67E-01	Control	6.1	44824	15	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986958	PP_0215		signal transduction protein	1.1	8.22E-01	0,75 g/l BuOH	7.0	45294	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
26986968	PP_0225		amino-acid ABC transporter ATP-binding protein YecC	1.1	7.52E-01	0,75 g/l BuOH	10.2	27596	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26986970	PP_0227		cystine transporter subunit	1.2	2.17E-01	0,75 g/l BuOH	8.7	28756	21	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26986977	PP_0234	oprE	outer membrane porin	1.6	1.92E-03	0,75 g/l BuOH	5.4	48317	12	Outer Membrane			
26986978	PP_0235	lsfA	peroxidase	1.6	2.14E-01	0,75 g/l BuOH	6.0	23948	9	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26986986	PP_0243	gshA	glutamate--cysteine ligase	1.3	2.10E-01	0,75 g/l BuOH	4.8	59067	6	Cytoplasmic	COG2918	Coenzyme metabolism	
26986988	PP_0245		S1 RNA-binding domain-containing protein	3.2	6.33E-02	0,75 g/l BuOH	8.7	94304	2	Cytoplasmic	COG2183	Transcription	
26986989	PP_0246	ompR	osmolarity response regulator	1.3	4.48E-01	0,75 g/l BuOH	5.9	27492	10	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26986995	PP_0252	hslO	Hsp33-like chaperonin	1.1	5.67E-01	Control	4.4	33472	6	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
26987002	PP_0260	nudE	ADP-ribose diphosphatase NudE	1.5	2.42E-01	0,75 g/l BuOH	4.5	20947	3	Cytoplasmic			
26987003	PP_0261	cysQ	3'(2'),5'-bisphosphate nucleotidase	1.4	1.84E-01	0,75 g/l BuOH	4.3	28452	2	Cytoplasmic	COG1218	Inorganic ion transport and metabolism	
26987007	PP_0265		dTDP-4-dehydrorhamnose 3,5-epimerase	7.3	7.63E-01	Control	6.2	20315	2	Unknown	COG1898	Cell envelope biogenesis, outer membrane	
26987008	PP_0266		agmatine deiminase	1.4	4.67E-02	Control	4.7	40837	2	Cytoplasmic	COG2957	Amino acid transport and metabolism	
26987010	PP_0268	oprQ	outer membrane porin	1.5	8.67E-03	0,75 g/l BuOH	6.1	47787	11	Outer Membrane			
26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding protein	1.2	5.39E-01	0,75 g/l BuOH	5.2	27869	23	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987025	PP_0283		amino acid ABC transporter ATP-binding protein	1.3	7.03E-02	0,75 g/l BuOH	7.7	28381	6	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism	
26987029	PP_0287		AsmA family protein	1.5	2.95E-01	0,75 g/l BuOH	6.0	80277	6	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987031	PP_0289	hisB	imidazoleglycerol-phosphate dehydratase	1.4	2.44E-02	0,75 g/l BuOH	6.4	23420	5	Cytoplasmic	COG0131	Amino acid transport and metabolism	
26987032	PP_0290	hisH	imidazole glycerol phosphate synthase subunit HisH	1.4	5.85E-02	0,75 g/l BuOH	6.4	23535	6	Cytoplasmic	COG0118	Amino acid transport and metabolism	
26987034	PP_0292	hisA	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-cart	1.5	4.48E-02	0,75 g/l BuOH	4.9	25907	5	Cytoplasmic	COG0106	Amino acid transport and metabolism	
26987035	PP_0293	hisF	imidazole glycerol phosphate synthase subunit HisF	1.6	9.85E-02	0,75 g/l BuOH	5.0	27131	6	Cytoplasmic	COG0107	Amino acid transport and metabolism	
26987036	PP_0294		glycine betaine/L-proline ABC transporter ATP-binding subunit	1.2	3.87E-01	Control	7.9	43724	5	Cytoplasmic Membrane	COG4175	Amino acid transport and metabolism	
26987038	PP_0296		glycine betaine/L-proline ABC transporter periplasmic protein	1.0	9.19E-01	Control	6.6	34568	13	Unknown	COG2113	Amino acid transport and metabolism	
26987046	PP_0304		hypothetical protein	1.2	4.43E-01	Control	7.6	35771	2	Periplasmic	COG2113	Amino acid transport and metabolism	
26987050	PP_0308		membrane dipeptidase	1.5	2.35E-01	0,75 g/l BuOH	5.4	35978	2	Cytoplasmic	COG2355	Amino acid transport and metabolism	
26987063	PP_0321		threonine aldolase	1.5	9.26E-02	0,75 g/l BuOH	5.4	38068	8	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987064	PP_0322	glyA-1	serine hydroxymethyltransferase	1.2	5.52E-01	0,75 g/l BuOH	6.4	44555	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987067	PP_0325	soxA	sarcosine oxidase, alpha subunit family	2.2	1.53E-02	Control	7.6	109175	6	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987068	PP_0326	soxG	sarcosine oxidase, gamma subunit family	1.2	2.06E-01	Control	7.3	22961	5	Cytoplasmic	COG4583	Amino acid transport and metabolism	
26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	1.1	2.19E-01	Control	6.6	42328	9	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
26987077	PP_0335		glutathione S-transferase family protein	1.1	7.03E-01	Control	6.4	23174	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	1.4	2.68E-01	0,75 g/l BuOH	4.7	24565	5	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.3	7.68E-01	0,75 g/l BuOH	5.3	55654	24	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.1	3.60E-01	Control	5.6	99332	60	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.3	3.05E-02	Control	5.3	109432	19	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987086	PP_0344	waaP	lipopolysaccharide kinase	1.1	6.22E-01	Control	10.2	30807	2	Cytoplasmic			

26987089	PP_0347		hypothetical protein	1.1	6.93E-01	0,75 g/l BuOH	7.4	53779	2	Cytoplasmic		
26987098	PP_0356	glcB	malate synthase G	1.4	3.73E-01	0,75 g/l BuOH	5.8	78346	12	Cytoplasmic	COG2225	Energy production and conversion
26987099	PP_0357		ACT domain-containing protein	4.9	5.74E-01	Control	4.5	19023	2	Cytoplasmic	COG2716	Amino acid transport and metabolism
26987106	PP_0364	bioH	carboxylesterase	1.9	6.53E-02	Control	4.8	26344	3	Cytoplasmic	COG0596	General function prediction only
26987108	PP_0366	bioD	dithiobiotin synthetase	1.1	9.46E-01	0,75 g/l BuOH	5.3	23871	9	Cytoplasmic	COG0132	Coenzyme metabolism
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.0	6.50E-01	0,75 g/l BuOH	5.8	65541	24	Cytoplasmic	COG1960	Lipid metabolism
26987112	PP_0370		acyl-CoA dehydrogenase domain-containing protein	1.1	4.95E-01	Control	4.9	63592	6	Cytoplasmic	COG1960	Lipid metabolism
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	10.3	2.25E-03	0,75 g/l BuOH	6.8	29075	13	Cytoplasmic	COG5424	Coenzyme metabolism
26987121	PP_0379	pqqB	pyrroloquinoline quinone biosynthesis protein PqqB	4.4	5.27E-03	0,75 g/l BuOH	5.5	33331	5	Cytoplasmic	COG1235	General function prediction only
26987124	PP_0382		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	1.1	9.09E-01	0,75 g/l BuOH	4.9	29311	3	Cytoplasmic	COG0388	General function prediction only
26987128	PP_0386		sensory box protein	2.8	1.77E-04	Control	5.6	139392	14	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.3	6.61E-02	0,75 g/l BuOH	4.6	69396	22	Cytoplasmic	COG0568	Transcription
26987132	PP_0390	gcp	DNA-binding/iron metalloprotein/AP endonuclease	1.1	3.80E-01	Control	4.8	36606	2	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones
26987137	PP_0395		SpoVR family protein	1.1	6.63E-01	0,75 g/l BuOH	5.4	61330	13	Cytoplasmic	COG2719	Function unknown
26987138	PP_0396		hypothetical protein	1.3	9.66E-02	Control	7.0	50488	8	Cytoplasmic	COG2718	Function unknown
26987139	PP_0397		serine protein kinase, PrkA	1.1	2.50E-01	0,75 g/l BuOH	5.8	73782	45	Cytoplasmic	COG2766	Signal transduction mechanisms
26987143	PP_0401	ksgA	dimethyladenosine transferase	1.0	7.68E-01	0,75 g/l BuOH	8.5	29666	2	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis
26987145	PP_0403	surA	survival protein SurA	1.3	1.86E-01	0,75 g/l BuOH	5.2	49082	12	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones
26987146	PP_0405		aminoglycoside phosphotransferase	1.1	8.10E-01	0,75 g/l BuOH	4.8	38238	2	Cytoplasmic	COG3178	General function prediction only
26987147	PP_0406		nucleotidyl transferase	1.0	8.79E-01	0,75 g/l BuOH	6.0	23814	4	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane
26987151	PP_0410	uhpA	LuxR family two component transcriptional regulator	1.5	6.67E-02	0,75 g/l BuOH	7.2	22750	3	Cytoplasmic	COG2197	Signal transduction mechanisms
26987153	PP_0412		polyamine ABC transporter periplasmic protein	1.1	2.01E-01	0,75 g/l BuOH	5.3	37801	12	Periplasmic	COG0687	Amino acid transport and metabolism
26987156	PP_0415	rpe	ribulose-phosphate 3-epimerase	1.4	4.60E-01	0,75 g/l BuOH	5.6	27672	4	Cytoplasmic	COG0036	Carbohydrate transport and metabolism
26987158	PP_0417	trpE	anthranilate synthase component I	1.3	6.61E-03	0,75 g/l BuOH	4.8	54406	13	Cytoplasmic	COG0147	Amino acid transport and metabolism
26987161	PP_0420	trpG	anthranilate synthase component II	2.0	3.80E-01	0,75 g/l BuOH	6.2	21677	2	Cytoplasmic	COG0512	Amino acid transport and metabolism
26987162	PP_0421	trpD	anthranilate phosphoribosyltransferase	1.7	8.50E-02	0,75 g/l BuOH	5.6	37245	5	Cytoplasmic	COG0547	Amino acid transport and metabolism
26987163	PP_0422	trpC	indole-3-glycerol-phosphate synthase	1.2	3.39E-01	0,75 g/l BuOH	4.7	30433	9	Cytoplasmic	COG0134	Amino acid transport and metabolism
26987171	PP_0430		hypothetical protein	1.5	1.89E-02	Control	6.7	33680	3	Unknown	COG2070	General function prediction only
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.1	8.43E-01	0,75 g/l BuOH	6.8	36277	11	Cytoplasmic	COG0002	Amino acid transport and metabolism
26987175	PP_0434	anmK	anhydro-N-acetylmuramic acid kinase	2.7	5.85E-02	0,75 g/l BuOH	5.8	38235	3	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones
26987177	PP_0436	tyrS	tyrosyl-tRNA synthetase	1.4	2.15E-01	0,75 g/l BuOH	5.5	44287	10	Cytoplasmic	COG0162	Translation, ribosomal structure and biogenesis
26987181	PP_0440	tuf	elongation factor Tu	1.7	7.54E-02	0,75 g/l BuOH	5.0	43495	24	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis
26987183	PP_0442	nusG	transcription antitermination protein NusG	1.7	3.77E-01	0,75 g/l BuOH	6.3	20048	2	Cytoplasmic	COG0250	Transcription
26987185	PP_0444	rplA	50S ribosomal protein L1	1.2	6.06E-01	0,75 g/l BuOH	10.1	24251	18	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.3	1.73E-01	Control	5.5	150992	93	Cytoplasmic	COG0085	Transcription
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.2	4.19E-01	Control	7.2	154797	80	Cytoplasmic	COG0086	Transcription
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.4	9.09E-01	Control	10.8	17578	2	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis
26987192	PP_0451	fusA	elongation factor G	1.2	4.68E-01	0,75 g/l BuOH	4.9	78817	60	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis
26987193	PP_0452	tuf	elongation factor Tu	1.3	1.43E-01	0,75 g/l BuOH	5.0	43478	43	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis
26987196	PP_0455	rplD	50S ribosomal protein L4	1.2	6.05E-01	0,75 g/l BuOH	10.3	21811	9	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis
26987198	PP_0457	rplB	50S ribosomal protein L2	1.2	3.53E-01	Control	11.7	29669	17	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis
26987207	PP_0466	rplE	50S ribosomal protein L5	1.1	4.59E-01	0,75 g/l BuOH	10.3	20329	14	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis
26987210	PP_0469	rplF	50S ribosomal protein L6	1.3	4.17E-01	0,75 g/l BuOH	10.4	19143	12	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis
26987211	PP_0470	rplR	50S ribosomal protein L18	1.9	1.19E-01	0,75 g/l BuOH	10.9	12628	3	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.2	6.84E-01	0,75 g/l BuOH	10.6	17666	3	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.3	6.81E-02	0,75 g/l BuOH	10.4	47853	5	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.1	7.27E-01	0,75 g/l BuOH	10.5	23056	16	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.3	8.07E-02	0,75 g/l BuOH	4.7	36629	20	Cytoplasmic	COG0202	Transcription
26987223	PP_0482		bacterioferritin	2.4	7.24E-01	0,75 g/l BuOH	4.6	17972	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism
26987224	PP_0483	uvrA	excinuclease ABC subunit A	1.6	5.16E-02	Control	7.0	104378	13	Cytoplasmic	COG0178	DNA replication, recombination, and repair
26987226	PP_0485	ssb	single-stranded DNA-binding protein	1.5	5.05E-01	0,75 g/l BuOH	6.0	20059	6	Cytoplasmic	COG0629	DNA replication, recombination, and repair
26987233	PP_0493	selA	selenocysteine synthase	1.5	1.26E-01	0,75 g/l BuOH	7.7	51723	2	Cytoplasmic	COG1921	seryl-tRNASer selenium transferase
26987240	PP_0501		NAD-dependent epimerase/dehydratase	1.1	7.83E-01	0,75 g/l BuOH	5.2	33325	7	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane
26987249	PP_0510	trx-1	thioredoxin	1.3	2.77E-01	0,75 g/l BuOH	4.6	31822	6	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones
26987253	PP_0515	ribE-1	riboflavin synthase subunit alpha	1.1	6.44E-01	0,75 g/l BuOH	6.5	23597	3	Cytoplasmic	COG0307	Coenzyme metabolism
26987259	PP_0521		hypothetical protein	1.0	7.68E-01	Control	6.4	28523	3	Unknown		
26987260	PP_0522	ribA	GTP cyclohydrolase II	1.2	1.08E-01	0,75 g/l BuOH	7.0	22350	4	Cytoplasmic	COG0807	Coenzyme metabolism
26987266	PP_0528	ispA	polyprenyl synthetase	1.2	4.88E-01	0,75 g/l BuOH	4.9	31352	2	Cytoplasmic	COG0142	Coenzyme metabolism
26987276	PP_0538	ppa	inorganic pyrophosphatase	1.5	2.96E-01	0,75 g/l BuOH	4.6	19189	7	Cytoplasmic	COG0221	Energy production and conversion
26987280	PP_0542		ethanolamine ammonia-lyase small subunit	1.4	2.00E-01	Control	6.9	29573	5	Cytoplasmic	COG4302	Amino acid transport and metabolism
26987281	PP_0543	eutB	ethanolamine ammonia lyase large subunit	3.4	2.49E-01	0,75 g/l BuOH	5.0	49939	3	Cytoplasmic	COG4303	Amino acid transport and metabolism
26987283	PP_0545		aldehyde dehydrogenase family protein	1.3	2.34E-01	0,75 g/l BuOH	5.9	55268	33	Cytoplasmic	COG1012	Energy production and conversion
26987285	PP_0547	mpl	UDP-N-acetylmuramate	1.4	1.94E-01	0,75 g/l BuOH	6.1	48202	6	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane
26987288	PP_0550		hypothetical protein	1.1	5.73E-01	Control	7.6	23787	9	Cytoplasmic	COG0739	Cell envelope biogenesis, outer membrane
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.1	3.94E-01	0,75 g/l BuOH	6.5	49088	19	Cytoplasmic	COG4339	Lipid metabolism
26987297	PP_0559	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	1.9	4.93E-01	0,75 g/l BuOH	4.7	16186	5	Unknown	COG0511	Lipid metabolism
26987302	PP_0564		hypothetical protein	1.1	4.12E-01	Control	6.6	40223	6	Unknown	COG5345	Function unknown
26987305	PP_0567	speA	arginine decarboxylase	1.4	3.21E-01	Control	5.3	71043	7	Unknown	COG1166	Amino acid transport and metabolism
26987308	PP_0570		alpha-2-macroglobulin domain protein	1.6	2.22E-02	Control	5.2	178472	37	Unknown	COG2373	General function prediction only
26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.1	5.43E-01	0,75 g/l BuOH	7.5	47782	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
26987320	PP_0582		acetyl-CoA acetyltransferase	1.1	4.19E-01	0,75 g/l BuOH	8.3	45543	2	Cytoplasmic	COG0183	Lipid metabolism
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.1	5.32E-01	Control	5.0	69953	23	Cytoplasmic Membrane	COG0840	Cell motility and secretion
26987329	PP_0591	add	adenosine deaminase	1.1	6.29E-01	Control	4.8	35845	4	Cytoplasmic	COG1816	Nucleotide transport and metabolism
26987330	PP_0592		short chain dehydrogenase	1.2	9.45E-01	Control	6.0	24627	4	Extracellular	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
26987332	PP_0594		TetR family transcriptional regulator	1.2	3.13E-01	0,75 g/l BuOH	7.6	27446	2	Cytoplasmic	COG1309	Transcription
26987334	PP_0596		beta alanine--pyruvate transaminase	1.7	2.63E-01	0,75 g/l BuOH	6.8	48529	4	Cytoplasmic	COG0161	Coenzyme metabolism
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.4	2.69E-03	0,75 g/l BuOH	5.9	53498	8	Cytoplasmic	COG1012	Energy production and conversion
26987339	PP_0602	ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	1.0	9.46E-01	0,75 g/l BuOH	9.7	34827	5	Cytoplasmic	COG0196	Coenzyme metabolism
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.1	4.99E-01	Control	6.0	105800	39	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis
26987343	PP_0606	ispH	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.2	5.59E-01	Control	4.7	34543	2	Cytoplasmic	COG0761	Lipid metabolism
26987352	PP_0615		branched chain amino acid ABC transporter ATP-binding protein	1.4	1.61E-01	Control	9.6	25813	2	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism
26987359	PP_0622		competence lipoprotein ComL	1.5	1.15E-01	0,75 g/l BuOH	4.8	38410	3	Unknown	COG4105	General function prediction only
26987360	PP_0624		hypothetical protein	1.8	1.89E-01	0,75 g/l BuOH	6.1	26401	2	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.0	1.19E-01	0,75 g/l BuOH	5.2	94861	42	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
26987364	PP_0628		hypothetical protein	1.0	8.93E-01	0,75 g/l BuOH	9.1	24364	2	Cytoplasmic		
26987367	PP_0631	coaE	dephospho-CoA kinase	1.2	6.35E-01	0,75 g/l BuOH	6.6	22652	4	Cytoplasmic	COG0237	Coenzyme metabolism
26987376	PP_0640		hypothetical protein	1.5	1.97E-01	0,75 g/l BuOH	6.6	44093	4	Cytoplasmic Membrane		
26987390	PP_0654	mdh	malate dehydrogenase	1.4	4.74E-01	0,75 g/l BuOH	5.1	29434	3	Cytoplasmic	COG0039	Energy production and conversion
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.4	2.75E-01	0,75 g/l BuOH	6.2	44897	24	Cytoplasmic	COG0112	Amino acid transport and metabolism
26987408	PP_0672		sensory box protein	4.2	2.62E-02	0,75 g/l BuOH	5.7	144317	4	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26987410	PP_0674		ABC transporter ATP-binding protein	1.2	5.15E-01	0,75 g/l BuOH	5.3	61860	23	Cytoplasmic	COG0488	General function prediction only
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.5	8.61E-02	0,75 g/l BuOH	6.5	48871	8	Unknown	COG0334	Amino acid transport and metabolism
26987416	PP_0680		ATP-dependent protease	2.6	2.72E-02	0,75 g/l BuOH	4.5	89677	11	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones
26987420	PP_0684	fklB-1	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.5	8.12E-01	0,75 g/l BuOH	4.4	21678	5	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones
26987423	PP_0687	ispB	polyprenyl synthetase	1.1	4.06E-01	0,75 g/l BuOH	4.8	35269	7	Cytoplasmic	COG0142	Coenzyme metabolism

26987426	PP_0690	obgE	GTPase ObgE	1.3	3.03E-01	0,75 g/l BuOH	4.5	44825	7	Cytoplasmic	COG0536	General function prediction only	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.2	8.82E-01	0,75 g/l BuOH	7.8	39661	3	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987429	PP_0693		hypothetical protein	1.5	8.01E-02	Control	5.1	106556	17	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26987441	PP_0705		DNA-3-methyladenine glycosylase II	1.1	7.23E-01	0,75 g/l BuOH	6.4	22893	2	Unknown	COG0122	DNA replication, recombination, and repair	
26987443	PP_0707		MscS mechanosensitive ion channel	1.3	1.58E-01	0,75 g/l BuOH	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	1.6	1.20E-01	Control	5.3	23026	16	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	1.3	4.93E-01	Control	10.5	31284	8	Cytoplasmic	COG2326	Function unknown	
26987455	PP_0719		GTP-dependent nucleic acid-binding protein EngD	1.2	5.18E-01	0,75 g/l BuOH	4.7	39962	6	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
26987456	PP_0720	pth	peptidyl-tRNA hydrolase	1.5	1.31E-01	0,75 g/l BuOH	10.1	20949	5	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.2	3.89E-01	0,75 g/l BuOH	6.4	23242	12	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.9	3.21E-03	0,75 g/l BuOH	5.9	34192	10	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987460	PP_0724	lolB	outer membrane lipoprotein LolB	1.1	6.94E-01	0,75 g/l BuOH	8.2	22895	5	Unknown	COG3017	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	1.2	3.05E-01	Control	4.6	63994	4	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987471	PP_0735		molybdopterin biosynthesis protein MoeB	1.2	6.05E-01	0,75 g/l BuOH	5.1	26584	2	Cytoplasmic	COG0476	Coenzyme metabolism	
26987478	PP_0742		hypothetical protein	1.0	9.81E-01	0,75 g/l BuOH	6.2	36114	6	Unknown	COG3380	General function prediction only	
26987479	PP_0743		NAD-dependent epimerase/dehydratase	1.3	2.58E-01	Control	9.7	33119	4	Cytoplasmic Membrane	COG1090	General function prediction only	
26987482	PP_0746	upp	uracil phosphoribosyltransferase	1.0	9.50E-01	0,75 g/l BuOH	7.1	23000	6	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	1.9	3.49E-02	0,75 g/l BuOH	8.4	54282	8	Cytoplasmic	COG0579	General function prediction only	
26987492	PP_0756		phospholipid/glycerol acyltransferase	1.3	2.30E-02	0,75 g/l BuOH	8.3	47784	4	Cytoplasmic			
26987495	PP_0759		hypothetical protein	1.1	5.90E-01	0,75 g/l BuOH	7.0	29743	8	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987498	PP_0762	hprA	glycerate dehydrogenase	1.4	1.07E-01	0,75 g/l BuOH	6.1	34094	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	1.1	9.91E-01	0,75 g/l BuOH	5.5	62125	11	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	1.0	9.06E-01	0,75 g/l BuOH	5.0	67937	19	Outer Membrane			
26987502	PP_0766		hypothetical protein	1.0	8.09E-01	Control	9.6	50572	36	Unknown			
26987504	PP_0768		response regulator/hypothetical protein	1.3	2.16E-01	0,75 g/l BuOH	8.4	59272	14	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987505	PP_0769		histidine kinase	1.4	2.58E-01	0,75 g/l BuOH	4.6	25229	8	Cytoplasmic	COG0642	Signal transduction mechanisms	
26987509	PP_0773		OmpA/MotB domain protein	1.3	5.37E-01	0,75 g/l BuOH	9.5	24753	11	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987510	PP_0774	pta	phosphate acetyltransferase	1.2	8.15E-01	0,75 g/l BuOH	5.2	74642	2	Cytoplasmic Membrane	COG0280	Energy production and conversion	
26987515	PP_0779		methyl-accepting chemotaxis transducer/sensory box protein	1.1	5.30E-01	0,75 g/l BuOH	6.2	49856	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987522	PP_0786	trxB	thioredoxin reductase	1.2	2.81E-01	0,75 g/l BuOH	5.1	33841	7	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
26987523	PP_0787	nadC	nicotinate-nucleotide pyrophosphorylase	1.7	7.84E-02	0,75 g/l BuOH	5.2	30163	8	Cytoplasmic	COG0157	Coenzyme metabolism	
26987525	PP_0789	ampD	N-acetyl-anhydromuranmyl-L-alanine amidase	1.2	6.99E-01	0,75 g/l BuOH	5.9	21294	2	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26987528	PP_0792	fruR	DNA-binding transcriptional regulator FruR	1.5	1.74E-01	0,75 g/l BuOH	6.7	36210	2	Cytoplasmic	COG1609	Transcription	
26987529	PP_0793	fruB	phosphoenolpyruvate-protein phosphotransferase	1.9	6.69E-02	Control	4.8	101497	18	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding protein	1.4	1.66E-01	Control	9.2	79558	3	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987542	PP_0806		surface adhesion protein	2.3	2.41E-01	Control	3.5	615675	14	Extracellular			
26987553	PP_0817		aminotransferase	1.9	4.08E-02	Control	8.1	44996	4	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26987559	PP_0823	selD	selenophosphate synthetase	2.6	2.92E-02	0,75 g/l BuOH	5.4	36245	3	Unknown	COG0709	Amino acid transport and metabolism	
26987560	PP_0824		phosphonate ABC transporter periplasmic phosphonate-binding protein	1.3	1.53E-01	0,75 g/l BuOH	8.6	31104	13	Periplasmic	COG3221	Inorganic ion transport and metabolism	
26987569	PP_0833	tgt	queuine tRNA-ribosyltransferase	2.3	6.46E-01	0,75 g/l BuOH	6.8	41335	2	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.3	1.10E-01	0,75 g/l BuOH	9.6	66913	10	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	5.7	6.98E-03	0,75 g/l BuOH	4.8	32758	2	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.3	2.08E-01	0,75 g/l BuOH	6.6	29753	6	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.1	5.58E-01	0,75 g/l BuOH	6.2	44468	18	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987582	PP_0846	hscA	chaperone protein HscA	1.5	3.67E-02	0,75 g/l BuOH	4.7	65888	3	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26987589	PP_0853	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.0	9.68E-01	0,75 g/l BuOH	6.2	39687	7	Cytoplasmic	COG0821	Lipid metabolism	
26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.3	6.02E-02	0,75 g/l BuOH	5.1	47738	14	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
26987591	PP_0855		hypothetical protein	2.9	1.74E-01	0,75 g/l BuOH	4.6	22514	2	Unknown	COG2976	Function unknown	
26987592	PP_0856		hypothetical protein	1.3	4.41E-01	0,75 g/l BuOH	4.7	40737	8	Outer Membrane	COG1520	Function unknown	
26987593	PP_0857	engA	GTP-binding protein EngA	1.3	3.85E-01	0,75 g/l BuOH	9.2	54154	11	Cytoplasmic Membrane	COG1160	General function prediction only	
26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	1.4	1.23E-01	0,75 g/l BuOH	6.5	29780	3	Cytoplasmic	COG0388	General function prediction only	
26987600	PP_0864		ornithine decarboxylase	1.1	4.30E-01	0,75 g/l BuOH	4.7	41535	5	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26987608	PP_0872	prfC	peptide chain release factor 3	1.2	3.88E-01	Control	6.2	59713	3	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
26987615	PP_0879	dppD	oligopeptide/dipeptide ABC transporter ATPase subunit	1.3	1.32E-01	Control	6.3	34914	8	Cytoplasmic Membrane	COG0444	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987617	PP_0881	dppB	alkaline phosphatase	1.4	5.70E-01	Control	8.4	36980	6	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987618	PP_0882	dppA	dipeptide ABC transporter periplasmic dipeptide-binding protein	1.2	2.08E-01	Control	7.4	60974	5	Periplasmic	COG0747	Amino acid transport and metabolism	
26987620	PP_0884		dipeptide ABC transporter periplasmic peptide-binding protein	1.7	4.02E-03	Control	7.3	59564	3	Periplasmic	COG0747	Amino acid transport and metabolism	
26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	1.0	7.23E-01	Control	7.1	60366	29	Periplasmic	COG0747	Amino acid transport and metabolism	
26987622	PP_0886		hypothetical protein	1.0	8.99E-01	Control	8.4	25634	4	Periplasmic	COG3471	Function unknown	
26987624	PP_0888		two component transcriptional regulator, Fis family	1.3	4.91E-01	0,75 g/l BuOH	5.0	20775	5	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription
26987629	PP_0893		intracellular protease, PfpI family	1.1	8.59E-01	0,75 g/l BuOH	5.5	21071	4	Cytoplasmic	COG0693	General function prediction only	
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.5	3.02E-01	0,75 g/l BuOH	4.9	54767	21	Cytoplasmic	COG1951	Energy production and conversion	
26987637	PP_0901	colR	winged helix family two component transcriptional regulator	1.8	8.61E-01	Control	6.2	25489	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987640	PP_0904		lipopolysaccharide kinase	1.6	2.76E-01	0,75 g/l BuOH	8.6	26976	1	Cytoplasmic			
26987642	PP_0906		multidrug efflux protein	3.9	1.84E-03	Control	4.8	110352	3	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26987645	PP_0909		hypothetical protein	1.0	8.05E-01	Control	6.4	38380	6	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.2	8.89E-01	0,75 g/l BuOH	4.4	47019	19	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.1	6.80E-01	0,75 g/l BuOH	5.8	78578	6	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987651	PP_0915	sodB	superoxide dismutase	1.7	5.09E-01	Control	5.8	21938	6	Periplasmic	COG0605	Inorganic ion transport and metabolism	
26987656	PP_0920	xenB	NADH:flavin oxidoreductase/NADH oxidase	1.7	1.82E-01	Control	5.3	37805	2	Cytoplasmic	COG1902	Energy production and conversion	
26987661	PP_0925		hypothetical protein	1.1	6.03E-01	0,75 g/l BuOH	5.8	31410	3	Unknown			
26987666	PP_0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.1	6.10E-01	0,75 g/l BuOH	4.8	52678	10	Cytoplasmic	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.4	2.29E-02	0,75 g/l BuOH	6.2	51518	16	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987670	PP_0934	mreC	rod shape-determining protein MreC	1.1	9.24E-01	0,75 g/l BuOH	7.8	35514	2	Unknown	COG1792	Cell envelope biogenesis, outer membrane	
26987672	PP_0936	maf	Maf-like protein	1.2	7.41E-01	0,75 g/l BuOH	4.7	21232	2	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
26987673	PP_0937	cafA	ribonuclease, Rne/Rng family	2.3	6.68E-02	0,75 g/l BuOH	5.2	54840	4	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26987674	PP_0938		hypothetical protein	1.4	2.44E-01	0,75 g/l BuOH	6.2	138482	5	Outer Membrane	COG3164	Function unknown	
26987675	PP_0939		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	1.8	9.23E-02	Control	6.5	30410	2	Cytoplasmic	COG0388	General function prediction only	
26987676	PP_0940	tldD	tldD protein	1.2	5.09E-01	0,75 g/l BuOH	4.9	50161	6	Cytoplasmic	COG0312	General function prediction only	
26987677	PP_0941		hypothetical protein	2.1	3.95E-01	0,75 g/l BuOH	9.5	20239	2	Cytoplasmic	COG3028	Function unknown	
26987678	PP_0942	pmbA	pmbA protein	1.1	7.21E-01	0,75 g/l BuOH	5.0	48296	7	Cytoplasmic	COG0312	General function prediction only	
26987685	PP_0949		hypothetical protein	1.1	9.32E-01	0,75 g/l BuOH	6.2	32097	3	Cytoplasmic	COG1660	General function prediction only	
26987688	PP_0952	rpoN	RNA polymerase factor sigma-54	1.5	9.24E-01	0,75 g/l BuOH	4.4	56215	3	Cytoplasmic	COG1508	Transcription	
26987689	PP_0953		ABC transporter ATP-binding protein	1.5	3.34E-01	0,75 g/l BuOH	7.0	26579	6	Cytoplasmic	COG1137	General function prediction only	
26987691	PP_0955		hypothetical protein	1.2	7.99E-01	0,75 g/l BuOH	6.5	21349	2	Cytoplasmic	COG3117	Function unknown	
26987693	PP_0957		KpsF/GutQ family protein	1.1	8.60E-01	0,75 g/l BuOH	5.6	34397	4	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
26987695	PP_0959	ttg2B	hypothetical protein	1.0	9.92E-01	0,75 g/l BuOH	8.2	28489	4	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987697	PP_0961	ttg2D	toluene tolerance family protein	1.1	8.39E-01	0,75 g/l BuOH	9.7	23751	9	Unknown	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.3	5.08E-02	0,75 g/l BuOH	5.2	44973	12	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.1	7.25E-01	Control	8.4	22938	10	Cytoplasmic	COG0040	Amino acid transport and metabolism	
26987702	PP_0966	hisD	histidinol dehydrogenase	1.6	1.04E-01	0,75 g/l BuOH	5.1	47605	6	Cytoplasmic	COG0141	Amino acid transport and metabolism	
26987703	PP_0967	hisC	histidinol-phosphate aminotransferase	1.1	6.30E-01	Control	4.9	38768	5	Cytoplasmic	COG0079	Amino acid transport and metabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.3	1.43E-01	Control	5.1	107495	36	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.4	5.01E-02	0,75 g/l BuOH	7.4	52433	25	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.0	7.39E-01	Control	9.7	41323	2	Cytoplasmic Membrane	COG0795	General function prediction only	

26987722	PP_0986	gcvT-1	glycine cleavage system T protein	1.1	5.90E-01	Control	6.4	40319	3	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	1.6	7.10E-02	Control	5.5	33423	10	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	1.2	2.16E-01	Control	6.3	37911	27	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	1.1	3.33E-01	Control	5.7	46462	37	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	1.3	7.77E-02	Control	9.1	51061	4	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	1.0	9.58E-01	0,75 g/l BuOH	7.0	36057	20	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	1.2	1.91E-01	0,75 g/l BuOH	6.4	65359	25	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	1.2	2.91E-01	Control	6.5	33904	14	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987748	PP_1012	gltR-2	winged helix family two component transcriptional regulator	1.5	2.20E-01	0,75 g/l BuOH	6.4	27124	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987750	PP_1014		hypothetical protein	1.2	1.95E-01	0,75 g/l BuOH	6.4	45472	12	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	1.3	6.15E-02	0,75 g/l BuOH	6.2	45449	59	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	1.2	5.58E-01	0,75 g/l BuOH	10.1	33781	9	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	1.3	3.62E-01	Control	9.9	30428	3	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	1.3	5.69E-02	0,75 g/l BuOH	6.7	41895	15	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	1.0	7.47E-01	Control	5.9	49646	36	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	1.1	2.03E-01	Control	6.8	55000	21	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	1.3	1.21E-01	Control	6.7	25476	15	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1.2	2.68E-01	Control	5.4	25004	8	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.5	1.79E-02	0,75 g/l BuOH	5.1	61712	20	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987762	PP_1026		M24/M37 family peptidase	1.1	6.38E-01	0,75 g/l BuOH	10.9	29756	2	Unknown	COG0739	Cell envelope biogenesis, outer membrane	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.3	2.55E-01	0,75 g/l BuOH	7.0	51765	22	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.2	3.25E-01	0,75 g/l BuOH	5.2	58204	18	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.2	4.47E-01	Control	4.7	140818	51	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987792	PP_1056		iron-chelator utilization protein	1.2	8.55E-02	Control	5.2	28123	2	Cytoplasmic	COG2375	Inorganic ion transport and metabolism	
26987794	PP_1058		hypothetical protein	1.5	9.62E-02	Control	9.5	117041	8	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987804	PP_1068		amino acid ABC transporter ATP-binding protein	1.5	7.44E-01	Control	8.2	28149	5	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.0	9.32E-01	0,75 g/l BuOH	8.9	33428	31	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987810	PP_1074	glpR	DeoR family transcriptional regulator	1.4	1.47E-01	0,75 g/l BuOH	5.7	27749	3	Cytoplasmic	COG1349	Transcription	Carbohydrate transport and metabolism
26987811	PP_1075	glpK	glycerol kinase	1.2	1.72E-01	Control	4.9	55282	4	Cytoplasmic	COG0554	Energy production and conversion	
26987818	PP_1082	bfr	bacterioferritin	2.9	5.68E-01	0,75 g/l BuOH	4.4	17971	8	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.2	5.35E-01	0,75 g/l BuOH	4.9	21730	18	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987821	PP_1085	rnt	ribonuclease T	1.8	3.49E-01	0,75 g/l BuOH	5.3	22457	2	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
26987822	PP_1086	pyrC	dihydroorotase	1.1	6.40E-01	0,75 g/l BuOH	6.9	38414	5	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
26987823	PP_1087		OmpA family outer membrane protein	1.2	5.23E-01	Control	10.0	34341	13	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987824	PP_1088	argG	argininosuccinate synthase	1.4	8.38E-02	0,75 g/l BuOH	5.1	45164	21	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.1	2.80E-01	0,75 g/l BuOH	5.5	75186	14	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987834	PP_1098		ATP-binding Mrp/Nbp35 family protein	1.7	2.09E-01	0,75 g/l BuOH	4.8	38207	3	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
26987836	PP_1100	dcd	deoxycytidine triphosphate deaminase	1.0	6.34E-01	Control	5.4	21233	3	Cytoplasmic	COG0717	Nucleotide transport and metabolism	
26987840	PP_1104		succinylglutamate desuccinylase/aspartoacylase	1.1	9.54E-01	Control	6.3	40904	2	Cytoplasmic	COG3608	General function prediction only	
26987844	PP_1108		acylase	1.3	3.09E-01	Control	8.7	88728	12	Periplasmic	COG2366	General function prediction only	
26987847	PP_1111		synthetase	1.0	8.63E-01	Control	6.0	29406	5	Cytoplasmic	COG2872	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	1.1	9.08E-01	0,75 g/l BuOH	7.6	32597	11	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	1.1	7.38E-01	0,75 g/l BuOH	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.2	4.65E-01	Control	4.7	27345	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987862	PP_1126		Beta-agarase	1.9	4.27E-01	0,75 g/l BuOH	6.6	86407	3	Periplasmic			
26987865	PP_1129	pdxH	pyridoxamine 5'-phosphate oxidase	1.1	9.71E-01	Control	6.4	24581	7	Cytoplasmic	COG0259	Coenzyme metabolism	
26987867	PP_1131		17 kDa surface antigen	1.2	4.87E-01	Control	9.3	15682	5	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987870	PP_1134		FAD dependent oxidoreductase	1.3	4.17E-01	Control	6.9	58398	3	Cytoplasmic	COG2509	General function prediction only	
26987873	PP_1137	braG	branched chain amino acid ABC transporter ATP-binding protein	1.1	5.13E-01	0,75 g/l BuOH	7.6	25545	8	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
26987874	PP_1138	livG	leucine/isoleucine/valine transporter ATP-binding subunit	1.1	4.37E-01	Control	9.7	28280	8	Cytoplasmic	COG0411	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.4	5.91E-04	0,75 g/l BuOH	6.4	39402	32	Periplasmic	COG0683	Amino acid transport and metabolism	
26987879	PP_1143		3-hydroxyisobutyrate dehydrogenase	1.1	9.34E-01	0,75 g/l BuOH	5.8	30664	5	Unknown	COG2084	Lipid metabolism	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	2.0	3.88E-02	Control	4.8	105994	16	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987893	PP_1157		acetolactate synthase	1.0	7.80E-01	0,75 g/l BuOH	6.1	60059	9	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26987897	PP_1162		glutathione S-transferase family protein	1.0	8.29E-01	0,75 g/l BuOH	6.8	22677	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.4	3.53E-01	0,75 g/l BuOH	4.5	46989	9	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.2	4.61E-01	Control	5.7	106948	30	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987919	PP_1184		dienelactone hydrolase	1.1	7.26E-01	0,75 g/l BuOH	6.8	28722	11	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26987935	PP_1200	kup	Kup system potassium uptake protein	2.1	8.14E-03	Control	7.9	68568	2	Cytoplasmic Membrane	COG3158	Inorganic ion transport and metabolism	
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.7	2.45E-01	0,75 g/l BuOH	5.0	63623	17	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.8	4.99E-02	0,75 g/l BuOH	4.6	46120	23	Outer Membrane			
26987945	PP_1210		DNA-binding stress protein	1.1	5.72E-01	Control	5.0	17861	2	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.2	2.09E-01	0,75 g/l BuOH	5.1	66568	27	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987949	PP_1214		hypothetical protein	1.2	9.75E-01	0,75 g/l BuOH	4.4	26842	2	Cytoplasmic	COG0217	Function unknown	
26987951	PP_1216	ruvA	Holliday junction DNA helicase RuvA	1.2	4.25E-01	0,75 g/l BuOH	8.5	22384	2	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.5	1.96E-01	0,75 g/l BuOH	6.3	25310	6	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.3	1.09E-01	0,75 g/l BuOH	9.8	47431	8	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.1	4.23E-01	0,75 g/l BuOH	4.9	17833	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987960	PP_1225		radical SAM domain protein	1.5	5.65E-02	Control	4.9	24096	3	Cytoplasmic	COG0602	Posttranslational modification, protein turnover, chaperones	
26987961	PP_1226	exsB	exsB protein	1.1	7.04E-01	0,75 g/l BuOH	4.7	23961	4	Cytoplasmic	COG0603	General function prediction only	
26987965	PP_1230		hypothetical protein	1.7	3.46E-02	0,75 g/l BuOH	5.1	53328	2	Cytoplasmic Membrane	COG5339	Function unknown	
26987967	PP_1232		hypothetical protein	1.1	5.49E-01	0,75 g/l BuOH	6.9	53219	7	Unknown	COG4783	General function prediction only	
26987971	PP_1236		glycine cleavage system transcriptional repressor	1.4	3.98E-01	0,75 g/l BuOH	4.8	20529	2	Cytoplasmic	COG2716	Amino acid transport and metabolism	
26987972	PP_1237	dapA	dihydrodipicolinate synthase	1.0	8.13E-01	0,75 g/l BuOH	6.0	31654	10	Cytoplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
26987973	PP_1238		lipoprotein	1.0	7.95E-01	0,75 g/l BuOH	4.8	40784	12	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.1	5.96E-01	0,75 g/l BuOH	5.1	26916	14	Cytoplasmic	COG0152	Nucleotide transport and metabolism	
26987981	PP_1246		hypothetical protein	1.1	7.11E-01	Control	6.0	65952	2	Unknown	COG5373	Function unknown	
26988009	PP_1274		short chain dehydrogenase	1.3	7.35E-02	0,75 g/l BuOH	10.2	28618	6	Cytoplasmic	COG0300	General function prediction only	
26988026	PP_1291		PhoH family protein	1.0	9.61E-01	0,75 g/l BuOH	5.7	51856	13	Cytoplasmic	COG1875	General function prediction only	
26988031	PP_1296	estB	carboxylesterase	1.1	6.97E-01	0,75 g/l BuOH	4.9	24402	5	Cytoplasmic Membrane	COG0400	General function prediction only	
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.1	4.72E-01	0,75 g/l BuOH	5.6	36424	27	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988033	PP_1298	aapQ	polar amino acid ABC transporter inner membrane subunit	1.1	7.00E-01	0,75 g/l BuOH	10.2	43229	4	Cytoplasmic Membrane	COG4597	Amino acid transport and metabolism	
26988035	PP_1300	aapP	general amino acid ABC transporter ATP-binding protein	1.1	6.14E-01	0,75 g/l BuOH	7.6	28879	6	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26988037	PP_1302		hypothetical protein	1.0	6.02E-01	0,75 g/l BuOH	5.8	27492	3	Cytoplasmic	COG0327	Function unknown	
26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2	1.1	1.98E-01	Control	6.8	35284	10	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.2	7.21E-01	0,75 g/l BuOH	5.6	69049	18	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988046	PP_1311		tryptophanyl-tRNA synthetase	1.1	8.43E-01	0,75 g/l BuOH	5.4	49297	5	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
26988049	PP_1314		aldo/keto reductase family oxidoreductase	1.2	3.32E-01	0,75 g/l BuOH	6.5	38777	12	Cytoplasmic	COG0667	Energy production and conversion	
26988052	PP_1317	petA	ubiquinol-cytochrome c reductase, iron-sulfur subunit	1.1	7.40E-01	0,75 g/l BuOH	7.5	20855	12	Cytoplasmic Membrane	COG0723	Energy production and conversion	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	1.0	9.83E-01	Control	8.4	45901	9	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.2	5.08E-01	0,75 g/l BuOH	7.1	29032	9	Unknown	COG2857	Energy production and conversion	
26988055	PP_1320	sspA	stringent starvation protein A	1.3	2.21E-01	0,75 g/l BuOH	6.4	23566	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988060	PP_1325		LppC family lipoprotein	1.2	3.42E-01	0,75 g/l BuOH	7.5	64637	22	Cytoplasmic Membrane	COG3107	General function prediction only	
26988061	PP_1326		uroporphyrin-III C/tetrapyrrole methyltransferase	1.0	7.88E-01	0,75 g/l BuOH	5.4	31389	3	Cytoplasmic	COG0313	General function prediction only	
26988063	PP_1329	mraW	S-adenosyl-methyltransferase MraW	1.2	3.79E-01	0,75 g/l BuOH	7.2	34314	5	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane	

26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.2	2.68E-01	0,75 g/l BuOH	5.3	53602	23	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligas	1.3	1.76E-01	0,75 g/l BuOH	6.6	46750	12	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
26988069	PP_1335	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	1.5	1.45E-01	0,75 g/l BuOH	5.7	48300	6	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane	
26988072	PP_1338	murC	UDP-N-acetylmuramate--L-alanine ligase	1.1	4.72E-01	0,75 g/l BuOH	6.3	52166	4	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
26988073	PP_1339	ddl	D-alanine--D-alanine ligase	1.1	7.50E-01	Control	4.7	34131	5	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	1.0	7.17E-01	0,75 g/l BuOH	4.9	47444	10	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988076	PP_1342	ftsZ	cell division protein FtsZ	1.0	8.60E-01	Control	4.7	41830	10	Cytoplasmic	COG0206	Cell division and chromosome partitioning	
26988077	PP_1343	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	1.2	5.74E-01	0,75 g/l BuOH	4.8	33269	7	Cytoplasmic	COG0774	Cell envelope biogenesis, outer membrane	
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	2.2	4.03E-01	Control	5.0	42236	5	Cytoplasmic	COG1364	Amino acid transport and metabolism	
26988081	PP_1347		glutathione S-transferase family protein	1.0	8.23E-01	Control	5.3	23247	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988082	PP_1348		hypothetical protein	1.6	6.15E-01	0,75 g/l BuOH	5.5	34390	2	Cytoplasmic	COG0352	Coenzyme metabolism	
26988086	PP_1352		nucleotide-binding protein	1.3	7.09E-01	Control	7.4	18561	10	Cytoplasmic	COG1666	Function unknown	
26988092	PP_1358		hypothetical protein	1.2	1.32E-01	0,75 g/l BuOH	7.8	32006	10	Unknown	COG0748	Inorganic ion transport and metabolism	
26988095	PP_1361	groEL	chaperonin GroEL	1.1	2.77E-01	0,75 g/l BuOH	4.7	56743	40	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	1.5	4.88E-01	0,75 g/l BuOH	6.7	52057	22	Cytoplasmic	COG0469	Carbohydrate transport and metabolism	
26988101	PP_1367	purU	formyltetrahydrofolate deformylase	1.0	9.48E-01	0,75 g/l BuOH	6.6	32376	6	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.2	2.87E-01	0,75 g/l BuOH	4.8	67652	14	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988106	PP_1372		hypothetical protein	1.5	5.47E-02	Control	6.5	52321	12	Unknown	COG0433	Replication, recombination, and repair	
26988109	PP_1375	pcaR	pca regulon regulatory protein	1.7	8.52E-02	Control	7.2	31741	2	Cytoplasmic	COG1414	Transcription	
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	1.3	1.15E-01	0,75 g/l BuOH	6.5	48194	6	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase	1.1	4.02E-01	0,75 g/l BuOH	5.1	28656	7	Unknown	COG0596	General function prediction only	
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.7	1.21E-01	0,75 g/l BuOH	5.1	52864	9	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	2.2	8.51E-03	Control	5.3	112835	6	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	1.3	3.46E-01	0,75 g/l BuOH	4.9	31783	4	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26988126	PP_1392		NAD-dependent epimerase/dehydratase	1.4	1.51E-01	0,75 g/l BuOH	8.0	21985	4	Unknown	COG2910	General function prediction only	
26988145	PP_1412		enoyl-CoA hydratase/isomerase	1.3	4.75E-01	Control	6.5	40490	4	Cytoplasmic	COG1024	Lipid metabolism	
26988151	PP_1418		tricarboxylate transport protein TctC	1.1	5.11E-01	0,75 g/l BuOH	6.6	34981	6	Periplasmic	COG3181	Function unknown	
26988156	PP_1423		hypothetical protein	1.7	3.72E-02	0,75 g/l BuOH	6.0	33350	3	Unknown	COG0354	General function prediction only	
26988159	PP_1426	nadB	L-aspartate oxidase	1.1	7.61E-01	0,75 g/l BuOH	5.8	59215	2	Cytoplasmic	COG0029	Coenzyme metabolism	
26988160	PP_1427	algU	RNA polymerase sigma factor AlgU	1.3	3.02E-01	0,75 g/l BuOH	5.2	22282	8	Cytoplasmic	COG1595	Transcription	
26988162	PP_1429	algN	sigma E regulatory protein, MucB/RseB	1.2	1.23E-01	0,75 g/l BuOH	6.6	34982	4	Periplasmic	COG3026	Signal transduction mechanisms	
26988163	PP_1430	algY	protease Do	1.8	1.73E-01	0,75 g/l BuOH	6.6	52617	13	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
26988164	PP_1431	lepA	GTP-binding protein LepA	1.2	5.00E-01	Control	5.5	66116	4	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.3	8.47E-01	Control	9.2	32060	2	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988167	PP_1434	era	GTP-binding protein Era	1.4	3.42E-01	Control	6.9	34243	2	Cytoplasmic Membrane	COG1159	General function prediction only	
26988169	PP_1436	pdxJ	pyridoxine 5'-phosphate synthase	1.3	2.31E-01	0,75 g/l BuOH	6.2	26737	4	Cytoplasmic	COG0854	Coenzyme metabolism	
26988176	PP_1443	lon-1	ATP-dependent protease La	1.0	9.59E-01	Control	6.4	89794	10	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.1	2.24E-01	Control	6.0	86581	12	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.3	3.34E-01	0,75 g/l BuOH	5.7	42575	15	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	35.6	1.04E-01	0,75 g/l BuOH	9.0	45563	2	Cytoplasmic Membrane			
26988194	PP_1461	ffh	signal recognition particle protein	1.5	5.82E-02	0,75 g/l BuOH	10.7	58232	5	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
26988202	PP_1469	dsbC	thiol:disulfide interchange protein DsbC	2.3	1.92E-01	0,75 g/l BuOH	7.9	27601	2	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
26988203	PP_1470	hom	homoserine dehydrogenase	1.7	1.21E-01	0,75 g/l BuOH	5.1	46194	11	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.5	3.28E-02	0,75 g/l BuOH	6.2	51645	21	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	1.0	7.78E-01	0,75 g/l BuOH	5.8	40626	17	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.3	3.52E-01	0,75 g/l BuOH	5.7	50918	14	Unknown	COG1012	Energy production and conversion	
26988219	PP_1486		polyamine ABC transporter periplasmic polyamine-binding protein	1.1	2.67E-01	0,75 g/l BuOH	6.4	41728	16	Periplasmic	COG0687	Amino acid transport and metabolism	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.4	3.48E-01	0,75 g/l BuOH	4.7	58605	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988223	PP_1490		methyltransferase, CheR-like	1.8	2.08E-01	0,75 g/l BuOH	8.6	46889	2	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
26988224	PP_1491		chemotaxis protein CheW	2.0	2.65E-02	Control	6.9	23549	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26988227	PP_1494		response regulator/GGDEF domain-containing protein	1.4	3.74E-01	Control	5.7	37046	5	Cytoplasmic	COG3706	Signal transduction mechanisms	
26988228	PP_1496	lysS	lysyl-tRNA synthetase	1.5	1.69E-02	0,75 g/l BuOH	5.0	57137	20	Cytoplasmic	COG1190	Translation, ribosomal structure and biogenesis	
26988231	PP_1499		hypothetical protein	1.1	5.72E-01	0,75 g/l BuOH	6.3	49645	2	Cytoplasmic	COG3930	Function unknown	
26988234	PP_1502		OmpA/MotB domain protein	1.9	4.86E-02	0,75 g/l BuOH	9.5	28964	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.4	1.01E-01	Control	6.6	96963	21	Cytoplasmic	COG2352	Energy production and conversion	
26988238	PP_1506	adk	adenylate kinase	1.2	6.81E-01	0,75 g/l BuOH	5.7	23222	11	Cytoplasmic	COG0563	Nucleotide transport and metabolism	
26988239	PP_1507		hypothetical protein	1.1	8.61E-01	Control	6.0	23544	2	Unknown	COG1214	Posttranslational modification, protein turnover, chaperones	
26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	1.2	5.33E-01	Control	4.2	29130	8	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26988245	PP_1513		hypothetical protein	1.5	3.01E-01	0,75 g/l BuOH	9.0	27864	2	Cytoplasmic			
26988258	PP_1526		beta-(1-3)-glucosyl transferase	1.2	6.34E-01	0,75 g/l BuOH	8.1	97324	6	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism	
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.5	6.74E-01	0,75 g/l BuOH	5.6	35858	7	Unknown	COG2171	Amino acid transport and metabolism	
26988320	PP_1588		succinyldiaminopimelate transaminase	1.3	9.37E-02	0,75 g/l BuOH	5.4	43759	6	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988321	PP_1589	glnD	PII uridylyl-transferase	1.8	2.56E-02	Control	5.9	102620	13	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones	
26988322	PP_1590	map	methionine aminopeptidase	1.1	5.02E-01	0,75 g/l BuOH	6.6	28956	7	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.1	6.97E-01	0,75 g/l BuOH	9.3	27023	16	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.2	3.07E-01	0,75 g/l BuOH	4.9	30432	20	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988325	PP_1593	pyrH	uridylate kinase	1.4	4.38E-01	0,75 g/l BuOH	6.2	26484	7	Cytoplasmic	COG0528	Nucleotide transport and metabolism	
26988326	PP_1594	frr	ribosome recycling factor	1.2	6.13E-01	0,75 g/l BuOH	8.9	20152	14	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis	
26988327	PP_1595	uppS	undecaprenyl diphosphate synthase	1.3	4.27E-01	0,75 g/l BuOH	8.5	27951	5	Cytoplasmic	COG0020	Lipid metabolism	
26988331	PP_1599		surface antigen family outer membrane protein	2.0	8.20E-02	0,75 g/l BuOH	4.7	86513	12	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988334	PP_1602	fabZ	(3R)-hydroxymyristoyl-ACP dehydratase	1.7	2.45E-01	Control	6.3	18409	6	Cytoplasmic	COG0764	Lipid metabolism	
26988335	PP_1603	lpxA	UDP-N-acetylglucosamine acyltransferase	1.4	1.55E-01	0,75 g/l BuOH	6.9	28107	2	Cytoplasmic	COG1043	acyl carrier protein	
26988338	PP_1606	dnaE	DNA polymerase III subunit alpha	1.5	4.34E-01	0,75 g/l BuOH	5.3	130923	6	Cytoplasmic	COG0587	DNA replication, recombination, and repair	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.7	1.63E-02	0,75 g/l BuOH	6.0	35135	15	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.2	3.57E-01	0,75 g/l BuOH	5.8	59474	27	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988343	PP_1611	kdsA-1	2-dehydro-3-deoxyphosphooctonate aldolase	1.1	6.17E-01	0,75 g/l BuOH	5.8	31034	12	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.2	6.00E-01	0,75 g/l BuOH	4.7	45490	19	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.0	8.96E-01	Control	6.3	39364	3	Cytoplasmic	COG1062	Energy production and conversion	
26988349	PP_1617		S-formylglutathione hydrolase	1.0	9.18E-01	Control	6.4	31637	2	Unknown	COG0627	General function prediction only	
26988353	PP_1621	pcm	protein-L-isoaspartate O-methyltransferase	1.1	8.48E-01	0,75 g/l BuOH	7.1	25497	3	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones	
26988354	PP_1622	nlpD	peptidase M23B	1.2	4.49E-01	Control	11.0	27506	5	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988355	PP_1623	rpoS	RNA polymerase sigma factor RpoS	2.1	3.27E-01	0,75 g/l BuOH	4.9	38175	8	Cytoplasmic	COG0568	Transcription	
26988357	PP_1625		ferrodoxin, 4Fe-4S	1.0	9.88E-01	0,75 g/l BuOH	3.7	12047	2	Cytoplasmic	COG1146	Energy production and conversion	
26988361	PP_1629	recA	recombinase A	1.0	8.62E-01	0,75 g/l BuOH	5.3	37545	8	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988367	PP_1635		LuxR family two component transcriptional regulator	1.9	1.75E-02	0,75 g/l BuOH	4.8	23481	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26988370	PP_1638	fpr	oxidoreductase FAD/NAD(P)-binding domain protein	1.1	2.88E-01	0,75 g/l BuOH	5.1	29710	5	Cytoplasmic	COG1018	Energy production and conversion	
26988373	PP_1641		C32 tRNA thiolase	1.3	2.75E-01	0,75 g/l BuOH	6.8	31043	4	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
26988381	PP_1649	ldhA	D-lactate dehydrogenase	1.0	6.20E-01	0,75 g/l BuOH	6.6	37126	5	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26988382	PP_1650	gacS	multi-sensor hybrid histidine kinase	1.4	2.79E-02	0,75 g/l BuOH	5.4	100653	6	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26988386	PP_1654	cysM	cysteine synthase B	1.2	2.34E-01	Control	4.9	32305	7	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26988388	PP_1656	relA	(p)ppGpp synthetase I, SpoT/RelA	1.1	6.16E-01	Control	7.9	83609	13	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26988390	PP_1658		hypothetical protein	1.1	6.29E-01	0,75 g/l BuOH	9.6	20470	2	Cytoplasmic	COG3122	Function unknown	
26988391	PP_1659		hypothetical protein	2.0	4.80E-03	Control	5.9	48336	21	Periplasmic			
26988392	PP_1660		hypothetical protein	2.7	1.94E-01	Control	5.1	19178	3	Cytoplasmic Membrane			
26988393	PP_1661		dehydrogenase subunit	2.3	5.15E-03	Control	5.5	81020	43	Extracellular	COG2303	Amino acid transport and metabolism	

26988395	PP_1663		hypothetical protein	1.2	4.51E-01	0,75 g/l BuOH	9.2	26313	9	Periplasmic			
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	1.0	7.32E-01	Control	4.6	36942	9	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
26988398	PP_1666		hypothetical protein	1.1	4.10E-01	0,75 g/l BuOH	5.5	37790	2	Unknown	COG3249	Function unknown	
26988400	PP_1668		DNA replication initiation factor	1.3	1.45E-01	0,75 g/l BuOH	8.7	26586	6	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
26988404	PP_1672	cobO	cob(I)yrinic acid a,c-diamide adenosyltransferase	1.1	5.36E-01	0,75 g/l BuOH	7.7	22602	8	Cytoplasmic	COG2109	Coenzyme metabolism	
26988418	PP_1686		glutathione peroxidase	1.4	8.01E-01	Control	8.9	22309	3	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
26988434	PP_1702	rdgC	recombination associated protein	1.2	5.37E-01	Control	4.6	34283	3	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.2	8.50E-01	0,75 g/l BuOH	4.8	26520	11	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988451	PP_1719	prc	carboxyl-terminal protease	1.1	4.69E-01	0,75 g/l BuOH	7.1	79096	31	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26988452	PP_1720		alcohol dehydrogenase, zinc-containing	1.2	3.11E-01	0,75 g/l BuOH	4.7	33921	6	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26988453	PP_1721		HAD superfamily hydrolase	1.2	4.74E-01	0,75 g/l BuOH	4.5	24571	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26988454	PP_1722		ABC transporter ATP-binding protein	2.5	5.16E-02	0,75 g/l BuOH	8.0	36445	2	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26988457	PP_1725		type I phosphodiesterase/nucleotide pyrophosphatase	1.4	8.22E-02	0,75 g/l BuOH	6.4	31520	3	Cytoplasmic	COG1524	General function prediction only	
26988458	PP_1726		ABC transporter periplasmic protein	1.2	1.66E-01	Control	6.0	38636	21	Unknown	COG1840	Inorganic ion transport and metabolism	
26988464	PP_1733	minD	septum site-determining protein MinD	1.0	9.86E-01	Control	6.2	29650	16	Cytoplasmic	COG2894	Cell division and chromosome partitioning	
26988465	PP_1734	minC	septum formation inhibitor	1.0	9.71E-01	0,75 g/l BuOH	8.9	29680	2	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
26988472	PP_1741		substrate-binding region of ABC-type glycine betaine transport system	1.1	7.33E-01	Control	9.6	31215	2	Periplasmic	COG2113	Amino acid transport and metabolism	
26988474	PP_1743	actP	acetate permease	4.5	1.24E-02	0,75 g/l BuOH	9.6	58972	2	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	1.4	6.36E-03	0,75 g/l BuOH	8.2	57637	10	Cytoplasmic	COG2326	Function unknown	
26988486	PP_1755	fumC-2	fumarate hydratase	1.2	3.77E-01	0,75 g/l BuOH	6.4	49131	23	Cytoplasmic	COG0114	Energy production and conversion	
26988490	PP_1759		DSBA oxidoreductase	1.1	7.82E-01	0,75 g/l BuOH	4.7	21492	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
26988492	PP_1761		sensory box protein/GGDEF family protein	1.2	4.63E-01	Control	6.8	108193	5	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26988494	PP_1763		short chain dehydrogenase	1.1	7.06E-01	Control	4.7	26253	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988495	PP_1764		phosphoglycolate phosphatase	1.0	8.59E-01	0,75 g/l BuOH	4.5	24373	4	Cytoplasmic	COG0546	General function prediction only	
26988496	PP_1765	ubiG	3-demethylubiquinone-9 3-methyltransferase	1.1	6.66E-01	0,75 g/l BuOH	5.7	26084	4	Cytoplasmic	COG2227	Coenzyme metabolism	
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.3	1.65E-01	Control	4.7	102037	34	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988499	PP_1768	serC	phosphoserine aminotransferase	1.1	6.91E-01	0,75 g/l BuOH	5.1	39911	10	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
26988500	PP_1769	pheA	chorismate mutase	1.2	3.19E-02	0,75 g/l BuOH	6.4	40816	11	Cytoplasmic	COG0077	Amino acid transport and metabolism	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransl	1.1	3.87E-01	Control	6.4	79133	10	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988502	PP_1771	cmk	cytidylate kinase	1.3	2.54E-01	Control	4.9	24691	8	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
26988506	PP_1775		beta-lactamase domain protein	1.6	2.33E-01	Control	6.5	52195	4	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1.3	5.57E-01	0,75 g/l BuOH	5.2	52989	6	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP_1780		mannosyltransferase	1.8	1.42E-02	Control	5.8	180042	21	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988514	PP_1783	rmlA	glucose-1-phosphate thymidylyltransferase	1.1	4.96E-01	0,75 g/l BuOH	4.9	32517	6	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
26988515	PP_1784	rmlD	dTDP-4-dehydrorhamnose reductase	1.1	4.02E-01	Control	6.7	32131	5	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	1.5	4.57E-02	0,75 g/l BuOH	6.1	40690	8	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	1.3	6.74E-02	Control	6.4	128499	19	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988518	PP_1787		hypothetical protein	1.1	5.37E-01	Control	5.3	37903	5	Unknown			
26988521	PP_1790		acylneuraminate cytidylyltransferase	1.1	5.97E-01	0,75 g/l BuOH	6.4	26350	3	Cytoplasmic	COG1083	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	1.2	8.96E-01	0,75 g/l BuOH	5.9	58534	12	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988523	PP_1792		glycosyl transferase, group 2 family protein	1832.5	4.42E-03	0,75 g/l BuOH	6.5	88305	2	Cytoplasmic	COG1216	General function prediction only	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.1	4.60E-01	0,75 g/l BuOH	6.4	40124	13	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988530	PP_1800	rmd	oxidoreductase Rmd	1.0	9.16E-01	0,75 g/l BuOH	7.2	32310	6	Unknown	COG1089	Cell envelope biogenesis, outer membrane	
26988537	PP_1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase	1.0	9.54E-01	0,75 g/l BuOH	6.0	30469	6	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
26988545	PP_1815	pyrF	orotidine 5'-phosphate decarboxylase	1.3	1.70E-01	0,75 g/l BuOH	4.9	24551	4	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
26988546	PP_1816		alcohol dehydrogenase, zinc-containing	1.0	9.45E-01	0,75 g/l BuOH	7.4	35802	9	Cytoplasmic	COG2130	General function prediction only	
26988549	PP_1819		methyl-accepting chemotaxis sensory transducer	1.4	3.46E-01	Control	4.7	68069	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988551	PP_1821		glutathione S-transferase family protein	1.5	4.06E-01	0,75 g/l BuOH	5.6	23207	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988553	PP_1823	folE	GTP cyclohydrolase I	1.1	4.73E-01	0,75 g/l BuOH	8.1	21388	2	Cytoplasmic	COG0302	Coenzyme metabolism	
26988556	PP_1826		isochorismatase superfamily hydrolase	2.6	4.66E-01	Control	7.6	21283	3	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988557	PP_1827		N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	1.2	5.96E-01	0,75 g/l BuOH	4.4	34094	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26988560	PP_1830	aroC	chorismate synthase	1.3	6.05E-01	0,75 g/l BuOH	6.5	38987	5	Cytoplasmic	COG0082	Amino acid transport and metabolism	
26988562	PP_1832		oxidase	1.3	4.27E-01	0,75 g/l BuOH	4.8	19469	3	Cytoplasmic	COG1791	Function unknown	
26988568	PP_1838		hypothetical protein	1.2	5.61E-01	0,75 g/l BuOH	6.8	76615	5	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988571	PP_1841		cytochrome c family protein	1.1	3.21E-01	Control	7.6	29246	2	Unknown	COG2010	Energy production and conversion	
26988572	PP_1842		amidotransferase	1.2	5.76E-01	0,75 g/l BuOH	4.9	27317	5	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
26988575	PP_1845		enoyl-CoA hydratase	1.6	1.28E-01	0,75 g/l BuOH	7.7	24641	9	Cytoplasmic	COG1024	Lipid metabolism	
26988588	PP_1858	efp	elongation factor P	1.4	8.20E-01	0,75 g/l BuOH	4.5	21303	5	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988596	PP_1866		phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	2.90E-01	0,75 g/l BuOH	6.4	49706	2	Cytoplasmic	COG3200	Amino acid transport and metabolism	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.6	3.56E-02	0,75 g/l BuOH	9.2	60924	17	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988600	PP_1870	tpm	thiopurine S-methyltransferase	1.1	7.12E-01	0,75 g/l BuOH	4.7	24365	6	Cytoplasmic			
26988601	PP_1871	htpX	heat shock protein HtpX	1.3	3.77E-01	0,75 g/l BuOH	7.2	32199	5	Cytoplasmic Membrane	COG0501	Posttranslational modification, protein turnover, chaperones	
26988602	PP_1872		aminotransferase AlaT	1.5	1.40E-01	0,75 g/l BuOH	5.8	44705	8	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988606	PP_1876		hypothetical protein	1.5	8.03E-02	0,75 g/l BuOH	8.8	38962	3	Cytoplasmic	COG2607	General function prediction only	
26988608	PP_1878		hypothetical protein	1.2	3.74E-01	0,75 g/l BuOH	7.3	290993	4	Cytoplasmic			
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	1.0	9.03E-01	Control	6.9	89194	28	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988624	PP_1894		glutathione S-transferase family protein	1.4	1.73E-01	0,75 g/l BuOH	5.0	23668	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26988625	PP_1895		ABC transporter ATP-binding protein	1.2	4.99E-01	0,75 g/l BuOH	7.1	34488	3	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26988628	PP_1898		MotA/TolQ/ExbB proton channel	1.1	9.89E-01	Control	7.0	24408	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26988632	PP_1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.2	5.57E-01	0,75 g/l BuOH	5.2	27809	2	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.1	8.34E-01	0,75 g/l BuOH	4.7	120904	31	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.0	7.31E-01	Control	6.4	36497	7	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988638	PP_1909	maf	Maf-like protein	2.2	9.42E-01	Control	4.9	22268	2	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.3	7.84E-01	0,75 g/l BuOH	4.7	32614	8	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.2	4.84E-01	0,75 g/l BuOH	6.0	25470	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988644	PP_1915	acpP	acyl carrier protein	2.8	5.58E-01	0,75 g/l BuOH	3.8	8712	2	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26988646	PP_1917	pabC	4-amino-4-deoxychorismate lyase	1.1	7.72E-01	Control	7.2	29486	3	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26988669	PP_1942		LysR family transcriptional regulator	1.1	4.89E-01	Control	5.8	36540	3	Cytoplasmic	COG0583	Transcription	
26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	1.0	8.16E-01	Control	5.3	27212	3	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988685	PP_1958		hypothetical protein	1.4	3.09E-01	0,75 g/l BuOH	8.0	30813	2	Cytoplasmic			
26988691	PP_1964		deoxynucleotide monophosphate kinase	1.1	7.88E-01	0,75 g/l BuOH	5.9	30146	4	Unknown			
26988696	PP_1970		lipoprotein	1.2	4.28E-01	0,75 g/l BuOH	4.9	22337	6	Unknown			
26988697	PP_1971		hypothetical protein	1.2	7.21E-01	0,75 g/l BuOH	4.5	21577	5	Cytoplasmic	COG3816	Function unknown	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.1	5.82E-01	0,75 g/l BuOH	5.9	43290	18	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.1	2.17E-01	0,75 g/l BuOH	5.6	56483	14	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988709	PP_1983		sensory box protein	2.4	2.75E-03	Control	5.7	128000	12	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	1.5	3.34E-01	0,75 g/l BuOH	5.6	51255	5	Cytoplasmic	COG0065	Amino acid transport and metabolism	
26988712	PP_1986	leuD	isopropylmalate isomerase small subunit	1.1	6.03E-01	0,75 g/l BuOH	5.3	24284	9	Cytoplasmic	COG0066	Amino acid transport and metabolism	
26988713	PP_1987		UbiE/COQ5 family methyltransferase	1.2	6.81E-01	Control	5.8	28181	3	Cytoplasmic	COG2226	Coenzyme metabolism	
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.2	5.40E-01	0,75 g/l BuOH	4.8	38824	8	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.1	7.03E-01	Control	5.3	40672	17	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.3	8.03E-01	0,75 g/l BuOH	3.9	96918	27	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.1	8.75E-01	0,75 g/l BuOH	7.8	32510	5	Cytoplasmic	COG0777	Lipid metabolism	
26988722	PP_1997	folC	FolC bifunctional protein	1.3	3.26E-01	0,75 g/l BuOH	4.8	46895	3	Cytoplasmic	COG0285	Coenzyme metabolism	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.4	2.40E-01	0,75 g/l BuOH	6.5	55400	12	Cytoplasmic	COG0034	Nucleotide transport and metabolism	

26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	1.4	6.95E-02	0,75 g/l BuOH	5.4	43284	4	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26988727	PP_2002		oxidoreductase	1.1	5.00E-01	0,75 g/l BuOH	6.6	27212	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988731	PP_2006		hypothetical protein	2.6	7.28E-03	Control	5.1	63743	38	Unknown			
26988732	PP_2007		P-47-related protein	1.7	8.92E-02	Control	5.8	44707	8	Unknown			
26988733	PP_2008	fadH	NADH:flavin oxidoreductase/NADH oxidase	1.6	3.33E-01	Control	7.0	73935	3	Cytoplasmic	COG1902	Energy production and conversion	
26988737	PP_2012	ppnK	inorganic polyphosphate/ATP-NAD kinase	1.1	8.29E-01	Control	7.0	34318	2	Cytoplasmic	COG0061	Coenzyme metabolism	
26988742	PP_2017	pepN	aminopeptidase N	1.1	6.37E-01	Control	4.8	99573	32	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988743	PP_2018		BNR domain-containing protein	1.2	3.80E-01	0,75 g/l BuOH	4.5	33691	6	Unknown	COG4447	General function prediction only	
26988744	PP_2019		hypothetical protein	1.9	1.91E-01	0,75 g/l BuOH	6.6	87732	6	Cytoplasmic Membrane	COG1033	General function prediction only	
26988746	PP_2021		hypothetical protein	1.1	2.13E-01	0,75 g/l BuOH	7.2	40684	3	Periplasmic	COG2706	Carbohydrate transport and metabolism	
26988749	PP_2024	sbcC	SMC domain protein	1.6	3.11E-01	0,75 g/l BuOH	5.5	136091	6	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26988757	PP_2032		ATPase	1.3	3.85E-01	0,75 g/l BuOH	5.0	35347	2	Cytoplasmic	COG0714	General function prediction only	
26988805	PP_2080		NAD-glutamate dehydrogenase	1.4	1.02E-01	Control	5.8	187043	68	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988806	PP_2081		hypothetical protein	1.2	3.80E-01	0,75 g/l BuOH	6.6	30824	4	Cytoplasmic	COG1806	Function unknown	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.5	8.30E-02	0,75 g/l BuOH	4.8	86015	39	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.4	4.43E-01	0,75 g/l BuOH	5.8	29111	6	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.2	2.82E-01	0,75 g/l BuOH	4.5	37012	27	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	1.3	8.37E-01	0,75 g/l BuOH	8.2	35545	5	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism	
26988823	PP_2098	dacB	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	1.2	2.13E-01	0,75 g/l BuOH	9.9	50799	4	Periplasmic	COG2027	Cell envelope biogenesis, outer membrane	
26988827	PP_2102		deoxyguanosinetriphosphate triphosphohydrolase-like protein	1.4	4.02E-01	Control	6.9	49908	3	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	1.0	8.33E-01	Control	6.0	57068	16	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988836	PP_2112	acnA	aconitate hydratase	1.2	5.12E-01	Control	5.7	99147	23	Cytoplasmic	COG1048	Energy production and conversion	
26988841	PP_2117	pdxB	erythronate-4-phosphate dehydrogenase	1.5	7.88E-02	0,75 g/l BuOH	5.1	41614	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26988847	PP_2123	moeA	molybdopterin biosynthesis MoeA protein	1.3	2.66E-01	0,75 g/l BuOH	5.1	43963	2	Cytoplasmic	COG0303	Coenzyme metabolism	
26988852	PP_2128	chev-2	chemotaxis protein CheV	1.0	8.71E-01	0,75 g/l BuOH	6.5	34556	5	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26988853	PP_2129		MOSC domain containing protein	1.2	1.08E-01	Control	5.5	29621	7	Cytoplasmic	COG3217	General function prediction only	
26988854	PP_2130		soluble lytic transglycosylase	1.7	1.91E-01	0,75 g/l BuOH	9.9	75337	10	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988855	PP_2131		ABC transporter ATP-binding protein	1.4	2.33E-01	0,75 g/l BuOH	5.1	71398	6	Cytoplasmic	COG0488	General function prediction only	
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.1	4.09E-01	0,75 g/l BuOH	5.9	77449	14	Cytoplasmic	COG1250	Lipid metabolism	
26988861	PP_2137	fadA	3-ketoacyl-CoA thiolase	1.1	6.33E-01	0,75 g/l BuOH	7.0	41556	2	Cytoplasmic	COG0183	Lipid metabolism	
26988863	PP_2139	topA	DNA topoisomerase I	1.2	2.80E-01	Control	8.0	97239	27	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
26988867	PP_2143	lexA-1	LexA repressor	1.1	7.89E-01	0,75 g/l BuOH	6.7	22147	6	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
26988868	PP_2144		TetR family transcriptional regulator	1.2	5.37E-01	0,75 g/l BuOH	9.8	26183	5	Cytoplasmic	COG1309	Transcription	
26988869	PP_2145	nagZ	beta-hexosaminidase	1.4	1.39E-01	0,75 g/l BuOH	6.3	36513	4	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
26988872	PP_2148	mfd	transcription-repair coupling factor	1.1	2.56E-01	Control	5.7	128301	13	Unknown	COG1197	DNA replication, recombination, and repair	Transcription
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.5	5.90E-02	0,75 g/l BuOH	7.7	53014	27	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	1.6	4.80E-01	0,75 g/l BuOH	7.7	50905	6	Cytoplasmic	COG1249	Energy production and conversion	
26988876	PP_2152		glycerophosphoryl diester phosphodiesterase	1.0	7.85E-01	0,75 g/l BuOH	7.5	26252	10	Cytoplasmic	COG0584	Energy production and conversion	
26988877	PP_2153		type IV pilus assembly PilZ	1.3	4.02E-01	0,75 g/l BuOH	5.0	21858	4	Cytoplasmic			
26988879	PP_2155	lolD	lipoprotein releasing system, ATP-binding protein	1.3	1.59E-01	0,75 g/l BuOH	7.3	25304	3	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26988882	PP_2158		two component heavy metal response transcriptional regulator	1.2	9.15E-01	Control	5.0	25354	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	1.1	9.70E-01	Control	6.5	30686	4	Cytoplasmic	COG2904	Function unknown	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.3	1.64E-01	0,75 g/l BuOH	5.3	26061	9	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988892	PP_2168	tal	transaldolase B	1.6	2.65E-02	0,75 g/l BuOH	5.0	33615	15	Unknown	COG0176	Carbohydrate transport and metabolism	
26988899	PP_2175		short-chain dehydrogenase/reductase SDR	1.1	3.51E-01	0,75 g/l BuOH	6.6	24818	3	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988908	PP_2184		NADH dehydrogenase (quinone)	1.1	4.91E-01	0,75 g/l BuOH	4.8	55160	2	Cytoplasmic	COG1894	Energy production and conversion	
26988909	PP_2185		formate dehydrogenase, alpha subunit	2.8	4.82E-02	Control	6.5	104885	3	Cytoplasmic	COG3383	General function prediction only	
26988911	PP_2187		universal stress protein	1.2	1.29E-01	0,75 g/l BuOH	6.3	31384	4	Cytoplasmic	COG0589	Signal transduction mechanisms	
26988919	PP_2195		periplasmic polyamine-binding protein	1.2	6.15E-01	0,75 g/l BuOH	5.5	39788	5	Periplasmic	COG0687	Amino acid transport and metabolism	
26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	2.0	3.02E-03	0,75 g/l BuOH	6.0	61223	9	Cytoplasmic	COG0365	Lipid metabolism	
26988938	PP_2214	fadB2x	short-chain dehydrogenase/reductase SDR	1.4	1.89E-01	0,75 g/l BuOH	6.7	26030	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988939	PP_2215	fadAx	acetyl-CoA acetyltransferase	1.3	4.56E-02	0,75 g/l BuOH	6.9	41382	7	Cytoplasmic	COG0183	Lipid metabolism	
26988941	PP_2217	fadB1x	enoyl-CoA hydratase/isomerase	1.4	2.26E-01	0,75 g/l BuOH	5.2	27668	11	Cytoplasmic	COG1024	Lipid metabolism	
26988957	PP_2233		isochorismatase superfamily hydrolase	2.8	1.40E-01	0,75 g/l BuOH	6.0	19296	9	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988962	PP_2238		peptidase M24	1.2	1.12E-02	0,75 g/l BuOH	5.4	68915	8	Unknown	COG0006	Amino acid transport and metabolism	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.3	2.29E-01	Control	5.1	68646	19	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988988	PP_2264		extracellular solute-binding protein, family 1	1.0	7.89E-01	0,75 g/l BuOH	5.6	65243	28	Unknown	COG1653	Carbohydrate transport and metabolism	
26988989	PP_2265	folD-2	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahy	1.2	2.01E-01	0,75 g/l BuOH	6.4	30623	5	Cytoplasmic	COG0190	Coenzyme metabolism	
26989016	PP_2292		hypothetical protein	1.1	4.44E-01	0,75 g/l BuOH	5.8	28522	12	Cytoplasmic			
26989023	PP_2299	tig	trigger factor	1.5	1.36E-01	0,75 g/l BuOH	4.5	49190	24	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
26989024	PP_2300	clpP	ATP-dependent Clp protease proteolytic subunit	1.0	9.80E-01	Control	5.6	23515	8	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.6	2.84E-01	0,75 g/l BuOH	4.8	48526	17	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
26989026	PP_2302	lon-2	ATP-dependent protease La	1.2	1.08E-01	Control	5.9	88722	31	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.1	7.88E-01	0,75 g/l BuOH	4.8	68580	10	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
26989031	PP_2307		CHAD domain containing protein	1.3	2.42E-01	Control	10.8	29498	8	Cytoplasmic	COG5607	Function unknown	
26989032	PP_2308		acyl-CoA thioesterase II	1.1	6.37E-01	Control	6.1	28745	5	Unknown	COG1946	Lipid metabolism	
26989035	PP_2311		TatD family hydrolase	1.4	3.29E-01	0,75 g/l BuOH	5.9	29409	3	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
26989044	PP_2320		ErfK/YbiS/YcfS/YnhG family protein	1.1	6.57E-01	Control	5.4	35051	8	Unknown	COG1376	Function unknown	
26989048	PP_2324	aroF-1	phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	1.31E-01	0,75 g/l BuOH	6.4	40260	7	Cytoplasmic	COG0722	Amino acid transport and metabolism	
26989051	PP_2327	cysB	transcriptional regulator CysB	1.0	7.74E-01	Control	6.7	35955	10	Cytoplasmic	COG0583	Transcription	
26989052	PP_2328	cysH	phosphoadenosine phosphosulfate reductase	1.4	2.71E-01	0,75 g/l BuOH	6.5	27896	9	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26989054	PP_2330		alpha-L-glutamate ligase-like protein	1.1	6.88E-01	Control	6.8	35904	2	Cytoplasmic			
26989055	PP_2331		hypothetical protein	1.0	8.30E-01	0,75 g/l BuOH	7.9	57064	5	Cytoplasmic Membrane			
26989058	PP_2334	prpB	2-methylisocitrate lyase	1.2	4.59E-01	Control	5.4	31811	9	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26989059	PP_2335		methylcitrate synthase	1.2	1.99E-01	Control	6.7	41995	14	Cytoplasmic	COG0372	Energy production and conversion	
26989060	PP_2336		aconitate hydratase	1.6	3.45E-02	Control	5.3	93961	11	Cytoplasmic	COG1048	Energy production and conversion	
26989061	PP_2337		hypothetical protein	1.5	3.48E-01	Control	5.2	41312	2	Cytoplasmic	COG2828	Function unknown	
26989062	PP_2338	prpD	2-methylcitrate dehydratase	1.1	5.18E-01	0,75 g/l BuOH	7.1	54860	13	Cytoplasmic	COG2079	General function prediction only	
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.2	4.48E-01	Control	5.0	93609	53	Cytoplasmic	COG1049	Energy production and conversion	
26989075	PP_2351		acetyl-CoA synthetase	1.1	9.63E-01	0,75 g/l BuOH	6.1	68868	2	Cytoplasmic	COG0365	Lipid metabolism	
26989080	PP_2356		phytochrome family protein	1.2	4.97E-01	Control	6.2	83859	4	Cytoplasmic Membrane	COG4251	Signal transduction mechanisms	
26989085	PP_2361	csuC	type 1 pili usher pathway chaperone CsuC	1.2	3.04E-01	Control	10.3	28448	7	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
26989088	PP_2364		hypothetical protein	1.7	1.70E-02	0,75 g/l BuOH	5.2	42461	6	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.4	9.57E-02	0,75 g/l BuOH	5.8	62191	26	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP_2375	metH	B12-dependent methionine synthase	1.1	3.83E-01	0,75 g/l BuOH	4.7	135408	30	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989102	PP_2378	yhgI	yhgI protein	1.4	2.93E-01	0,75 g/l BuOH	4.3	20955	3	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
26989119	PP_2396		hypothetical protein	1.2	8.77E-01	0,75 g/l BuOH	8.9	20592	13	Periplasmic			
26989159	PP_2436		LysR family transcriptional regulator	1.0	9.81E-01	0,75 g/l BuOH	9.4	35025	2	Cytoplasmic	COG0583	Transcription	
26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	1.6	1.94E-01	0,75 g/l BuOH	4.8	20507	10	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26989165	PP_2442		hypothetical protein	1.3	7.31E-02	0,75 g/l BuOH	5.2	23851	9	Cytoplasmic	COG3132	Function unknown	
26989170	PP_2447		hypothetical protein	1.1	9.99E-01	0,75 g/l BuOH	10.2	26784	3	Unknown			
26989176	PP_2453	ansA	L-asparaginase, type II	1.4	4.63E-01	0,75 g/l BuOH	7.9	38608	9	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
26989177	PP_2454	rbsB	monosaccharide-transporting ATPase	1.2	4.56E-01	0,75 g/l BuOH	5.9	33763	10	Periplasmic	COG1879	Carbohydrate transport and metabolism	
26989183	PP_2460		inosine/uridine-preferring nucleoside hydrolase	1.3	4.25E-01	0,75 g/l BuOH	6.2	34388	2	Unknown	COG1957	Nucleotide transport and metabolism	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.4	2.00E-01	0,75 g/l BuOH	5.8	72697	13	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	

26989189	PP_2466	infC	translation initiation factor IF-3	1.4	3.26E-01	0,75 g/l BuOH	10.0	20120	11	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	2.0	4.52E-01	0,75 g/l BuOH	12.1	13280	2	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989192	PP_2469	pheS	phenylalanyl-tRNA synthetase subunit alpha	1.2	1.16E-01	0,75 g/l BuOH	5.2	38082	7	Cytoplasmic	COG0016	Translation, ribosomal structure and biogenesis	
26989193	PP_2470	pheT	phenylalanyl-tRNA synthetase subunit beta	1.0	8.03E-01	Control	4.8	86617	20	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis	
26989197	PP_2474		glutathione S-transferase family protein	1.2	3.68E-01	Control	6.1	23793	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989198	PP_2475		TetR family transcriptional regulator	1.2	6.52E-01	0,75 g/l BuOH	6.4	22413	4	Cytoplasmic	COG1309	Transcription	
26989211	PP_2488		succinic-semialdehyde dehydrogenase	1.7	7.58E-02	Control	5.1	50254	2	Cytoplasmic	COG1012	Energy production and conversion	
26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	1.0	9.78E-01	0,75 g/l BuOH	6.5	45235	9	Cytoplasmic	COG2873	Amino acid transport and metabolism	
26989256	PP_2536		glutathione S-transferase family protein	1.1	5.15E-01	0,75 g/l BuOH	6.5	23574	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989258	PP_2538		hypothetical protein	1.1	5.78E-01	0,75 g/l BuOH	8.2	26353	2	Unknown			
26989260	PP_2540		short chain dehydrogenase/reductase family oxidoreductase	1.3	2.87E-01	0,75 g/l BuOH	7.7	26775	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989270	PP_2550		hypothetical protein	1.2	9.75E-01	0,75 g/l BuOH	4.6	25315	2	Cytoplasmic	COG0217	Function unknown	
26989274	PP_2554		4-hydroxyphenylpyruvate dioxygenase	1.4	3.83E-01	Control	5.0	70406	3	Cytoplasmic	COG3185	Amino acid transport and metabolism	General function prediction only
26989289	PP_2569		major facilitator transporter	1.8	3.61E-02	Control	9.0	60538	4	Cytoplasmic Membrane	COG2223	Inorganic ion transport and metabolism	
26989384	PP_2665	agmR	LuxR family two component transcriptional regulator	6.2	1.64E-02	0,75 g/l BuOH	5.9	24536	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26989387	PP_2668		efflux ABC transporter ATP-binding protein	20.9	8.92E-03	0,75 g/l BuOH	9.8	27178	5	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26989391	PP_2672		LuxR family DNA-binding response regulator	5.5	1.80E-03	0,75 g/l BuOH	8.3	23226	5	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26989392	PP_2673		pentapeptide repeat-containing protein	29.9	9.99E-03	0,75 g/l BuOH	5.3	23569	13	Extracellular	COG1357	Function unknown	
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	43.4	8.21E-04	0,75 g/l BuOH	7.0	69173	46	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989395	PP_2676		periplasmic protein	101.7	1.00E-02	0,75 g/l BuOH	6.5	34540	5	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26989396	PP_2677		hypothetical protein	25.5	4.41E-03	0,75 g/l BuOH	5.3	28059	7	Unknown			
26989397	PP_2678		beta-lactamase domain protein	23.7	1.37E-04	0,75 g/l BuOH	6.4	33711	8	Unknown	COG0491	General function prediction only	
26989398	PP_2679		quinoprotein ethanol dehydrogenase	103.6	2.60E-05	0,75 g/l BuOH	9.1	64883	7	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	16.5	1.08E-03	0,75 g/l BuOH	5.5	54903	26	Cytoplasmic	COG1012	Energy production and conversion	
26989402	PP_2683		PAS/PAC sensor hybrid histidine kinase	1.3	6.56E-02	0,75 g/l BuOH	6.6	62695	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1.4	3.05E-01	Control	6.3	38659	23	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26989418	PP_2699		hypothetical protein	2.1	9.02E-02	Control	6.5	40451	5	Cytoplasmic			
26989525	PP_2806		TetR family transcriptional regulator	1.5	6.59E-01	0,75 g/l BuOH	5.3	21294	5	Unknown	COG3226	Function unknown	
26989572	PP_2853		hypothetical protein	1.2	7.17E-01	0,75 g/l BuOH	4.5	46020	4	Unknown			
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	1.0	8.72E-01	0,75 g/l BuOH	5.7	58659	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989586	PP_2867		pyridine nucleotide-disulphide oxidoreductase family protein	1.7	3.88E-01	0,75 g/l BuOH	5.6	42483	3	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26989603	PP_2884		XRE family transcriptional regulator	1.7	5.09E-01	0,75 g/l BuOH	4.9	19995	2	Cytoplasmic	COG1396	Transcription	
26989609	PP_2890	xthA	exonuclease III	1.4	5.40E-01	0,75 g/l BuOH	6.7	30951	4	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
26989610	PP_2891		acetyltransferase	1.1	4.53E-01	0,75 g/l BuOH	7.6	25615	5	Cytoplasmic Membrane			
26989621	PP_2902		UDP-2,3-diacylglucosamine hydrolase	1.4	5.31E-01	0,75 g/l BuOH	8.7	27325	2	Cytoplasmic	COG2908	Function unknown	
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.5	2.16E-02	0,75 g/l BuOH	6.1	64654	10	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	1.4	2.19E-02	0,75 g/l BuOH	5.8	51676	5	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	1.2	4.52E-01	0,75 g/l BuOH	5.0	35225	8	Cytoplasmic	COG0113	Coenzyme metabolism	
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase	1.0	6.41E-01	0,75 g/l BuOH	8.0	59671	7	Unknown	COG0579	General function prediction only	
26989647	PP_2928		saccharopine dehydrogenase	1.7	9.21E-02	0,75 g/l BuOH	5.0	45363	4	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989651	PP_2932		amidase	1.2	6.96E-01	0,75 g/l BuOH	4.5	60346	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26989652	PP_2933		glutathione S-transferase YghU	1.4	2.73E-01	0,75 g/l BuOH	6.0	31202	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989661	PP_2942		response regulator	1.2	2.84E-01	Control	5.6	51291	5	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26989663	PP_2944		sensor histidine kinase	1.7	2.51E-01	Control	6.1	67470	4	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989738	PP_3019		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	1.0	9.34E-01	0,75 g/l BuOH	5.1	26214	6	Cytoplasmic	COG0388	General function prediction only	
26989790	PP_3071		acetoacetyl-CoA synthetase	1.2	3.26E-01	Control	6.4	72303	3	Cytoplasmic	COG0365	Lipid metabolism	
26989792	PP_3073	bdhA	3-hydroxybutyrate dehydrogenase	1.1	7.21E-01	0,75 g/l BuOH	6.9	26852	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989808	PP_3089		hypothetical protein	4.4	3.10E-01	Control	5.3	19453	7	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	1.7	2.36E-02	Control	6.8	138655	14	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989814	PP_3095		chaperone-associated ATPase	1.6	2.97E-02	Control	6.1	96474	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26989818	PP_3099		hypothetical protein	1.1	4.95E-01	0,75 g/l BuOH	4.9	56072	10	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989825	PP_3106		hypothetical protein	2.4	1.44E-02	Control	5.6	69529	19	Cytoplasmic	COG3501	Function unknown	
26989827	PP_3108		rhs-related protein	2.9	1.52E-02	Control	6.0	155811	36	Unknown	COG3209	Cell envelope biogenesis, outer membrane	
26989839	PP_3120		aldo/keto reductase family oxidoreductase	1.1	3.91E-01	0,75 g/l BuOH	6.4	27746	2	Cytoplasmic	COG0656	General function prediction only	
26989845	PP_3126		polysaccharide export protein	1.0	6.40E-01	Control	4.9	19528	6	Unknown	COG1596	Cell wall	membrane
26989846	PP_3127		lipopolysaccharide biosynthesis protein	1.0	9.65E-01	0,75 g/l BuOH	9.0	57141	24	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989847	PP_3128		protein-tyrosine kinase	1.1	6.92E-01	Control	7.1	29623	8	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
26989848	PP_3129	galE	UDP-glucose 4-epimerase	1.3	5.42E-02	Control	6.3	34967	5	Cytoplasmic	COG1087	Cell envelope biogenesis, outer membrane	
26989849	PP_3130		hypothetical protein	2.0	1.20E-02	Control	6.4	96618	5	Unknown			
26989850	PP_3131		hypothetical protein	2.0	1.96E-01	Control	10.2	56350	2	Cytoplasmic Membrane			
26989853	PP_3134		transferase hexapeptide repeat containing protein	1.6	9.00E-01	Control	9.9	25699	8	Cytoplasmic	COG0110	General function prediction only	
26989854	PP_3135		glycosyl transferase	1.2	1.02E-02	Control	8.6	35887	11	Cytoplasmic	COG1216	General function prediction only	
26989857	PP_3138		VirK domain-containing protein	1.7	3.18E-01	Control	8.6	37023	2	Unknown	COG2990	Function unknown	
26989858	PP_3139		glycosyl transferase, group 1 family protein	1.1	9.63E-01	0,75 g/l BuOH	7.9	44606	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26989859	PP_3140		glycosyl transferase, group 2 family protein	1.3	3.82E-01	Control	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989860	PP_3141		Wec8/TagA/CpsF family glycosyl transferase	1.1	7.93E-01	0,75 g/l BuOH	10.2	27576	6	Unknown	COG1922	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	1.3	2.89E-01	Control	9.7	29885	16	Unknown			
26989876	PP_3157		inositol monophosphatase family protein	1.1	7.02E-01	0,75 g/l BuOH	4.3	27793	5	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26989883	PP_3164	benD	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	2.8	4.11E-02	Control	6.0	27087	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989904	PP_3185	pet18	transcriptional activator, TenA family	1.3	1.93E-01	0,75 g/l BuOH	4.9	23859	3	Unknown	COG0819	Transcription	
26989905	PP_3186		transcriptional activator, TenA family	1.0	9.61E-01	0,75 g/l BuOH	4.8	24300	7	Cytoplasmic	COG0819	Transcription	
26989966	PP_3248		Dyp-type peroxidase family	1.3	6.30E-01	Control	4.6	31295	4	Unknown	COG2837	Inorganic ion transport and metabolism	
26989967	PP_3249		aldo/keto reductase	1.1	5.33E-01	0,75 g/l BuOH	8.2	29657	3	Cytoplasmic	COG0656	General function prediction only	
26990076	PP_3361		hypothetical protein	1.8	6.86E-02	Control	6.3	110896	5	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26990079	PP_3364		response regulator	1.7	1.46E-01	0,75 g/l BuOH	6.4	91750	4	Cytoplasmic	COG4251	Signal transduction mechanisms	
26990095	PP_3380	ptxS	PtxS family transcriptional regulator	1.1	8.37E-01	Control	6.9	36789	4	Cytoplasmic	COG1609	Transcription	
26990127	PP_3414		methyl-accepting chemotaxis transducer/sensory box protein	1.4	1.34E-01	Control	6.8	48686	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990144	PP_3431		ThiJ/Pfpl domain protein	1.2	4.06E-01	0,75 g/l BuOH	6.5	25246	12	Unknown	COG0693	General function prediction only	
26990154	PP_3441		hypothetical protein	1.1	8.73E-01	0,75 g/l BuOH	9.3	43139	4	Cytoplasmic			
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	1.1	7.00E-01	Control	6.2	59980	21	Cytoplasmic	COG1012	Energy production and conversion	
26990161	PP_3448	nfrB	bacteriophage N4 adsorption protein B	1.2	3.68E-01	0,75 g/l BuOH	7.4	82370	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26990172	PP_3459		hypothetical protein	10.1	1.74E-03	0,75 g/l BuOH	9.0	42365	4	Periplasmic			
26990203	PP_3491		enoly-coenzyme A hydratase/isomerase family protein	1.1	5.15E-01	Control	4.9	39382	6	Cytoplasmic	COG1024	Lipid metabolism	
26990204	PP_3492	acdA	acyl-CoA dehydrogenase domain-containing protein	1.1	4.19E-01	Control	5.7	41553	3	Cytoplasmic	COG1960	Lipid metabolism	
26990219	PP_3507	cobN	cobaltochelatase subunit CobN	1.3	6.83E-01	0,75 g/l BuOH	5.4	138545	4	Cytoplasmic	COG1429	Coenzyme metabolism	
26990220	PP_3508	cobW	cobalamin biosynthesis protein CobW	1.4	3.28E-01	0,75 g/l BuOH	4.6	38579	7	Cytoplasmic	COG0523	General function prediction only	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.5	3.00E-02	0,75 g/l BuOH	7.2	36863	14	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990242	PP_3530		hypothetical protein	1.2	3.09E-01	Control	6.2	31546	7	Cytoplasmic	COG3257	General function prediction only	
26990252	PP_3540	mvaB	hydroxymethylglutaryl-CoA lyase	1.1	4.00E-01	Control	5.4	31341	7	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26990258	PP_3546		PAS/PAC sensor hybrid histidine kinase	1.3	4.85E-01	0,75 g/l BuOH	5.0	76414	2	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	1.4	1.70E-01	0,75 g/l BuOH	6.0	26030	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990265	PP_3553		acyl-CoA synthetase	73.6	4.86E-04	0,75 g/l BuOH	6.4	59576	10	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990266	PP_3554		acyl-CoA dehydrogenase domain-containing protein	7.0	1.65E-04	0,75 g/l BuOH	5.5	63339	11	Cytoplasmic	COG1960	Lipid metabolism	
26990269	PP_3557		methyl-accepting chemotaxis transducer	1.1	5.82E-01	Control	4.7	76982	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990270	PP_3558		substrate-binding region of ABC-type glycine betaine transport system	1.4	5.23E-01	0,75 g/l BuOH	5.5	36928	4	Periplasmic	COG2113	Amino acid transport and metabolism	

26990275	PP_3563		hypothetical protein	1.1	4.46E-01	0,75 g/l BuOH	5.1	30285	3	Unknown	COG2340	Function unknown	
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	1.1	8.34E-01	0,75 g/l BuOH	6.9	85338	3	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990290	PP_3578		phosphoglucomutase	1.4	2.23E-02	0,75 g/l BuOH	5.6	58620	14	Unknown	COG0033	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	10.5	9.43E-01	0,75 g/l BuOH	5.2	53952	3	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990298	PP_3587	tpx	redoxin domain protein	3.1	5.94E-01	Control	4.7	17409	3	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.3	6.63E-02	0,75 g/l BuOH	5.9	43631	10	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990313	PP_3602		ketoglutarate semialdehyde dehydrogenase	1.4	5.72E-01	0,75 g/l BuOH	5.2	55538	11	Cytoplasmic	COG1012	Energy production and conversion	
26990314	PP_3603		GntR family transcriptional regulator	1.1	6.95E-01	0,75 g/l BuOH	9.0	28149	6	Cytoplasmic	COG2186	Transcription	
26990322	PP_3611		hypothetical protein	1.1	9.57E-01	0,75 g/l BuOH	9.7	20824	9	Unknown			
26990331	PP_3620		hypothetical protein	1.8	2.69E-01	0,75 g/l BuOH	4.3	81519	2	Cytoplasmic	COG1944	Function unknown	
26990333	PP_3622		isoquinoline 1-oxidoreductase, beta subunit	1.3	2.72E-01	Control	7.0	80889	17	Cytoplasmic Membrane	COG1529	Energy production and conversion	
26990347	PP_3636		sulfonate ABC transporter periplasmic sulfonate-binding protein	1.2	6.41E-01	0,75 g/l BuOH	7.3	43742	9	Cytoplasmic Membrane	COG0715	Inorganic ion transport and metabolism	
26990348	PP_3637		sulfonate ABC transporter ATP-binding protein	1.2	7.03E-02	Control	7.1	29618	2	Cytoplasmic Membrane	COG1116	Inorganic ion transport and metabolism	
26990349	PP_3638		acyl-CoA dehydrogenase	1.5	3.42E-01	0,75 g/l BuOH	6.1	38476	11	Cytoplasmic	COG1960	Lipid metabolism	
26990360	PP_3649		GntR family transcriptional regulator	1.1	4.53E-01	0,75 g/l BuOH	7.0	28178	3	Cytoplasmic	COG1802	Transcription	
26990362	PP_3651		GAF sensor hybrid histidine kinase	1.8	4.16E-01	0,75 g/l BuOH	4.9	79274	3	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26990373	PP_3662		decarboxylase family protein	1.0	5.16E-01	Control	6.7	50729	9	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	1.5	1.62E-02	Control	5.8	82061	44	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990380	PP_3669		LysR family transcriptional regulator	1.6	1.96E-01	Control	5.3	33285	2	Cytoplasmic	COG0583	Transcription	
26990389	PP_3680		hypothetical protein	1.6	1.63E-01	0,75 g/l BuOH	6.3	75093	8	Unknown	COG3593	DNA replication, recombination, and repair	
26990399	PP_3691		DNA helicase-related protein	1.6	2.84E-02	Control	5.0	245278	56	Unknown	COG1112	DNA replication, recombination, and repair	
26990400	PP_3692		hypothetical protein	2.1	2.02E-01	Control	8.0	98331	4	Cytoplasmic	COG4988	Energy production and conversion	Posttranslational modification, protein turnover, chaperones
26990402	PP_3694		hypothetical protein	1.3	4.29E-01	Control	7.6	35864	2	Cytoplasmic			
26990414	PP_3706		hypothetical protein	1.0	9.34E-01	0,75 g/l BuOH	5.7	35856	2	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26990421	PP_3713	catA	catechol 1,2-dioxygenase	1.2	2.44E-01	Control	5.1	34249	8	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26990448	PP_3742		glutathione S-transferase family protein	1.4	2.21E-01	0,75 g/l BuOH	6.4	24042	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26990459	PP_3754		beta-ketothiolase	1.3	2.14E-01	0,75 g/l BuOH	6.9	40988	11	Cytoplasmic	COG0183	Lipid metabolism	
26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	1.5	1.29E-01	0,75 g/l BuOH	6.3	30088	5	Cytoplasmic	COG1250	Lipid metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.8	9.05E-02	Control	4.9	129450	37	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990468	PP_3763		precorrin 6A synthase	1.2	6.51E-01	0,75 g/l BuOH	4.9	27798	2	Cytoplasmic	COG2243	Coenzyme metabolism	
26990480	PP_3775		sarcosine oxidase	1.3	4.85E-02	Control	6.4	41164	22	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777		hypothetical protein	2.3	2.11E-02	Control	5.2	31324	15	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	1.3	3.57E-01	Control	6.2	27714	18	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	1.2	7.23E-01	0,75 g/l BuOH	7.0	53071	11	Cytoplasmic	COG0635	Coenzyme metabolism	
26990488	PP_3783		hypothetical protein	1.4	1.94E-01	Control	5.8	34938	13	Cytoplasmic			
26990489	PP_3784		hypothetical protein	1.5	8.64E-02	Control	5.4	41070	13	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	1.6	3.80E-02	Control	6.5	50495	10	Cytoplasmic			
26990491	PP_3786		aminotransferase	1.1	5.10E-01	Control	6.4	44067	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990492	PP_3787		hypothetical protein	2.0	3.07E-02	Control	6.8	33215	4	Unknown	COG0332	acyl-carrier-protein	
26990495	PP_3790	dapF	diaminopimelate epimerase	1.1	4.82E-01	Control	6.0	29286	5	Cytoplasmic	COG0253	Amino acid transport and metabolism	
26990511	PP_3806		isochorismatase superfamily hydrolase	1.3	7.94E-01	Control	6.3	19515	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26990519	PP_3814		polyamine ABC transporter periplasmic polyamine-binding protein	1.3	9.83E-02	Control	5.2	37113	6	Periplasmic	COG0687	Amino acid transport and metabolism	
26990524	PP_3819	gor	glutathione reductase	1.6	5.48E-02	0,75 g/l BuOH	5.2	49180	5	Cytoplasmic	COG1249	Energy production and conversion	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.3	1.90E-01	0,75 g/l BuOH	5.3	30957	6	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990537	PP_3832		carbon storage regulator	4.7	3.19E-02	0,75 g/l BuOH	7.8	7271	2	Unknown	COG1551	Signal transduction mechanisms	
26990539	PP_3834		non-specific serine/threonine protein kinase	1.2	4.22E-01	0,75 g/l BuOH	6.6	51271	2	Cytoplasmic	COG0467	Signal transduction mechanisms	
26990544	PP_3839		alcohol dehydrogenase	1.1	9.60E-01	0,75 g/l BuOH	5.7	35397	10	Cytoplasmic	COG1064	General function prediction only	
26990627	PP_3922		periplasmic protease	1.8	6.28E-02	0,75 g/l BuOH	9.8	37502	4	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990631	PP_3926		short chain dehydrogenase	1.1	6.85E-01	0,75 g/l BuOH	7.4	26721	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990656	PP_3951	pcaI	3-oxoadipate CoA-transferase, subunit A	2.3	1.86E-02	Control	5.3	24319	2	Cytoplasmic	COG1788	Lipid metabolism	
26990659	PP_3954		periplasmic protein	1.3	1.38E-01	0,75 g/l BuOH	9.3	33239	15	Unknown	COG2358	General function prediction only	
26990693	PP_3988		hypothetical protein	1.3	4.96E-01	0,75 g/l BuOH	6.3	76259	13	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
26990704	PP_3999	cobA-2	uroporphyrin-III C-methyltransferase	1.0	8.33E-01	Control	6.8	49494	3	Cytoplasmic	COG0007	Coenzyme metabolism	
26990705	PP_4000	serS	seryl-tRNA synthetase	1.1	3.69E-01	0,75 g/l BuOH	5.1	46849	11	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
26990708	PP_4003	lolA	outer-membrane lipoprotein carrier protein	1.5	2.10E-01	0,75 g/l BuOH	9.5	25146	5	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	1.0	7.18E-01	0,75 g/l BuOH	6.4	91296	4	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.1	6.15E-01	Control	5.7	83310	18	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	1.0	8.46E-01	Control	5.4	45695	35	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.5	3.05E-01	0,75 g/l BuOH	5.4	79899	37	Cytoplasmic	COG2838	Energy production and conversion	
26990719	PP_4014	mnmA	tRNA-specific 2-thiouridylase MnmA	1.1	3.10E-01	0,75 g/l BuOH	5.5	41489	3	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
26990721	PP_4016	purB	adenylosuccinate lyase	1.8	1.65E-01	0,75 g/l BuOH	5.9	50555	13	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990726	PP_4021	est	alpha/beta hydrolase fold	1.6	7.99E-02	Control	6.1	30206	8	Cytoplasmic	COG0596	General function prediction only	
26990732	PP_4029	nudC	NADH pyrophosphatase	1.3	2.64E-01	0,75 g/l BuOH	5.0	30868	3	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
26990733	PP_4030		enoyl-CoA hydratase	1.1	4.74E-01	0,75 g/l BuOH	5.2	30613	6	Cytoplasmic	COG1024	Lipid metabolism	
26990737	PP_4034		allantoate amidohydrolase	1.3	5.14E-02	0,75 g/l BuOH	5.7	45010	21	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	1.0	6.07E-01	Control	7.9	53519	5	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP_4037		oxidoreductase	1.2	9.40E-02	Control	5.5	48815	30	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038		dihydropyrimidine dehydrogenase	1.1	6.70E-01	Control	5.1	46093	22	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990742	PP_4041		glycoside hydrolase 15-related	1.1	8.32E-01	0,75 g/l BuOH	6.4	69769	4	Cytoplasmic	COG3387	Carbohydrate transport and metabolism	
26990743	PP_4042	zwf-2	glucose-6-phosphate 1-dehydrogenase	1.6	1.54E-01	0,75 g/l BuOH	7.9	56311	2	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26990744	PP_4043	gnd	6-phosphogluconate dehydrogenase	1.0	7.64E-01	0,75 g/l BuOH	6.4	35366	5	Cytoplasmic	COG1023	Carbohydrate transport and metabolism	
26990751	PP_4050	glgA	glycogen synthase	2.2	8.65E-05	Control	6.0	57190	13	Cytoplasmic	COG0297	Carbohydrate transport and metabolism	
26990752	PP_4051		malto-oligosyltrehalose trehalohydrolase	1.4	1.18E-01	Control	6.0	64544	13	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990753	PP_4052	malQ	4-alpha-glucanotransferase	2.9	1.96E-02	Control	5.5	76475	24	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	2.8	5.85E-03	Control	6.6	103167	29	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	2.4	6.70E-04	Control	5.1	81044	22	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990759	PP_4058	glgB	glycogen branching enzyme	1.5	1.26E-01	0,75 g/l BuOH	5.9	82877	9	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990760	PP_4059		trehalose synthase	4.0	5.51E-02	Control	5.4	125589	10	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990761	PP_4060		alpha-amylase family protein	1.2	2.55E-01	Control	6.1	75542	7	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990764	PP_4063		AMP-binding domain protein	2.4	2.00E-01	Control	5.6	61594	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990765	PP_4064	ivd	acyl-CoA dehydrogenase domain-containing protein	1.1	6.75E-01	Control	7.2	46572	10	Cytoplasmic	COG1960	Lipid metabolism	
26990766	PP_4065		propionyl-CoA carboxylase	1.3	3.15E-01	Control	6.9	57504	5	Cytoplasmic	COG4799	Lipid metabolism	
26990767	PP_4066		gamma-carboxygeranoyl-CoA hydratase	1.5	1.14E-01	Control	5.5	30015	6	Cytoplasmic	COG1024	Lipid metabolism	
26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	1.5	2.98E-01	Control	5.8	69729	8	Cytoplasmic	COG4770	Lipid metabolism	
26990769	PP_4068		Cro/CI family transcriptional regulator	1.4	1.66E-01	0,75 g/l BuOH	4.9	26361	2	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
26990794	PP_4099	gacA	DNA-binding response regulator GacA	1.4	3.84E-01	Control	6.3	23138	4	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26990799	PP_4104		glutathione S-transferase family protein	1.3	9.52E-01	Control	7.8	26354	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26990806	PP_4111	fusA	elongation factor G	1.3	2.55E-01	Control	5.0	77832	19	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990809	PP_4115		NoIW domain protein	1.2	8.42E-01	0,75 g/l BuOH	6.7	29306	5	Unknown			
26990810	PP_4116	aceA	isocitrate lyase	3.1	1.87E-02	0,75 g/l BuOH	5.3	48633	13	Cytoplasmic	COG2224	Energy production and conversion	
26990814	PP_4120	nuoB	NADH dehydrogenase subunit B	1.0	7.33E-01	Control	4.9	25523	6	Cytoplasmic Membrane	COG0377	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.2	1.53E-01	0,75 g/l BuOH	6.5	67609	24	Cytoplasmic	COG0649	Energy production and conversion	
26990817	PP_4123	nuoF	NADH dehydrogenase I subunit F	1.2	2.90E-01	0,75 g/l BuOH	7.1	49135	13	Cytoplasmic	COG1894	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.1	5.78E-01	Control	5.9	97582	32	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	2.4	7.67E-01	0,75 g/l BuOH	6.1	37637	2	Cytoplasmic Membrane	COG1005	Energy production and conversion	

26990820	PP_4126	nuoI	NADH dehydrogenase subunit I	1.1	7.20E-01	Control	6.0	20517	4	Cytoplasmic	COG1143	Energy production and conversion
26990824	PP_4130	nuoM	NADH dehydrogenase subunit M	4.2	2.23E-02	0,75 g/l BuOH	8.2	55614	2	Cytoplasmic Membrane	COG1008	Energy production and conversion
26990832	PP_4138		NADPH-dependent FMN reductase	1.0	6.41E-01	Control	8.7	20354	11	Cytoplasmic	COG0431	General function prediction only
26990837	PP_4144	gloB	hydroxyacylglutathione hydrolase	1.5	1.76E-01	0,75 g/l BuOH	6.3	28767	2	Cytoplasmic	COG0491	General function prediction only
26990847	PP_4154		hypothetical protein	1.8	7.96E-02	Control	5.1	99530	2	Cytoplasmic	COG0160	Amino acid transport and metabolism
26990855	PP_4163		hypothetical protein	1.1	5.41E-01	Control	5.5	28880	3	Unknown		
26990861	PP_4169	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1.3	1.52E-01	0,75 g/l BuOH	6.6	36520	8	Cytoplasmic	COG0240	Energy production and conversion
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.3	2.56E-01	0,75 g/l BuOH	5.3	43264	14	Cytoplasmic	COG0304	Lipid metabolism
26990870	PP_4178		dienelactone hydrolase	1.1	7.59E-01	0,75 g/l BuOH	7.1	26269	12	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism
26990871	PP_4179	htpG	heat shock protein 90	1.0	9.21E-01	0,75 g/l BuOH	5.0	71610	37	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.2	4.66E-01	Control	6.2	30111	21	Cytoplasmic	COG0074	Energy production and conversion
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.0	6.73E-01	Control	6.1	41239	29	Cytoplasmic	COG0045	Energy production and conversion
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.2	7.78E-01	0,75 g/l BuOH	6.3	49912	22	Cytoplasmic	COG1249	Energy production and conversion
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.2	1.29E-01	0,75 g/l BuOH	5.1	42434	17	Cytoplasmic	COG0508	Energy production and conversion
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.2	1.74E-01	Control	6.5	106521	51	Cytoplasmic	COG0567	Energy production and conversion
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.2	4.51E-01	0,75 g/l BuOH	7.5	26000	16	Cytoplasmic Membrane	COG0479	Energy production and conversion
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.2	2.27E-02	0,75 g/l BuOH	6.2	63448	24	Cytoplasmic Membrane	COG1053	Energy production and conversion
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.5	1.40E-01	0,75 g/l BuOH	9.0	13579	2	Cytoplasmic Membrane	COG2142	Energy production and conversion
26990886	PP_4194	gltA	type II citrate synthase	1.6	1.25E-01	0,75 g/l BuOH	7.0	47622	23	Cytoplasmic	COG0372	Energy production and conversion
26990890	PP_4198		OmpA/MotB domain protein	1.0	8.31E-01	0,75 g/l BuOH	8.9	29694	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
26990892	PP_4200		hypothetical protein	1.4	3.78E-01	0,75 g/l BuOH	8.1	29611	2	Unknown	COG0834	Amino acid transport and metabolism
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	2.6	8.60E-03	0,75 g/l BuOH	4.9	31237	14	Unknown	COG2025	Energy production and conversion
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.4	2.82E-01	0,75 g/l BuOH	9.7	26361	17	Unknown	COG2086	Energy production and conversion
26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	1.5	6.86E-04	0,75 g/l BuOH	5.7	61082	17	Cytoplasmic	COG0644	Energy production and conversion
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.7	9.09E-01	0,75 g/l BuOH	5.5	89725	12	Outer Membrane	COG4773	Inorganic ion transport and metabolism
26990912	PP_4220		non-ribosomal peptide synthetase	7.9	6.56E-01	Control	5.2	287552	5	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism
26990928	PP_4237	dsbG	disulfide isomerase/thiol-disulfide oxidase	1.0	8.95E-01	0,75 g/l BuOH	8.6	27578	4	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones
26990940	PP_4249		hypothetical protein	1.2	2.86E-01	0,75 g/l BuOH	7.0	24715	3	Cytoplasmic	COG3571	General function prediction only
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	1.3	2.87E-01	0,75 g/l BuOH	9.6	53567	3	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.1	8.51E-01	Control	9.0	22637	11	Cytoplasmic	COG2993	Energy production and conversion
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.2	8.49E-02	0,75 g/l BuOH	5.2	35613	12	Unknown	COG2010	Energy production and conversion
26990956	PP_4265	anr	transcriptional regulator Anr	2.0	3.34E-01	0,75 g/l BuOH	6.5	27221	3	Cytoplasmic	COG0664	Signal transduction mechanisms
26990957	PP_4266	apt	adenine phosphoribosyltransferase	1.2	4.37E-01	0,75 g/l BuOH	4.6	20018	3	Cytoplasmic	COG0503	Nucleotide transport and metabolism
26990965	PP_4274	ligA	NAD-dependent DNA ligase LigA	3.1	3.01E-02	Control	5.3	84112	2	Cytoplasmic	COG0272	DNA replication, recombination, and repair
26990966	PP_4275	zipA	cell division protein ZipA	1.2	7.97E-01	0,75 g/l BuOH	6.0	35312	5	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning
26990967	PP_4276		chromosome segregation protein SMC	1.1	9.06E-01	0,75 g/l BuOH	4.7	131729	8	Cytoplasmic	COG1196	Cell division and chromosome partitioning
26990968	PP_4277		GntR family transcriptional regulator	1.2	3.70E-01	0,75 g/l BuOH	7.5	24972	8	Cytoplasmic	COG1802	Transcription
26990970	PP_4279	xdhB	xanthine dehydrogenase, XdhB subunit	1.6	1.17E-01	Control	6.4	88031	2	Cytoplasmic	COG4631	Nucleotide transport and metabolism
26990974	PP_4283		GntR family transcriptional regulator	1.4	1.07E-01	0,75 g/l BuOH	6.8	27912	6	Cytoplasmic	COG1802	Transcription
26990986	PP_4295		TetR family transcriptional regulator	1.5	1.15E-01	0,75 g/l BuOH	6.6	22721	5	Cytoplasmic	COG1309	Transcription
26990990	PP_4299	glxR	2-hydroxy-3-oxopropionate reductase	1.1	8.17E-01	Control	6.6	30864	3	Cytoplasmic	COG2084	Lipid metabolism
26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	1.2	4.37E-01	Control	6.3	36692	4	Periplasmic	COG1613	Inorganic ion transport and metabolism
26991006	PP_4315		PhzF family phenazine biosynthesis protein	1.2	9.22E-01	0,75 g/l BuOH	4.5	28437	7	Cytoplasmic	COG0384	General function prediction only
26991018	PP_4328		hypothetical protein	1.4	2.26E-01	Control	7.1	55477	5	Unknown		
26991022	PP_4332	cheW	purine-binding chemotaxis protein CheW	1.0	6.63E-01	Control	4.1	17784	2	Cytoplasmic	COG0835	Cell motility and secretion
26991026	PP_4336	motC	flagellar motor protein	1.1	6.50E-01	Control	4.9	25930	6	Cytoplasmic Membrane	COG1291	Cell motility and secretion
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	1.0	8.25E-01	Control	9.0	39451	9	Cytoplasmic	COG2201	Cell motility and secretion
26991028	PP_4338	cheA	chemotaxis protein CheA	1.1	9.31E-01	0,75 g/l BuOH	4.4	79674	26	Cytoplasmic	COG0643	Cell motility and secretion
26991029	PP_4339	cheZ	chemotaxis phosphatase, CheZ	1.0	9.77E-01	0,75 g/l BuOH	4.8	29533	14	Cytoplasmic	COG3143	Cell motility and secretion
26991032	PP_4342	fleN	flagellar number regulator FleN	1.1	4.70E-01	Control	8.0	29670	5	Cytoplasmic Membrane	COG0455	Cell motility
26991047	PP_4358	fliM	flagellar motor switch protein FliM	1.4	3.91E-01	Control	5.1	36011	2	Cytoplasmic	COG1868	Cell motility and secretion
26991052	PP_4363		response regulator receiver protein	1.0	5.10E-01	0,75 g/l BuOH	5.7	62118	4	Cytoplasmic	COG0745	Signal transduction mechanisms
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.6	1.04E-01	0,75 g/l BuOH	5.4	55551	13	Cytoplasmic	COG2204	Signal transduction mechanisms
26991067	PP_4378	fliC	flagellin FliC	4.4	2.13E-01	0,75 g/l BuOH	4.2	67846	29	Extracellular	COG1344	Cell motility and secretion
26991068	PP_4379		beta-ketoacyl-acyl-carrier-protein synthase I	1.1	5.89E-01	Control	4.8	33207	4	Cytoplasmic	COG0332	acyl-carrier-protein
26991069	PP_4380	flgL	flagellar hook-associated protein FlgL	2.6	3.24E-01	0,75 g/l BuOH	4.3	54938	3	Extracellular	COG1344	Cell motility and secretion
26991070	PP_4381	flgK	flagellar hook-associated protein FlgK	2.9	9.32E-03	0,75 g/l BuOH	4.5	69628	2	Extracellular	COG1256	Cell motility and secretion
26991081	PP_4392	cheR	chemotaxis protein methyltransferase CheR	1.1	8.88E-01	0,75 g/l BuOH	9.3	31084	2	Cytoplasmic	COG1352	Cell motility and secretion
26991082	PP_4393	cheV-3	chemotaxis protein CheV	1.1	8.77E-01	0,75 g/l BuOH	6.2	34498	11	Cytoplasmic	COG0835	Cell motility and secretion
26991086	PP_4397		type IV pilus assembly PilZ	1.2	2.40E-01	0,75 g/l BuOH	6.7	28449	17	Cytoplasmic	COG5581	Signal transduction mechanisms
26991088	PP_4399		glutamine synthetase	1.8	8.81E-01	0,75 g/l BuOH	6.2	45023	2	Cytoplasmic	COG0174	Amino acid transport and metabolism
26991091	PP_4402	bkdA2	2-oxoisovalerate dehydrogenase, beta subunit	4.7	1.78E-01	0,75 g/l BuOH	5.2	37143	3	Cytoplasmic	COG0022	Energy production and conversion
26991116	PP_4428		amino acid ABC transporter periplasmic amino acid-binding protein	1.3	2.31E-01	0,75 g/l BuOH	5.8	30355	3	Periplasmic	COG0834	Amino acid transport and metabolism
26991134	PP_4448		hypothetical protein	1.0	6.63E-01	Control	6.0	66331	28	Cytoplasmic	COG0433	Replication, recombination, and repair
26991155	PP_4469	gmk-1	phosphate metabolism protein/1,5-bisphosphokinase (PRPP-forming) PhnN	1.0	9.34E-01	0,75 g/l BuOH	9.7	21513	3	Cytoplasmic	COG3709	Inorganic ion transport and metabolism
26991159	PP_4473		aspartate kinase	1.3	2.31E-01	0,75 g/l BuOH	5.0	44605	13	Cytoplasmic	COG0527	Amino acid transport and metabolism
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.3	3.17E-01	0,75 g/l BuOH	5.1	94711	36	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis
26991161	PP_4475	astE	succinylglutamate desuccinylase	1.2	4.27E-01	0,75 g/l BuOH	6.2	37580	8	Cytoplasmic	COG2988	Amino acid transport and metabolism
26991163	PP_4477	astB	succinylarginine dihydrolase	1.2	3.87E-03	0,75 g/l BuOH	6.4	48862	7	Cytoplasmic	COG3724	Amino acid transport and metabolism
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.1	3.80E-01	0,75 g/l BuOH	5.4	51330	4	Cytoplasmic	COG1012	Energy production and conversion
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminas	1.4	1.19E-01	0,75 g/l BuOH	6.5	43490	14	Cytoplasmic	COG4992	Amino acid transport and metabolism
26991169	PP_4483		basic amino acid ABC transporter ATP-binding protein	1.2	5.94E-01	0,75 g/l BuOH	7.8	28000	3	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism
26991172	PP_4486		cationic amino acid ABC transporter periplasmic protein	1.4	1.98E-01	0,75 g/l BuOH	8.1	28302	10	Periplasmic	COG0834	Amino acid transport and metabolism
26991173	PP_4487	acsA	acetyl-CoA synthetase	9.7	9.86E-04	0,75 g/l BuOH	6.4	71796	31	Cytoplasmic	COG0365	Lipid metabolism
26991184	PP_4499		SuaS/YciO/YrdC/YwlC family protein	1.6	1.85E-01	Control	5.6	24738	4	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis
26991191	PP_4506		nitroreductase	1.3	5.49E-01	0,75 g/l BuOH	6.6	19994	8	Unknown	COG0778	Energy production and conversion
26991193	PP_4508		AraC family transcriptional regulator	1.1	5.96E-01	0,75 g/l BuOH	6.8	39367	4	Cytoplasmic	COG2207	Transcription
26991202	PP_4517		hypothetical protein	1.3	5.48E-01	Control	3.8	21967	4	Cytoplasmic	COG3318	General function prediction only
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.2	2.92E-01	0,75 g/l BuOH	5.4	50393	23	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane
26991205	PP_4520		DTW domain containing protein	1.4	3.41E-01	Control	7.1	21779	2	Cytoplasmic	COG3148	Function unknown
26991206	PP_4521		aerotaxis receptor	1.1	2.96E-01	Control	6.4	56605	19	Cytoplasmic Membrane	COG0840	Cell motility and secretion
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.4	8.93E-02	0,75 g/l BuOH	10.3	48478	6	Cytoplasmic	COG0513	DNA replication, recombination, and repair
26991223	PP_4539		LysR family transcriptional regulator	1.5	3.05E-01	0,75 g/l BuOH	7.1	33901	4	Cytoplasmic	COG0583	Transcription
26991224	PP_4540		alpha/beta fold family hydrolase	1.0	8.17E-01	0,75 g/l BuOH	7.4	30640	2	Cytoplasmic	COG0596	General function prediction only
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.2	1.76E-01	0,75 g/l BuOH	5.7	42326	14	Cytoplasmic	COG0332	acyl-carrier-protein
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	1.2	4.60E-01	0,75 g/l BuOH	8.3	146950	11	Cytoplasmic	COG1643	DNA replication, recombination, and repair
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	1.1	5.56E-01	Control	7.7	61812	4	Cytoplasmic	COG0318	Lipid metabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	1.1	5.02E-01	Control	7.8	61658	9	Cytoplasmic	COG0318	Lipid metabolism
26991235	PP_4551		alpha/beta fold family hydrolase	1.6	2.59E-01	0,75 g/l BuOH	7.3	34587	2	Cytoplasmic	COG2267	Lipid metabolism
26991249	PP_4565	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	1.1	4.37E-01	Control	5.3	65954	2	Cytoplasmic	COG4579	Signal transduction mechanisms
26991254	PP_4570		hypothetical protein	1.1	2.79E-02	Control	10.1	35846	5	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones
26991255	PP_4571	cysK	cysteine synthase A	1.1	4.42E-01	0,75 g/l BuOH	5.5	34357	9	Cytoplasmic	COG0031	Amino acid transport and metabolism
26991257	PP_4573		ATPase AAA	1.0	8.94E-01	0,75 g/l BuOH	5.8	32146	14	Cytoplasmic	COG0714	General function prediction only
26991261	PP_4577		LamB/YcsF family protein	1.1	8.73E-01	Control	5.8	27871	4	Cytoplasmic	COG1540	General function prediction only
26991265	PP_4581		hypothetical protein	1.5	1.87E-01	0,75 g/l BuOH	6.2	28647	3	Cytoplasmic	COG0121	General function prediction only

26991272	PP_4588		nitroreductase	1.1	6.56E-01	0,75 g/l BuOH	6.0	21997	10	Unknown	COG0778	Energy production and conversion	
26991275	PP_4591	rnd	ribonuclease D	1.2	7.66E-02	0,75 g/l BuOH	5.5	42668	3	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
26991286	PP_4602		AraC family transcriptional regulator	1.1	6.71E-01	0,75 g/l BuOH	8.9	31224	4	Cytoplasmic	COG2207	Transcription	
26991303	PP_4619		maleylacetoacetate isomerase	1.1	6.68E-01	0,75 g/l BuOH	6.2	22876	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26991316	PP_4632		short chain dehydrogenase	1.5	1.17E-01	0,75 g/l BuOH	7.8	26619	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26991319	PP_4635		trans-2-enoyl-CoA reductase	1.0	6.88E-01	0,75 g/l BuOH	5.0	44265	20	Cytoplasmic	COG3007	Function unknown	
26991325	PP_4641	cstA	carbon starvation protein CstA	1.0	8.90E-01	Control	9.0	73763	8	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991330	PP_4646		oxidoreductase FAD/NAD(P)-binding domain protein	1.2	3.57E-01	0,75 g/l BuOH	5.2	28960	7	Cytoplasmic	COG1018	Energy production and conversion	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	1.7	3.30E-01	0,75 g/l BuOH	9.1	53016	6	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	1.5	2.59E-01	0,75 g/l BuOH	9.4	26835	3	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26991341	PP_4657		metallopeptidase, zinc binding	2.9	8.35E-02	0,75 g/l BuOH	6.7	34400	3	Unknown	COG2321	General function prediction only	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.2	7.18E-01	0,75 g/l BuOH	4.8	68764	13	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991343	PP_4659	ggt-2	gamma-glutamyltransferase	1.1	6.87E-01	0,75 g/l BuOH	6.0	59835	12	Periplasmic	COG0405	Amino acid transport and metabolism	
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	1.0	9.94E-01	0,75 g/l BuOH	6.1	30321	8	Cytoplasmic	COG2084	Lipid metabolism	
26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	1.2	8.26E-02	0,75 g/l BuOH	6.0	54367	9	Cytoplasmic	COG1012	Energy production and conversion	
26991357	PP_4673	recB	exodeoxyribonuclease V, beta subunit	2.3	2.42E-01	Control	6.0	137490	2	Cytoplasmic	COG1074	DNA replication, recombination, and repair	
26991361	PP_4677	pssA-2	CDP-diacylglycerol--serine O-phosphatidyltransferase	1.0	8.37E-01	Control	9.2	30359	2	Cytoplasmic Membrane	COG1183	Lipid metabolism	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	9.02E-01	0,75 g/l BuOH	5.4	36370	26	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.3	3.32E-01	0,75 g/l BuOH	6.8	62781	28	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26991366	PP_4682		hypothetical protein	1.3	9.18E-01	0,75 g/l BuOH	8.2	27215	4	Unknown	COG4783	General function prediction only	
26991368	PP_4684		hypothetical protein	1.4	7.19E-02	0,75 g/l BuOH	5.1	56095	6	Cytoplasmic	COG2187	Function unknown	
26991373	PP_4689		periplasmic protein	1.1	8.11E-01	Control	7.1	30685	6	Periplasmic	COG4558	Inorganic ion transport and metabolism	
26991376	PP_4692		hypothetical protein	1.1	5.03E-01	0,75 g/l BuOH	6.5	42505	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis family	5.6	1.03E-01	0,75 g/l BuOH	5.3	52585	5	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991381	PP_4697	pcnB	poly(A) polymerase	1.1	6.77E-01	0,75 g/l BuOH	9.6	52721	3	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis	
26991383	PP_4699	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.2	4.90E-01	Control	5.8	27762	5	Unknown	COG0413	Coenzyme metabolism	
26991384	PP_4700	panC	pantoate--beta-alanine ligase	1.3	1.31E-01	Control	7.7	31189	5	Cytoplasmic	COG0414	Coenzyme metabolism	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.2	2.90E-01	0,75 g/l BuOH	6.8	61455	18	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	1.4	1.03E-01	Control	6.5	71251	12	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	2.1	7.14E-03	Control	5.6	107252	25	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.2	4.65E-01	0,75 g/l BuOH	4.9	75010	33	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.2	2.83E-01	Control	6.8	91460	36	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP_4713	nusA	transcription elongation factor NusA	1.2	1.36E-01	0,75 g/l BuOH	4.3	54673	18	Cytoplasmic	COG0195	Transcription	
26991398	PP_4715	tpiA	triosephosphate isomerase	1.1	7.25E-01	0,75 g/l BuOH	4.7	25991	6	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
26991399	PP_4716	glmM	phosphoglucosamine mutase	2.3	2.87E-01	0,75 g/l BuOH	6.0	47744	2	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.6	4.72E-02	0,75 g/l BuOH	5.4	69722	15	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	1.4	5.03E-02	0,75 g/l BuOH	5.8	40574	7	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
26991408	PP_4725	dapB	dihydrodipicolinate reductase	1.0	7.34E-01	Control	5.9	28423	5	Cytoplasmic	COG0289	Amino acid transport and metabolism	
26991409	PP_4726	dnaJ	chaperone protein DnaJ	1.1	7.60E-01	Control	6.7	40181	5	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.1	9.75E-01	0,75 g/l BuOH	4.6	68800	56	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991411	PP_4728	grpE	heat shock protein GrpE	1.2	8.08E-01	0,75 g/l BuOH	4.7	20531	5	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
26991414	PP_4731	omlA	SmpA/OmlA domain protein	2.6	4.32E-01	0,75 g/l BuOH	4.4	19586	3	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991423	PP_4740	hsdR	type I restriction-modification system, R subunit	1.2	2.31E-01	Control	5.2	89615	10	Cytoplasmic	COG4096	Defense mechanisms	
26991429	PP_4748		amino acid ABC transporter periplasmic amino acid-binding protein	1.4	2.57E-01	0,75 g/l BuOH	5.4	28338	4	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991434	PP_4753		N-methylproline demethylase	1.2	3.83E-01	0,75 g/l BuOH	6.5	75215	9	Cytoplasmic	COG1902	Energy production and conversion	
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	1.1	9.34E-01	0,75 g/l BuOH	6.2	35615	6	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26991443	PP_4762	tesB	acyl-CoA thioesterase II	1.5	4.64E-01	0,75 g/l BuOH	6.1	32319	7	Cytoplasmic	COG1946	Lipid metabolism	
161378119	PP_4779		AMP nucleosidase	1.4	2.12E-01	0,75 g/l BuOH	6.8	54498	8	Cytoplasmic	COG0775	Nucleotide transport and metabolism	
26991460	PP_4780		acyl-CoA dehydrogenase domain-containing protein	1.0	7.42E-01	Control	6.6	59803	8	Cytoplasmic	COG1960	Lipid metabolism	
26991462	PP_4782	thiD	phosphomethylpyrimidine kinase	1.6	1.40E-01	0,75 g/l BuOH	5.1	28338	3	Cytoplasmic	COG0351	Coenzyme metabolism	
26991463	PP_4783	thiE	thiamine-phosphate pyrophosphorylase	1.3	3.92E-01	0,75 g/l BuOH	7.6	21702	2	Unknown	COG0352	Coenzyme metabolism	
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.2	2.92E-02	0,75 g/l BuOH	5.7	45178	10	Cytoplasmic	COG0001	Coenzyme metabolism	
26991469	PP_4789		CBS domain containing protein	1.0	6.15E-01	0,75 g/l BuOH	4.7	31393	7	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.1	5.27E-01	Control	5.6	96697	29	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B	1.5	3.60E-01	0,75 g/l BuOH	6.1	22414	11	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991478	PP_4798		lytic murein transglycosylase	1.8	5.47E-02	0,75 g/l BuOH	7.7	48000	4	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991481	PP_4801	lipB	lipoate-protein ligase B	1.3	2.46E-01	0,75 g/l BuOH	6.0	23689	3	Cytoplasmic	COG0321	Coenzyme metabolism	
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.2	1.69E-01	0,75 g/l BuOH	6.6	42288	7	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane	
26991490	PP_4810	nadD	nicotinic acid mononucleotide adenylyltransferase	1.2	4.41E-01	0,75 g/l BuOH	5.6	25291	2	Cytoplasmic	COG1057	Coenzyme metabolism	
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.2	3.50E-02	0,75 g/l BuOH	6.1	45417	7	Cytoplasmic	COG0014	Amino acid transport and metabolism	
26991494	PP_4814		ATP-dependent protease La	1.2	5.20E-01	0,75 g/l BuOH	4.1	21846	5	Cytoplasmic	COG2802	General function prediction only	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cycloh	1.5	1.34E-01	0,75 g/l BuOH	6.5	57695	20	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.1	4.19E-01	0,75 g/l BuOH	4.7	45837	9	Cytoplasmic	COG0151	Nucleotide transport and metabolism	
26991504	PP_4824		integral membrane sensor hybrid histidine kinase	1.4	1.72E-01	Control	6.6	101587	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26991528	PP_4848		DnaJ family curved-DNA-binding protein	1.1	4.06E-01	Control	9.8	34808	12	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
26991539	PP_4859		TetR family transcriptional regulator	1.4	1.55E-01	0,75 g/l BuOH	7.7	23426	2	Cytoplasmic	COG1309	Transcription	
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	1.0	9.87E-01	0,75 g/l BuOH	6.3	27400	6	Cytoplasmic	COG4221	General function prediction only	
26991543	PP_4863		branched chain amino acid ABC transporter ATP-binding protein	1.7	1.65E-01	0,75 g/l BuOH	9.3	26312	10	Unknown	COG0410	Amino acid transport and metabolism	
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	1.1	8.27E-01	0,75 g/l BuOH	6.6	32427	4	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	1.8	3.25E-03	0,75 g/l BuOH	6.2	40270	23	Periplasmic	COG0683	Amino acid transport and metabolism	
26991549	PP_4869	nadE	NAD synthetase	1.0	9.30E-01	0,75 g/l BuOH	5.6	29273	9	Cytoplasmic	COG0171	Coenzyme metabolism	
26991550	PP_4870		azurin	2.4	8.57E-02	0,75 g/l BuOH	6.9	16028	2	Periplasmic	COG3241	Energy production and conversion	
26991554	PP_4874	rplI	50S ribosomal protein L9	1.4	5.40E-01	Control	5.3	15466	2	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis	
26991558	PP_4879		RNA methyltransferase	1.5	5.33E-02	0,75 g/l BuOH	6.8	27014	8	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.2	2.70E-01	Control	7.9	96688	24	Cytoplasmic	COG0557	Transcription	
26991560	PP_4881		iron ABC transporter periplasmic iron-binding protein	1.1	5.73E-01	0,75 g/l BuOH	5.0	36800	7	Periplasmic	COG1840	Inorganic ion transport and metabolism	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	1.9	1.58E-03	0,75 g/l BuOH	6.1	71958	17	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.2	3.91E-01	0,75 g/l BuOH	5.6	46833	17	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991568	PP_4890	hisZ	ATP phosphoribosyltransferase regulatory subunit	1.1	5.48E-01	0,75 g/l BuOH	4.7	42935	5	Cytoplasmic	COG3705	Amino acid transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.0	9.93E-01	0,75 g/l BuOH	9.8	33001	17	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.2	5.10E-01	0,75 g/l BuOH	5.1	44762	15	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991573	PP_4895	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	1.1	6.49E-01	0,75 g/l BuOH	7.1	35447	2	Cytoplasmic	COG0324	Translation, ribosomal structure and biogenesis	
26991580	PP_4902	orn	oligoribonuclease	1.4	4.88E-01	0,75 g/l BuOH	5.8	20787	7	Cytoplasmic	COG1949	RNA processing and modification	
26991582	PP_4904	motB	flagellar motor protein MotB	1.1	5.55E-01	Control	4.8	37802	6	Cytoplasmic Membrane	COG1360	Cell motility and secretion	
26991583	PP_4905		flagellar motor protein MotA	1.4	3.38E-02	Control	6.2	30312	3	Cytoplasmic Membrane	COG1291	Cell motility and secretion	
26991584	PP_4906		metal-dependent hydrolase HDOD	1.2	1.94E-01	0,75 g/l BuOH	7.7	57677	3	Unknown			
26991585	PP_4907	rhdA-2	rhodanese domain protein	1.2	3.39E-01	0,75 g/l BuOH	6.1	29517	8	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.4	1.10E-01	0,75 g/l BuOH	8.6	31547	5	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991587	PP_4909	serB	phosphoserine phosphatase SerB	1.0	8.05E-01	0,75 g/l BuOH	5.1	45033	2	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991588	PP_4910		hypothetical protein	1.7	8.58E-01	0,75 g/l BuOH	4.7	53632	2	Cytoplasmic	COG3726	General function prediction only	
26991589	PP_4911		hypothetical protein	1.6	1.12E-01	0,75 g/l BuOH	8.5	27337	3	Periplasmic	COG3009	Function unknown	
26991593	PP_4915	parE	DNA topoisomerase IV subunit B	1.3	3.83E-01	Control	6.2	69556	3	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
26991597	PP_4919		NUDIX hydrolase	1.3	2.28E-01	0,75 g/l BuOH	4.7	23607	7	Cytoplasmic			
26991600	PP_4922	thiC	thiamine biosynthesis protein ThiC	1.6	3.01E-01	0,75 g/l BuOH	5.7	69727	11	Cytoplasmic	COG0422	Coenzyme metabolism	
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.1	3.93E-01	0,75 g/l BuOH	5.2	52637	8	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion

26991609	PP_4931		FAD dependent oxidoreductase	1.1	5.04E-01	0,75 g/l BuOH	7.2	42015	6	Cytoplasmic	COG0578	Energy production and conversion
26991610	PP_4932		aldo/keto reductase	1.0	7.52E-01	Control	6.4	29123	3	Cytoplasmic	COG0667	Energy production and conversion
26991611	PP_4933		hypothetical protein	1.1	8.16E-01	Control	10.0	37000	2	Unknown		
26991612	PP_4934		bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase	1.3	5.35E-02	0,75 g/l BuOH	5.8	49970	8	Cytoplasmic	COG2870	Cell envelope biogenesis, outer membrane
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.5	3.68E-01	0,75 g/l BuOH	7.6	66279	8	Cytoplasmic Membrane	COG1132	Defense mechanisms
26991615	PP_4937		toluene tolerance protein	1.7	2.86E-01	0,75 g/l BuOH	10.4	25956	4	Cytoplasmic		
26991616	PP_4938		glycosyl transferase	1.3	3.69E-01	0,75 g/l BuOH	9.4	41783	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane
26991617	PP_4939		hypothetical protein	1.2	5.09E-01	0,75 g/l BuOH	7.1	28978	3	Cytoplasmic		
26991622	PP_4944		carbamoyltransferase	1.0	9.61E-01	0,75 g/l BuOH	7.2	65646	10	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate d	1.3	4.02E-02	Control	6.3	142580	38	Cytoplasmic	COG4230	Energy production and conversion
26991627	PP_4949		TldD/PmbA family protein	1.4	4.94E-02	0,75 g/l BuOH	6.6	55611	3	Unknown	COG0312	General function prediction only
26991628	PP_4950		hypothetical protein	1.8	2.04E-01	0,75 g/l BuOH	4.9	47741	2	Unknown	COG0312	General function prediction only
26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PA	1.2	8.46E-01	0,75 g/l BuOH	4.8	78896	17	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.0	7.83E-01	Control	5.6	38453	19	Cytoplasmic	COG0191	Carbohydrate transport and metabolism
26991641	PP_4963	pgk	phosphoglycerate kinase	1.1	2.20E-01	0,75 g/l BuOH	4.9	40005	15	Cytoplasmic	COG0126	Carbohydrate transport and metabolism
26991643	PP_4965	tktA	transketolase	1.1	8.45E-01	0,75 g/l BuOH	5.0	72463	32	Cytoplasmic	COG0021	Carbohydrate transport and metabolism
26991644	PP_4966		ArsR family transcriptional regulator	1.5	1.62E-01	Control	6.4	36148	7	Cytoplasmic	COG2226	Coenzyme metabolism
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.0	8.62E-01	0,75 g/l BuOH	5.1	42779	22	Cytoplasmic	COG0192	Coenzyme metabolism
26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	1.5	1.31E-01	Control	6.2	32979	12	Cytoplasmic	COG0685	Amino acid transport and metabolism
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	1.9	1.69E-01	0,75 g/l BuOH	10.7	68073	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991658	PP_4981		hypothetical protein	1.6	6.75E-01	Control	8.8	22129	11	Unknown	COG2353	Function unknown
26991665	PP_4988		chemotaxis protein CheA	1.6	2.05E-02	Control	4.7	180005	7	Unknown	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991670	PP_4993	gshB	glutathione synthetase	1.3	5.72E-02	0,75 g/l BuOH	5.1	35254	5	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26991675	PP_4998	pyrB	aspartate carbamoyltransferase catalytic subunit	1.2	3.22E-01	0,75 g/l BuOH	7.1	36344	5	Cytoplasmic	COG0540	Nucleotide transport and metabolism
26991676	PP_4999	pyrC	dihydroorotase	1.3	4.01E-01	0,75 g/l BuOH	5.4	44116	2	Cytoplasmic	COG0044	Nucleotide transport and metabolism
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.0	8.17E-01	Control	5.7	49982	15	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	1.1	3.79E-01	0,75 g/l BuOH	7.4	62241	22	Cytoplasmic	COG3243	Lipid metabolism
26991682	PP_5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	1.1	5.70E-01	Control	9.6	62722	9	Cytoplasmic	COG3243	Lipid metabolism
26991683	PP_5006		TetR family transcriptional regulator	1.5	3.55E-01	0,75 g/l BuOH	5.3	23055	3	Cytoplasmic	COG1309	Transcription
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.2	1.40E-01	Control	10.9	26214	15	Cytoplasmic	COG3937	Function unknown
26991688	PP_5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.2	2.93E-01	0,75 g/l BuOH	9.5	28397	11	Cytoplasmic	COG2226	Coenzyme metabolism
26991689	PP_5012		hypothetical protein	1.4	6.11E-02	0,75 g/l BuOH	5.4	22983	3	Unknown	COG3165	Function unknown
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.2	8.53E-01	0,75 g/l BuOH	4.9	69017	33	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991698	PP_5022		amino acid ABC transporter ATP-binding protein	1.1	4.97E-01	0,75 g/l BuOH	7.6	27004	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26991700	PP_5024		amino acid ABC transporter periplasmic amino acid-binding protein	1.4	4.63E-01	0,75 g/l BuOH	8.6	29848	15	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.3	1.05E-01	0,75 g/l BuOH	8.3	95875	5	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991702	PP_5026	mdoG	glucan biosynthesis protein G	1.0	9.60E-01	0,75 g/l BuOH	6.5	62340	8	Periplasmic	COG3131	Inorganic ion transport and metabolism	
26991704	PP_5028	pip	proline iminopeptidase	2.0	1.63E-03	0,75 g/l BuOH	6.2	36589	13	Cytoplasmic	COG0596	General function prediction only	
26991711	PP_5035	hutC	histidine utilization repressor	1.2	5.53E-01	0,75 g/l BuOH	6.6	27624	2	Cytoplasmic	COG2188	Transcription	
26991715	PP_5039		hypothetical protein	2.1	6.05E-01	0,75 g/l BuOH	4.8	23220	4	Unknown	COG3803	Function unknown	
26991716	PP_5040	fbp	fructose-1,6-bisphosphatase	1.0	9.42E-01	0,75 g/l BuOH	5.9	37246	6	Cytoplasmic	COG0158	Carbohydrate transport and metabolism	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.1	9.43E-02	0,75 g/l BuOH	6.4	92004	24	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.7	6.67E-01	0,75 g/l BuOH	5.3	67157	15	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.0	7.57E-01	Control	5.1	51740	21	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991724	PP_5048	ntrC	nitrogen metabolism transcriptional regulator NtrC	1.4	6.10E-01	0,75 g/l BuOH	6.0	53114	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991732	PP_5056	pgm	phosphoglyceromutase	1.1	3.19E-01	0,75 g/l BuOH	4.9	55180	12	Cytoplasmic	COG0696	Carbohydrate transport and metabolism	
26991734	PP_5058		carboxyl-terminal protease	1.4	3.11E-01	0,75 g/l BuOH	5.6	46333	12	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26991739	PP_5063	betB	betaine aldehyde dehydrogenase	1.2	5.22E-01	0,75 g/l BuOH	4.8	52986	4	Cytoplasmic	COG1012	Energy production and conversion	
26991740	PP_5064	betA	choline dehydrogenase	2.2	3.83E-02	0,75 g/l BuOH	6.8	62544	3	Cytoplasmic Membrane	COG2303	Amino acid transport and metabolism	
26991750	PP_5074	hemE	uroporphyrinogen decarboxylase	1.2	7.20E-01	0,75 g/l BuOH	6.7	38883	2	Cytoplasmic	COG0407	Coenzyme metabolism	
26991751	PP_5075	gltD	glutamate synthase subunit beta	1.5	5.95E-01	0,75 g/l BuOH	6.3	51819	6	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.6	4.57E-03	Control	6.2	161772	41	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP_5077		sporulation domain protein	1.2	2.48E-01	0,75 g/l BuOH	7.1	55434	5	Unknown	COG3267	Intracellular trafficking and secretion	
26991754	PP_5078	aroB	3-dehydroquinate synthase	1.5	5.06E-01	0,75 g/l BuOH	6.0	39485	6	Cytoplasmic	COG0337	Amino acid transport and metabolism	
26991760	PP_5084		penicillin-binding protein, 1A family	1.8	1.87E-01	0,75 g/l BuOH	7.2	89193	3	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP_5085	maeB	malic enzyme	1.4	1.55E-01	0,75 g/l BuOH	4.9	45127	29	Cytoplasmic	COG0281	Energy production and conversion	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.4	1.86E-02	0,75 g/l BuOH	5.7	63668	18	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991770	PP_5094		alanine racemase domain protein	1.3	2.10E-01	0,75 g/l BuOH	6.8	24192	8	Cytoplasmic	COG0325	General function prediction only	
26991771	PP_5095	proC-2	pyrroline-5-carboxylate reductase	1.2	3.12E-01	0,75 g/l BuOH	4.7	28258	7	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26991776	PP_5100		deoxyribonucleotide triphosphate pyrophosphatase	1.6	9.30E-01	Control	5.9	21303	2	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
26991779	PP_5103	trmB	tRNA (guanine-N(7)-)-methyltransferase	1.1	6.91E-01	Control	7.3	27203	3	Cytoplasmic	COG0220	General function prediction only	
26991780	PP_5104	thiG	thiazole synthase	1.2	5.89E-01	0,75 g/l BuOH	5.8	28917	8	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
26991786	PP_5110	ftsE	cell division ATP-binding protein FtsE	1.2	3.86E-01	0,75 g/l BuOH	11.0	24830	6	Cytoplasmic Membrane	COG2884	Cell division and chromosome partitioning	
26991787	PP_5111	ftsY	signal recognition particle-docking protein FtsY	4.8	4.49E-01	0,75 g/l BuOH	4.9	51680	7	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
26991788	PP_5112		peptidase M16 domain protein	1.2	3.46E-01	0,75 g/l BuOH	5.9	50095	2	Periplasmic	COG0612	General function prediction only	
26991790	PP_5114		hypothetical protein	1.4	1.73E-01	0,75 g/l BuOH	8.2	22311	2	Unknown	COG0742	DNA replication, recombination, and repair	
26991794	PP_5118		rhodanese domain protein	1.1	8.44E-01	0,75 g/l BuOH	5.6	30750	11	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991796	PP_5120		conifer aldehyde dehydrogenase	1.4	4.07E-01	Control	9.2	52453	6	Cytoplasmic	COG1012	Energy production and conversion	
26991803	PP_5127		hypothetical protein	1.3	2.98E-03	0,75 g/l BuOH	6.9	44126	2	Cytoplasmic	COG1092	General function prediction only	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.3	3.42E-01	0,75 g/l BuOH	5.8	65671	21	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991817	PP_5141	thyA	thymidylate synthase	1.0	7.32E-01	Control	5.4	36772	2	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
26991820	PP_5144		hypothetical protein	1.2	3.90E-01	0,75 g/l BuOH	5.3	26452	4	Unknown	COG3332	Function unknown	
26991821	PP_5145	ptsP	PTSINtr with GAF domain, PtsP	1.2	5.13E-01	0,75 g/l BuOH	5.3	83337	21	Cytoplasmic	COG3605	Signal transduction mechanisms	
26991823	PP_5147		HAD superfamily hydrolase	1.3	2.40E-01	0,75 g/l BuOH	4.7	24940	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991826	PP_5150	rpiA	ribose-5-phosphate isomerase A	1.2	4.20E-01	0,75 g/l BuOH	4.9	23496	7	Unknown	COG0120	Carbohydrate transport and metabolism	
26991829	PP_5153		fumarylacetoacetate (FAA) hydrolase	1.1	8.11E-01	Control	4.7	23906	3	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
26991830	PP_5154		FAD linked oxidase domain protein	1.2	3.38E-01	0,75 g/l BuOH	5.2	49990	2	Cytoplasmic	COG0277	Energy production and conversion	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.3	2.08E-01	0,75 g/l BuOH	6.3	44339	20	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991836	PP_5160		hypothetical protein	1.2	5.55E-01	0,75 g/l BuOH	8.9	27008	4	Cytoplasmic Membrane			
26991839	PP_5163		acetyltransferase	1.0	6.27E-01	0,75 g/l BuOH	6.1	20366	2	Cytoplasmic	COG0110	General function prediction only	
26991847	PP_5171	cysP	sulfate ABC transporter periplasmic sulfate-binding protein	2.2	1.07E-01	0,75 g/l BuOH	9.0	37491	2	Periplasmic	COG1613	Inorganic ion transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	2.1	4.93E-03	Control	5.4	112277	11	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991850	PP_5174		RND efflux transporter	1.1	3.05E-01	0,75 g/l BuOH	5.5	38032	6	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991851	PP_5175		efflux transporter RND family, MFP subunit	1.0	8.81E-01	Control	6.5	38304	7	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991853	PP_5177	potI	ornithine carbamoyltransferase	3.3	3.99E-02	Control	10.0	32247	2	Cytoplasmic Membrane	COG1177	Amino acid transport and metabolism	
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	1.2	1.15E-01	Control	6.5	42472	9	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26991856	PP_5180	potF-1	putrescine ABC transporter periplasmic putrescine-binding protein	1.1	7.47E-01	0,75 g/l BuOH	8.0	39788	7	Periplasmic	COG0687	Amino acid transport and metabolism	
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.1	9.95E-01	0,75 g/l BuOH	6.4	40068	23	Periplasmic	COG0687	Amino acid transport and metabolism	
26991858	PP_5182		aminotransferase	1.4	1.73E-01	0,75 g/l BuOH	6.2	49871	9	Cytoplasmic	COG0161	Coenzyme metabolism	
26991859	PP_5183		glutamine synthetase	1.3	6.30E-01	0,75 g/l BuOH	4.8	50877	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991860	PP_5184		glutamine synthetase	1.2	6.66E-01	0,75 g/l BuOH	4.5	50974	10	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991861	PP_5185	argA	N-acetylglutamate synthase	1.3	2.66E-03	0,75 g/l BuOH	5.9	47440	3	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991862	PP_5186	argE	acetylornithine deacetylase	1.6	2.37E-02	0,75 g/l BuOH	4.9	41425	2	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26991863	PP_5187		adenylate cyclase	1.2	1.40E-01	0,75 g/l BuOH	5.6	52133	4	Cytoplasmic	COG3025	Function unknown	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.2	5.99E-01	0,75 g/l BuOH	6.3	104037	15	Cytoplasmic	COG1003	Amino acid transport and metabolism	

26991870	PP_5194	gcvT	glycine cleavage system aminomethyltransferase T	1.2	1.09E-01	0,75 g/l BuOH	5.3	39379	4	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26991876	PP_5200	pepP	peptidase M24	1.2	4.63E-01	0,75 g/l BuOH	5.8	49171	2	Cytoplasmic	COG0006	Amino acid transport and metabolism	
26991877	PP_5201		hypothetical protein	1.5	4.36E-01	0,75 g/l BuOH	3.9	19468	3	Unknown	COG3079	Function unknown	
26991879	PP_5203		5-formyltetrahydrofolate cyclo-ligase	1.0	9.80E-01	Control	11.8	23687	3	Cytoplasmic	COG0212	Coenzyme metabolism	
26991882	PP_5206		secretion protein HlyD family protein	1.1	5.60E-01	Control	9.6	34522	8	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26991883	PP_5207		ABC transporter ATP-binding protein/permease	1.1	6.80E-01	0,75 g/l BuOH	7.8	98772	2	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26991886	PP_5210		alcohol dehydrogenase, zinc-containing	1.3	2.51E-01	0,75 g/l BuOH	7.6	33856	6	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26991890	PP_5214	rho	transcription termination factor Rho	1.4	3.49E-03	0,75 g/l BuOH	8.2	47041	24	Cytoplasmic	COG1158	Transcription	
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.1	5.88E-01	0,75 g/l BuOH	6.9	55958	9	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991893	PP_5217	ppk	polyphosphate kinase	1.0	7.38E-01	Control	7.8	81732	15	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
26991896	PP_5220	elbB	isoprenoid biosynthesis protein with amidotransferase-like domain	1.6	2.29E-01	0,75 g/l BuOH	5.0	23391	4	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
26991903	PP_5227	lysA-2	diaminopimelate decarboxylase	1.2	9.13E-02	0,75 g/l BuOH	4.9	45213	3	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26991904	PP_5228	dapF	diaminopimelate epimerase	1.1	7.22E-01	0,75 g/l BuOH	8.2	31487	3	Cytoplasmic	COG0253	Amino acid transport and metabolism	
26991905	PP_5229		hypothetical protein	1.1	5.21E-01	0,75 g/l BuOH	6.1	26395	4	Cytoplasmic	COG3159	Function unknown	
26991907	PP_5231		HAD superfamily hydrolase	1.4	1.19E-01	0,75 g/l BuOH	5.1	25611	4	Cytoplasmic	COG1011	General function prediction only	
26991928	PP_5252		amidohydrolase 3	1.2	1.54E-01	Control	6.4	72743	15	Unknown	COG1574	General function prediction only	
26991934	PP_5258		aldehyde dehydrogenase family protein	1.0	9.08E-01	Control	5.4	53106	9	Cytoplasmic	COG1012	Energy production and conversion	
26991941	PP_5265	xpt	xanthine phosphoribosyltransferase	2.1	2.73E-01	Control	6.1	20386	7	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
26991954	PP_5278		aldehyde dehydrogenase family protein	1.2	4.33E-03	0,75 g/l BuOH	5.5	53053	9	Cytoplasmic	COG1012	Energy production and conversion	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.4	3.26E-01	0,75 g/l BuOH	12.3	8922	2	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991959	PP_5283		periplasmic dipeptide-binding protein	1.3	9.19E-02	0,75 g/l BuOH	8.5	57512	6	Periplasmic	COG0747	Amino acid transport and metabolism	
26991964	PP_5288		phosphomannomutase	1.3	6.61E-02	0,75 g/l BuOH	5.0	50271	5	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991965	PP_5289	argB	acetylglutamate kinase	1.2	2.94E-01	0,75 g/l BuOH	5.7	31953	12	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991967	PP_5291	pyrE	orotate phosphoribosyltransferase	1.4	1.41E-01	0,75 g/l BuOH	4.9	23079	5	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
26991968	PP_5292	crc	exodeoxyribonuclease III Xth	1.3	3.21E-01	0,75 g/l BuOH	4.9	29786	2	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
26991970	PP_5294	rph	ribonuclease PH	1.4	9.69E-01	0,75 g/l BuOH	5.9	25723	3	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis	
26991972	PP_5296	gmk	guanylate kinase	1.3	3.04E-01	0,75 g/l BuOH	6.4	23184	4	Cytoplasmic	COG0194	Nucleotide transport and metabolism	
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	1.2	3.07E-01	Control	9.2	78603	9	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991979	PP_5303		endoribonuclease	6.8	1.05E-01	0,75 g/l BuOH	4.8	13508	2	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
26991980	PP_5304		lipoprotein	1.1	6.74E-01	0,75 g/l BuOH	5.1	26284	2	Unknown			
26991982	PP_5306	exbB	ferric siderophore transport system protein ExbB	1.2	8.42E-01	Control	9.5	33260	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26991985	PP_5309		LysR family transcriptional regulator	1.1	7.08E-01	0,75 g/l BuOH	7.0	33763	8	Cytoplasmic	COG0583	Transcription	
26991987	PP_5311		signal transduction protein	2.0	2.22E-01	0,75 g/l BuOH	5.9	51775	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
26991996	PP_5320	phoB	transcriptional regulator	1.2	5.68E-01	0,75 g/l BuOH	5.2	27080	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26992001	PP_5325	phoU	phosphate transporter PhoU	1.0	7.54E-01	0,75 g/l BuOH	5.0	28893	4	Cytoplasmic	COG0704	Inorganic ion transport and metabolism	
26992005	PP_5329	pstS	phosphate ABC transporter phosphate-binding protein	1.5	6.63E-02	0,75 g/l BuOH	9.4	34955	7	Cytoplasmic Membrane	COG0226	Inorganic ion transport and metabolism	
26992008	PP_5332		aldose 1-epimerase	1.1	5.72E-01	Control	4.7	33226	3	Cytoplasmic	COG0676	Carbohydrate transport and metabolism	
26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.1	4.22E-01	0,75 g/l BuOH	5.2	38702	4	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
26992014	PP_5338	aspA	aspartate ammonia-lyase	1.1	8.80E-01	0,75 g/l BuOH	5.9	51562	8	Cytoplasmic	COG1027	Amino acid transport and metabolism	
26992017	PP_5341		ABC transporter periplasmic polyamine-binding protein	1.0	8.63E-01	0,75 g/l BuOH	8.8	40667	4	Periplasmic	COG0687	Amino acid transport and metabolism	
26992021	PP_5345		acetyltransferase	1.1	6.38E-01	0,75 g/l BuOH	6.0	25042	5	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.3	3.27E-02	0,75 g/l BuOH	5.3	65626	32	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	1.4	3.78E-02	0,75 g/l BuOH	6.5	51942	20	Cytoplasmic	COG0439	Lipid metabolism	
26992028	PP_5352	uvrD	DNA-dependent helicase II	1.5	7.28E-01	0,75 g/l BuOH	6.2	81692	3	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
26992029	PP_5353		hypothetical protein	1.4	4.58E-01	0,75 g/l BuOH	7.2	30672	4	Cytoplasmic Membrane	COG4395	Function unknown	
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	1.3	4.10E-01	0,75 g/l BuOH	5.9	48114	4	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	3.2	1.30E-02	Control	6.0	49353	4	Cytoplasmic	COG1249	Energy production and conversion	
26992054	PP_5378		cytochrome c family protein	2.2	1.70E-01	Control	6.4	27551	3	Unknown			
26992056	PP_5380	copA	copper resistance protein A	1.9	3.05E-01	Control	6.0	74225	3	Periplasmic	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
26992059	PP_5383	copR	two component heavy metal response transcriptional regulator	2.1	3.18E-01	0,75 g/l BuOH	5.5	25141	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26992070	PP_5395		hypothetical protein	1.3	6.89E-02	Control	5.6	31623	10	Cytoplasmic	COG1568	General function prediction only	
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.1	5.50E-01	Control	6.0	66312	4	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
26992086	PP_5411	glmU	UDP-N-acetylglucosamine pyrophosphorylase	1.3	4.32E-02	0,75 g/l BuOH	6.7	48471	10	Cytoplasmic	COG1207	Cell envelope biogenesis, outer membrane	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.6	7.94E-02	0,75 g/l BuOH	4.6	49359	40	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.0	9.22E-01	0,75 g/l BuOH	9.2	31464	13	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.2	2.72E-02	0,75 g/l BuOH	5.2	55352	32	Cytoplasmic	COG0056	Energy production and conversion	
26992091	PP_5416	atpH	F0F1 ATP synthase subunit delta	1.1	7.50E-01	Control	5.7	19197	3	Cytoplasmic	COG0712	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.5	3.39E-01	0,75 g/l BuOH	5.3	16898	3	Cytoplasmic Membrane	COG0711	Energy production and conversion	
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	5.2	3.12E-01	Control	6.7	31712	3	Cytoplasmic Membrane	COG0356	Energy production and conversion	
148545375	Pput_0118		hypothetical protein	1.1	7.21E-01	0,75 g/l BuOH	4.7	23815	2	Cytoplasmic			
148545524	Pput_0268		phosphoenolpyruvate carboxykinase	1.4	1.84E-01	0,75 g/l BuOH	5.0	55582	22	Cytoplasmic	COG1866	Energy production and conversion	
148545739	Pput_0487	rplC	50S ribosomal protein L3	1.1	4.89E-01	0,75 g/l BuOH	10.7	22603	11	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis	
148546201	Pput_0958		hypothetical protein	1.0	9.41E-01	0,75 g/l BuOH	6.3	30928	2	Unknown			
148547308	Pput_2086		hypothetical protein	1.1	3.09E-01	0,75 g/l BuOH	5.7	21520	2	Cytoplasmic			
148547528	Pput_2307		hypothetical protein	8.5	7.23E-04	0,75 g/l BuOH	7.4	58966	6	Periplasmic			
148548380	Pput_3170		trans-aconitate 2-methyltransferase	1.2	2.97E-01	0,75 g/l BuOH	6.2	29082	3	Cytoplasmic	COG4106	General function prediction only	
148549264	Pput_4058		hypothetical protein	3.5	1.24E-01	Control	5.7	17801	3	Cytoplasmic Membrane			
148549523	Pput_4318		hypothetical protein	1.8	9.02E-02	0,75 g/l BuOH	7.9	44604	2	Cytoplasmic			
148549632	Pput_4430		ATP-dependent RNA helicase RhlB	1.2	3.06E-01	0,75 g/l BuOH	8.4	53170	5	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	1.2	6.03E-02	Control	5.4	51447	25	Cytoplasmic	COG0499	Coenzyme metabolism	
148550089	Pput_4887		2-polyprenylphenol 6-hydroxylase	1.0	8.02E-01	Control	9.3	61664	2	Cytoplasmic Membrane	COG0661	General function prediction only	
24986476				1.5	5.70E-01	0,75 g/l BuOH			54				
313498081				1.1	4.44E-01	0,75 g/l BuOH			28				
24981839				1.1	5.75E-01	0,75 g/l BuOH			15				
152973457				36.1	1.83E-01	0,75 g/l BuOH			13				
310644212				78.5	1.47E-01	0,75 g/l BuOH			12				
377576294				9.0	4.37E-01	0,75 g/l BuOH			12				
377576277				14.5	4.47E-01	0,75 g/l BuOH			10				
377579435				241.6	2.30E-01	0,75 g/l BuOH			10				
354585430				26.4	1.13E-01	0,75 g/l BuOH			10				
354585434				192.3	1.50E-02	0,75 g/l BuOH			10				
308070977				19.3	1.13E-02	0,75 g/l BuOH			9				
313498324				1.2	1.96E-01	0,75 g/l BuOH			9				
377576439				8.8	4.94E-01	0,75 g/l BuOH			9				
24987101				1.0	9.56E-01	0,75 g/l BuOH			9				
261406039				69.5	4.89E-02	0,75 g/l BuOH			9				
254521045				1.2	7.27E-01	0,75 g/l BuOH			10				
377579124				107.9	1.65E-01	0,75 g/l BuOH			9				
24981833				1.9	2.73E-01	0,75 g/l BuOH			8				
24986054				1.3	4.32E-01	0,75 g/l BuOH			7				
377579693				141.6	3.34E-01	0,75 g/l BuOH			8				
16801615				29.4	1.34E-02	0,75 g/l BuOH			6				
377577374				8.8	3.77E-01	0,75 g/l BuOH			6				
377576355				9.9	4.71E-01	0,75 g/l BuOH			6				
315646628				82.3	6.02E-02	0,75 g/l BuOH			6				

24986535	1.3	7.92E-02	0,75 g/l BuOH	6
377578097	162.4	3.52E-01	0,75 g/l BuOH	4
354581590	39.6	1.23E-01	0,75 g/l BuOH	4
24981896	1.5	2.35E-01	0,75 g/l BuOH	5
298682197	82.6	1.01E-03	0,75 g/l BuOH	5
104780459	1.5	1.95E-01	0,75 g/l BuOH	5
377579911	8.5	5.38E-01	0,75 g/l BuOH	5
377579920	16.9	2.03E-01	0,75 g/l BuOH	5
24985446	1.3	2.98E-01	0,75 g/l BuOH	5
337744926	18.8	4.45E-02	0,75 g/l BuOH	6
334137473	63.2	6.78E-02	0,75 g/l BuOH	5
24981908	2.0	7.20E-02	0,75 g/l BuOH	5
24983623	1.1	4.58E-01	0,75 g/l BuOH	5
377576497	207.3	4.15E-01	0,75 g/l BuOH	5
377578292	43.3	6.23E-02	0,75 g/l BuOH	5
377578621	45.9	4.47E-01	0,75 g/l BuOH	5
377578099	63.9	9.03E-01	0,75 g/l BuOH	5
296102816	20.2	9.44E-02	0,75 g/l BuOH	5
261340754	35.9	2.98E-01	0,75 g/l BuOH	5
156935823	30.1	7.99E-01	0,75 g/l BuOH	5
308068146	388.4	1.91E-02	0,75 g/l BuOH	4
354582832	24.2	3.64E-02	0,75 g/l BuOH	4
283787348	53.5	1.93E-01	0,75 g/l BuOH	4
190572930	1.5	3.72E-01	0,75 g/l BuOH	4
354582719	6.6	4.20E-02	0,75 g/l BuOH	4
377578821	25.9	1.61E-01	0,75 g/l BuOH	4
377578749	47.2	4.48E-01	0,75 g/l BuOH	4
260597147	38.0	2.86E-01	0,75 g/l BuOH	4
354582092	77.6	1.18E-02	0,75 g/l BuOH	4
377578495	11.0	4.52E-01	0,75 g/l BuOH	4
315649653	111.0	1.59E-02	0,75 g/l BuOH	4
308069633	66.2	5.85E-02	0,75 g/l BuOH	4
377576216	12.2	3.12E-01	0,75 g/l BuOH	5
261823229	Infinity	1.38E-01	0,75 g/l BuOH	4
377576845	7.4	5.72E-01	0,75 g/l BuOH	4
308071147	24.6	1.44E-01	0,75 g/l BuOH	4
313501129	1.4	4.30E-01	0,75 g/l BuOH	4
377578400	250.8	4.71E-01	0,75 g/l BuOH	3
375308212	12.9	1.04E-01	0,75 g/l BuOH	3
253575746	37.6	6.10E-02	0,75 g/l BuOH	3
261346935	12.5	3.01E-01	0,75 g/l BuOH	3
269200099	1.8	1.92E-01	0,75 g/l BuOH	3
315649715	953.2	3.09E-02	0,75 g/l BuOH	3
377579856	30.8	1.69E-01	0,75 g/l BuOH	3
304316878	19.4	5.57E-02	0,75 g/l BuOH	3
116667412	11.8	5.21E-01	0,75 g/l BuOH	3
374322939	1168.3	1.60E-02	0,75 g/l BuOH	3
261406205	9.4	2.24E-03	0,75 g/l BuOH	3
377577662	44.4	5.82E-01	0,75 g/l BuOH	3
251794236	66.2	1.52E-02	0,75 g/l BuOH	3
261405470	229.1	9.53E-03	0,75 g/l BuOH	3
261408990	55.8	1.09E-02	0,75 g/l BuOH	3
354580128	1030.8	2.68E-02	0,75 g/l BuOH	3
365846643	306.7	9.19E-01	0,75 g/l BuOH	3
261409551	21.2	3.35E-02	0,75 g/l BuOH	3
261409528	18.6	4.33E-02	0,75 g/l BuOH	3
188532975	286.6	6.98E-01	0,75 g/l BuOH	2
260451185	428.5	3.42E-01	0,75 g/l BuOH	3
377577022	1067.4	2.74E-02	0,75 g/l BuOH	3
259906930	1.2	9.19E-01	0,75 g/l BuOH	3
317046845	151.8	1.34E-01	0,75 g/l BuOH	3
251796396	47.2	3.87E-02	0,75 g/l BuOH	3
308069292	217.6	1.38E-01	0,75 g/l BuOH	3
304405022	32.9	6.92E-02	0,75 g/l BuOH	3
354586098	12.6	4.32E-02	0,75 g/l BuOH	3
261406245	52.9	4.97E-02	0,75 g/l BuOH	3
261409493	326.9	3.65E-02	0,75 g/l BuOH	3
377577317	160.2	2.24E-01	0,75 g/l BuOH	3
333371015	Infinity	1.43E-03	0,75 g/l BuOH	1
251796660	1391.1	2.41E-01	0,75 g/l BuOH	2
253576477	126.5	6.82E-01	0,75 g/l BuOH	2
304406615	178.6	1.92E-02	0,75 g/l BuOH	2
138896640	9.1	4.67E-02	0,75 g/l BuOH	2
377577602	58.6	8.87E-04	0,75 g/l BuOH	3
261407773	Infinity	1.98E-03	0,75 g/l BuOH	2
261404073	11485.7	2.85E-03	0,75 g/l BuOH	2
260770896	4.7	2.00E-01	0,75 g/l BuOH	2
24982083	1.2	4.66E-01	0,75 g/l BuOH	2
135596	3.1	3.46E-01	0,75 g/l BuOH	2
377576376	21.8	7.48E-01	0,75 g/l BuOH	2
123440765	1.5	8.06E-01	0,75 g/l BuOH	2
152973456	37.5	1.18E-01	0,75 g/l BuOH	2
261341225	4.5	2.89E-01	0,75 g/l BuOH	2
260595953	7.5	8.66E-01	0,75 g/l BuOH	2
297787753	24.3	2.51E-01	0,75 g/l BuOH	2
261338832	3.6	2.15E-01	0,75 g/l BuOH	2
253577368	48.5	9.11E-03	0,75 g/l BuOH	2
377576592	69.3	4.15E-01	0,75 g/l BuOH	2
253576329	49.6	5.96E-02	0,75 g/l BuOH	2
377577824	18.6	6.63E-01	0,75 g/l BuOH	2
319787927	2.1	9.93E-01	0,75 g/l BuOH	2
377576167	4.7	8.34E-01	0,75 g/l BuOH	2
261409679	Infinity	1.16E-01	0,75 g/l BuOH	1
261407922	Infinity	8.39E-04	0,75 g/l BuOH	2
320539767	18.7	1.31E-01	0,75 g/l BuOH	2

168335361	Infinity	1.89E-03	0,75 g/l BuOH	2
302870826	814.3	1.18E-01	0,75 g/l BuOH	2
377577192	22.2	3.32E-01	0,75 g/l BuOH	2
377577075	51.3	1.67E-01	0,75 g/l BuOH	2
374605319	185.3	3.03E-01	0,75 g/l BuOH	2
156935308	34.8	9.11E-01	0,75 g/l BuOH	2
167465045	143.2	1.36E-01	0,75 g/l BuOH	2
377579853	Infinity	3.74E-01	0,75 g/l BuOH	1
377578145	140.1	1.10E-01	0,75 g/l BuOH	2
24986578	1.3	3.80E-01	0,75 g/l BuOH	2
366158573	2.3	4.58E-01	0,75 g/l BuOH	2
377579828	18.8	1.22E-01	0,75 g/l BuOH	2
354723915	799.5	4.51E-02	0,75 g/l BuOH	2
260596078	11.0	4.19E-01	0,75 g/l BuOH	2
261343037	155.8	8.64E-01	0,75 g/l BuOH	2
308069724	418.7	2.20E-02	0,75 g/l BuOH	2
85060262	57.4	1.15E-01	0,75 g/l BuOH	2
261342208	55.0	8.78E-01	0,75 g/l BuOH	1
119944441	95.5	5.78E-01	0,75 g/l BuOH	1
24986088	1.4	6.60E-01	0,75 g/l BuOH	2
261409688	115.3	5.44E-03	0,75 g/l BuOH	2
261409360	20.6	3.16E-02	0,75 g/l BuOH	2
304407346	43.6	9.03E-02	0,75 g/l BuOH	1
253574173	12.3	3.10E-02	0,75 g/l BuOH	1
37526691	134.7	8.76E-04	0,75 g/l BuOH	2
212640607	248.4	1.34E-02	0,75 g/l BuOH	2
197285722	114.6	3.75E-01	0,75 g/l BuOH	3
308068359	36.9	1.07E-01	0,75 g/l BuOH	2
377578625	41.3	2.50E-01	0,75 g/l BuOH	2
253576627	568.1	6.68E-02	0,75 g/l BuOH	2
24983268	1.0	8.24E-01	Control	34
24982804	1.2	2.38E-01	Control	26
313496770	1.1	9.02E-01	Control	20
254522278	1.5	6.52E-01	Control	11
190575345	1.9	7.51E-01	Control	8
24982353	1.0	6.80E-01	Control	7
190572988	1.1	9.58E-01	Control	7
190574492	1.1	6.67E-01	Control	6
190572101	1.5	7.74E-01	Control	6
24982449	1.1	4.76E-01	Control	5
113866733	25.3	1.81E-01	Control	5
228957652	74.2	1.87E-01	Control	4
113868033	499.1	1.73E-01	Control	4
118476855	174.9	8.32E-02	Control	3
344208107	1.2	9.40E-01	Control	3
113866501	3.1	1.32E-01	Control	3
113868357	363.5	7.73E-01	Control	3
261824796	1.0	9.14E-01	Control	2
190575561	1.3	8.15E-01	Control	2
254521740	1.1	8.59E-01	Control	2
331702725	1.6	3.54E-01	Control	1
113868360	1242.9	6.81E-01	Control	3
113868358	106.0	9.47E-01	Control	2
113868595	555.8	3.89E-02	Control	2
113869100	103.0	8.41E-01	Control	2
206970137	102.3	8.25E-02	Control	2

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986746	PP_0001	parB	parB-like partition protein	1.1	9.11E-01	7,5 g/l BuOH	6.5	32390	Cytoplasmic	11	COG1475	Transcription	
26986747	PP_0002		ParA family protein	1.8	2.04E-01	Control	6.7	28919	Cytoplasmic Membrane	3	COG1192	Cell division and chromosome partitioning	
26986748	PP_0003	gidB	16S rRNA methyltransferase GidB	1.6	4.87E-01	Control	7.1	24063	Unknown	2	COG0357	Cell envelope biogenesis, outer membrane	
26986749	PP_0004	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	1.0	5.63E-01	Control	6.4	69567	Cytoplasmic	2	COG0445	Cell cycle control, cell division, chromosome partitioning	
26986750	PP_0005	trmE	tRNA modification GTPase TrmE	1.2	1.39E-01	7,5 g/l BuOH	5.0	48963	Cytoplasmic	4	COG0486	General function prediction only	
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.7	2.25E-01	Control	9.1	61919	Cytoplasmic Membrane	7	COG0706	Intracellular trafficking and secretion	
26986755	PP_0010	dnaA	chromosomal replication initiation protein	1.4	1.01E-01	Control	8.3	56473	Cytoplasmic	2	COG0593	DNA replication, recombination, and repair	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.5	7.48E-02	Control	4.9	40718	Cytoplasmic	13	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.2	3.50E-01	7,5 g/l BuOH	5.8	90030	Unknown	17	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.2	2.02E-01	Control	6.1	31236	Cytoplasmic	14			
26986764	PP_0019		hypothetical protein	1.0	7.07E-01	7,5 g/l BuOH	4.8	24854	Unknown	6			
26986765	PP_0020		hypothetical protein	1.3	1.79E-01	Control	4.9	33146	Cytoplasmic	4			
26986774	PP_0029	czrR-1	DNA-binding response regulator CzrR	4.7	4.14E-02	Control	6.1	25537	Cytoplasmic	3	COG0745	Signal transduction mechanisms	Transcription
26986797	PP_0052		beta-lactamase domain protein	1.7	4.07E-02	Control	5.5	32706	Cytoplasmic	4	COG0491	General function prediction only	
26986802	PP_0057		major facilitator family transporter	22.3	2.10E-01	7,5 g/l BuOH	9.3	58758	Cytoplasmic Membrane	2	COG2814	Carbohydrate transport and metabolism	
26986803	PP_0058		phospholipid/glycerol acyltransferase	5.0	1.10E-01	Control	###	29094	Cytoplasmic Membrane	2	COG0204	Lipid metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	2.4	7.88E-03	7,5 g/l BuOH	4.9	75112	Cytoplasmic	18	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.5	1.20E-01	Control	4.8	36024	Cytoplasmic	5	COG0752	Translation, ribosomal structure and biogenesis	
26986808	PP_0063		lipid A biosynthesis lauroyl acyltransferase	1.1	7.69E-01	7,5 g/l BuOH	###	32840	Cytoplasmic Membrane	2	COG1560	Cell envelope biogenesis, outer membrane	
26986813	PP_0068	def	peptide deformylase	1.6	5.28E-01	Control	5.1	19410	Cytoplasmic	3	COG0242	Translation, ribosomal structure and biogenesis	
26986815	PP_0070		Sua5/YciO/YrdC/YwlC family protein	1.4	5.35E-01	Control	6.1	20493	Cytoplasmic	2	COG0009	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	1.6	1.08E-01	Control	8.1	34224	Cytoplasmic	15	COG0604	Energy production and conversion	General function prediction only
26986818	PP_0073	hemF	coproporphyrinogen III oxidase	1.2	4.79E-01	7,5 g/l BuOH	5.6	34393	Cytoplasmic	4	COG0408	Coenzyme metabolism	
26986819	PP_0074	aroE	shikimate 5-dehydrogenase	1.5	2.21E-01	7,5 g/l BuOH	5.0	29289	Cytoplasmic	4	COG0169	Amino acid transport and metabolism	
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1.9	8.72E-02	Control	5.0	28482	Cytoplasmic	8	COG0159	Amino acid transport and metabolism	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	1.2	1.36E-01	Control	6.4	44046	Cytoplasmic	6	COG0133	Amino acid transport and metabolism	
26986831	PP_0086		hypothetical protein	4.6	3.71E-02	7,5 g/l BuOH	7.9	7959	Unknown	4	COG3360	Function unknown	
26986839	PP_0094		HAD superfamily hydrolase	1.6	3.23E-01	7,5 g/l BuOH	5.1	24540	Cytoplasmic	3	COG0546	General function prediction only	
26986841	PP_0096	prlC	oligopeptidase A	1.6	2.43E-02	7,5 g/l BuOH	5.0	75721	Cytoplasmic	22	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.8	2.97E-02	Control	6.8	26001	Cytoplasmic	20	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	2.2	1.70E-02	Control	6.8	42059	Cytoplasmic Membrane	8	COG1622	Energy production and conversion	
26986851	PP_0106		cytochrome c oxidase, subunit III	1.3	3.94E-01	Control	8.7	33623	Cytoplasmic Membrane	3	COG1845	Energy production and conversion	
26986856	PP_0111		electron transport protein SCO1/SenC	3.5	8.46E-01	Control	8.2	22960	Cytoplasmic Membrane	5	COG1999	General function prediction only	
26986857	PP_0112		metal ABC transporter periplasmic protein	1.1	5.24E-01	Control	7.8	27711	Cytoplasmic Membrane	16	COG1464	Inorganic ion transport and metabolism	
26986861	PP_0116		lipoprotein	1.2	4.11E-01	7,5 g/l BuOH	7.4	25597	Unknown	9			
26986868	PP_0123	polA	DNA polymerase I	1.8	1.47E-01	Control	5.1	99607	Cytoplasmic	14	COG0749	DNA replication, recombination, and repair	
26986869	PP_0124	engB	ribosome biogenesis GTP-binding protein YsxC	1.3	7.28E-02	Control	9.6	23440	Cytoplasmic	9	COG0218	General function prediction only	
26986871	PP_0126		cytochrome c4	2.2	1.24E-01	Control	8.0	21260	Periplasmic	4	COG2863	Energy production and conversion	
26986872	PP_0127		DsbA family thiol:disulfide interchange protein	1.2	5.06E-01	Control	7.1	23073	Periplasmic	5	COG1651	Posttranslational modification, protein turnover, chaperones	
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.0	6.50E-01	Control	9.6	29387	Cytoplasmic	2	COG3023	Cell envelope biogenesis, outer membrane	
26986878	PP_0133	algB	two component, sigma54 specific, transcriptional regulator, Fis family	1.7	2.43E-01	7,5 g/l BuOH	5.4	49604	Cytoplasmic	3	COG2204	Signal transduction mechanisms	
26986884	PP_0139		lipoprotein	3.3	2.12E-02	Control	9.5	23212	Unknown	4	COG3218	General function prediction only	
26986885	PP_0140		hypothetical protein	1.1	8.95E-01	7,5 g/l BuOH	5.4	33062	Unknown	3	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26986886	PP_0141		ABC transporter ATP-binding protein	1.6	9.14E-02	Control	6.7	28270	Cytoplasmic Membrane	3	COG1127	Secondary metabolites biosynthesis, transport, and catabolism	
26986887	PP_0142		hypothetical protein	4.7	5.24E-02	Control	5.3	40379	Cytoplasmic Membrane	2	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.4	5.50E-01	7,5 g/l BuOH	7.3	50185	Cytoplasmic Membrane	2	COG1282	Energy production and conversion	
26986902	PP_0158	gcdH	acyl-CoA dehydrogenase domain-containing protein	6.9	9.65E-02	Control	6.2	43242	Cytoplasmic	4	COG1960	Lipid metabolism	
26986907	PP_0163		GntR family transcriptional regulator	1.0	6.46E-01	7,5 g/l BuOH	7.3	25518	Cytoplasmic	4	COG1802	Transcription	
26986909	PP_0165		GGDEF domain-containing protein	1.5	2.67E-01	Control	6.3	71284	Cytoplasmic Membrane	7	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.1	6.02E-01	Control	7.8	51116	Cytoplasmic Membrane	4	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.3	2.67E-01	Control	7.7	78583	Cytoplasmic Membrane	18	COG2274	Defense mechanisms	
26986912	PP_0168		surface adhesion protein	9.3	2.12E-04	Control	3.9	888214	Extracellular	22	COG2931	Secondary metabolites biosynthesis, transport, and catabolism	
26986917	PP_0173		transcriptional factor-related protein	1.3	5.55E-01	7,5 g/l BuOH	###	23493	Unknown	3			
26986927	PP_0183		glutathione S-transferase family protein	1.1	5.26E-01	Control	5.4	24438	Cytoplasmic	10	COG0625	Posttranslational modification, protein turnover, chaperones	
26986928	PP_0184	argH	argininosuccinate lyase	1.4	2.31E-01	Control	5.4	52061	Cytoplasmic	13	COG0165	Amino acid transport and metabolism	
26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	1.8	5.55E-02	Control	6.5	27422	Cytoplasmic	12	COG3279	Transcription	Signal transduction mechanisms
26986930	PP_0186	hemC	porphobilinogen deaminase	2.0	1.97E-01	Control	5.1	33440	Cytoplasmic	2	COG0181	Coenzyme metabolism	
26986931	PP_0187	hemD	uroporphyrinogen-III synthase	1.1	6.91E-01	7,5 g/l BuOH	6.8	27045	Unknown	2	COG1587	Coenzyme metabolism	
26986932	PP_0188		uroporphyrin-III C-methyltransferase	1.9	3.30E-01	7,5 g/l BuOH	4.8	40556	Cytoplasmic Membrane	12	COG2959	Coenzyme metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.1	6.65E-01	Control	9.6	46030	Cytoplasmic Membrane	8	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	1.8	6.73E-02	Control	###	32300	Cytoplasmic	6			
26986940	PP_0196		ABC transporter ATP-binding protein	2.2	2.12E-02	7,5 g/l BuOH	5.7	70615	Cytoplasmic	5	COG0488	General function prediction only	
26986947	PP_0203		hypothetical protein	1.2	5.17E-01	Control	5.9	62682	Unknown	19	COG0624	Amino acid transport and metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.1	7.90E-02	Control	5.2	51549	Cytoplasmic	25	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	2.0	1.01E-02	Control	6.1	44824	Cytoplasmic	15	COG0160	Amino acid transport and metabolism	
26986958	PP_0215		signal transduction protein	1.1	7.26E-01	7,5 g/l BuOH	7.0	45294	Cytoplasmic	2	COG1639	Signal transduction mechanisms	
26986968	PP_0225		amino-acid ABC transporter ATP-binding protein YecC	1.5	2.21E-01	Control	###	27596	Cytoplasmic Membrane	3	COG1126	Amino acid transport and metabolism	
26986970	PP_0227		cystine transporter subunit	1.3	1.48E-01	7,5 g/l BuOH	8.7	28756	Periplasmic	24	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26986977	PP_0234	oprE	outer membrane porin	1.3	5.55E-01	7,5 g/l BuOH	5.4	48317	Outer Membrane	12			
26986978	PP_0235	lsfA	peroxidase	1.2	4.36E-01	7,5 g/l BuOH	6.0	23948	Cytoplasmic	10	COG0450	Posttranslational modification, protein turnover, chaperones	
26986986	PP_0243	gshA	glutamate--cysteine ligase	1.6	7.23E-02	Control	4.8	59067	Cytoplasmic	7	COG2918	Coenzyme metabolism	
26986989	PP_0246	ompR	osmolarity response regulator	1.1	5.78E-01	7,5 g/l BuOH	5.9	27492	Cytoplasmic	12	COG0745	Signal transduction mechanisms	Transcription
26986991	PP_0248	rimK	alpha-L-glutamate ligase, RimK family	1.4	8.27E-01	7,5 g/l BuOH	###	32629	Cytoplasmic	3	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26986995	PP_0252	hslO	Hsp33-like chaperonin	1.5	2.33E-02	Control	4.4	33472	Cytoplasmic	11	COG1281	Posttranslational modification, protein turnover, chaperones	
26987002	PP_0260	nudE	ADP-ribose diphosphatase NudE	1.9	2.32E-01	Control	4.5	20947	Cytoplasmic	2			
26987003	PP_0261	cysQ	3'(2'),5'-bisphosphate nucleotidase	1.8	1.84E-01	Control	4.3	28452	Cytoplasmic	2	COG1218	Inorganic ion transport and metabolism	
26987005	PP_0263		two component, sigma54 specific, transcriptional regulator, Fis family	2.5	1.92E-01	7,5 g/l BuOH	5.9	50990	Cytoplasmic	4	COG2204	Signal transduction mechanisms	
26987008	PP_0266		agmatine deiminase	1.8	2.21E-02	Control	4.7	40837	Cytoplasmic	2	COG2957	Amino acid transport and metabolism	
26987010	PP_0268	oprQ	outer membrane porin	1.6	7.59E-02	Control	6.1	47787	Outer Membrane	9			
26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding protein	1.3	1.61E-01	Control	5.2	27869	Periplasmic	22	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987025	PP_0283		amino acid ABC transporter ATP-binding protein	1.3	3.37E-01	Control	7.7	28381	Cytoplasmic Membrane	4	COG4598	Amino acid transport and metabolism	
26987029	PP_0287		AsmA family protein	1.1	9.93E-01	7,5 g/l BuOH	6.0	80277	Unknown	10	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	310.2	2.91E-02	7,5 g/l BuOH	8.5	58780	Cytoplasmic Membrane	3			
26987031	PP_0289	hisB	imidazoleglycerol-phosphate dehydratase	1.3	2.81E-01	7,5 g/l BuOH	6.4	23420	Cytoplasmic	5	COG0131	Amino acid transport and metabolism	
26987032	PP_0290	hisH	imidazole glycerol phosphate synthase subunit HisH	1.3	5.99E-01	7,5 g/l BuOH	6.4	23535	Cytoplasmic	7	COG0118	Amino acid transport and metabolism	
26987034	PP_0292	hisA	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	2.1	3.57E-02	7,5 g/l BuOH	4.9	25907	Cytoplasmic	7	COG0106	Amino acid transport and metabolism	
26987035	PP_0293	hisF	imidazole glycerol phosphate synthase subunit HisF	1.3	3.90E-01	7,5 g/l BuOH	5.0	27131	Cytoplasmic	5	COG0107	Amino acid transport and metabolism	
26987036	PP_0294		glycine betaine/L-proline ABC transporter ATP-binding subunit	4.1	5.42E-02	Control	7.9	43724	Cytoplasmic Membrane	4	COG4175	Amino acid transport and metabolism	
26987038	PP_0296		glycine betaine/L-proline ABC transporter periplasmic protein	2.4	1.06E-02	Control	6.6	34568	Unknown	14	COG2113	Amino acid transport and metabolism	
26987046	PP_0304		hypothetical protein	12.0	1.19E-01	Control	7.6	35771	Periplasmic	2	COG2113	Amino acid transport and metabolism	
26987050	PP_0308		membrane dipeptidase	1.6	2.44E-01	7,5 g/l BuOH	5.4	35978	Cytoplasmic	3	COG2355	Amino acid transport and metabolism	
26987063	PP_0321		threonine aldolase	1.6	3.45E-02	7,5 g/l BuOH	5.4	38068	Cytoplasmic	8	COG2008	Amino acid transport and metabolism	
26987067	PP_0325	soxA	sarcosine oxidase, alpha subunit family	1.9	5.75E-03	Control	7.6	109175	Cytoplasmic	7	COG0404	Amino acid transport and metabolism	
26987068	PP_0326	soxG	sarcosine oxidase, gamma subunit family	2.6	1.05E-01	Control	7.3	22961	Cytoplasmic	4	COG4583	Amino acid transport and metabolism	
26987070	PP_0328	fdhA	formaldehyde dehydrogenase, glutathione-independent	7.1	4.52E-02	Control	6.6	42328	Cytoplasmic	7	COG1063	Amino acid transport and metabolism	General function prediction only
26987077	PP_0335		glutathione S-transferase family protein	1.0	8.31E-01	Control	6.4	23174	Cytoplasmic	8	COG0625	Posttranslational modification, protein turnover, chaperones	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	2.4	1.56E-01	Control	4.7	24565	Unknown	7	COG0225	Posttranslational modification, protein turnover, chaperones	
26987079	PP_0337		diguanylate cyclase/phosphodiesterase with PAS/PAC and GAF sensor(s)	1.6	2.09E-01	Control	6.1	100753	Cytoplasmic Membrane	3	COG5001	Signal transduction mechanisms	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.6	5.13E-03	Control	5.3	55654	Cytoplasmic	20	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.9	8.28E-03	Control	5.6	99332	Cytoplasmic	62	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	1.5	2.69E-01	Control	5.3	109432	Cytoplasmic	21	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987086	PP_0344	waaP	lipopolysaccharide kinase	1.9	2.12E-01	Control	###	30807	Cytoplasmic	2			
26987089	PP_0347		hypothetical protein	2.7	4.29E-02	Control	7.4	53779	Cytoplasmic	3			
26987098	PP_0356	glcB	malate synthase G	7.8	4.36E-04	7,5 g/l BuOH	5.8	78346	Cytoplasmic	25	COG2225	Energy production and conversion	
26987101	PP_0359		serine/threonine protein kinase	2.3	5.23E-01	7,5 g/l BuOH	5.7	38203	Cytoplasmic	2	COG2334	General function prediction only	
26987104	PP_0362	bioB	biotin synthase	1.3	2.96E-01	7,5 g/l BuOH	5.6	38950	Cytoplasmic	4	COG0502	Coenzyme metabolism	
26987106	PP_0364	bioH	carboxylesterase	3.4	4.50E-02	Control	4.8	26344	Cytoplasmic	3	COG0596	General function prediction only	
26987108	PP_0366	bioD	dithiobiotin synthetase	3.0	7.75E-03	Control	5.3	23871	Cytoplasmic	9	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	2.1	1.46E-02	Control	5.8	65541	Cytoplasmic	25	COG1960	Lipid metabolism	
26987112	PP_0370		acyl-CoA dehydrogenase domain-containing protein	2.9	8.08E-03	Control	4.9	63592	Cytoplasmic	7	COG1960	Lipid metabolism	
26987117	PP_0375		prolyl oligopeptidase family protein	39.6	8.47E-03	7,5 g/l BuOH	6.0	67549	Cytoplasmic	4	COG1506	Amino acid transport and metabolism	
26987118	PP_0376	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	17.9	4.24E-05	7,5 g/l BuOH	6.5	42507	Cytoplasmic	5	COG0535	General function prediction only	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	19.6	2.26E-04	7,5 g/l BuOH	6.8	29075	Cytoplasmic	20	COG5424	Coenzyme metabolism	

26987121	PP_0379	pqqB	pyrroloquinoline quinone biosynthesis protein PqqB	19.0	1.48E-04	7,5 g/l BuOH	5.5	33331	Cytoplasmic	14	COG1235	General function prediction only	
26987124	PP_0382		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	3.0	2.63E-01	Control	4.9	29311	Cytoplasmic	2	COG0388	General function prediction only	
26987128	PP_0386		sensory box protein	4.3	6.89E-03	Control	5.6	139392	Cytoplasmic Membrane	8	COG5001	Signal transduction mechanisms	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	2.2	4.44E-02	7,5 g/l BuOH	4.6	69396	Cytoplasmic	25	COG0568	Transcription	
26987130	PP_0388	dnaG	DNA primase	2.5	2.54E-01	7,5 g/l BuOH	6.8	73829	Cytoplasmic	1	COG0358	DNA replication, recombination, and repair	
26987132	PP_0390	gcp	DNA-binding/iron metalloprotein/AP endonuclease	3.6	1.83E-02	Control	4.8	36606	Extracellular	2	COG0533	Posttranslational modification, protein turnover, chaperones	
26987137	PP_0395		SpoVR family protein	3.3	3.66E-02	Control	5.4	61330	Cytoplasmic	13	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	2.8	8.10E-03	Control	7.0	50488	Cytoplasmic	9	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	1.6	8.29E-03	7,5 g/l BuOH	5.8	73782	Cytoplasmic	46	COG2766	Signal transduction mechanisms	
26987143	PP_0401	kspA	dimethyladenosine transferase	1.4	3.17E-01	Control	8.5	29666	Cytoplasmic	2	COG0030	Translation, ribosomal structure and biogenesis	
26987145	PP_0403	surA	survival protein SurA	2.2	1.24E-01	7,5 g/l BuOH	5.2	49082	Periplasmic	14	COG0760	Posttranslational modification, protein turnover, chaperones	
26987146	PP_0405		aminoglycoside phosphotransferase	2.1	1.55E-03	7,5 g/l BuOH	4.8	38238	Cytoplasmic	5	COG3178	General function prediction only	
26987147	PP_0406		nucleotidyl transferase	1.3	4.18E-01	Control	6.0	23814	Cytoplasmic	3	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
26987151	PP_0410	uhpA	LuxR family two component transcriptional regulator	1.3	5.99E-02	7,5 g/l BuOH	7.2	22750	Cytoplasmic	3	COG2197	Signal transduction mechanisms	Transcription
26987153	PP_0412		polyamine ABC transporter periplasmic protein	2.2	6.26E-02	Control	5.3	37801	Periplasmic	12	COG0687	Amino acid transport and metabolism	
26987156	PP_0415	rpe	ribulose-phosphate 3-epimerase	1.4	2.41E-01	7,5 g/l BuOH	5.6	27672	Cytoplasmic	4	COG0036	Carbohydrate transport and metabolism	
26987158	PP_0417	trpE	anthranilate synthase component I	1.5	2.36E-01	Control	4.8	54406	Cytoplasmic	8	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
26987159	PP_0418		GDSL family lipase	1.1	7.17E-01	7,5 g/l BuOH	4.4	67175	Outer Membrane	2	COG3240	Lipid metabolism	General function prediction only
26987161	PP_0420	trpG	anthranilate synthase component II	2.4	2.29E-01	Control	6.2	21677	Cytoplasmic	3	COG0512	Amino acid transport and metabolism	Coenzyme metabolism
26987162	PP_0421	trpD	anthranilate phosphoribosyltransferase	1.3	4.60E-01	Control	5.6	37245	Cytoplasmic	4	COG0547	Amino acid transport and metabolism	
26987163	PP_0422	trpC	indole-3-glycerol-phosphate synthase	1.1	4.47E-01	7,5 g/l BuOH	4.7	30433	Cytoplasmic	12	COG0134	Amino acid transport and metabolism	
26987171	PP_0430		hypothetical protein	2.6	8.07E-03	Control	6.7	33680	Unknown	4	COG2070	General function prediction only	
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.3	3.66E-01	Control	6.8	36277	Cytoplasmic	13	COG0002	Amino acid transport and metabolism	
26987177	PP_0436	tyrS	tyrosyl-tRNA synthetase	1.3	1.57E-01	7,5 g/l BuOH	5.5	44287	Cytoplasmic	13	COG0162	Translation, ribosomal structure and biogenesis	
26987181	PP_0440	tuf	elongation factor Tu	1.3	1.51E-01	7,5 g/l BuOH	5.0	43495	Cytoplasmic	25	COG0050	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.8	4.64E-03	Control	###	24251	Cytoplasmic	22	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	19.3	2.81E-02	7,5 g/l BuOH	###	17686	Cytoplasmic	4	COG0244	Translation, ribosomal structure and biogenesis	
26987187	PP_0446	rplL	50S ribosomal protein L7/L12	34.5	4.40E-02	7,5 g/l BuOH	4.4	12599	Unknown	2	COG0222	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	2.1	4.77E-02	Control	5.5	150992	Cytoplasmic	92	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	2.1	4.66E-02	Control	7.2	154797	Cytoplasmic	82	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	2.6	9.07E-02	7,5 g/l BuOH	###	13727	Cytoplasmic	2	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	8.8	1.13E-01	7,5 g/l BuOH	###	17578	Cytoplasmic	4	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.0	7.08E-01	Control	4.9	78817	Cytoplasmic	52	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.1	5.26E-01	Control	5.0	43478	Cytoplasmic	50	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.2	3.83E-01	Control	###	21811	Cytoplasmic	8	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	2.2	4.50E-02	Control	###	29669	Cytoplasmic	17	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	5.1	1.43E-01	7,5 g/l BuOH	###	15373	Cytoplasmic	2	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	9.1	2.40E-01	7,5 g/l BuOH	###	13410	Cytoplasmic	2	COG0093	Translation, ribosomal structure and biogenesis	
26987206	PP_0465	rplX	50S ribosomal protein L24	133.6	6.92E-02	7,5 g/l BuOH	###	11329	Cytoplasmic	4	COG0198	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.3	3.04E-01	7,5 g/l BuOH	###	20329	Cytoplasmic	12	COG0094	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	4.6	1.35E-01	7,5 g/l BuOH	###	13975	Cytoplasmic	3	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.4	3.39E-01	Control	###	19143	Cytoplasmic	13	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	7.5	4.40E-03	7,5 g/l BuOH	###	12628	Cytoplasmic	4	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	3.3	2.26E-01	7,5 g/l BuOH	###	17666	Cytoplasmic	7	COG0098	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	15.8	5.38E-02	7,5 g/l BuOH	###	15189	Cytoplasmic	5	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.2	7.06E-01	Control	###	47853	Cytoplasmic Membrane	6	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	5.0	7.00E-02	7,5 g/l BuOH	###	13256	Cytoplasmic	3	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	2.1	3.49E-01	7,5 g/l BuOH	###	13660	Cytoplasmic	3	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.5	2.22E-01	Control	###	23056	Cytoplasmic	17	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.1	2.35E-01	7,5 g/l BuOH	4.7	36629	Cytoplasmic	20	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	8.5	4.91E-02	7,5 g/l BuOH	###	14363	Cytoplasmic	4	COG0203	Translation, ribosomal structure and biogenesis	
26987224	PP_0483	uvrA	excinuclease ABC subunit A	1.0	7.59E-01	Control	7.0	104378	Cytoplasmic	12	COG0178	DNA replication, recombination, and repair	
26987226	PP_0485	ssb	single-stranded DNA-binding protein	1.6	9.53E-01	Control	6.0	20059	Cytoplasmic	6	COG0629	DNA replication, recombination, and repair	
26987233	PP_0493	selA	selenocysteine synthase	1.2	1.51E-01	Control	7.7	51723	Cytoplasmic	2	COG1921	seryl-tRNASer selenium transferase	
26987240	PP_0501		NAD-dependent epimerase/dehydratase	1.2	2.32E-01	Control	5.2	33325	Cytoplasmic	5	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987249	PP_0510	trx-1	thioredoxin	1.3	8.75E-02	7,5 g/l BuOH	4.6	31822	Cytoplasmic	9	COG3118	Posttranslational modification, protein turnover, chaperones	
26987252	PP_0514	ribD	riboflavin biosynthesis protein RibD	1.9	5.86E-02	Control	7.7	39816	Cytoplasmic	2	COG0117	Coenzyme metabolism	
26987253	PP_0515	ribE-1	riboflavin synthase subunit alpha	2.5	1.03E-01	Control	6.5	23597	Cytoplasmic	2	COG0307	Coenzyme metabolism	
26987259	PP_0521		hypothetical protein	1.0	8.09E-01	7,5 g/l BuOH	6.4	28523	Unknown	3			
26987260	PP_0522	ribA	GTP cyclohydrolase II	1.1	5.93E-01	Control	7.0	22350	Cytoplasmic	4	COG0807	Coenzyme metabolism	
26987266	PP_0528	ispA	polyprenyl synthetase	5.2	1.40E-01	7,5 g/l BuOH	4.9	31352	Cytoplasmic	2	COG0142	Coenzyme metabolism	
26987276	PP_0538	ppa	inorganic pyrophosphatase	1.2	7.27E-01	7,5 g/l BuOH	4.6	19189	Cytoplasmic	8	COG0221	Energy production and conversion	
26987280	PP_0542		ethanolamine ammonia-lyase small subunit	2.0	6.35E-02	Control	6.9	29573	Cytoplasmic	5	COG4302	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	2.4	8.63E-04	7,5 g/l BuOH	5.9	55268	Cytoplasmic	35	COG1012	Energy production and conversion	
26987285	PP_0547	mpl	UDP-N-acetylmuramate	1.6	6.15E-02	Control	6.1	48202	Cytoplasmic	5	COG0773	Cell envelope biogenesis, outer membrane	
26987288	PP_0550		hypothetical protein	2.8	7.63E-02	Control	7.6	23787	Cytoplasmic	8	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987293	PP_0555	acoA	pyruvate dehydrogenase (acetyl-transferring)	2.1	1.35E-01	7,5 g/l BuOH	5.0	34676	Cytoplasmic	2	COG1071	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.7	1.22E-01	Control	6.5	49088	Cytoplasmic	22	COG0439	Lipid metabolism	
26987297	PP_0559	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	1.0	8.45E-01	Control	4.7	16186	Unknown	4	COG0511	Lipid metabolism	
26987298	PP_0560	aroQ-1	3-dehydroquinate dehydratase	138.4	4.47E-02	7,5 g/l BuOH	6.9	16491	Cytoplasmic	3	COG0757	Amino acid transport and metabolism	
26987302	PP_0564		hypothetical protein	1.4	2.57E-01	7,5 g/l BuOH	6.6	40223	Unknown	12	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	1.2	4.24E-01	Control	5.3	71043	Unknown	9	COG1166	Amino acid transport and metabolism	
26987308	PP_0570		alpha-2-macroglobulin domain protein	2.4	1.57E-03	Control	5.2	178472	Unknown	35	COG2373	General function prediction only	
26987312	PP_0574		LuxR family DNA-binding response regulator	2.2	6.66E-02	Control	5.1	29040	Cytoplasmic	3	COG2197	Signal transduction mechanisms	Transcription
26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.7	3.74E-01	7,5 g/l BuOH	7.5	47782	Cytoplasmic	10	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987320	PP_0582		acetyl-CoA acetyltransferase	2.2	9.69E-02	Control	8.3	45543	Cytoplasmic	2	COG0183	Lipid metabolism	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.1	7.78E-01	7,5 g/l BuOH	5.0	69953	Cytoplasmic Membrane	24	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	6.8	2.30E-03	Control	6.6	83475	Cytoplasmic Membrane	3	COG2217	Inorganic ion transport and metabolism	
26987329	PP_0591	add	adenosine deaminase	1.2	5.92E-01	7,5 g/l BuOH	4.8	35845	Cytoplasmic	6	COG1816	Nucleotide transport and metabolism	
26987330	PP_0592		short chain dehydrogenase	1.4	3.12E-01	Control	6.0	24627	Extracellular	4	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987332	PP_0594		TetR family transcriptional regulator	2.0	1.72E-01	Control	7.6	27446	Cytoplasmic	2	COG1309	Transcription	
26987334	PP_0596		beta alanine--pyruvate transaminase	2.2	1.74E-02	7,5 g/l BuOH	6.8	48529	Cytoplasmic	8	COG0161	Coenzyme metabolism	
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.2	1.36E-01	Control	5.9	53498	Cytoplasmic	9	COG1012	Energy production and conversion	
26987336	PP_0599		hypothetical protein	2.9	1.87E-02	Control	9.6	83247	Unknown	3	COG3008	General function prediction only	
26987339	PP_0602	ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	1.7	1.11E-01	Control	9.7	34827	Cytoplasmic	5	COG0196	Coenzyme metabolism	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.2	4.22E-01	Control	6.0	105800	Cytoplasmic	38	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP_0622		competence lipoprotein ComL	3.7	9.61E-02	7,5 g/l BuOH	4.8	38410	Unknown	11	COG4105	General function prediction only	
26987360	PP_0624		hypothetical protein	1.2	3.86E-01	7,5 g/l BuOH	6.1	26401	Unknown	3	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.8	7.31E-02	7,5 g/l BuOH	5.2	94861	Cytoplasmic	48	COG0542	Posttranslational modification, protein turnover, chaperones	
26987367	PP_0631	coaE	dephospho-CoA kinase	1.2	3.01E-01	7,5 g/l BuOH	6.6	22652	Cytoplasmic	5	COG0237	Coenzyme metabolism	
26987376	PP_0640		hypothetical protein	2.7	1.02E-01	Control	6.6	44093	Cytoplasmic Membrane	6			
26987390	PP_0654	mdh	malate dehydrogenase	2.1	6.58E-03	Control	5.1	29434	Cytoplasmic	5	COG0039	Energy production and conversion	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.5	9.39E-02	Control	6.2	44897	Cytoplasmic	22	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.7	3.61E-02	7,5 g/l BuOH	5.3	61860	Cytoplasmic	26	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.2	6.58E-02	7,5 g/l BuOH	6.5	48871	Unknown	10	COG0334	Amino acid transport and metabolism	
26987415	PP_0679		hypothetical protein	1.8	1.66E-02	7,5 g/l BuOH	7.6	18133	Cytoplasmic Membrane	2			
26987416	PP_0680		ATP-dependent protease	1.9	1.97E-03	7,5 g/l BuOH	4.5	89677	Cytoplasmic	11	COG1067	Posttranslational modification, protein turnover, chaperones	
26987420	PP_0684	fklB-1	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.9	2.73E-01	Control	4.4	21678	Cytoplasmic	5	COG0545	Posttranslational modification, protein turnover, chaperones	
26987423	PP_0687	ispB	polyprenyl synthetase	2.1	9.99E-02	Control	6.8	35269	Cytoplasmic	6	COG0142	Coenzyme metabolism	
26987426	PP_0690	obgE	GTPase ObgE	1.5	2.03E-01	7,5 g/l BuOH	4.5	44825	Cytoplasmic	8	COG0536	General function prediction only	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.1	8.93E-01	Control	7.8	39661	Cytoplasmic	3	COG0263	Amino acid transport and metabolism	
26987429	PP_0693		hypothetical protein	1.3	3.52E-01	Control	5.1	106556	Cytoplasmic	10	COG0419	DNA replication, recombination, and repair	
26987443	PP_0707		MscS mechanosensitive ion channel	1.4	3.15E-01	Control	9.9	92124	Cytoplasmic Membrane	5	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	4.8	8.74E-04	Control	5.3	23026	Unknown	16	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	2.3	2.47E-02	Control	###	31284	Cytoplasmic	5	COG2326	Function unknown	
26987455	PP_0719		GTP-dependent nucleic acid-binding protein EngD	1.8	1.84E-01	Control	4.7	39962	Cytoplasmic	6	COG0012	Translation, ribosomal structure and biogenesis	
26987456	PP_0720	pth	peptidyl-tRNA hydrolase	1.1	6.13E-01	Control	###	20949	Cytoplasmic	6	COG0193	Translation, ribosomal structure and biogenesis	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.0	9.14E-01	Control	6.4	23242	Cytoplasmic	13	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.2	4.41E-01	Control	5.9	34192	Cytoplasmic	14	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987460	PP_0724	lolB	outer membrane lipoprotein LolB	1.5	8.48E-02	7,5 g/l BuOH	8.2	22895	Unknown	4	COG3017	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	4.1	4.27E-02	7,5 g/l BuOH	4.6	63994	Cytoplasmic	11	COG5010	Intracellular trafficking and secretion	
26987468	PP_0732	hemA	glutamyl-tRNA reductase	1.3	5.55E-01	Control	5.5	46305	Cytoplasmic	2	COG0373	Coenzyme metabolism	
26987478	PP_0742		hypothetical protein	1.0	9.37E-01	7,5 g/l BuOH	6.2	36114	Unknown	6	COG3380	General function prediction only	
26987479	PP_0743		NAD-dependent epimerase/dehydratase	3.4	6.95E-02	Control	9.7	33119	Cytoplasmic Membrane	5	COG1090	General function prediction only	

5.2.3.3 GeLCMSMS_P_putida_KT2440_7.5g_BuOH_Tabelle

26987482	PP 0746	upp	uracil phosphoribosyltransferase	1.5	2.72E-01	Control	7.1	23000	Cytoplasmic	9	COG0035	Nucleotide transport and metabolism	
26987487	PP 0751	mqo-1	malate:quinone oxidoreductase	2.7	2.59E-04	7,5 g/l BuOH	8.4	54282	Cytoplasmic	12	COG0579	General function prediction only	
26987492	PP 0756		phospholipid/glycerol acyltransferase	1.3	7.19E-02	7,5 g/l BuOH	8.3	47784	Cytoplasmic	4			
26987495	PP 0759		hypothetical protein	1.1	9.82E-01	7,5 g/l BuOH	7.0	29743	Unknown	9	COG0501	Posttranslational modification, protein turnover, chaperones	
26987498	PP 0762	hprA	glycerate dehydrogenase	2.1	8.92E-02	7,5 g/l BuOH	6.1	34094	Cytoplasmic	3	COG1052	Energy production and conversion	Coenzyme metabolism
26987499	PP 0763		long-chain-fatty-acid--CoA ligase	2.0	1.01E-01	Control	5.5	62125	Cytoplasmic	13	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP 0765		hypothetical protein	1.7	2.93E-02	Control	5.0	67937	Outer Membrane	25			
26987502	PP 0766		hypothetical protein	1.8	7.98E-04	Control	9.6	50572	Unknown	37			
26987504	PP 0768		response regulator/hypothetical protein	2.1	1.05E-01	Control	8.4	59272	Cytoplasmic	15	COG3437	Transcription	Signal transduction mechanisms
26987505	PP 0769		histidine kinase	1.0	8.11E-01	Control	4.6	25229	Cytoplasmic	10	COG0642	Signal transduction mechanisms	
26987509	PP 0773		OmpA/MotB domain protein	2.7	6.76E-02	7,5 g/l BuOH	9.5	24753	Outer Membrane	14	COG2885	Cell envelope biogenesis, outer membrane	
26987510	PP 0774	pta	phosphate acetyltransferase	4.0	9.87E-02	Control	5.2	74642	Cytoplasmic Membrane	4	COG0280	Energy production and conversion	
26987515	PP 0779		methyl-accepting chemotaxis transducer/sensory box protein	1.1	5.69E-01	Control	6.2	49856	Cytoplasmic Membrane	3	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987522	PP 0786	trxB	thioredoxin reductase	1.9	7.38E-02	Control	5.1	33841	Unknown	11	COG0492	Posttranslational modification, protein turnover, chaperones	
26987523	PP 0787	nadC	nicotinate-nucleotide pyrophosphorylase	1.6	1.38E-01	Control	5.2	30163	Cytoplasmic	10	COG0157	Coenzyme metabolism	
26987528	PP 0792	fruR	DNA-binding transcriptional regulator FruR	3.3	1.36E-01	7,5 g/l BuOH	6.7	36210	Cytoplasmic	5	COG1609	Transcription	
26987529	PP 0793	fruB	phosphoenolpyruvate-protein phosphotransferase	3.7	1.45E-03	Control	4.8	101497	Cytoplasmic	11	COG1080	Carbohydrate transport and metabolism	
26987530	PP 0794	fruK	1-phosphofructokinase	2.3	1.81E-01	Control	6.0	33188	Cytoplasmic	3	COG1105	Carbohydrate transport and metabolism	
26987538	PP 0802	chev-1	chemotaxis protein CheV	1.2	7.69E-01	Control	6.1	32223	Cytoplasmic	3	COG0835	Cell motility and secretion	Signal transduction mechanisms
26987540	PP 0804		protein secretion ABC efflux system, permease and ATP-binding protein	1.3	6.57E-01	7,5 g/l BuOH	9.2	79558	Cytoplasmic Membrane	2	COG2274	Defense mechanisms	
26987541	PP 0805		TolC family type I secretion outer membrane protein	1.6	3.15E-01	Control	5.8	51839	Outer Membrane	2	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26987542	PP 0806		surface adhesion protein	7.8	2.58E-02	Control	3.5	615675	Extracellular	13			
26987548	PP 0812	cyoA	ubiquinol oxidase subunit 2	10.5	6.00E-04	7,5 g/l BuOH	6.7	34557	Cytoplasmic Membrane	4	COG1622	Energy production and conversion	
26987553	PP 0817		aminotransferase	2.1	9.54E-02	Control	8.1	44996	Cytoplasmic	7	COG0436	Amino acid transport and metabolism	
26987559	PP 0823	selD	selenophosphate synthetase	1.1	6.73E-01	Control	5.4	36245	Unknown	3	COG0709	Amino acid transport and metabolism	
26987560	PP 0824		phosphonate ABC transporter periplasmic phosphonate-binding protein	1.3	2.53E-01	Control	8.6	31104	Periplasmic	13	COG3221	Inorganic ion transport and metabolism	
26987571	PP 0835	secD	preprotein translocase subunit SecD	1.1	4.69E-01	Control	9.6	66913	Cytoplasmic Membrane	9	COG0342	Intracellular trafficking and secretion	
26987574	PP 0838	suhB	inositol-phosphate phosphatase	1.4	2.50E-01	Control	6.6	29753	Cytoplasmic	8	COG0483	Carbohydrate transport and metabolism	
26987575	PP 0839		RNA methyltransferase	1.5	2.00E-01	7,5 g/l BuOH	6.6	27468	Cytoplasmic	2	COG0565	Translation, ribosomal structure and biogenesis	
26987576	PP 0840	cysE	serine O-acetyltransferase	3.6	1.53E-01	7,5 g/l BuOH	6.7	28206	Cytoplasmic	2	COG1045	Amino acid transport and metabolism	
26987578	PP 0842	iscS	cysteine desulfurase	1.5	2.14E-01	Control	6.2	44468	Cytoplasmic	16	COG1104	Amino acid transport and metabolism	
26987582	PP 0846	hscA	chaperone protein HscA	1.4	5.62E-02	Control	4.7	65888	Cytoplasmic	5	COG0443	Posttranslational modification, protein turnover, chaperones	
26987588	PP 0852		Cro/CI family transcriptional regulator	1.8	3.22E-01	7,5 g/l BuOH	5.6	34931	Unknown	3	COG1426	Function unknown	
26987589	PP 0853	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.2	2.17E-01	Control	6.2	39687	Cytoplasmic	10	COG0821	Lipid metabolism	
26987590	PP 0854	hisS	histidyl-tRNA synthetase	1.3	2.10E-01	7,5 g/l BuOH	5.1	47738	Cytoplasmic	17	COG0124	Translation, ribosomal structure and biogenesis	
26987591	PP 0855		hypothetical protein	1.4	3.68E-01	7,5 g/l BuOH	4.6	22514	Unknown	3	COG2976	Function unknown	
26987592	PP 0856		hypothetical protein	2.4	5.76E-02	Control	4.7	40737	Outer Membrane	5	COG1520	Function unknown	
26987593	PP 0857	engA	GTP-binding protein EngA	1.4	3.13E-01	Control	9.2	54154	Cytoplasmic Membrane	12	COG1160	General function prediction only	
26987595	PP 0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2.7	9.91E-02	Control	6.5	29780	Cytoplasmic	4	COG0388	General function prediction only	
26987615	PP 0879	dppD	oligopeptide/dipeptide ABC transporter ATPase subunit	4.7	7.48E-02	Control	6.3	34914	Cytoplasmic Membrane	3	COG0444	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987617	PP 0881	dppB	alkaline phosphatase	19.2	1.01E-01	Control	8.4	36980	Cytoplasmic Membrane	7	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987618	PP 0882	dppA	dipeptide ABC transporter periplasmic dipeptide-binding protein	7.0	1.12E-04	Control	7.4	60974	Periplasmic	4	COG0747	Amino acid transport and metabolism	
26987620	PP 0884		dipeptide ABC transporter periplasmic peptide-binding protein	11.9	4.03E-03	Control	7.3	59564	Periplasmic	5	COG0747	Amino acid transport and metabolism	
26987621	PP 0885		dipeptide ABC transporter periplasmic peptide-binding protein	1.4	3.81E-02	Control	7.1	60366	Periplasmic	36	COG0747	Amino acid transport and metabolism	
26987622	PP 0886		hypothetical protein	2.2	1.22E-01	7,5 g/l BuOH	8.4	25634	Periplasmic	6	COG3471	Function unknown	
26987624	PP 0888		two component transcriptional regulator, Fis family	1.5	1.02E-01	Control	5.0	20775	Cytoplasmic	5	COG4567	Signal transduction mechanisms	Transcription
26987629	PP 0893		intracellular protease, PfpI family	1.7	1.52E-01	7,5 g/l BuOH	5.5	21071	Cytoplasmic	5	COG0693	General function prediction only	
26987633	PP 0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	1.2	2.65E-01	Control	4.9	54767	Cytoplasmic	18	COG1951	Energy production and conversion	
26987637	PP 0901	colR	winged helix family two component transcriptional regulator	1.5	1.99E-01	Control	6.2	25489	Cytoplasmic	4	COG0745	Signal transduction mechanisms	Transcription
26987640	PP 0904		lipopolysaccharide kinase	1.1	8.36E-01	7,5 g/l BuOH	8.6	26976	Cytoplasmic	1			
26987642	PP 0906		multidrug efflux protein	8.3	5.80E-04	Control	4.8	110352	Cytoplasmic Membrane	4	COG0841	Defense mechanisms	
26987643	PP 0907		RND efflux membrane fusion protein-related protein	2.7	3.05E-01	Control	9.7	43537	Cytoplasmic Membrane	2	COG0845	Cell envelope biogenesis, outer membrane	
26987645	PP 0909		hypothetical protein	1.3	1.31E-01	7,5 g/l BuOH	6.4	38380	Unknown	6	COG3489	General function prediction only	
26987649	PP 0913		hypothetical protein	1.5	3.78E-01	Control	4.4	47019	Outer Membrane	21	COG3487	Inorganic ion transport and metabolism	
26987650	PP 0914		GGDEF domain-containing protein	1.2	5.42E-01	7,5 g/l BuOH	5.8	78578	Cytoplasmic Membrane	6	COG5001	Signal transduction mechanisms	
26987651	PP 0915	sodB	superoxide dismutase	1.5	6.62E-01	Control	5.8	21938	Periplasmic	8	COG0605	Inorganic ion transport and metabolism	
26987655	PP 0919		hypothetical protein	1.9	2.37E-01	7,5 g/l BuOH	###	18933	Unknown	5			
26987661	PP 0925		hypothetical protein	2.0	1.38E-01	Control	5.8	31410	Unknown	5			
26987666	PP 0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.8	1.71E-01	Control	4.8	52678	Cytoplasmic	14	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP 0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.4	1.88E-01	Control	6.2	51518	Cytoplasmic	14	COG0154	Translation, ribosomal structure and biogenesis	
26987673	PP 0937	cafA	ribonuclease, Rne/Rng family	1.1	7.73E-01	7,5 g/l BuOH	5.2	54840	Cytoplasmic	4	COG1530	Translation, ribosomal structure and biogenesis	
26987674	PP 0938		hypothetical protein	4.3	5.34E-02	Control	6.2	138482	Outer Membrane	4	COG3164	Function unknown	
26987676	PP 0940	tldD	tldD protein	1.6	5.29E-01	7,5 g/l BuOH	4.9	50161	Cytoplasmic	9	COG0312	General function prediction only	
26987677	PP 0941		hypothetical protein	2.5	9.58E-01	Control	9.5	20239	Cytoplasmic	2	COG3028	Function unknown	
26987678	PP 0942	pmbA	pmbA protein	3.3	5.05E-02	Control	5.0	48296	Cytoplasmic	8	COG0312	General function prediction only	
26987685	PP 0949		hypothetical protein	1.7	4.77E-03	Control	6.2	32097	Cytoplasmic	5	COG1660	General function prediction only	
26987688	PP 0952	rpoN	RNA polymerase factor sigma-54	2.6	4.27E-01	7,5 g/l BuOH	4.4	56215	Cytoplasmic	6	COG1508	Transcription	
26987689	PP 0953		ABC transporter ATP-binding protein	1.7	2.94E-02	Control	7.0	26579	Cytoplasmic	6	COG1137	General function prediction only	
26987691	PP 0955		hypothetical protein	8.3	7.80E-01	Control	6.5	21349	Cytoplasmic	2	COG3117	Function unknown	
26987693	PP 0957		KpsF/GutQ family protein	1.4	2.76E-01	Control	5.6	34397	Cytoplasmic	7	COG0794	Cell envelope biogenesis, outer membrane	
26987695	PP 0959	ttg2B	hypothetical protein	4.3	5.87E-02	Control	8.2	28489	Cytoplasmic Membrane	4	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987697	PP 0961	ttg2D	toluene tolerance family protein	1.0	9.42E-01	Control	9.7	23751	Unknown	9	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
26987700	PP 0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.2	4.29E-01	Control	5.2	44973	Cytoplasmic	8	COG0766	Cell envelope biogenesis, outer membrane	
26987701	PP 0965	hisG	ATP phosphoribosyltransferase catalytic subunit	1.4	3.20E-01	Control	8.4	22938	Cytoplasmic	11	COG0040	Amino acid transport and metabolism	
26987702	PP 0966	hisD	histidinol dehydrogenase	1.4	2.94E-01	Control	5.1	47605	Cytoplasmic	5	COG0141	Amino acid transport and metabolism	
26987703	PP 0967	hisC	histidinol-phosphate aminotransferase	1.7	6.32E-02	Control	4.9	38768	Cytoplasmic	10	COG0079	Amino acid transport and metabolism	
26987709	PP 0973	ndpA	nucleoid-associated protein NdpA	1.6	1.11E-02	7,5 g/l BuOH	5.6	37617	Cytoplasmic	5	COG3081	General function prediction only	
26987713	PP 0977	valS	valyl-tRNA synthetase	1.1	6.57E-01	7,5 g/l BuOH	5.1	107495	Cytoplasmic	33	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP 0980	pepA	leucyl aminopeptidase	1.8	1.02E-01	Control	7.4	52433	Cytoplasmic	29	COG0260	Amino acid transport and metabolism	
26987718	PP 0982		permease YjgP/YjgQ family protein	5.1	1.27E-02	Control	9.7	41323	Cytoplasmic Membrane	2	COG0795	General function prediction only	
26987721	PP 0985		cold-shock domain-contain protein	1.3	9.80E-01	7,5 g/l BuOH	###	18586	Cytoplasmic	2	COG1278	Transcription	
26987722	PP 0986	gcvT-1	glycine cleavage system T protein	3.5	3.86E-02	Control	6.4	40319	Cytoplasmic	5	COG0404	Amino acid transport and metabolism	
26987735	PP 0999	arcC	carbamate kinase	4.0	1.83E-04	Control	5.5	33423	Cytoplasmic	11	COG0549	Amino acid transport and metabolism	
26987736	PP 1000	argI	ornithine carbamoyltransferase	3.5	3.67E-03	Control	6.3	37911	Cytoplasmic	29	COG0078	Amino acid transport and metabolism	
26987737	PP 1001	arcA	arginine deiminase	3.0	8.71E-04	Control	5.7	46462	Cytoplasmic	42	COG2235	Amino acid transport and metabolism	
26987738	PP 1002	arcD	arginine/ornithine antiporter	5.7	7.04E-02	Control	9.1	51061	Cytoplasmic Membrane	4	COG0531	Amino acid transport and metabolism	
26987745	PP 1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	9.1	1.52E-03	Control	7.0	36057	Cytoplasmic	18	COG0057	Carbohydrate transport and metabolism	
26987746	PP 1010	edd	phosphogluconate dehydratase	4.1	7.42E-03	Control	6.4	65359	Cytoplasmic	27	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP 1011	glk	glucokinase	2.7	8.74E-03	Control	6.5	33904	Cytoplasmic	13	COG0837	Carbohydrate transport and metabolism	
26987748	PP 1012	gltR-2	winged helix family two component transcriptional regulator	2.5	7.07E-03	Control	6.4	27124	Cytoplasmic	2	COG0745	Signal transduction mechanisms	Transcription
26987749	PP 1013		integral membrane sensor signal transduction histidine kinase	16.6	6.43E-02	Control	7.3	54020	Cytoplasmic Membrane	2	COG0642	Signal transduction mechanisms	
26987750	PP 1014		hypothetical protein	1.9	1.87E-01	Control	6.4	45472	Unknown	11	COG2942	Carbohydrate transport and metabolism	
26987751	PP 1015		sugar ABC transporter periplasmic sugar-binding protein	1.3	9.21E-01	7,5 g/l BuOH	6.2	45449	Periplasmic	62	COG1653	Carbohydrate transport and metabolism	
26987752	PP 1016		binding-protein-dependent transport systems inner membrane component	1.0	5.49E-01	7,5 g/l BuOH	###	33781	Cytoplasmic Membrane	11	COG1175	Carbohydrate transport and metabolism	
26987753	PP 1017		binding-protein-dependent transport systems inner membrane component	2.1	1.04E-01	Control	9.9	30428	Cytoplasmic Membrane	3	COG0395	Carbohydrate transport and metabolism	
26987754	PP 1018		sugar ABC transporter ATP-binding subunit	1.1	4.79E-01	Control	6.7	41895	Cytoplasmic Membrane	20	COG3839	Carbohydrate transport and metabolism	
26987755	PP 1019	oprB-1	porin B	1.4	2.87E-01	Control	5.9	49646	Outer Membrane	37	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP 1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	2.3	9.99E-03	Control	6.8	55000	Cytoplasmic	21	COG0364	Carbohydrate transport and metabolism	
26987759	PP 1023	pgl	6-phosphogluconolactonase	2.4	3.43E-02	Control	6.7	25476	Unknown	13	COG0363	Carbohydrate transport and metabolism	
26987760	PP 1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	3.5	2.83E-03	Control	5.4	25004	Cytoplasmic	8	COG0800	Carbohydrate transport and metabolism	
26987761	PP 1025	leuA	2-isopropylmalate synthase	1.4	8.58E-02	7,5 g/l BuOH	5.1	61712	Cytoplasmic	25	COG0119	Amino acid transport and metabolism	
26987767	PP 1031	guaB	inosine 5'-monophosphate dehydrogenase	1.4	9.93E-02	Control	7.0	51765	Cytoplasmic	26	COG0516	Nucleotide transport and metabolism	
26987768	PP 1032	guaA	GMP synthase	2.4	6.36E-02	Control	5.2	58204	Cytoplasmic	22	COG0519	Nucleotide transport and metabolism	
26987773	PP 1037	purL	phosphoribosylformylglycinamidine synthase	2.1	4.53E-03	Control	4.7	140818	Cytoplasmic	50	COG0046	Nucleotide transport and metabolism	
26987792	PP 1056		iron-chelator utilization protein	1.7	1.05E-01	Control	5.2	28123	Cytoplasmic	2	COG2375	Inorganic ion transport and metabolism	
26987794	PP 1058		hypothetical protein	1.7	1.37E-01	Control	9.5	117041	Unknown	8	COG0744	Cell envelope biogenesis, outer membrane	
26987796	PP 1060		glutamate synthase, large subunit	1.7	8.14E-01	7,5 g/l BuOH	8.1	59136	Cytoplasmic	2	COG0069	Amino acid transport and metabolism	
26987799	PP 1063	metR-1	transcriptional activator MetR	1.0	7.56E-01	Control	6.2	33975	Cytoplasmic	3	COG0583	Transcription	
26987804	PP 1068		amino acid ABC transporter ATP-binding protein	2.3	1.55E-01	Control	8.2	28149	Cytoplasmic Membrane	4	COG1126	Amino acid transport and metabolism	
26987807	PP 1071		amino acid ABC transporter periplasmic amino acid-binding protein	1.2	1.50E-01	Control	8.9	33428	Periplasmic	37	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987810	PP 1074	glpR	DeoR family transcriptional regulator	2.1	1.82E-01	Control	5.7	27749	Cytoplasmic	4	COG1349	Transcription	Carbohydrate transport and metabolism
26987811	PP 1075	glpK	glycerol kinase	1.3	1.98E-01	Control	4.9	55282	Cytoplasmic	4	COG0554	Energy production and conversion	
26987815	PP 1079	argF	ornithine carbamoyltransferase	1.6	2.09E-01	Control	5.7	34433	Cytoplasmic	3	COG0078	Amino acid transport and metabolism	
26987818	PP 1082	bfr	bacterioferritin	1.5	3.02E-01	7,5 g/l BuOH	4.4	17971	Cytoplasmic	6	COG2193	Inorganic ion transport and metabolism	

26987820	PP_1084		anti-oxidant AhpCTSA family protein	2.5	3.74E-02	Control	4.9	21730	Cytoplasmic	18	COG0450	Posttranslational modification, protein turnover, chaperones	
26987822	PP_1086	pyrC	dihydroorotase	1.3	3.54E-01	Control	6.9	38414	Cytoplasmic	6	COG0418	Nucleotide transport and metabolism	
26987823	PP_1087		OmpA family outer membrane protein	1.1	6.04E-01	Control	###	34341	Outer Membrane	15	COG2885	Cell envelope biogenesis, outer membrane	
26987824	PP_1088	argG	argininosuccinate synthase	1.0	7.17E-01	Control	5.1	45164	Cytoplasmic	16	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.4	1.80E-01	7,5 g/l BuOH	5.5	75186	Cytoplasmic	22	COG0143	Translation, ribosomal structure and biogenesis	
26987834	PP_1098		ATP-binding Mrp/Nbp35 family protein	1.0	7.75E-01	Control	4.8	38207	Cytoplasmic Membrane	2	COG0489	Cell division and chromosome partitioning	
26987836	PP_1100	dcd	deoxycytidine triphosphate deaminase	2.5	6.51E-01	Control	5.4	21233	Cytoplasmic	2	COG0717	Nucleotide transport and metabolism	
26987840	PP_1104		succinylglutamate desuccinylase/aspartoacylase	1.6	2.51E-01	Control	6.3	40904	Cytoplasmic	4	COG3608	General function prediction only	
26987844	PP_1108		acylase	1.7	1.79E-01	Control	8.7	88728	Periplasmic	13	COG2366	General function prediction only	
26987847	PP_1111		synthetase	3.8	2.53E-02	Control	6.0	29406	Cytoplasmic	6	COG2872	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	5.6	3.77E-03	Control	7.6	32597	Cytoplasmic	10	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	2.1	4.69E-02	Control	5.0	24084	Outer Membrane	9	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	1.4	3.43E-01	Control	4.7	27345	Outer Membrane	6	COG2885	Cell envelope biogenesis, outer membrane	
26987862	PP_1126		Beta-agarase	1.6	1.47E-01	Control	6.6	86407	Periplasmic	3			
26987865	PP_1129	pdxH	pyridoxamine 5'-phosphate oxidase	1.5	2.21E-01	Control	6.4	24581	Cytoplasmic	8	COG0259	Coenzyme metabolism	
26987867	PP_1131		17 kDa surface antigen	1.2	7.83E-01	7,5 g/l BuOH	9.3	15682	Outer Membrane	2	COG3133	Cell envelope biogenesis, outer membrane	
26987873	PP_1137	braG	branched chain amino acid ABC transporter ATP-binding protein	2.1	1.36E-01	Control	7.6	25545	Cytoplasmic Membrane	7	COG0410	Amino acid transport and metabolism	
26987874	PP_1138	livG	leucine/isoleucine/valine transporter ATP-binding subunit	2.7	1.23E-01	Control	9.7	28280	Cytoplasmic	9	COG0411	Amino acid transport and metabolism	
26987875	PP_1139	livM	leucine/isoleucine/valine transporter permease subunit	2.8	4.41E-01	7,5 g/l BuOH	###	46299	Cytoplasmic Membrane	2	COG4177	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.4	6.58E-02	7,5 g/l BuOH	6.4	39402	Periplasmic	36	COG0683	Amino acid transport and metabolism	
26987879	PP_1143		3-hydroxyisobutyrate dehydrogenase	1.6	3.39E-01	Control	5.8	30664	Unknown	3	COG2084	Lipid metabolism	
26987880	PP_1144		GGDEF domain-containing protein	Infinity	3.88E-05	Control	6.8	82754	Cytoplasmic Membrane	2	COG5001	Signal transduction mechanisms	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	2.3	4.04E-02	Control	4.8	105994	Cytoplasmic	14	COG0553	Transcription	DNA replication, recombination, and repair
26987893	PP_1157		acetolactate synthase	1.7	1.49E-01	Control	6.1	60059	Cytoplasmic	8	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26987897	PP_1162		glutathione S-transferase family protein	1.0	7.99E-01	7,5 g/l BuOH	6.8	22677	Cytoplasmic	3	COG0625	Posttranslational modification, protein turnover, chaperones	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.0	7.31E-01	Control	4.5	46989	Cytoplasmic	8	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	1.3	2.50E-01	Control	5.7	106948	Cytoplasmic	33	COG0209	Nucleotide transport and metabolism	
26987919	PP_1184		dienelactone hydrolase	1.5	8.65E-02	Control	6.8	28722	Unknown	12	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26987920	PP_1185	oprH	outer membrane protein H1	45.6	5.35E-02	7,5 g/l BuOH	6.8	21501	Outer Membrane	2			
26987935	PP_1200	kup	Kup system potassium uptake protein	16.8	3.34E-02	Control	7.9	68568	Cytoplasmic Membrane	2	COG3158	Inorganic ion transport and metabolism	
26987940	PP_1205	proS	prolyl-tRNA synthetase	1.2	3.76E-01	7,5 g/l BuOH	5.0	63623	Cytoplasmic	21	COG0442	Translation, ribosomal structure and biogenesis	
26987941	PP_1206	oprD	outer membrane porin	1.6	2.12E-01	Control	4.6	46120	Outer Membrane	24			
26987945	PP_1210		DNA-binding stress protein	3.0	4.65E-01	7,5 g/l BuOH	5.0	17861	Cytoplasmic	5	COG0783	Inorganic ion transport and metabolism	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.7	4.96E-02	7,5 g/l BuOH	5.1	66568	Cytoplasmic	30	COG0173	Translation, ribosomal structure and biogenesis	
26987949	PP_1214		hypothetical protein	1.1	8.92E-01	7,5 g/l BuOH	4.4	26842	Cytoplasmic	4	COG0217	Function unknown	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.4	4.14E-01	7,5 g/l BuOH	6.3	25310	Cytoplasmic Membrane	7	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.3	3.29E-01	Control	9.8	47431	Unknown	10	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	5.9	1.55E-01	7,5 g/l BuOH	4.9	17833	Outer Membrane	5	COG2885	Cell envelope biogenesis, outer membrane	
26987960	PP_1225		radical SAM domain protein	1.3	3.69E-01	Control	4.9	24096	Cytoplasmic	2	COG0602	Posttranslational modification, protein turnover, chaperones	
26987961	PP_1226	exsB	exsB protein	1.7	2.54E-01	Control	4.7	23961	Cytoplasmic	5	COG0603	General function prediction only	
26987965	PP_1230		hypothetical protein	1.7	1.84E-01	Control	5.1	53328	Cytoplasmic Membrane	3	COG5339	Function unknown	
26987967	PP_1232		hypothetical protein	1.5	1.84E-01	Control	6.9	53219	Unknown	3	COG4783	General function prediction only	
26987972	PP_1237	dapA	dihydrodipicolinate synthase	1.0	9.23E-01	Control	6.0	31654	Cytoplasmic	13	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
26987973	PP_1238		lipoprotein	1.9	2.39E-01	7,5 g/l BuOH	4.8	40784	Unknown	15	COG3317	Cell envelope biogenesis, outer membrane	
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.6	1.02E-01	Control	5.1	26916	Cytoplasmic	16	COG0152	Nucleotide transport and metabolism	
26987981	PP_1246		hypothetical protein	2.3	1.36E-01	7,5 g/l BuOH	6.0	65952	Unknown	3	COG5373	Function unknown	
26988009	PP_1274		short chain dehydrogenase	1.4	3.98E-01	Control	###	28618	Cytoplasmic	8	COG0300	General function prediction only	
26988026	PP_1291		PhoH family protein	2.5	1.22E-02	Control	5.7	51856	Cytoplasmic	14	COG1875	General function prediction only	
26988031	PP_1296	estB	carboxylesterase	2.2	9.49E-02	Control	4.9	24402	Cytoplasmic Membrane	3	COG0400	General function prediction only	
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	2.5	3.29E-03	Control	5.6	36424	Periplasmic	27	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988033	PP_1298	aapQ	polar amino acid ABC transporter inner membrane subunit	6.3	4.56E-02	Control	###	43229	Cytoplasmic Membrane	4	COG4597	Amino acid transport and metabolism	
26988035	PP_1300	aapP	general amino acid ABC transporter ATP-binding protein	4.4	3.51E-02	Control	7.6	28879	Cytoplasmic Membrane	6	COG1126	Amino acid transport and metabolism	
26988037	PP_1302		hypothetical protein	1.3	1.48E-01	7,5 g/l BuOH	5.8	27492	Cytoplasmic	7	COG0327	Function unknown	
26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2	1.5	1.68E-01	Control	6.8	35284	Cytoplasmic	9	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	1.2	4.79E-01	Control	5.6	69049	Cytoplasmic	18	COG2895	Inorganic ion transport and metabolism	
26988046	PP_1311		tryptophanyl-tRNA synthetase	1.1	5.65E-01	Control	5.4	49297	Cytoplasmic	6	COG0180	Translation, ribosomal structure and biogenesis	
26988047	PP_1312		AFG1-family ATPase	1.2	5.08E-01	Control	6.8	42094	Cytoplasmic	2	COG1485	General function prediction only	
26988049	PP_1314		aldo/keto reductase family oxidoreductase	1.2	3.67E-01	7,5 g/l BuOH	6.5	38777	Cytoplasmic	11	COG0667	Energy production and conversion	
26988050	PP_1315	rplM	50S ribosomal protein L13	9.2	1.54E-01	7,5 g/l BuOH	###	15862	Unknown	5	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	5.9	3.84E-02	7,5 g/l BuOH	###	14592	Cytoplasmic	3	COG0103	Translation, ribosomal structure and biogenesis	
26988052	PP_1317	petA	ubiquinol-cytochrome c reductase, iron-sulfur subunit	1.3	1.80E-01	Control	7.5	20855	Cytoplasmic Membrane	11	COG0723	Energy production and conversion	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	4.3	5.76E-02	Control	8.4	45901	Cytoplasmic Membrane	8	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	1.2	2.39E-01	Control	7.1	29032	Unknown	10	COG2857	Energy production and conversion	
26988060	PP_1325		LppC family lipoprotein	1.5	2.79E-01	7,5 g/l BuOH	7.5	64637	Cytoplasmic Membrane	23	COG3107	General function prediction only	
26988061	PP_1326		uroporphyrin-III C/tetrapyrrole methyltransferase	1.6	3.13E-02	7,5 g/l BuOH	5.4	31389	Cytoplasmic	6	COG0313	General function prediction only	
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	1.7	1.20E-02	Control	5.3	53602	Cytoplasmic	20	COG0769	Cell envelope biogenesis, outer membrane	
26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.7	1.01E-01	Control	6.6	46750	Cytoplasmic	12	COG0770	Cell envelope biogenesis, outer membrane	
26988069	PP_1335	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	2.0	2.13E-02	Control	5.7	48300	Cytoplasmic	3	COG0771	Cell envelope biogenesis, outer membrane	
26988073	PP_1339	ddl	D-alanine--D-alanine ligase	3.0	4.93E-02	Control	4.7	34131	Cytoplasmic	6	COG1181	Cell envelope biogenesis, outer membrane	
26988075	PP_1341	ftsA	cell division protein FtsA	2.5	4.43E-02	Control	4.9	47444	Cytoplasmic	12	COG0849	Cell division and chromosome partitioning	
26988076	PP_1342	ftsZ	cell division protein FtsZ	1.3	1.47E-01	7,5 g/l BuOH	4.7	41830	Cytoplasmic	12	COG0206	Cell division and chromosome partitioning	
26988077	PP_1343	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	1.3	2.43E-01	7,5 g/l BuOH	4.8	33269	Cytoplasmic	9	COG0774	Cell envelope biogenesis, outer membrane	
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	3.8	1.35E-01	Control	5.0	42236	Cytoplasmic	7	COG1364	Amino acid transport and metabolism	
26988081	PP_1347		glutathione S-transferase family protein	2.1	8.93E-01	Control	5.3	23247	Cytoplasmic	9	COG0625	Posttranslational modification, protein turnover, chaperones	
26988082	PP_1348		hypothetical protein	2.2	1.06E-01	Control	5.5	34390	Cytoplasmic	2	COG0352	Coenzyme metabolism	
26988086	PP_1352		nucleotide-binding protein	1.2	4.02E-01	7,5 g/l BuOH	7.4	18561	Cytoplasmic	11	COG1666	Function unknown	
26988092	PP_1358		hypothetical protein	1.3	2.35E-01	Control	7.8	32006	Unknown	10	COG0748	Inorganic ion transport and metabolism	
26988095	PP_1361	groEL	chaperonin GroEL	1.7	7.89E-02	7,5 g/l BuOH	4.7	56743	Cytoplasmic	56	COG0459	Posttranslational modification, protein turnover, chaperones	
26988096	PP_1362	pykA	pyruvate kinase	2.7	2.25E-02	Control	6.7	52057	Cytoplasmic	23	COG0469	Carbohydrate transport and metabolism	
26988100	PP_1366		transcriptional regulator MvaT, P16 subunit	47.1	3.25E-02	7,5 g/l BuOH	###	14184	Cytoplasmic	4			
26988101	PP_1367	purU	formyltetrahydrofolate deformylase	1.2	3.62E-01	Control	6.6	32376	Cytoplasmic	8	COG0788	Nucleotide transport and metabolism	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.1	6.87E-01	7,5 g/l BuOH	4.8	67652	Cytoplasmic Membrane	14	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988106	PP_1372		hypothetical protein	1.5	2.25E-01	7,5 g/l BuOH	6.5	52321	Unknown	17	COG0433	Replication, recombination, and repair	
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	2.1	1.01E-01	7,5 g/l BuOH	6.5	48194	Cytoplasmic	10	COG0015	Nucleotide transport and metabolism	
26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase	1.0	7.82E-01	Control	5.1	28656	Unknown	9	COG0596	General function prediction only	
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.1	8.93E-01	7,5 g/l BuOH	5.1	52864	Outer Membrane	8	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.1	5.01E-01	Control	5.3	112835	Cytoplasmic Membrane	5	COG0841	Defense mechanisms	
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	4.3	3.20E-02	Control	4.9	31783	Cytoplasmic	6	COG2513	Carbohydrate transport and metabolism	
26988126	PP_1392		NAD-dependent epimerase/dehydratase	1.2	6.61E-01	7,5 g/l BuOH	8.0	21985	Unknown	5	COG2910	General function prediction only	
26988137	PP_1403	bglX	periplasmic beta-glucosidase	1.3	3.20E-01	Control	6.1	83414	Periplasmic	2	COG1472	Carbohydrate transport and metabolism	
26988140	PP_1406		hypothetical protein	1.3	8.85E-01	7,5 g/l BuOH	7.8	37042	Unknown	2			
26988145	PP_1412		enoyl-CoA hydratase/isomerase	2.2	1.58E-01	Control	6.5	40490	Cytoplasmic	4	COG1024	Lipid metabolism	
26988151	PP_1418		tricarboxylate transport protein TctC	1.1	5.73E-01	Control	6.6	34981	Periplasmic	7	COG3181	Function unknown	
26988156	PP_1423		hypothetical protein	2.1	1.70E-01	Control	6.0	33350	Unknown	3	COG0354	General function prediction only	
26988159	PP_1426	nadB	L-aspartate oxidase	1.3	3.70E-01	Control	5.8	59215	Cytoplasmic	3	COG0029	Coenzyme metabolism	
26988160	PP_1427	algU	RNA polymerase sigma factor AlgU	2.3	1.28E-02	7,5 g/l BuOH	5.2	22282	Cytoplasmic	8	COG1595	Transcription	
26988162	PP_1429	algN	sigma E regulatory protein, MucB/RseB	1.3	2.12E-01	7,5 g/l BuOH	6.6	34982	Periplasmic	6	COG3026	Signal transduction mechanisms	
26988163	PP_1430	algY	protease Do	1.0	9.85E-01	Control	6.6	52617	Periplasmic	10	COG0265	Posttranslational modification, protein turnover, chaperones	
26988164	PP_1431	lepA	GTP-binding protein LepA	3.0	1.13E-01	Control	5.5	66116	Cytoplasmic Membrane	5	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.5	1.84E-01	7,5 g/l BuOH	9.2	32060	Cytoplasmic Membrane	6	COG0681	Intracellular trafficking and secretion	
26988167	PP_1434	era	GTP-binding protein Era	2.0	2.62E-01	Control	6.9	34243	Cytoplasmic Membrane	3	COG1159	General function prediction only	
26988169	PP_1436	pdxJ	pyridoxine 5'-phosphate synthase	1.1	4.29E-01	7,5 g/l BuOH	6.2	26737	Cytoplasmic	8	COG0854	Coenzyme metabolism	
26988176	PP_1443	lon-1	ATP-dependent protease La	1.4	3.05E-01	Control	6.4	89794	Cytoplasmic	10	COG0466	Posttranslational modification, protein turnover, chaperones	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	3.3	2.11E-02	Control	6.0	86581	Cytoplasmic Membrane	13	COG4993	Carbohydrate transport and metabolism	
26988187	PP_1454		anhydrase family 3 protein	2.1	1.86E-01	7,5 g/l BuOH	6.5	18548	Cytoplasmic	3	COG0663	General function prediction only	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	2.2	8.56E-02	Control	5.7	42575	Cytoplasmic Membrane	14	COG0027	Nucleotide transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	9.5	7.38E-01	7,5 g/l BuOH	9.0	45563	Cytoplasmic Membrane	4			
26988194	PP_1461	ffh	signal recognition particle protein	1.3	2.24E-01	7,5 g/l BuOH	###	58232	Cytoplasmic Membrane	4	COG0541	Intracellular trafficking and secretion	
26988198	PP_1465	rplS	50S ribosomal protein L19	64.9	1.76E-02	7,5 g/l BuOH	###	13012	Cytoplasmic	5	COG0335	Translation, ribosomal structure and biogenesis	
26988202	PP_1469	dsbC	thiol:disulfide interchange protein DsbC	2.0	3.93E-01	7,5 g/l BuOH	7.9	27601	Periplasmic	2	COG1651	Posttranslational modification, protein turnover, chaperones	
26988203	PP_1470	hom	homoserine dehydrogenase	1.6	3.29E-02	7,5 g/l BuOH	5.1	46194	Cytoplasmic	12	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	2.0	2.25E-02	7,5 g/l BuOH	6.2	51645	Cytoplasmic	23	COG0498	Amino acid transport and metabolism	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	2.1	1.92E-02	Control	5.8	40626	Cytoplasmic	18	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	1.8	1.13E-01	Control	5.7	50918	Unknown	10	COG1012	Energy production and conversion	

26988219	PP_1486		polyamine ABC transporter periplasmic polyamine-binding protein	1.5	9.12E-02	Control	6.4	41728	Periplasmic	15	COG0687	Amino acid transport and metabolism	
26988220	PP_1487		hypothetical protein	1.2	8.01E-01	Control	6.5	24063	Cytoplasmic Membrane	2	COG2979	Function unknown	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.2	7.10E-01	7,5 g/l BuOH	4.7	58605	Cytoplasmic Membrane	8	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988225	PP_1492		chemotaxis protein CheA	1.0	7.55E-01	7,5 g/l BuOH	5.0	83257	Cytoplasmic	2	COG0643	Cell motility and secretion	Signal transduction mechanisms
26988227	PP_1494		response regulator/GGDEF domain-containing protein	1.9	1.23E-01	Control	5.7	37046	Cytoplasmic	5	COG3706	Signal transduction mechanisms	
26988228	PP_1496	lysS	lysyl-tRNA synthetase	1.0	6.32E-01	7,5 g/l BuOH	5.0	57137	Cytoplasmic	20	COG1190	Translation, ribosomal structure and biogenesis	
26988231	PP_1499		hypothetical protein	1.7	1.56E-01	7,5 g/l BuOH	6.3	49645	Cytoplasmic	3	COG3930	Function unknown	
26988234	PP_1502		OmpA/MotB domain protein	6.7	2.65E-02	7,5 g/l BuOH	9.5	28964	Outer Membrane	10	COG2885	Cell envelope biogenesis, outer membrane	
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	1.5	1.34E-02	Control	6.6	96963	Cytoplasmic	17	COG2352	Energy production and conversion	
26988238	PP_1506	adk	adenylate kinase	1.8	1.39E-01	7,5 g/l BuOH	5.7	23222	Cytoplasmic	15	COG0563	Nucleotide transport and metabolism	
26988239	PP_1507		hypothetical protein	2.4	8.43E-02	Control	6.0	23544	Unknown	2	COG1214	Posttranslational modification, protein turnover, chaperones	
26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	1.5	2.94E-01	Control	4.2	29130	Cytoplasmic	9	COG2513	Carbohydrate transport and metabolism	
26988245	PP_1513		hypothetical protein	1.1	9.86E-01	7,5 g/l BuOH	9.0	27864	Cytoplasmic	3			
26988258	PP_1526		beta-(1-3)-glucosyl transferase	1.1	8.38E-01	Control	8.1	97324	Cytoplasmic Membrane	4	COG5309	Carbohydrate transport and metabolism	
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.7	1.60E-02	7,5 g/l BuOH	5.6	35858	Unknown	6	COG2171	Amino acid transport and metabolism	
26988320	PP_1588		succinyldiaminopimelate transaminase	1.2	4.53E-01	7,5 g/l BuOH	5.4	43759	Cytoplasmic	6	COG0436	Amino acid transport and metabolism	
26988321	PP_1589	glnD	PII uridylyl-transferase	2.7	3.89E-02	Control	5.9	102620	Cytoplasmic	13	COG2844	Posttranslational modification, protein turnover, chaperones	
26988322	PP_1590	map	methionine aminopeptidase	1.4	1.45E-01	Control	6.6	28956	Cytoplasmic	9	COG0024	Translation, ribosomal structure and biogenesis	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.3	1.75E-01	Control	9.3	27023	Cytoplasmic	20	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.1	6.37E-01	7,5 g/l BuOH	4.9	30432	Cytoplasmic	30	COG0264	Translation, ribosomal structure and biogenesis	
26988325	PP_1593	pyrH	uridylate kinase	1.6	1.90E-01	Control	6.2	26484	Cytoplasmic	10	COG0528	Nucleotide transport and metabolism	
26988326	PP_1594	frr	ribosome recycling factor	1.0	8.26E-01	Control	8.9	20152	Cytoplasmic	11	COG0233	Translation, ribosomal structure and biogenesis	
26988327	PP_1595	uppS	undecaprenyl diphosphate synthase	1.5	1.77E-01	Control	8.5	27951	Cytoplasmic	6	COG0020	Lipid metabolism	
26988331	PP_1599		surface antigen family outer membrane protein	2.6	2.73E-03	7,5 g/l BuOH	4.7	86513	Outer Membrane	12	COG4775	Cell envelope biogenesis, outer membrane	
26988335	PP_1603	lpxA	UDP-N-acetylglucosamine acyltransferase	1.7	1.75E-01	Control	6.9	28107	Cytoplasmic	2	COG1043	acyl carrier protein	
26988338	PP_1606	dnaE	DNA polymerase III subunit alpha	2.8	6.61E-03	Control	5.3	130923	Cytoplasmic	3	COG0587	DNA replication, recombination, and repair	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.4	4.66E-02	7,5 g/l BuOH	6.0	35135	Cytoplasmic	20	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.4	2.34E-01	Control	5.8	59474	Cytoplasmic	26	COG0504	Nucleotide transport and metabolism	
26988343	PP_1611	kdsA-1	2-dehydro-3-deoxyphosphooctonate aldolase	2.1	4.22E-02	Control	5.8	31034	Cytoplasmic	10	COG2877	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.4	3.84E-01	7,5 g/l BuOH	4.7	45490	Cytoplasmic	22	COG0148	Carbohydrate transport and metabolism	
26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.7	2.10E-01	Control	6.3	39364	Cytoplasmic	5	COG1062	Energy production and conversion	
26988353	PP_1621	pcm	protein-L-isoaspartate O-methyltransferase	1.4	2.18E-01	Control	7.1	25497	Cytoplasmic	4	COG2518	Posttranslational modification, protein turnover, chaperones	
26988354	PP_1622	nlpD	peptidase M23B	1.1	6.99E-01	Control	###	27506	Outer Membrane	4	COG0739	Cell envelope biogenesis, outer membrane	
26988355	PP_1623	rpoS	RNA polymerase sigma factor RpoS	2.3	4.27E-03	7,5 g/l BuOH	4.9	38175	Cytoplasmic	12	COG0568	Transcription	
26988357	PP_1625		ferrodoxin, 4Fe-4S	2.0	1.50E-01	Control	3.7	12047	Cytoplasmic	2	COG1146	Energy production and conversion	
26988361	PP_1629	recA	recombinase A	2.0	8.98E-02	Control	5.3	37545	Cytoplasmic	9	COG0468	DNA replication, recombination, and repair	
26988367	PP_1635		LuxR family two component transcriptional regulator	1.5	9.64E-01	7,5 g/l BuOH	4.8	23481	Cytoplasmic	9	COG2197	Signal transduction mechanisms	Transcription
26988370	PP_1638	fpr	oxidoreductase FAD/NAD(P)-binding domain protein	1.2	2.49E-01	Control	5.1	29710	Cytoplasmic	7	COG1018	Energy production and conversion	
26988373	PP_1641		C32 tRNA thiolase	1.3	5.35E-01	7,5 g/l BuOH	6.8	31043	Cytoplasmic	3	COG0037	Cell cycle control, cell division, chromosome partitioning	
26988374	PP_1642		hypothetical protein	1.4	7.93E-01	7,5 g/l BuOH	9.1	25287	Unknown	2	COG2818	DNA replication, recombination, and repair	
26988381	PP_1649	ldhA	D-lactate dehydrogenase	2.7	1.19E-01	Control	6.6	37126	Cytoplasmic	6	COG1052	Energy production and conversion	Coenzyme metabolism
26988382	PP_1650	gacS	multi-sensor hybrid histidine kinase	1.2	2.46E-01	7,5 g/l BuOH	5.4	100653	Cytoplasmic Membrane	7	COG0642	Signal transduction mechanisms	
26988386	PP_1654	cysM	cysteine synthase B	1.7	4.28E-02	Control	4.9	32305	Cytoplasmic	4	COG0031	Amino acid transport and metabolism	
26988388	PP_1656	relA	(p)ppGpp synthetase I, SpoT/RelA	1.2	4.80E-01	Control	7.9	83609	Cytoplasmic	17	COG0317	Signal transduction mechanisms	Transcription
26988390	PP_1658		hypothetical protein	1.4	3.19E-01	7,5 g/l BuOH	9.6	20470	Cytoplasmic	2	COG3122	Function unknown	
26988391	PP_1659		hypothetical protein	5.2	1.21E-02	Control	5.9	48336	Periplasmic	23			
26988392	PP_1660		hypothetical protein	11.0	3.02E-03	Control	5.1	19178	Cytoplasmic Membrane	3			
26988393	PP_1661		dehydrogenase subunit	4.0	7.58E-03	Control	5.5	81020	Extracellular	47	COG2303	Amino acid transport and metabolism	
26988395	PP_1663		hypothetical protein	1.3	3.58E-01	Control	9.2	26313	Periplasmic	8			
26988396	PP_1664	purN	phosphoribosylglycinamide formyltransferase	2.4	9.73E-02	Control	6.7	23338	Cytoplasmic	2	COG0299	Nucleotide transport and metabolism	
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	2.0	4.76E-02	Control	4.6	36942	Cytoplasmic	10	COG0150	Nucleotide transport and metabolism	
26988398	PP_1666		hypothetical protein	2.4	5.00E-01	7,5 g/l BuOH	5.5	37790	Unknown	4	COG3249	Function unknown	
26988400	PP_1668		DNA replication initiation factor	1.0	9.18E-01	7,5 g/l BuOH	8.7	26586	Cytoplasmic	8	COG0593	DNA replication, recombination, and repair	
26988404	PP_1672	cobO	cob(I)yrinic acid a,c-diamide adenosyltransferase	1.6	4.93E-01	Control	7.7	22602	Cytoplasmic	7	COG2109	Coenzyme metabolism	
26988405	PP_1673	cobB	cobyrinic acid a,c-diamide synthase	4.0	2.75E-01	7,5 g/l BuOH	6.3	45776	Cytoplasmic	2	COG1797	Coenzyme metabolism	
26988418	PP_1686		glutathione peroxidase	3.3	4.64E-01	Control	8.9	22309	Periplasmic	3	COG0386	Posttranslational modification, protein turnover, chaperones	
26988429	PP_1697		GntR family transcriptional regulator	3.4	8.10E-02	7,5 g/l BuOH	8.7	34197	Cytoplasmic	2	COG2188	Transcription	
26988434	PP_1702	rdgC	recombination associated protein	1.1	5.29E-01	7,5 g/l BuOH	4.6	34283	Cytoplasmic	5	COG2974	DNA replication, recombination, and repair	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	2.0	2.71E-03	7,5 g/l BuOH	4.8	26520	Cytoplasmic	14	COG0545	Posttranslational modification, protein turnover, chaperones	
26988451	PP_1719	prc	carboxyl-terminal protease	1.1	3.06E-01	Control	7.1	79096	Cytoplasmic Membrane	28	COG0793	Cell envelope biogenesis, outer membrane	
26988452	PP_1720		alcohol dehydrogenase, zinc-containing	1.3	3.37E-01	Control	4.7	33921	Cytoplasmic Membrane	7	COG0604	Energy production and conversion	General function prediction only
26988453	PP_1721		HAD superfamily hydrolase	2.3	7.80E-02	Control	4.5	24571	Cytoplasmic	2	COG0560	Amino acid transport and metabolism	
26988457	PP_1725		type I phosphodiesterase/nucleotide pyrophosphatase	2.4	1.28E-01	Control	6.4	31520	Cytoplasmic	4	COG1524	General function prediction only	
26988458	PP_1726		ABC transporter periplasmic protein	1.2	3.56E-01	Control	6.0	38636	Unknown	22	COG1840	Inorganic ion transport and metabolism	
26988462	PP_1730		aminopeptidase 2	1.4	7.83E-02	Control	5.6	46996	Cytoplasmic	3	COG1362	Amino acid transport and metabolism	
26988464	PP_1733	minD	septum site-determining protein MinD	2.2	8.90E-02	Control	6.2	29650	Cytoplasmic	20	COG2894	Cell division and chromosome partitioning	
26988465	PP_1734	minC	septum formation inhibitor	4.7	1.40E-03	Control	8.9	29680	Cytoplasmic	3	COG0850	Cell division and chromosome partitioning	
26988472	PP_1741		substrate-binding region of ABC-type glycine betaine transport system	2.0	2.95E-01	Control	9.6	31215	Periplasmic	4	COG2113	Amino acid transport and metabolism	
26988474	PP_1743	actP	acetate permease	28.6	2.79E-03	7,5 g/l BuOH	9.6	58972	Cytoplasmic Membrane	4	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	2.1	6.83E-02	Control	8.2	57637	Cytoplasmic	10	COG2326	Function unknown	
26988486	PP_1755	fumC-2	fumarate hydratase	1.3	4.38E-01	7,5 g/l BuOH	6.4	49131	Cytoplasmic	20	COG0114	Energy production and conversion	
26988490	PP_1759		DSBA oxidoreductase	1.0	7.63E-01	Control	4.7	21492	Unknown	4	COG3531	Posttranslational modification, protein turnover, chaperones	
26988492	PP_1761		sensory box protein/GGDEF family protein	1.1	6.11E-01	Control	6.8	108193	Cytoplasmic Membrane	5	COG2200	Signal transduction mechanisms	
26988494	PP_1763		short chain dehydrogenase	2.4	1.21E-03	Control	4.7	26253	Cytoplasmic	4	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988495	PP_1764		phosphoglycolate phosphatase	1.3	2.68E-01	Control	4.5	24373	Cytoplasmic	7	COG0546	General function prediction only	
26988496	PP_1765	ubiG	3-demethylubiquinone-9 3-methyltransferase	1.9	9.06E-02	Control	5.7	26084	Cytoplasmic	4	COG2227	Coenzyme metabolism	
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.3	9.07E-02	Control	4.7	102037	Cytoplasmic	30	COG0188	DNA replication, recombination, and repair	
26988499	PP_1768	serC	phosphoserine aminotransferase	1.4	1.17E-01	Control	5.1	39911	Cytoplasmic	10	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
26988500	PP_1769	pheA	chorismate mutase	1.3	3.49E-01	Control	6.4	40816	Cytoplasmic	11	COG0077	Amino acid transport and metabolism	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	2.1	1.09E-01	Control	6.4	79133	Cytoplasmic	11	COG0128	Amino acid transport and metabolism	
26988502	PP_1771	cmk	cytidylate kinase	1.3	3.84E-01	Control	4.9	24691	Cytoplasmic	9	COG0283	Nucleotide transport and metabolism	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	1.8	2.78E-02	Control	5.2	52989	Cytoplasmic	6	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP_1780		mannosyltransferase	2.2	2.56E-02	Control	5.8	180042	Cytoplasmic	23	COG0438	Cell envelope biogenesis, outer membrane	
26988514	PP_1783	rmlA	glucose-1-phosphate thymidylyltransferase	2.7	1.06E-03	Control	4.9	32517	Cytoplasmic	11	COG1209	Cell envelope biogenesis, outer membrane	
26988515	PP_1784	rmlD	dTDP-4-dehydrorhamnose reductase	3.5	9.49E-02	Control	6.7	32131	Cytoplasmic	4	COG1091	Cell envelope biogenesis, outer membrane	
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	1.0	7.68E-01	7,5 g/l BuOH	6.1	40690	Cytoplasmic	6	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	1.9	2.03E-02	Control	6.4	128499	Cytoplasmic	17	COG0438	Cell envelope biogenesis, outer membrane	
26988518	PP_1787		hypothetical protein	2.4	4.04E-02	Control	5.3	37903	Unknown	7			
26988521	PP_1790		acylneuraminate cytidylyltransferase	1.8	7.93E-03	Control	6.4	26350	Cytoplasmic	3	COG1083	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	2.2	6.78E-03	Control	5.9	58534	Cytoplasmic	13	COG0119	Amino acid transport and metabolism	
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.3	2.81E-01	Control	6.4	40124	Cytoplasmic	18	COG1089	Cell envelope biogenesis, outer membrane	
26988530	PP_1800	rmd	oxidoreductase Rmd	2.5	4.83E-02	Control	7.2	32310	Unknown	7	COG1089	Cell envelope biogenesis, outer membrane	
26988537	PP_1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase	1.3	5.30E-02	Control	6.0	30469	Cytoplasmic	9	COG2877	Cell envelope biogenesis, outer membrane	
26988545	PP_1815	pyrF	orotidine 5'-phosphate decarboxylase	2.4	6.10E-02	Control	4.9	24551	Cytoplasmic	7	COG0284	Nucleotide transport and metabolism	
26988546	PP_1816		alcohol dehydrogenase, zinc-containing	3.7	2.15E-02	Control	7.4	35802	Cytoplasmic	6	COG2130	General function prediction only	
26988549	PP_1819		methyl-accepting chemotaxis sensory transducer	1.3	3.16E-01	Control	4.7	68069	Cytoplasmic Membrane	7	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988551	PP_1821		glutathione S-transferase family protein	1.1	6.95E-01	7,5 g/l BuOH	5.6	23207	Cytoplasmic	6	COG0625	Posttranslational modification, protein turnover, chaperones	
26988556	PP_1826		isochorismatase superfamily hydrolase	10.7	6.04E-02	Control	7.6	21283	Cytoplasmic	4	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26988558	PP_1828		hypothetical protein	5.0	8.89E-02	Control	7.7	29758	Cytoplasmic	2			
26988560	PP_1830	aroC	chorismate synthase	2.3	5.60E-02	7,5 g/l BuOH	6.5	38987	Cytoplasmic	7	COG0082	Amino acid transport and metabolism	
26988562	PP_1832		oxidase	3.2	1.68E-02	7,5 g/l BuOH	4.8	19469	Cytoplasmic	6	COG1791	Function unknown	
26988568	PP_1838		hypothetical protein	3.0	1.72E-02	7,5 g/l BuOH	6.8	76615	Cytoplasmic Membrane	7	COG1368	Cell envelope biogenesis, outer membrane	
26988571	PP_1841		cytochrome c family protein	5.4	1.19E-02	Control	7.6	29246	Unknown	3	COG2010	Energy production and conversion	
26988572	PP_1842		amidotransferase	1.5	1.40E-01	Control	4.9	27317	Cytoplasmic	6	COG0518	Nucleotide transport and metabolism	
26988575	PP_1845		enoyl-CoA hydratase	2.0	1.13E-01	Control	7.7	24641	Cytoplasmic	10	COG1024	Lipid metabolism	
26988588	PP_1858	efp	elongation factor P	2.1	2.39E-01	Control	4.5	21303	Cytoplasmic	8	COG0231	Translation, ribosomal structure and biogenesis	
26988589	PP_1859	ohr	OsmC family protein	3.7	1.89E-01	7,5 g/l BuOH	6.8	14665	Cytoplasmic	2	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.0	8.38E-01	7,5 g/l BuOH	9.2	60924	Cytoplasmic	16	COG0513	DNA replication, recombination, and repair	Transcription
26988600	PP_1870	tpm	thiopurine S-methyltransferase	3.1	1.75E-02	Control	4.7	24365	Cytoplasmic	4			
26988601	PP_1871	htpX	heat shock protein HtpX	1.4	1.72E-01	7,5 g/l BuOH	7.2	32199	Cytoplasmic Membrane	7	COG0501	Posttranslational modification, protein turnover, chaperones	
26988602	PP_1872		aminotransferase AlaT	1.5	2.08E-02	7,5 g/l BuOH	5.8	44705	Cytoplasmic	8	COG0436	Amino acid transport and metabolism	
26988606	PP_1876		hypothetical protein	1.7	1.54E-01	7,5 g/l BuOH	8.8	38962	Cytoplasmic	3	COG2607	General function prediction only	
26988608	PP_1878		hypothetical protein	1.5	1.40E-01	7,5 g/l BuOH	7.3	29093	Cytoplasmic	7			
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	2.5	1.60E-02	Control	6.9	89194	Cytoplasmic Membrane	25	COG1960	Lipid metabolism	

26988624	PP_1894		glutathione S-transferase family protein	1.9	1.07E-01	Control	5.0	23668	Cytoplasmic	4	COG0625	Posttranslational modification, protein turnover, chaperones		
26988625	PP_1895		ABC transporter ATP-binding protein	1.1	7.37E-01	7,5 g/l BuOH	7.1	34488	Cytoplasmic Membrane	3	COG1131	Defense mechanisms		
26988632	PP_1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.2	3.57E-01	Control	5.2	27809	Cytoplasmic	8	COG1212	Cell envelope biogenesis, outer membrane		
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.1	9.28E-01	Control	4.7	120904	Cytoplasmic	33	COG1530	Translation, ribosomal structure and biogenesis		
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.0	7.27E-01	Control	6.4	36497	Cytoplasmic Membrane	6	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion	
26988638	PP_1909	maf	Maf-like protein	4.0	5.14E-01	Control	4.9	22268	Cytoplasmic	2	COG0424	Cell division and chromosome partitioning		
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.0	9.72E-01	7,5 g/l BuOH	4.7	32614	Cytoplasmic	11	COG0331	Lipid metabolism		
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.0	8.10E-01	7,5 g/l BuOH	6.0	25470	Cytoplasmic	12	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988644	PP_1915	acpP	acyl carrier protein	1.7	4.09E-01	Control	3.8	8712	Cytoplasmic	2	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
26988645	PP_1916	fabF	3-oxoacyl-(acyl carrier protein) synthase II	2.0	2.46E-01	Control	5.8	43152	Cytoplasmic Membrane	2	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
26988646	PP_1917	pabC	4-amino-4-deoxychorismate lyase	2.3	7.33E-02	Control	7.2	29486	Cytoplasmic	4	COG0115	Amino acid transport and metabolism	Coenzyme metabolism	
26988668	PP_1941		hypothetical protein	1.2	6.96E-01	7,5 g/l BuOH	7.8	23098	Unknown	2	COG1309	Transcription		
26988669	PP_1942		LysR family transcriptional regulator	4.0	1.15E-01	Control	5.8	36540	Cytoplasmic	2	COG0583	Transcription		
26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	3.2	5.98E-02	Control	5.3	27212	Unknown	7	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988691	PP_1964		deoxynucleotide monophosphate kinase	1.9	1.46E-01	Control	5.9	30146	Unknown	5				
26988696	PP_1970		lipoprotein	1.4	6.18E-01	Control	4.9	22337	Unknown	8				
26988697	PP_1971		hypothetical protein	1.3	3.05E-01	Control	4.5	21577	Cytoplasmic	5	COG3816	Function unknown		
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.3	3.22E-01	Control	5.9	43290	Cytoplasmic	21	COG1448	Amino acid transport and metabolism		
26988700	PP_1974	uvrB	excinuclease ABC subunit B	4.6	3.25E-02	Control	4.9	76034	Cytoplasmic	2	COG0556	DNA replication, recombination, and repair		
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.6	5.60E-02	7,5 g/l BuOH	5.6	56483	Cytoplasmic	15	COG0008	Translation, ribosomal structure and biogenesis		
26988709	PP_1983		sensory box protein	4.1	3.03E-03	Control	5.7	128000	Cytoplasmic Membrane	12	COG5001	Signal transduction mechanisms		
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	1.1	7.04E-01	7,5 g/l BuOH	5.6	51255	Cytoplasmic	5	COG0065	Amino acid transport and metabolism		
26988712	PP_1986	leuD	isopropylmalate isomerase small subunit	1.1	7.49E-01	Control	5.3	24284	Cytoplasmic	10	COG0066	Amino acid transport and metabolism		
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	1.3	3.90E-02	Control	4.8	38824	Cytoplasmic	7	COG0473	Amino acid transport and metabolism		
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.5	1.75E-01	Control	5.3	40672	Cytoplasmic	21	COG0136	Amino acid transport and metabolism		
26988719	PP_1993		peptidoglycan-binding LysM	1.0	9.70E-01	7,5 g/l BuOH	3.9	96918	Unknown	22	COG3170	Cell motility and secretion	Intracellular trafficking and secretion	
26988720	PP_1995	trpF	N-(5'-phosphoribosyl)anthranilate isomerase	1.6	1.54E-02	7,5 g/l BuOH	5.3	21886	Cytoplasmic	2	COG0135	Amino acid transport and metabolism		
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.2	5.76E-01	Control	7.8	32510	Cytoplasmic	9	COG0777	Lipid metabolism		
26988725	PP_2000	purF	amidophosphoribosyltransferase	2.0	8.70E-02	Control	6.5	55400	Cytoplasmic	9	COG0034	Nucleotide transport and metabolism		
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	2.5	7.28E-02	Control	5.4	43284	Cytoplasmic	4	COG0626	Amino acid transport and metabolism		
26988727	PP_2002		oxidoreductase	1.0	6.59E-01	7,5 g/l BuOH	6.6	27212	Cytoplasmic	3	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988731	PP_2006		hypothetical protein	14.2	3.25E-04	Control	5.1	63743	Unknown	39				
26988732	PP_2007		P-47-related protein	11.0	1.41E-04	Control	5.8	44707	Unknown	8				
26988733	PP_2008	fadH	NADH:flavin oxidoreductase/NADH oxidase	1.2	3.80E-01	Control	7.0	73935	Cytoplasmic	4	COG1902	Energy production and conversion		
26988742	PP_2017	pepN	aminopeptidase N	1.7	2.01E-02	Control	4.8	99573	Cytoplasmic	30	COG0308	Amino acid transport and metabolism		
26988743	PP_2018		BNR domain-containing protein	1.2	3.49E-01	7,5 g/l BuOH	4.5	33691	Unknown	4	COG4447	General function prediction only		
26988744	PP_2019		hypothetical protein	1.1	5.28E-01	7,5 g/l BuOH	6.6	87732	Cytoplasmic Membrane	5	COG1033	General function prediction only		
26988746	PP_2021		hypothetical protein	5.4	1.02E-01	Control	7.2	40684	Periplasmic	2	COG2706	Carbohydrate transport and metabolism		
26988749	PP_2024	sbcC	SMC domain protein	1.3	2.93E-01	7,5 g/l BuOH	5.5	136091	Cytoplasmic	7	COG0419	DNA replication, recombination, and repair		
26988757	PP_2032		ATPase	1.0	8.37E-01	Control	5.0	35347	Cytoplasmic	3	COG0714	General function prediction only		
26988799	PP_2074		LysR family transcriptional regulator	1.2	5.73E-01	Control	6.5	34029	Cytoplasmic	2	COG0583	Transcription		
26988805	PP_2080		NAD-glutamate dehydrogenase	1.6	2.40E-02	Control	5.8	187043	Cytoplasmic Membrane	65	COG2902	Amino acid transport and metabolism		
26988806	PP_2081		hypothetical protein	2.1	1.06E-01	Control	6.6	30824	Cytoplasmic	7	COG1806	Function unknown		
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.9	4.30E-03	7,5 g/l BuOH	4.8	86015	Cytoplasmic	42	COG0574	Carbohydrate transport and metabolism		
26988809	PP_2084	menG	ribonuclease activity regulator protein RraA	5.0	1.27E-02	7,5 g/l BuOH	4.6	17646	Cytoplasmic	2	COG0684	Coenzyme metabolism		
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.0	9.73E-01	Control	5.8	29111	Cytoplasmic Membrane	6				
26988814	PP_2089	oprF	OmpF family protein	1.5	1.32E-04	Control	4.5	37012	Outer Membrane	24	COG2885	Cell envelope biogenesis, outer membrane		
26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	2.3	8.95E-01	7,5 g/l BuOH	8.2	35545	Cytoplasmic Membrane	2	COG0167	Nucleotide transport and metabolism		
26988823	PP_2098	dacB	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	1.4	7.86E-02	Control	9.9	50799	Periplasmic	3	COG2027	Cell envelope biogenesis, outer membrane		
26988827	PP_2102		deoxyguanosinetriphosphate triphosphohydrolase-like protein	2.2	2.11E-02	Control	6.9	49908	Cytoplasmic	2	COG0232	Nucleotide transport and metabolism		
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	2.4	5.88E-03	Control	6.0	57068	Cytoplasmic Membrane	14	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26988836	PP_2112	acnA	aconitate hydratase	1.2	2.61E-01	Control	5.7	99147	Cytoplasmic	19	COG1048	Energy production and conversion		
26988841	PP_2117	pdxB	erythronate-4-phosphate dehydrogenase	1.3	3.26E-01	Control	5.1	41614	Cytoplasmic	3	COG0111	Amino acid transport and metabolism		
26988852	PP_2128	chev-2	chemotaxis protein CheV	3.5	6.16E-02	Control	6.5	34556	Cytoplasmic Membrane	13	COG0835	Cell motility and secretion	Signal transduction mechanisms	
26988853	PP_2129		MOSC domain containing protein	1.1	1.52E-01	7,5 g/l BuOH	5.5	29621	Cytoplasmic	10	COG3217	General function prediction only		
26988854	PP_2130		soluble lytic transglycosylase	1.8	2.24E-01	Control	9.9	75337	Periplasmic	4	COG0741	Cell envelope biogenesis, outer membrane		
26988855	PP_2131		ABC transporter ATP-binding protein	2.5	1.36E-03	7,5 g/l BuOH	5.1	71398	Cytoplasmic	9	COG0488	General function prediction only		
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.2	4.45E-01	Control	5.9	77449	Cytoplasmic	16	COG1250	Lipid metabolism		
26988863	PP_2139	topA	DNA topoisomerase I	1.3	4.44E-01	Control	8.0	97239	Cytoplasmic	28	COG0550	DNA replication, recombination, and repair		
26988867	PP_2143	lexA-1	LexA repressor	4.5	3.10E-02	Control	6.7	22147	Cytoplasmic	5	COG1974	Transcription	Signal transduction mechanisms	
26988868	PP_2144		TetR family transcriptional regulator	1.4	3.92E-01	Control	9.8	26183	Cytoplasmic	5	COG1309	Transcription		
26988869	PP_2145	nagZ	beta-hexosaminidase	1.1	6.25E-01	Control	6.3	36513	Cytoplasmic	3	COG1472	Carbohydrate transport and metabolism		
26988870	PP_2146		Snf2/Rad54 family helicase	1.1	4.40E-01	Control	6.1	75232	Cytoplasmic	2	COG0553	Transcription	DNA replication, recombination, and repair	
26988872	PP_2148	mfd	transcription-repair coupling factor	2.5	1.69E-01	Control	5.7	128301	Unknown	7	COG1197	DNA replication, recombination, and repair	Transcription	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.4	1.33E-01	7,5 g/l BuOH	7.7	53014	Cytoplasmic	21	COG0057	Carbohydrate transport and metabolism		
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	2.3	8.27E-02	7,5 g/l BuOH	7.7	50905	Cytoplasmic	7	COG1249	Energy production and conversion		
26988876	PP_2152		glycerophosphoryl diester phosphodiesterase	2.4	1.31E-01	Control	7.5	26252	Cytoplasmic	11	COG0584	Energy production and conversion		
26988877	PP_2153		type IV pilus assembly PilZ	1.4	3.07E-01	Control	5.0	21858	Cytoplasmic	2				
26988879	PP_2155	lolD	lipoprotein releasing system, ATP-binding protein	1.7	3.00E-01	7,5 g/l BuOH	7.3	25304	Cytoplasmic Membrane	3	COG1136	Defense mechanisms		
26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	2.1	9.59E-02	Control	6.5	30686	Cytoplasmic	4	COG2904	Function unknown		
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.0	8.92E-01	7,5 g/l BuOH	5.3	26061	Outer Membrane	9	COG2853	Cell envelope biogenesis, outer membrane		
26988892	PP_2168	tal	transaldolase B	2.4	1.78E-02	7,5 g/l BuOH	5.0	33615	Unknown	16	COG0176	Carbohydrate transport and metabolism		
26988899	PP_2175		short-chain dehydrogenase/reductase SDR	2.3	8.92E-02	Control	6.6	24818	Unknown	3	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988909	PP_2185		formate dehydrogenase, alpha subunit	7.1	1.12E-01	Control	6.5	104885	Cytoplasmic	3	COG3383	General function prediction only		
26988911	PP_2187		universal stress protein	1.9	4.20E-03	Control	6.3	31384	Cytoplasmic	5	COG0589	Signal transduction mechanisms		
26988919	PP_2195		periplasmic polyamine-binding protein	1.4	2.42E-01	7,5 g/l BuOH	5.5	39788	Periplasmic	5	COG0687	Amino acid transport and metabolism		
26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	1.1	8.60E-01	7,5 g/l BuOH	6.0	61223	Cytoplasmic	5	COG0365	Lipid metabolism		
26988938	PP_2214	fadB2x	short-chain dehydrogenase/reductase SDR	1.0	6.00E-01	Control	6.7	26030	Cytoplasmic	5	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
26988939	PP_2215	fadAx	acetyl-CoA acetyltransferase	1.2	6.70E-01	7,5 g/l BuOH	6.9	41382	Cytoplasmic	8	COG0183	Lipid metabolism		
26988940	PP_2216		acyl-CoA dehydrogenase domain-containing protein	1.4	5.67E-02	7,5 g/l BuOH	4.9	40529	Cytoplasmic	3	COG1960	Lipid metabolism		
26988941	PP_2217	fadB1x	enoyl-CoA hydratase/isomerase	1.9	1.35E-01	Control	5.2	27668	Cytoplasmic	12	COG1024	Lipid metabolism		
26988957	PP_2233		isochorismatase superfamily hydrolase	26.4	3.19E-03	7,5 g/l BuOH	6.0	19296	Cytoplasmic	17	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
26988962	PP_2238		peptidase M24	1.2	1.82E-01	Control	5.4	68915	Unknown	9	COG0006	Amino acid transport and metabolism		
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.3	1.70E-01	Control	5.1	68646	Cytoplasmic Membrane	19	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26988988	PP_2264		extracellular solute-binding protein, family 1	1.7	1.15E-01	Control	5.6	65243	Unknown	31	COG1653	Carbohydrate transport and metabolism		
26988989	PP_2265	folD-2	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	2.2	1.39E-01	Control	6.4	30623	Cytoplasmic	5	COG0190	Coenzyme metabolism		
26989016	PP_2292		hypothetical protein	1.3	2.79E-01	Control	5.8	28522	Cytoplasmic	14				
26989023	PP_2299	tig	trigger factor	1.2	6.88E-01	7,5 g/l BuOH	4.5	49190	Cytoplasmic	20	COG0544	Posttranslational modification, protein turnover, chaperones		
26989024	PP_2300	clpP	ATP-dependent Clp protease proteolytic subunit	2.1	7.36E-02	Control	5.6	23515	Cytoplasmic	12	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion	
26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.8	2.05E-01	7,5 g/l BuOH	4.8	48526	Cytoplasmic	23	COG1219	Posttranslational modification, protein turnover, chaperones		
26989026	PP_2302	lon-2	ATP-dependent protease La	1.0	9.18E-01	7,5 g/l BuOH	5.9	88722	Cytoplasmic	28	COG0466	Posttranslational modification, protein turnover, chaperones		
26989027	PP_2303	hupB	histone family protein DNA-binding protein	68.4	2.89E-02	7,5 g/l BuOH	###	9250	Cytoplasmic	2	COG0776	DNA replication, recombination, and repair		
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.7	1.79E-03	7,5 g/l BuOH	4.8	68580	Cytoplasmic Membrane	11	COG0760	Posttranslational modification, protein turnover, chaperones		
26989031	PP_2307		CHAD domain containing protein	1.3	4.02E-01	7,5 g/l BuOH	###	29498	Cytoplasmic	10	COG5607	Function unknown		
26989032	PP_2308		acyl-CoA thioesterase II	2.1	1.84E-02	Control	6.1	28745	Unknown	5	COG1946	Lipid metabolism		
26989044	PP_2320		ErfK/YbiS/YcfS/YnhG family protein	1.2	5.90E-01	7,5 g/l BuOH	5.4	35051	Unknown	11	COG1376	Function unknown		
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	79.2	4.99E-02	7,5 g/l BuOH	8.5	8801	Outer Membrane	3				
26989048	PP_2324	aroF-1	phospho-2-dehydro-3-deoxyheptonate aldolase	1.7	9.39E-02	7,5 g/l BuOH	6.4	40260	Cytoplasmic	7	COG0722	Amino acid transport and metabolism		
26989051	PP_2327	cysB	transcriptional regulator CysB	2.2	7.50E-02	Control	6.7	35955	Cytoplasmic	8	COG0583	Transcription		
26989052	PP_2328	cysH	phosphoadenosine phosphosulfate reductase	1.0	7.07E-01	7,5 g/l BuOH	6.5	27896	Cytoplasmic	8	COG0175	Amino acid transport and metabolism	Coenzyme metabolism	
26989054	PP_2330		alpha-L-glutamate ligase-like protein	1.3	5.30E-01	7,5 g/l BuOH	6.8	35904	Cytoplasmic	2				
26989055	PP_2331		hypothetical protein	2.1	1.68E-01	Control	7.9	57064	Cytoplasmic Membrane	3				
26989058	PP_2334	prpB	2-methylisocitrate lyase	1.6	6.08E-02	Control	5.4	31811	Cytoplasmic	8	COG2513	Carbohydrate transport and metabolism		
26989059	PP_2335		methylcitrate synthase	4.1	4.60E-02	Control	6.7	41995	Cytoplasmic	16	COG0372	Energy production and conversion		
26989060	PP_2336		aconitate hydratase	3.5	2.85E-02	Control	5.3	93961	Cytoplasmic	17	COG1048	Energy production and conversion		
26989061	PP_2337		hypothetical protein	25.9	2.51E-03	Control	5.2	41312	Cytoplasmic	2	COG2828	Function unknown		
26989062	PP_2338	prpD	2-methylcitrate dehydratase	2.5	1.16E-02	Control	7.1	54860	Cytoplasmic	12	COG2079	General function prediction only		
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.2	8.06E-02	7,5 g/l BuOH	5.0	93609	Cytoplasmic	50	COG1049	Energy production and conversion		
26989075	PP_2351		acetyl-CoA synthetase	2.8	1.87E-01	7,5 g/l BuOH	6.1	68868	Cytoplasmic	7	COG0365	Lipid metabolism		
26989078	PP_2354		multi-sensor hybrid histidine kinase	1.1	5.53E-01	Control	5.0	88511	Cytoplasmic Membrane	3	COG4191	Signal transduction mechanisms		
26989080	PP_2356		phytochrome family protein	2.1	1.73E-01	7,5 g/l BuOH	6.2	83859	Cytoplasmic Membrane	2	COG4251	Signal transduction mechanisms		
26989085	PP_2361	csuC	type 1 pili usher pathway chaperone CsuC	5.0	1.89E-03	Control	###	28448	Unknown	8	COG3121	Cell motility and secretion	Intracellular trafficking and secretion	
26989088	PP_2364		hypothetical protein	1.2	5.22E-01	Control	5.2	42461	Unknown	8	COG2866	Amino acid transport and metabolism		
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.0	9.97E-01	7,5 g/l BuOH	5.8	62191	Cytoplasmic	26	COG0155	Inorganic ion transport and metabolism		

26989099	PP_2375	metH	B12-dependent methionine synthase		1.0	9.72E-01	7,5 g/l BuOH	4.7	135408	Cytoplasmic	31	COG1410	Amino acid transport and metabolism		
26989102	PP_2378	yhgI	yhgI protein		1.7	3.41E-02	Control	4.3	20955	Cytoplasmic	4	COG0694	Posttranslational modification, protein turnover, chaperones		
26989119	PP_2396		hypothetical protein		1.2	5.10E-01	Control	8.9	20592	Periplasmic	9				
26989144	PP_2421		acetyltransferase		8.5	1.25E-02	7,5 g/l BuOH	8.3	20697	Cytoplasmic	3	COG0456	General function prediction only		
26989145	PP_2422		alkylhydroperoxidase-like protein	Infinity		4.51E-05	7,5 g/l BuOH	7.4	12135	Unknown	2	COG0599	Function unknown		
26989159	PP_2436		LysR family transcriptional regulator		4.2	1.53E-01	Control	9.4	35025	Cytoplasmic	4	COG0583	Transcription		
26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit		1.4	1.96E-01	7,5 g/l BuOH	4.8	20507	Cytoplasmic	8	COG0450	Posttranslational modification, protein turnover, chaperones		
26989165	PP_2442		hypothetical protein		1.1	7.71E-01	7,5 g/l BuOH	5.2	23851	Cytoplasmic	10	COG3132	Function unknown		
26989170	PP_2447		hypothetical protein		1.3	5.65E-01	Control	###	26784	Unknown	2				
26989176	PP_2453	ansA	L-asparaginase, type II		1.0	8.90E-01	7,5 g/l BuOH	7.9	38608	Periplasmic	8	COG0252	Amino acid transport and metabolism		Translation, ribosomal structure and biogenesis
26989177	PP_2454	rbsB	monosaccharide-transporting ATPase		1.3	4.59E-01	7,5 g/l BuOH	5.9	33763	Periplasmic	12	COG1879	Carbohydrate transport and metabolism		
26989183	PP_2460		inosine/uridine-preferring nucleoside hydrolase		1.9	1.95E-01	Control	6.2	34388	Unknown	3	COG1957	Nucleotide transport and metabolism		
26989188	PP_2465	thrS	threonyl-tRNA synthetase		2.0	2.88E-04	7,5 g/l BuOH	5.8	72697	Cytoplasmic	13	COG0441	Translation, ribosomal structure and biogenesis		
26989189	PP_2466	infC	translation initiation factor IF-3		1.7	2.81E-02	7,5 g/l BuOH	###	20120	Cytoplasmic	11	COG0290	Translation, ribosomal structure and biogenesis		
26989191	PP_2468	rplT	50S ribosomal protein L20		5.5	2.92E-01	7,5 g/l BuOH	###	13280	Cytoplasmic	3	COG0292	Translation, ribosomal structure and biogenesis		
26989192	PP_2469	pheS	phenylalanyl-tRNA synthetase subunit alpha		1.4	7.86E-02	7,5 g/l BuOH	5.2	38082	Cytoplasmic	8	COG0016	Translation, ribosomal structure and biogenesis		
26989193	PP_2470	pheT	phenylalanyl-tRNA synthetase subunit beta		1.1	5.21E-01	Control	4.8	86617	Cytoplasmic	25	COG0072	Translation, ribosomal structure and biogenesis		
26989197	PP_2474		glutathione S-transferase family protein		1.6	6.51E-02	Control	6.1	23793	Cytoplasmic	4	COG0625	Posttranslational modification, protein turnover, chaperones		
26989198	PP_2475		TetR family transcriptional regulator		1.3	9.36E-01	7,5 g/l BuOH	6.4	22413	Cytoplasmic	2	COG1309	Transcription		
26989211	PP_2488		succinic-semialdehyde dehydrogenase		1.5	2.72E-01	Control	5.1	50254	Cytoplasmic	2	COG1012	Energy production and conversion		
26989228	PP_2505		GAF domain/GGDEF domain-containing protein		2.7	1.75E-02	Control	6.0	38522	Cytoplasmic	2	COG3706	Signal transduction mechanisms		
26989230	PP_2507		short chain dehydrogenase/reductase family oxidoreductase		1.1	6.54E-01	Control	4.8	25476	Unknown	2	COG0300	General function prediction only		
26989244	PP_2524		HD domain-containing protein		1.7	2.10E-01	Control	6.5	24016	Cytoplasmic	2	COG1418	General function prediction only		
26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase		1.5	1.39E-01	Control	6.5	45235	Cytoplasmic	11	COG2873	Amino acid transport and metabolism		
26989256	PP_2536		glutathione S-transferase family protein		2.2	1.31E-01	Control	6.5	23574	Cytoplasmic	5	COG0625	Posttranslational modification, protein turnover, chaperones		
26989260	PP_2540		short chain dehydrogenase/reductase family oxidoreductase		1.9	4.43E-01	Control	7.7	26775	Cytoplasmic	2	COG1028	Secondary metabolites biosynthesis, transport, and catabolism		General function prediction only
26989265	PP_2545		trans-aconitate 2-methyltransferase		1.4	5.84E-01	7,5 g/l BuOH	6.8	30767	Cytoplasmic	5	COG4106	General function prediction only		
26989270	PP_2550		hypothetical protein		2.7	2.00E-01	Control	4.6	25315	Cytoplasmic	2	COG0217	Function unknown		
26989274	PP_2554		4-hydroxyphenylpyruvate dioxygenase		1.7	1.81E-01	Control	5.0	70406	Cytoplasmic	4	COG3185	Amino acid transport and metabolism		General function prediction only
26989289	PP_2569		major facilitator transporter		25.4	9.66E-02	Control	9.0	60538	Cytoplasmic Membrane	2	COG2223	Inorganic ion transport and metabolism		
26989307	PP_2588		aminotransferase		59.7	9.36E-02	7,5 g/l BuOH	6.5	50854	Cytoplasmic	2	COG0161	Coenzyme metabolism		
26989381	PP_2662		hypothetical protein		24.1	5.87E-03	7,5 g/l BuOH	4.3	42858	Outer Membrane	20				
26989382	PP_2663		hypothetical protein		46.9	9.66E-06	7,5 g/l BuOH	6.3	42469	Cytoplasmic	14	COG3287	Function unknown		
26989383	PP_2664		PAS/PAC sensor hybrid histidine kinase		80.3	1.17E-05	7,5 g/l BuOH	6.6	73094	Cytoplasmic Membrane	18	COG0642	Signal transduction mechanisms		
26989384	PP_2665	aqmR	LuxR family two component transcriptional regulator		13.4	6.11E-03	7,5 g/l BuOH	5.9	24536	Cytoplasmic	9	COG2197	Signal transduction mechanisms		Transcription
26989387	PP_2668		efflux ABC transporter ATP-binding protein		57.8	5.15E-04	7,5 g/l BuOH	9.8	27178	Cytoplasmic Membrane	10	COG1131	Defense mechanisms		
26989388	PP_2669		YVTN family beta-propeller repeat-containing protein		61.3	2.18E-03	7,5 g/l BuOH	6.2	36051	Unknown	11	COG3391	Function unknown		
26989391	PP_2672		LuxR family DNA-binding response regulator		28.2	1.43E-01	7,5 g/l BuOH	8.3	23226	Cytoplasmic	4	COG2197	Signal transduction mechanisms		Transcription
26989392	PP_2673		pentapeptide repeat-containing protein		56.9	2.90E-04	7,5 g/l BuOH	5.3	23569	Extracellular	17	COG1357	Function unknown		
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase		125.2	2.63E-04	7,5 g/l BuOH	7.0	69173	Periplasmic	69	COG4993	Carbohydrate transport and metabolism		
26989394	PP_2675		cytochrome c-type protein		86.7	4.65E-04	7,5 g/l BuOH	4.9	16280	Unknown	7	COG2010	Energy production and conversion		
26989395	PP_2676		periplasmic protein		133.1	2.67E-04	7,5 g/l BuOH	6.5	34540	Unknown	17	COG0834	Amino acid transport and metabolism		Signal transduction mechanisms
26989396	PP_2677		hypothetical protein		53.9	2.13E-04	7,5 g/l BuOH	5.3	28059	Unknown	11				
26989397	PP_2678		beta-lactamase domain protein		35.8	7.40E-06	7,5 g/l BuOH	6.4	33711	Unknown	16	COG0491	General function prediction only		
26989398	PP_2679		quinoprotein ethanol dehydrogenase		23.5	2.00E-04	7,5 g/l BuOH	9.1	64883	Periplasmic	26	COG4993	Carbohydrate transport and metabolism		
26989399	PP_2680		aldehyde dehydrogenase family protein		62.9	3.47E-04	7,5 g/l BuOH	5.5	54903	Cytoplasmic	45	COG1012	Energy production and conversion		
26989402	PP_2683		PAS/PAC sensor hybrid histidine kinase		2.8	1.76E-03	7,5 g/l BuOH	6.6	62695	Cytoplasmic Membrane	13	COG0642	Signal transduction mechanisms		
26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		1.1	4.45E-01	Control	6.3	38659	Cytoplasmic	29	COG0620	Amino acid transport and metabolism		
26989418	PP_2699		hypothetical protein		1.9	1.21E-01	Control	6.5	40451	Cytoplasmic	7				
26989420	PP_2701		LysR family transcriptional regulator		3.3	1.03E-01	Control	8.4	34726	Cytoplasmic	2	COG0583	Transcription		
26989432	PP_2713		DNA-binding response regulator		1.9	2.92E-01	7,5 g/l BuOH	5.2	24701	Cytoplasmic	2	COG0745	Signal transduction mechanisms		Transcription
26989525	PP_2806		TetR family transcriptional regulator		5.0	2.39E-01	Control	5.3	21294	Unknown	2	COG3226	Function unknown		
26989545	PP_2826	mexT	transcriptional regulator MexT		1.7	8.01E-01	7,5 g/l BuOH	6.7	33299	Cytoplasmic Membrane	3	COG0583	Transcription		
26989546	PP_2827		alcohol dehydrogenase, zinc-containing		1.1	5.90E-01	Control	5.4	36735	Cytoplasmic	2	COG0604	Energy production and conversion		General function prediction only
26989572	PP_2853		hypothetical protein		2.5	4.00E-02	Control	4.5	46020	Unknown	3				
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer		1.5	1.13E-01	Control	5.7	58659	Cytoplasmic Membrane	16	COG0840	Cell motility and secretion		Signal transduction mechanisms
26989581	PP_2862	uppP	undecaprenyl pyrophosphate phosphatase		11.1	1.75E-02	Control	7.8	30730	Cytoplasmic Membrane	2	COG1968	Lipid transport and metabolism		
26989586	PP_2867		pyridine nucleotide-disulphide oxidoreductase family protein		1.1	6.44E-01	Control	5.6	42483	Cytoplasmic Membrane	3	COG1252	Energy production and conversion		
26989609	PP_2890	xthA	exonuclease III		1.3	4.06E-01	7,5 g/l BuOH	6.7	30951	Cytoplasmic	4	COG0708	DNA replication, recombination, and repair		
26989610	PP_2891		acetyltransferase		1.5	2.38E-01	Control	7.6	25615	Cytoplasmic Membrane	3				
26989622	PP_2903	ppiB	peptidyl-prolyl cis-trans isomerase B		5.5	1.21E-01	7,5 g/l BuOH	6.5	18200	Cytoplasmic	2	COG0652	Posttranslational modification, protein turnover, chaperones		
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase		1.8	1.96E-03	7,5 g/l BuOH	6.1	64654	Cytoplasmic	10	COG0008	Translation, ribosomal structure and biogenesis		
26989624	PP_2905	cysS	cysteinyl-tRNA synthetase		1.5	1.90E-01	Control	5.8	51676	Cytoplasmic	5	COG0215	Translation, ribosomal structure and biogenesis		
26989627	PP_2908		DNA-binding transcriptional regulator CsiR		3.1	9.80E-02	Control	7.9	25953	Cytoplasmic	2	COG1802	Transcription		
26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase		1.6	9.89E-02	7,5 g/l BuOH	5.0	35225	Cytoplasmic	8	COG0113	Coenzyme metabolism		
26989635	PP_2916	ribE-2	riboflavin synthase subunit alpha		1.5	3.28E-01	Control	4.9	22902	Cytoplasmic	2	COG0307	Coenzyme metabolism		
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase		2.4	1.34E-02	Control	8.0	59671	Unknown	10	COG0579	General function prediction only		
26989647	PP_2928		saccharopine dehydrogenase		1.3	4.29E-01	Control	5.0	45363	Cytoplasmic	8	COG1748	Amino acid transport and metabolism		
26989648	PP_2929	nspC	carboxynorspermidine decarboxylase		2.3	1.15E-01	7,5 g/l BuOH	4.9	41026	Cytoplasmic	3	COG0019	Amino acid transport and metabolism		
26989651	PP_2932		amidase		2.0	3.12E-03	7,5 g/l BuOH	4.5	60346	Cytoplasmic	6	COG0154	Translation, ribosomal structure and biogenesis		
26989652	PP_2933		glutathione S-transferase YghU		2.1	5.33E-02	7,5 g/l BuOH	6.0	31202	Cytoplasmic	4	COG0625	Posttranslational modification, protein turnover, chaperones		
26989661	PP_2942		response regulator		1.1	6.21E-01	Control	5.6	51291	Cytoplasmic	4	COG3437	Transcription		Signal transduction mechanisms
26989663	PP_2944		sensor histidine kinase		7.9	4.66E-02	Control	6.1	67470	Cytoplasmic Membrane	2	COG4191	Signal transduction mechanisms		
26989738	PP_3019		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase		2.6	1.04E-01	Control	5.1	26214	Cytoplasmic	6	COG0388	General function prediction only		
26989743	PP_3024		hypothetical protein		3.9	5.43E-02	Control	###	45171	Cytoplasmic	2				
26989790	PP_3071		acetoacetyl-CoA synthetase		3.3	5.51E-02	Control	6.4	72303	Cytoplasmic	2	COG0365	Lipid metabolism		
26989792	PP_3073	bdhA	3-hydroxybutyrate dehydrogenase		3.2	1.09E-01	Control	6.9	26852	Cytoplasmic	5	COG1028	Secondary metabolites biosynthesis, transport, and catabolism		General function prediction only
26989807	PP_3088		hypothetical protein		18.3	6.21E-02	7,5 g/l BuOH	4.4	39853	Unknown	2	COG3515	Intracellular trafficking, secretion, and vesicular transport		
26989808	PP_3089		hypothetical protein		10.7	5.29E-02	Control	5.3	19453	Extracellular	9	COG3157	Intracellular trafficking, secretion, and vesicular transport		
26989809	PP_3090		OmpA domain-containing protein		3.2	1.62E-01	7,5 g/l BuOH	9.0	93143	Cytoplasmic Membrane	6	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989810	PP_3091		hypothetical protein		1.6	6.17E-01	7,5 g/l BuOH	6.8	138655	Cytoplasmic Membrane	17	COG3523	Intracellular trafficking, secretion, and vesicular transport		
26989811	PP_3092		hypothetical protein		4.1	9.93E-02	7,5 g/l BuOH	5.7	26868	Cytoplasmic	5	COG3455	Intracellular trafficking, secretion, and vesicular transport		
26989813	PP_3094		hypothetical protein		19.3	1.24E-01	7,5 g/l BuOH	4.7	25945	Unknown	6	COG3521	Intracellular trafficking, secretion, and vesicular transport		
26989814	PP_3095		chaperone-associated ATPase		4.5	2.90E-02	7,5 g/l BuOH	6.1	96474	Cytoplasmic	25	COG0542	Posttranslational modification, protein turnover, chaperones		
26989818	PP_3099		hypothetical protein		6.0	4.30E-02	7,5 g/l BuOH	4.9	56072	Cytoplasmic	27	COG3517	Intracellular trafficking, secretion, and vesicular transport		
26989825	PP_3106		hypothetical protein		3.3	4.21E-03	Control	5.6	69529	Cytoplasmic	18	COG3501	Function unknown		
26989827	PP_3108		rhs-related protein		3.9	1.14E-02	Control	6.0	155811	Unknown	29	COG3209	Cell envelope biogenesis, outer membrane		
26989841	PP_3122		3-oxoacid CoA-transferase subunit A		6.7	2.47E-02	7,5 g/l BuOH	5.2	25125	Cytoplasmic	2	COG1788	Lipid metabolism		
26989845	PP_3126		polysaccharide export protein		16.0	9.42E-01	Control	4.9	19528	Unknown	4	COG1596	Cell wall		membrane
26989846	PP_3127		lipopolysaccharide biosynthesis protein		2.7	1.83E-02	Control	9.0	57141	Cytoplasmic Membrane	19	COG3206	Cell envelope biogenesis, outer membrane		
26989847	PP_3128		protein-tyrosine kinase		3.2	2.19E-02	Control	7.1	29623	Cytoplasmic Membrane	8	COG0489	Cell division and chromosome partitioning		
26989848	PP_3129	galE	UDP-glucose 4-epimerase		3.8	1.54E-02	Control	6.3	34967	Cytoplasmic	6	COG1087	Cell envelope biogenesis, outer membrane		
26989849	PP_3130		hypothetical protein		7.6	2.99E-02	Control	6.4	96618	Unknown	5				
26989852	PP_3133		GMC oxidoreductase		4.6	2.81E-02	Control	5.2	52611	Cytoplasmic	2	COG2303	Amino acid transport and metabolism		
26989853	PP_3134		transferase hexapeptide repeat containing protein		12.3	4.39E-02	Control	9.9	25699	Cytoplasmic	6	COG0110	General function prediction only		
26989854	PP_3135		glycosyl transferase		4.4	1.86E-02	Control	8.6	35887	Cytoplasmic	9	COG1216	General function prediction only		
26989857	PP_3138		VirK domain-containing protein		3.5	1.43E-01	Control	8.6	37023	Unknown	3	COG2990	Function unknown		
26989859	PP_3140		glycosyl transferase, group 2 family protein		3.9	7.88E-02	Control	9.4	43092	Cytoplasmic Membrane	2	COG1215	Cell envelope biogenesis, outer membrane		
26989860	PP_3141		WecB/TagA/CpsF family glycosyl transferase		2.8	6.40E-02	Control	###	27576	Unknown	6	COG1922	Cell envelope biogenesis, outer membrane		
26989864	PP_3145		hypothetical protein		1.5	1.25E-01	Control	9.7	29885	Unknown	20				
26989876	PP_3157		inositol monophosphatase family protein		2.5	2.48E-01	Control	4.3	27793	Cytoplasmic	3	COG0483	Carbohydrate transport and metabolism		
26989904	PP_3185	pet18	transcriptional activator, TenA family		1.1	9.59E-01	7,5 g/l BuOH	4.9	23859	Unknown	3	COG0819	Transcription		
26989905	PP_3186		transcriptional activator, TenA family		2.0	1.14E-01	Control	4.8	24300	Cytoplasmic	5	COG0819	Transcription		
26989966	PP_3248		Dyp-type peroxidase family		1.9	2.98E-02	7,5 g/l BuOH	4.6	31295	Unknown	6	COG2837	Inorganic ion transport and metabolism		
26989967	PP_3249		aldo/keto reductase		1.2	8.98E-02	7,5 g/l BuOH	8.2	29657	Cytoplasmic	2	COG0656	General function prediction only		
26990018	PP_3300		TetR family transcriptional regulator		2.3	1.58E-02	7,5 g/l BuOH	7.8	22603	Unknown	3	COG1309	Transcription		
26990076	PP_3361		hypothetical protein		1.9	1.11E-01	Control	6.3	110896	Cytoplasmic	3	COG0160	Amino acid transport and metabolism		
26990079	PP_3364		response regulator		1.9	1.03E-01	Control	6.4	91750	Cytoplasmic	6	COG4251	Signal transduction mechanisms		
26990095	PP_3380	ptxS	PtxS family transcriptional regulator		4.9	6.31E-02	Control	6.9	36789	Cytoplasmic	3	COG1609	Transcription		
26990118	PP_3404		alpha/beta hydrolase fold		1.1	4.91E-01	Control	8.3	31909	Cytoplasmic	2	COG0596	General function prediction only		
26990127	PP_3414		methyl-accepting chemotaxis transducer/sensory box protein		1.1	5.85E-01	Control	6.8	48686	Cytoplasmic Membrane	5	COG0840	Cell motility and secretion		Signal transduction mechanisms
26990144	PP_3431		Thi4/Pfpl domain protein		1.9	8.63E-03	Control	6.5	25246	Unknown	16	COG0693	General function prediction only		
26990154	PP_3441		hypothetical protein		2.5	3.24E-01	Control	9.3	43139	Cytoplasmic	2				
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase		3.9	2.99E-04	Control	6.2	59980	Cytoplasmic	20	COG1012	Energy production and conversion		

26990161	PP 3448	nfrB	bacteriophage N4 adsorption protein B	2.0	1.40E-01	Control	7.4	82370	Cytoplasmic Membrane	4	COG1215	Cell envelope biogenesis, outer membrane	
26990172	PP 3459		hypothetical protein	5.2	4.28E-01	7,5 g/l BuOH	9.0	42365	Periplasmic	8			
26990203	PP 3491		enoly-coenzyme A hydratase/isomerase family protein	1.0	8.64E-01	Control	4.9	39382	Cytoplasmic	5	COG1024	Lipid metabolism	
26990204	PP 3492	acdA	acyl-CoA dehydrogenase domain-containing protein	1.5	6.95E-02	Control	5.7	41553	Cytoplasmic	4	COG1960	Lipid metabolism	
26990219	PP 3507	cobN	cobaltochelatase subunit CobN	1.7	4.17E-01	7,5 g/l BuOH	5.4	138545	Cytoplasmic	5	COG1429	Coenzyme metabolism	
26990220	PP 3508	cobW	cobalamin biosynthesis protein CobW	1.4	2.20E-01	7,5 g/l BuOH	4.6	38579	Cytoplasmic	10	COG0523	General function prediction only	
26990223	PP 3511	ilvE	branched-chain amino acid aminotransferase	1.1	7.02E-01	Control	7.2	36863	Cytoplasmic	24	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990239	PP 3527		TetR family transcriptional regulator	2.0	9.66E-01	7,5 g/l BuOH	6.5	26116	Cytoplasmic	3	COG1309	Transcription	
26990242	PP 3530		hypothetical protein	1.4	3.17E-01	Control	6.2	31546	Cytoplasmic	4	COG3257	General function prediction only	
26990252	PP 3540	mvaB	hydroxymethylglutaryl-CoA lyase	1.3	3.68E-01	7,5 g/l BuOH	5.4	31341	Cytoplasmic	8	COG0119	Amino acid transport and metabolism	
26990258	PP 3546		PAS/PAC sensor hybrid histidine kinase	1.2	3.47E-01	Control	5.0	76414	Cytoplasmic Membrane	2	COG4191	Signal transduction mechanisms	
26990259	PP 3547		short chain dehydrogenase/reductase family oxidoreductase	1.1	6.03E-01	Control	6.0	26030	Cytoplasmic	8	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990265	PP 3553		acyl-CoA synthetase	40.2	6.29E-04	7,5 g/l BuOH	6.4	59576	Cytoplasmic	16	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990266	PP 3554		acyl-CoA dehydrogenase domain-containing protein	32.4	2.06E-03	7,5 g/l BuOH	5.5	63339	Cytoplasmic	20	COG1960	Lipid metabolism	
26990269	PP 3557		methyl-accepting chemotaxis transducer	1.2	3.36E-01	7,5 g/l BuOH	4.7	76982	Cytoplasmic Membrane	13	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990270	PP 3558		substrate-binding region of ABC-type glycine betaine transport system	1.2	7.51E-01	7,5 g/l BuOH	5.5	36928	Periplasmic	8	COG2113	Amino acid transport and metabolism	
26990275	PP 3563		hypothetical protein	2.7	5.47E-02	7,5 g/l BuOH	5.1	30285	Unknown	2	COG2340	Function unknown	
26990281	PP 3569		quinate dehydrogenase (pyrroloquinoline-quinone)	2.4	1.11E-01	Control	6.9	85338	Cytoplasmic Membrane	2	COG4993	Carbohydrate transport and metabolism	
26990290	PP 3578		phosphoglucomutase	1.3	3.27E-01	Control	5.6	58620	Unknown	12	COG0033	Carbohydrate transport and metabolism	
26990294	PP 3582		RND efflux transporter	14.9	5.67E-03	7,5 g/l BuOH	5.2	53952	Outer Membrane	2	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990298	PP 3587	tpx	redoxin domain protein	1.1	7.71E-01	Control	4.7	17409	Periplasmic	4	COG2077	Posttranslational modification, protein turnover, chaperones	
26990301	PP 3590	tyrB-2	aromatic amino acid aminotransferase	2.9	1.28E-02	7,5 g/l BuOH	5.9	43631	Cytoplasmic	16	COG1448	Amino acid transport and metabolism	
26990313	PP 3602		ketoglutarate semialdehyde dehydrogenase	1.5	1.45E-01	Control	5.2	55538	Cytoplasmic	12	COG1012	Energy production and conversion	
26990314	PP 3603		GntR family transcriptional regulator	1.1	7.30E-01	Control	9.0	28149	Cytoplasmic	5	COG2186	Transcription	
26990322	PP 3611		hypothetical protein	4.5	8.75E-03	Control	9.7	20824	Unknown	13			
26990333	PP 3622		isoquinoline 1-oxidoreductase, beta subunit	1.6	3.34E-02	Control	7.0	80889	Cytoplasmic Membrane	25	COG1529	Energy production and conversion	
26990334	PP 3623		gluconate 2-dehydrogenase acceptor subunit	1.6	1.78E-02	Control	7.2	47849	Cytoplasmic Membrane	3	COG2010	Energy production and conversion	
26990342	PP 3631		hypothetical protein	3309.3	1.97E-02	7,5 g/l BuOH	7.7	23586	Unknown	2	COG3103	Signal transduction mechanisms	
26990347	PP 3636		sulfonate ABC transporter periplasmic sulfonate-binding protein	1.5	2.05E-01	Control	7.3	43742	Cytoplasmic Membrane	10	COG0715	Inorganic ion transport and metabolism	
26990348	PP 3637		sulfonate ABC transporter ATP-binding protein	1.9	7.90E-02	Control	7.1	29618	Cytoplasmic Membrane	3	COG1116	Inorganic ion transport and metabolism	
26990349	PP 3638		acyl-CoA dehydrogenase	2.3	9.98E-04	Control	6.1	38476	Cytoplasmic	14	COG1960	Lipid metabolism	
26990355	PP 3644		luciferase family protein	1.6	1.88E-01	Control	5.4	38951	Cytoplasmic	2	COG2141	Energy production and conversion	
26990360	PP 3649		GntR family transcriptional regulator	2.2	5.35E-02	7,5 g/l BuOH	7.0	28178	Cytoplasmic	7	COG1802	Transcription	
26990367	PP 3656		aromatic compound-specific porin	37.9	3.24E-01	7,5 g/l BuOH	5.3	46672	Outer Membrane	3			
26990369	PP 3658		aromatic compound MFS transporter	Infinity	1.41E-01	7,5 g/l BuOH	9.5	48129	Cytoplasmic Membrane	2	COG2814	Carbohydrate transport and metabolism	
26990373	PP 3662		decarboxylase family protein	1.3	3.59E-01	7,5 g/l BuOH	6.7	50729	Cytoplasmic	10	COG1611	General function prediction only	
26990379	PP 3668		catalase/peroxidase HPI	1.4	7.78E-02	7,5 g/l BuOH	5.8	82061	Cytoplasmic	48	COG0376	Inorganic ion transport and metabolism	
26990380	PP 3669		LysR family transcriptional regulator	2.2	1.52E-01	Control	5.3	33285	Cytoplasmic	3	COG0583	Transcription	
26990389	PP 3680		hypothetical protein	1.6	2.26E-01	7,5 g/l BuOH	6.3	75093	Unknown	6	COG3593	DNA replication, recombination, and repair	
26990399	PP 3691		DNA helicase-related protein	1.5	2.46E-02	Control	5.0	245278	Unknown	57	COG1112	DNA replication, recombination, and repair	
26990400	PP 3692		hypothetical protein	6.9	2.82E-02	Control	8.0	98331	Cytoplasmic	3	COG4988	Energy production and conversion	Posttranslational modification, protein turnover, chaperones
26990414	PP 3706		hypothetical protein	1.8	2.25E-01	Control	5.7	35856	Cytoplasmic	2	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26990415	PP 3707		hypothetical protein	1.6	2.98E-01	Control	5.4	52925	Cytoplasmic	2			
26990421	PP 3713	catA	catechol 1,2-dioxygenase	1.2	9.22E-01	7,5 g/l BuOH	5.1	34249	Cytoplasmic	10	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26990448	PP 3742		glutathione S-transferase family protein	1.8	1.90E-01	Control	6.4	24042	Cytoplasmic	4	COG0625	Posttranslational modification, protein turnover, chaperones	
26990459	PP 3754		beta-ketothiolase	2.5	8.22E-03	7,5 g/l BuOH	6.9	40988	Cytoplasmic	18	COG0183	Lipid metabolism	
26990460	PP 3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	2.4	4.64E-01	7,5 g/l BuOH	6.3	30088	Cytoplasmic	9	COG1250	Lipid metabolism	
26990466	PP 3761		multi-sensor hybrid histidine kinase	2.2	1.89E-02	Control	4.9	129450	Cytoplasmic Membrane	29	COG0642	Signal transduction mechanisms	
26990468	PP 3763		precorrin 6A synthase	1.9	2.02E-01	Control	4.9	27798	Cytoplasmic	2	COG2243	Coenzyme metabolism	
26990471	PP 3766	gloA	lactoylglutathione lyase	3.5	4.98E-01	Control	5.0	19811	Cytoplasmic	2	COG0346	Amino acid transport and metabolism	
26990480	PP 3775		sarcosine oxidase	2.9	4.12E-04	Control	6.4	41164	Cytoplasmic	22	COG0665	Amino acid transport and metabolism	
26990482	PP 3777		hypothetical protein	8.7	3.21E-03	Control	5.2	31324	Cytoplasmic	17	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP 3778	proC-1	pyrroline-5-carboxylate reductase	3.5	4.41E-04	Control	6.2	27714	Cytoplasmic	22	COG0345	Amino acid transport and metabolism	
26990486	PP 3781		oxygen-independent coproporphyrinogen III oxidase family protein	1.5	1.97E-01	Control	7.0	53071	Cytoplasmic	9	COG0635	Coenzyme metabolism	
26990488	PP 3783		hypothetical protein	2.5	1.00E-02	Control	5.8	34938	Cytoplasmic	13			
26990489	PP 3784		hypothetical protein	2.9	6.90E-03	Control	5.4	41070	Unknown	13	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP 3785		hypothetical protein	4.3	6.93E-02	Control	6.5	50495	Cytoplasmic	10			
26990491	PP 3786		aminotransferase	2.8	1.66E-01	Control	6.4	44067	Cytoplasmic	3	COG0436	Amino acid transport and metabolism	
26990492	PP 3787		hypothetical protein	6.2	1.31E-02	Control	6.8	33215	Unknown	6	COG0332	acyl-carrier-protein	
26990493	PP 3788		non-ribosomal peptide synthetase	3.4	5.49E-02	7,5 g/l BuOH	6.7	56336	Cytoplasmic	2	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990495	PP 3790	dapF	diaminopimelate epimerase	3.3	1.04E-01	Control	6.0	29286	Cytoplasmic	4	COG0253	Amino acid transport and metabolism	
26990511	PP 3806		isochorismatase superfamily hydrolase	2.5	3.99E-01	Control	6.3	19515	Unknown	3	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26990519	PP 3814		polyamine ABC transporter periplasmic polyamine-binding protein	2.4	6.87E-04	Control	5.2	37113	Periplasmic	8	COG0687	Amino acid transport and metabolism	
26990524	PP 3819	gor	glutathione reductase	1.0	6.42E-01	Control	5.2	49180	Cytoplasmic	5	COG1249	Energy production and conversion	
26990526	PP 3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.5	1.32E-01	7,5 g/l BuOH	5.3	30957	Cytoplasmic	13	COG1210	Cell envelope biogenesis, outer membrane	
26990537	PP 3832		carbon storage regulator	3.3	8.13E-01	7,5 g/l BuOH	7.8	7271	Unknown	3	COG1551	Signal transduction mechanisms	
26990544	PP 3839		alcohol dehydrogenase	1.7	8.35E-03	Control	5.7	35397	Cytoplasmic	12	COG1064	General function prediction only	
26990627	PP 3922		periplasmic protease	2.4	1.02E-01	7,5 g/l BuOH	9.8	37502	Cytoplasmic Membrane	4	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990631	PP 3926		short chain dehydrogenase	1.8	1.89E-01	Control	7.4	26721	Cytoplasmic	7	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990659	PP 3954		periplasmic protein	1.7	3.72E-02	Control	9.3	33239	Unknown	15	COG2358	General function prediction only	
26990662	PP 3957		choline/carnitine/betaine transporter family protein	7.4	3.67E-01	7,5 g/l BuOH	7.6	72789	Cytoplasmic Membrane	2	COG1292	Cell envelope biogenesis, outer membrane	
26990673	PP 3968		sensor histidine kinase	1.1	7.92E-01	Control	5.0	40394	Cytoplasmic Membrane	2	COG0642	Signal transduction mechanisms	
26990693	PP 3988		hypothetical protein	1.1	4.04E-01	7,5 g/l BuOH	6.3	76259	Cytoplasmic	11	COG0323	DNA replication, recombination, and repair	
26990705	PP 4000	serS	seryl-tRNA synthetase	1.3	1.53E-01	Control	5.1	46849	Cytoplasmic	10	COG0172	Translation, ribosomal structure and biogenesis	
26990707	PP 4002		recombination factor protein RarA	2.1	6.95E-02	7,5 g/l BuOH	6.1	49147	Cytoplasmic	2	COG2256	DNA replication, recombination, and repair	
26990708	PP 4003	lolA	outer-membrane lipoprotein carrier protein	1.1	6.63E-01	Control	9.5	25146	Periplasmic	6	COG2834	Cell envelope biogenesis, outer membrane	
26990709	PP 4004	ftsK	cell divisionFtsK/SpoIIIE	1.3	5.18E-01	Control	6.4	91296	Cytoplasmic Membrane	3	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.1	6.08E-01	Control	5.7	83310	Cytoplasmic	18	COG0542	Posttranslational modification, protein turnover, chaperones	
26990716	PP 4011	icd	isocitrate dehydrogenase, NADP-dependent	2.2	1.36E-02	Control	5.4	45695	Unknown	33	COG0538	Energy production and conversion	
26990717	PP 4012		isocitrate dehydrogenase, NADP-dependent	2.4	1.21E-01	Control	5.4	79899	Cytoplasmic	36	COG2838	Energy production and conversion	
26990719	PP 4014	mnmA	tRNA-specific 2-thiouridylase MnmA	1.2	3.78E-01	Control	5.5	41489	Cytoplasmic	3	COG0482	Translation, ribosomal structure and biogenesis	
26990721	PP 4016	purB	adenylosuccinate lyase	1.0	9.48E-01	7,5 g/l BuOH	5.9	50555	Cytoplasmic	16	COG0015	Nucleotide transport and metabolism	
26990726	PP 4021	est	alpha/beta hydrolase fold	2.4	2.03E-02	Control	6.1	30206	Cytoplasmic	10	COG0596	General function prediction only	
26990732	PP 4029	nudC	NADH pyrophosphatase	7.2	6.16E-03	Control	5.0	30868	Cytoplasmic	2	COG2816	DNA replication, recombination, and repair	
26990733	PP 4030		enoyl-CoA hydratase	2.1	1.22E-01	Control	5.2	30613	Cytoplasmic	3	COG1024	Lipid metabolism	
26990737	PP 4034		allantoate amidohydrolase	1.6	7.15E-02	Control	5.7	45010	Cytoplasmic	25	COG0624	Amino acid transport and metabolism	
26990738	PP 4035		NCS1 nucleoside transporter	1.2	3.88E-01	Control	7.9	53519	Cytoplasmic Membrane	4	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP 4037		oxidoreductase	2.3	2.54E-02	Control	5.5	48815	Cytoplasmic	30	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP 4038		dihydropyrimidine dehydrogenase	2.6	3.55E-02	Control	5.1	46093	Cytoplasmic	22	COG0167	Nucleotide transport and metabolism	
26990742	PP 4041		glycoside hydrolase 15-related	3.8	7.10E-02	Control	6.4	69769	Cytoplasmic	4	COG3387	Carbohydrate transport and metabolism	
26990744	PP 4043	gnd	6-phosphogluconate dehydrogenase	1.6	5.31E-01	7,5 g/l BuOH	6.4	35366	Cytoplasmic	9	COG1023	Carbohydrate transport and metabolism	
26990751	PP 4050	glgA	glycogen synthase	7.2	2.21E-02	Control	6.0	57190	Cytoplasmic	12	COG0297	Carbohydrate transport and metabolism	
26990752	PP 4051		malto-oligosyltrehalose trehalohydrolase	2.2	6.70E-03	Control	6.0	64544	Cytoplasmic	12	COG0296	Carbohydrate transport and metabolism	
26990753	PP 4052	malQ	4-alpha-glucanotransferase	3.6	4.68E-02	Control	5.5	76475	Cytoplasmic	20	COG1640	Carbohydrate transport and metabolism	
26990754	PP 4053		maltooligosyl trehalose synthase	3.5	6.08E-05	Control	6.6	103167	Cytoplasmic	27	COG3280	Carbohydrate transport and metabolism	
26990756	PP 4055	glgX	glycogen debranching protein GlgX	6.9	2.55E-03	Control	5.1	81044	Cytoplasmic	21	COG1523	Carbohydrate transport and metabolism	
26990759	PP 4058	glgB	glycogen branching enzyme	1.2	4.54E-01	Control	5.9	82877	Cytoplasmic	8	COG0296	Carbohydrate transport and metabolism	
26990760	PP 4059		trehalose synthase	8.0	2.16E-02	Control	5.4	125589	Cytoplasmic	7	COG0366	Carbohydrate transport and metabolism	
26990761	PP 4060		alpha-amylase family protein	1.8	1.02E-01	Control	6.1	75542	Cytoplasmic	10	COG0366	Carbohydrate transport and metabolism	
26990764	PP 4063		AMP-binding domain protein	2.3	2.26E-01	Control	5.6	61594	Cytoplasmic	4	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990765	PP 4064	ivd	acyl-CoA dehydrogenase domain-containing protein	2.2	2.28E-02	Control	7.2	46572	Cytoplasmic	10	COG1960	Lipid metabolism	
26990766	PP 4065		propionyl-CoA carboxylase	6.7	5.79E-03	Control	6.9	57504	Cytoplasmic	7	COG4799	Lipid metabolism	
26990767	PP 4066		gamma-carboxygeranoyl-CoA hydratase	3.1	2.14E-02	Control	5.5	30015	Cytoplasmic	8	COG1024	Lipid metabolism	
26990768	PP 4067		acetyl-CoA carboxylase, biotin carboxylase	3.0	3.30E-02	Control	5.8	69729	Cytoplasmic	8	COG4770	Lipid metabolism	
26990769	PP 4068		Cro/CI family transcriptional regulator	1.9	8.75E-02	Control	4.9	26361	Cytoplasmic	2	COG1974	Transcription	Signal transduction mechanisms
26990794	PP 4099	gacA	DNA-binding response regulator GacA	4.9	4.62E-02	Control	6.3	23138	Cytoplasmic	4	COG2197	Signal transduction mechanisms	Transcription
26990799	PP 4104		glutathione S-transferase family protein	1.7	1.02E-01	7,5 g/l BuOH	7.8	26354	Cytoplasmic	4	COG0625	Posttranslational modification, protein turnover, chaperones	
26990806	PP 4111	fusA	elongation factor G	2.1	9.51E-02	Control	5.0	77832	Cytoplasmic	23	COG0480	Translation, ribosomal structure and biogenesis	
26990809	PP 4115		NolW domain protein	2.9	8.51E-02	Control	6.7	29306	Unknown	4			
26990810	PP 4116	aceA	isocitrate lyase	80.9	1.47E-03	7,5 g/l BuOH	5.3	48633	Cytoplasmic	43	COG2224	Energy production and conversion	
26990814	PP 4120	nuoB	NADH dehydrogenase subunit B	2.1	6.37E-02	Control	4.9	25523	Cytoplasmic Membrane	6	COG0377	Energy production and conversion	
26990815	PP 4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.6	2.18E-01	Control	6.5	67609	Cytoplasmic	22	COG0649	Energy production and conversion	
26990817	PP 4123	nuoF	NADH dehydrogenase I subunit F	1.4	2.26E-02	Control	7.1	49135	Cytoplasmic	14	COG1894	Energy production and conversion	
26990818	PP 4124	nuoG	NADH dehydrogenase subunit G	2.1	6.41E-02	Control	5.9	97582	Unknown	30	COG1034	Energy production and conversion	

26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	3.1	1.40E-01	Control	6.1	37637	Cytoplasmic Membrane	2	COG1005	Energy production and conversion	
26990820	PP_4126	nuoI	NADH dehydrogenase subunit I	2.3	9.80E-01	Control	6.0	20517	Cytoplasmic	4	COG1143	Energy production and conversion	
26990832	PP_4138		NADPH-dependent FMN reductase	1.4	8.92E-01	Control	8.7	20354	Cytoplasmic	10	COG0431	General function prediction only	
26990837	PP_4144	gloB	hydroxyacylglutathione hydrolase	1.1	9.91E-01	Control	6.3	28767	Cytoplasmic	2	COG0491	General function prediction only	
26990840	PP_4147		peptide ABC transporter periplamic peptide-binding protein	1.9	1.23E-02	Control	7.2	69637	Periplasmic	2	COG4166	Amino acid transport and metabolism	
26990855	PP_4163		hypothetical protein	1.2	2.64E-01	Control	5.5	28880	Unknown	3			
26990861	PP_4169	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1.0	9.46E-01	7,5 g/l BuOH	6.6	36520	Cytoplasmic	11	COG0240	Energy production and conversion	
26990866	PP_4174	fabA	3-hydroxydecanoyl-(acyl carrier protein) dehydratase	2.7	1.12E-01	7,5 g/l BuOH	6.5	18791	Cytoplasmic	2	COG0764	Lipid metabolism	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.4	1.22E-01	Control	5.3	43264	Cytoplasmic	13	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990870	PP_4178		dienelactone hydrolase	1.3	5.96E-03	Control	7.1	26269	Cytoplasmic	14	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26990871	PP_4179	htpG	heat shock protein 90	2.2	9.13E-04	7,5 g/l BuOH	5.0	71610	Cytoplasmic	46	COG0326	Posttranslational modification, protein turnover, chaperones	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.2	2.88E-02	Control	6.2	30111	Cytoplasmic	23	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.7	3.79E-02	Control	6.1	41239	Cytoplasmic	25	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.7	1.30E-02	Control	6.3	49912	Cytoplasmic	25	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.0	6.35E-01	Control	5.1	42434	Cytoplasmic	19	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.3	1.83E-01	Control	6.5	106521	Cytoplasmic	46	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.0	9.42E-01	Control	7.5	26000	Cytoplasmic Membrane	14	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.1	9.60E-01	7,5 g/l BuOH	6.2	63448	Cytoplasmic Membrane	24	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.5	7.02E-01	7,5 g/l BuOH	9.0	13579	Cytoplasmic Membrane	2	COG2142	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	2.5	4.02E-03	7,5 g/l BuOH	7.0	47622	Cytoplasmic	28	COG0372	Energy production and conversion	
26990890	PP_4198		OmpA/MotB domain protein	1.4	5.16E-01	7,5 g/l BuOH	8.9	29694	Outer Membrane	5	COG2885	Cell envelope biogenesis, outer membrane	
26990892	PP_4200		hypothetical protein	1.6	2.16E-01	7,5 g/l BuOH	8.1	29611	Unknown	2	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.6	3.28E-02	7,5 g/l BuOH	4.9	31237	Unknown	18	COG2025	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.2	7.41E-01	7,5 g/l BuOH	9.7	26361	Unknown	18	COG2086	Energy production and conversion	
26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	5.6	1.37E-02	7,5 g/l BuOH	5.7	61082	Cytoplasmic	19	COG0644	Energy production and conversion	
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	16.9	2.63E-01	Control	5.5	89725	Outer Membrane	5	COG4773	Inorganic ion transport and metabolism	
26990911	PP_4219	ppsD	non-ribosomal siderophore peptide synthetase	37.6	8.21E-02	Control	5.5	382081	Unknown	3	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990912	PP_4220		non-ribosomal peptide synthetase	34.2	8.60E-01	Control	5.2	287552	Unknown	6	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990928	PP_4237	dsbG	disulfide isomerase/thiol-disulfide oxidase	1.3	5.25E-01	Control	8.6	27578	Periplasmic	3	COG1651	Posttranslational modification, protein turnover, chaperones	
26990940	PP_4249		hypothetical protein	1.3	4.53E-01	Control	7.0	24715	Cytoplasmic	3	COG3571	General function prediction only	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	2.1	4.46E-02	Control	9.6	53567	Cytoplasmic Membrane	4	COG3278	Posttranslational modification, protein turnover, chaperones	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	1.1	3.47E-01	7,5 g/l BuOH	9.0	22637	Cytoplasmic	10	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	1.3	3.25E-01	7,5 g/l BuOH	5.2	35613	Unknown	16	COG2010	Energy production and conversion	
26990956	PP_4265	anr	transcriptional regulator Anr	1.2	7.07E-01	7,5 g/l BuOH	6.5	27221	Cytoplasmic	3	COG0664	Signal transduction mechanisms	
26990957	PP_4266	apt	adenine phosphoribosyltransferase	1.7	1.68E-01	Control	4.6	20018	Cytoplasmic	4	COG0503	Nucleotide transport and metabolism	
26990960	PP_4269	dnaX	DNA polymerase III subunits gamma and tau	2.1	1.70E-01	7,5 g/l BuOH	4.4	74471	Cytoplasmic	1	COG2812	DNA replication, recombination, and repair	
26990965	PP_4274	ligA	NAD-dependent DNA ligase LigA	1.0	9.12E-01	7,5 g/l BuOH	5.3	84112	Cytoplasmic	4	COG0272	DNA replication, recombination, and repair	
26990966	PP_4275	zipA	cell division protein ZipA	1.8	5.36E-01	7,5 g/l BuOH	6.0	35312	Cytoplasmic Membrane	10	COG3115	Cell division and chromosome partitioning	
26990967	PP_4276		chromosome segregation protein SMC	2.7	3.83E-02	Control	4.7	131729	Cytoplasmic	7	COG1196	Cell division and chromosome partitioning	
26990968	PP_4277		GntR family transcriptional regulator	1.0	9.65E-01	7,5 g/l BuOH	7.5	24972	Cytoplasmic	9	COG1802	Transcription	
26990970	PP_4279	xdhB	xanthine dehydrogenase, XdhB subunit	2.2	1.03E-01	Control	6.4	88031	Cytoplasmic	2	COG4631	Nucleotide transport and metabolism	
26990974	PP_4283		GntR family transcriptional regulator	1.1	6.51E-01	Control	6.8	27912	Cytoplasmic	9	COG1802	Transcription	
26990977	PP_4286		polysaccharide deacetylase family protein	1.2	5.24E-01	Control	5.9	35315	Cytoplasmic	3	COG0726	Carbohydrate transport and metabolism	
26990978	PP_4287		hypothetical protein	1.3	3.46E-01	7,5 g/l BuOH	4.9	19028	Cytoplasmic	2	COG3195	Function unknown	
26990985	PP_4294		hypothetical protein	12.0	7.63E-01	7,5 g/l BuOH	7.2	31614	Cytoplasmic Membrane	2	COG2354	Function unknown	
26990986	PP_4295		TetR family transcriptional regulator	1.1	6.02E-01	7,5 g/l BuOH	6.6	22721	Cytoplasmic	4	COG1309	Transcription	
26990989	PP_4298	hyi	hydroxypyruvate isomerase	1.4	4.78E-02	7,5 g/l BuOH	5.0	29057	Cytoplasmic	9	COG3622	Carbohydrate transport and metabolism	
26990990	PP_4299	glxR	2-hydroxy-3-oxopropionate reductase	1.6	3.28E-01	Control	6.6	30864	Cytoplasmic	4	COG2084	Lipid metabolism	
26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	1.1	5.85E-01	Control	6.3	36692	Periplasmic	4	COG1613	Inorganic ion transport and metabolism	
26991006	PP_4315		PhzF family phenazine biosynthesis protein	3.6	1.68E-02	Control	4.5	28437	Cytoplasmic	7	COG0384	General function prediction only	
26991013	PP_4323	ccmE	cytochrome c-type biogenesis protein CcmE	15.5	4.76E-02	7,5 g/l BuOH	9.5	16115	Unknown	2	COG2332	Posttranslational modification, protein turnover, chaperones	
26991018	PP_4328		hypothetical protein	1.6	1.20E-01	Control	7.1	55477	Unknown	6			
26991022	PP_4332	cheW	purine-binding chemotaxis protein CheW	1.2	7.30E-01	7,5 g/l BuOH	4.1	17784	Cytoplasmic	2	COG0835	Cell motility and secretion	Signal transduction mechanisms
26991026	PP_4336	motC	flagellar motor protein	4.0	3.95E-02	Control	4.9	25930	Cytoplasmic Membrane	5	COG1291	Cell motility and secretion	
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	1.1	4.39E-01	Control	9.0	39451	Cytoplasmic	7	COG2201	Cell motility and secretion	Signal transduction mechanisms
26991028	PP_4338	cheA	chemotaxis protein CheA	4.9	4.20E-02	Control	4.4	79674	Cytoplasmic	24	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991029	PP_4339	cheZ	chemotaxis phosphatase, CheZ	1.0	9.56E-01	Control	4.8	29533	Cytoplasmic	18	COG3143	Cell motility and secretion	Signal transduction mechanisms
26991032	PP_4342	fleN	flagellar number regulator FleN	2.1	8.75E-02	Control	8.0	29670	Cytoplasmic Membrane	6	COG0455	Cell motility	
26991047	PP_4358	fliM	flagellar motor switch protein FliM	4.5	3.64E-02	Control	5.1	36011	Cytoplasmic	4	COG1868	Cell motility and secretion	
26991052	PP_4363		response regulator receiver protein	1.2	5.31E-01	Control	5.7	62118	Cytoplasmic	2	COG0745	Signal transduction mechanisms	Transcription
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.0	8.84E-01	Control	5.4	55551	Cytoplasmic	9	COG2204	Signal transduction mechanisms	
26991067	PP_4378	fliC	flagellin FliC	3.7	7.28E-02	Control	4.2	67846	Extracellular	18	COG1344	Cell motility and secretion	
26991068	PP_4379		beta-ketoacyl-acyl-carrier-protein synthase I	1.9	8.40E-02	Control	4.8	33207	Cytoplasmic	6	COG0332	acyl-carrier-protein	
26991074	PP_4385	flgG	flagellar basal body rod protein FlgG	3.1	2.98E-01	Control	4.1	27562	Extracellular	2	COG4786	Cell motility and secretion	
26991081	PP_4392	cheR	chemotaxis protein methyltransferase CheR	2.2	1.53E-01	Control	9.3	31084	Cytoplasmic	5	COG1352	Cell motility and secretion	Signal transduction mechanisms
26991082	PP_4393	cheV-3	chemotaxis protein CheV	2.7	8.26E-02	Control	6.2	34498	Cytoplasmic	14	COG0835	Cell motility and secretion	Signal transduction mechanisms
26991086	PP_4397		type IV pilus assembly PilZ	1.9	6.10E-02	Control	6.7	28449	Cytoplasmic	22	COG5581	Signal transduction mechanisms	
26991088	PP_4399		glutamine synthetase	1.3	3.53E-01	7,5 g/l BuOH	6.2	45023	Cytoplasmic	3	COG0174	Amino acid transport and metabolism	
26991116	PP_4428		amino acid ABC transporter periplasmic amino acid-binding protein	1.8	2.25E-01	Control	5.8	30355	Periplasmic	5	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991134	PP_4448		hypothetical protein	1.1	7.05E-02	Control	6.0	66331	Cytoplasmic	29	COG0433	Replication, recombination, and repair	
26991146	PP_4460		LysR family transcriptional regulator	3.4	2.69E-01	Control	###	34163	Cytoplasmic	2	COG0583	Transcription	
26991155	PP_4469	gmk-1	phosphonate metabolism protein/1,5-bisphosphokinase (PRPP-forming) PhnN	2.3	4.78E-02	7,5 g/l BuOH	9.7	21513	Cytoplasmic	4	COG3709	Inorganic ion transport and metabolism	
26991159	PP_4473		aspartate kinase	1.1	5.74E-01	Control	5.0	44605	Cytoplasmic	11	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.3	1.06E-01	7,5 g/l BuOH	5.1	94711	Cytoplasmic	36	COG0013	Translation, ribosomal structure and biogenesis	
26991161	PP_4475	astE	succinylglutamate desuccinylase	2.8	2.20E-02	Control	6.2	37580	Cytoplasmic	10	COG2988	Amino acid transport and metabolism	
26991163	PP_4477	astB	succinylarginine dihydrolase	1.5	2.65E-01	Control	6.4	48862	Cytoplasmic	3	COG3724	Amino acid transport and metabolism	
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.7	1.02E-01	Control	5.4	51330	Cytoplasmic	4	COG1012	Energy production and conversion	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	1.2	2.74E-02	7,5 g/l BuOH	6.5	43490	Cytoplasmic	18	COG4992	Amino acid transport and metabolism	
26991169	PP_4483		basic amino acid ABC transporter ATP-binding protein	1.1	4.99E-01	7,5 g/l BuOH	7.8	28000	Cytoplasmic Membrane	6	COG4598	Amino acid transport and metabolism	
26991172	PP_4486		cationic amino acid ABC transporter periplasmic protein	1.1	5.64E-01	Control	8.1	28302	Periplasmic	11	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991173	PP_4487	acsA	acetyl-CoA synthetase	44.7	1.31E-04	7,5 g/l BuOH	6.4	71796	Cytoplasmic	45	COG0365	Lipid metabolism	
26991184	PP_4499		SuaS/YciO/YrdC/YwlC family protein	5.6	2.57E-02	Control	5.6	24738	Cytoplasmic	3	COG0009	Translation, ribosomal structure and biogenesis	
26991191	PP_4506		nitroreductase	1.6	3.41E-01	7,5 g/l BuOH	6.6	19994	Unknown	4	COG0778	Energy production and conversion	
26991202	PP_4517		hypothetical protein	1.1	7.29E-01	Control	3.8	21967	Cytoplasmic	4	COG1318	General function prediction only	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.5	3.94E-01	7,5 g/l BuOH	5.4	50393	Outer Membrane	27	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	2.1	2.26E-03	Control	6.4	56605	Cytoplasmic Membrane	21	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.7	1.38E-01	Control	###	48478	Cytoplasmic	5	COG0513	DNA replication, recombination, and repair	Transcription
26991223	PP_4539		LysR family transcriptional regulator	1.8	2.21E-01	Control	7.1	33901	Cytoplasmic	4	COG0583	Transcription	
26991224	PP_4540		alpha/beta fold family hydrolase	4.0	2.50E-03	Control	7.4	30640	Cytoplasmic	3	COG0596	General function prediction only	
26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.5	1.38E-01	Control	5.7	42326	Cytoplasmic	14	COG0332	acyl-carrier-protein	
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	1.7	1.69E-01	Control	8.3	146950	Cytoplasmic	9	COG1643	DNA replication, recombination, and repair	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	3.3	5.96E-03	Control	7.7	61812	Cytoplasmic	7	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	1.4	3.65E-01	Control	7.8	61658	Cytoplasmic	14	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991235	PP_4551		alpha/beta fold family hydrolase	1.0	7.92E-01	Control	7.3	34587	Cytoplasmic	2	COG2267	Lipid metabolism	
26991249	PP_4565	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	2.9	7.54E-02	Control	5.3	65954	Cytoplasmic	3	COG4579	Signal transduction mechanisms	
26991254	PP_4570		hypothetical protein	1.8	1.82E-01	Control	###	35846	Cytoplasmic Membrane	2	COG3555	Posttranslational modification, protein turnover, chaperones	
26991255	PP_4571	cysK	cysteine synthase A	1.5	9.05E-02	Control	5.5	34357	Cytoplasmic	12	COG0031	Amino acid transport and metabolism	
26991257	PP_4573		ATPase AAA	1.2	3.64E-01	7,5 g/l BuOH	5.8	32146	Cytoplasmic	15	COG0714	General function prediction only	
26991261	PP_4577		LamB/YcsF family protein	1.1	8.18E-01	Control	5.8	27871	Cytoplasmic	5	COG1540	General function prediction only	
26991265	PP_4581		hypothetical protein	2.2	6.58E-02	Control	6.2	28647	Cytoplasmic	4	COG0121	General function prediction only	
26991267	PP_4583		oligopeptidase B	1.0	6.57E-01	Control	4.7	75818	Unknown	2	COG1770	Amino acid transport and metabolism	
26991272	PP_4588		nitroreductase	1.6	1.46E-01	Control	6.0	21997	Unknown	10	COG0778	Energy production and conversion	
26991275	PP_4591	rnd	ribonuclease D	1.7	3.50E-02	7,5 g/l BuOH	5.5	42668	Cytoplasmic	2	COG0349	Translation, ribosomal structure and biogenesis	
26991286	PP_4602		AraC family transcriptional regulator	1.1	2.09E-01	Control	8.9	31224	Cytoplasmic	4	COG2207	Transcription	
26991303	PP_4619		maleylacetoacetate isomerase	3.8	1.23E-01	Control	6.2	22876	Cytoplasmic	2	COG0625	Posttranslational modification, protein turnover, chaperones	
26991316	PP_4632		short chain dehydrogenase	1.4	2.18E-01	7,5 g/l BuOH	7.8	26619	Cytoplasmic	4	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26991319	PP_4635		trans-2-enoyl-CoA reductase	1.2	3.96E-01	Control	5.0	44265	Cytoplasmic	20	COG3007	Function unknown	
26991325	PP_4641	cstA	carbon starvation protein CstA	1.9	1.45E-01	Control	9.0	73763	Cytoplasmic Membrane	9	COG1966	Signal transduction mechanisms	
26991330	PP_4646		oxidoreductase FAD/NAD(P)-binding domain protein	1.7	7.24E-02	Control	5.2	28960	Cytoplasmic	7	COG1018	Energy production and conversion	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	2.6	1.09E-01	Control	9.1	53016	Cytoplasmic Membrane	5	COG1271	Energy production and conversion	
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	1.1	8.81E-01	Control	9.4	26835	Cytoplasmic	3	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26991341	PP_4657		metallopeptidase, zinc binding	2.7	7.17E-02	Control	6.7	34400	Unknown	7	COG2321	General function prediction only	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.1	7.41E-01	Control	4.8	68764	Unknown	13	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991343	PP_4659	ggt-2	gamma-glutamyltransferase	1.5	1.82E-01	7,5 g/l BuOH	6.0	59835	Periplasmic	13	COG0405	Amino acid transport and metabolism	

26991350	PP 4666	mmsB	3-hydroxyisobutyrate dehydrogenase		1.6	1.49E-02	Control	6.1	30321	Cytoplasmic	8	COG2084	Lipid metabolism	
26991351	PP 4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase		1.7	6.59E-02	Control	6.0	54367	Cytoplasmic	9	COG1012	Energy production and conversion	
26991358	PP 4674	recC	exodeoxyribonuclease V, gamma subunit		3.1	1.12E-01	Control	5.3	130394	Unknown	2	COG1330	DNA replication, recombination, and repair	
26991361	PP 4677	pssA-2	CDP-diacylglycerol--serine O-phosphatidyltransferase		2.5	9.99E-02	Control	9.2	30359	Cytoplasmic Membrane	3	COG1183	Lipid metabolism	
26991362	PP 4678	ilvC	ketol-acid reductoisomerase		1.1	6.48E-01	Control	5.4	36370	Cytoplasmic	28	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP 4680	ilvB	acetolactate synthase 3 catalytic subunit		1.0	8.41E-01	7,5 g/l BuOH	6.8	62781	Cytoplasmic	30	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26991366	PP 4682		hypothetical protein		1.8	4.02E-01	Control	8.2	27215	Unknown	5	COG4783	General function prediction only	
26991367	PP 4683	mrcB	penicillin-binding protein 1B		97.6	3.45E-02	7,5 g/l BuOH	9.5	85156	Cytoplasmic Membrane	2	COG0744	Cell envelope biogenesis, outer membrane	
26991368	PP 4684		hypothetical protein		2.0	1.10E-02	Control	5.1	56095	Cytoplasmic	9	COG2187	Function unknown	
26991373	PP 4689		periplasmic protein		1.8	2.94E-01	Control	7.1	30685	Periplasmic	7	COG4558	Inorganic ion transport and metabolism	
26991380	PP 4696		two component, sigma54 specific, transcriptional regulator, Fis family		3.5	1.04E-01	Control	5.3	52585	Cytoplasmic	2	COG2204	Signal transduction mechanisms	
26991381	PP 4697	pcnB	poly(A) polymerase		2.4	1.65E-01	Control	9.6	52721	Cytoplasmic	3	COG0617	Translation, ribosomal structure and biogenesis	
26991383	PP 4699	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase		3.5	2.60E-02	Control	5.8	27762	Unknown	4	COG0413	Coenzyme metabolism	
26991384	PP 4700	panC	pantoate--beta-alanine ligase		3.8	2.14E-03	Control	7.7	31189	Cytoplasmic	7	COG0414	Coenzyme metabolism	
26991385	PP 4701	pgi	glucose-6-phosphate isomerase		1.3	2.94E-01	Control	6.8	61455	Cytoplasmic	16	COG0166	Carbohydrate transport and metabolism	
26991386	PP 4702	acsB	acetyl-CoA synthetase		2.8	7.88E-02	Control	6.5	71251	Cytoplasmic	12	COG0365	Lipid metabolism	
26991388	PP 4704		hypothetical protein		2.7	1.48E-02	Control	5.6	107252	Outer Membrane	20	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP 4708	pnp	polynucleotide phosphorylase/polyadenylase		1.1	6.38E-01	7,5 g/l BuOH	4.9	75010	Cytoplasmic	31	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP 4712	infB	translation initiation factor IF-2		1.9	4.87E-02	Control	6.8	91460	Cytoplasmic	34	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP 4713	nusA	transcription elongation factor NusA		1.7	2.86E-02	7,5 g/l BuOH	4.3	54673	Cytoplasmic	22	COG0195	Transcription	
26991398	PP 4715	tpiA	triosephosphate isomerase		1.3	3.99E-01	7,5 g/l BuOH	4.7	25991	Cytoplasmic	9	COG0149	Carbohydrate transport and metabolism	
26991400	PP 4717	folP	dihydropteroate synthase		2.5	2.20E-02	Control	5.4	30274	Cytoplasmic	2	COG0294	Coenzyme metabolism	
26991401	PP 4718	ftsH	ATP-dependent metalloprotease FtsH		1.9	1.46E-02	7,5 g/l BuOH	5.4	69722	Cytoplasmic Membrane	15	COG0465	Posttranslational modification, protein turnover, chaperones	
26991402	PP 4719	rrmJ	ribosomal RNA methyltransferase RrmJ/FtsJ		1.5	6.96E-01	Control	8.5	23164	Cytoplasmic	2	COG0293	Translation, ribosomal structure and biogenesis	
26991407	PP 4724	carA	carbamoyl phosphate synthase small subunit		1.6	5.90E-02	7,5 g/l BuOH	5.8	40574	Cytoplasmic	8	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
26991408	PP 4725	dapB	dihydrodipicolinate reductase		1.8	1.92E-01	Control	5.9	28423	Cytoplasmic	7	COG0289	Amino acid transport and metabolism	
26991409	PP 4726	dnaJ	chaperone protein DnaJ		1.9	2.54E-01	Control	6.7	40181	Cytoplasmic	5	COG0484	Posttranslational modification, protein turnover, chaperones	
26991410	PP 4727	dnaK	molecular chaperone DnaK		1.6	2.85E-01	7,5 g/l BuOH	4.6	68800	Cytoplasmic	51	COG0443	Posttranslational modification, protein turnover, chaperones	
26991411	PP 4728	grpE	heat shock protein GrpE		1.4	1.90E-01	Control	4.7	20531	Cytoplasmic	7	COG0576	Posttranslational modification, protein turnover, chaperones	
26991414	PP 4731	omlA	SmpA/OmlA domain protein		3.0	4.82E-01	7,5 g/l BuOH	4.4	19586	Outer Membrane	6	COG2913	Cell envelope biogenesis, outer membrane	
26991423	PP 4740	hsdR	type I restriction-modification system, R subunit		1.7	2.46E-02	Control	5.2	89615	Cytoplasmic	11	COG4096	Defense mechanisms	
26991429	PP 4748		amino acid ABC transporter periplasmic amino acid-binding protein		1.0	9.47E-01	7,5 g/l BuOH	5.4	28338	Unknown	4	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991434	PP 4753		N-methylproline demethylase		1.5	5.88E-01	7,5 g/l BuOH	6.5	75215	Cytoplasmic	11	COG1902	Energy production and conversion	
26991441	PP 4760		alcohol dehydrogenase, zinc-containing		2.5	1.10E-01	Control	6.2	35615	Cytoplasmic Membrane	6	COG0604	Energy production and conversion	General function prediction only
26991443	PP 4762	tesB	acyl-CoA thioesterase II		1.4	1.13E-01	Control	6.1	32319	Cytoplasmic	6	COG1946	Lipid metabolism	
161378119	PP 4779		AMP nucleosidase		4.8	2.29E-02	Control	6.8	54498	Cytoplasmic	7	COG0775	Nucleotide transport and metabolism	
26991460	PP 4780		acyl-CoA dehydrogenase domain-containing protein		3.8	2.78E-04	Control	6.6	59803	Cytoplasmic	5	COG1960	Lipid metabolism	
26991462	PP 4782	thiD	phosphomethylpyrimidine kinase		2.2	9.16E-02	7,5 g/l BuOH	5.1	28338	Cytoplasmic	5	COG0351	Coenzyme metabolism	
26991463	PP 4783	thiE	thiamine-phosphate pyrophosphorylase		1.2	2.73E-01	Control	7.6	21702	Unknown	3	COG0352	Coenzyme metabolism	
26991464	PP 4784	hemL	glutamate-1-semialdehyde aminotransferase		2.0	1.04E-01	Control	5.7	45178	Cytoplasmic	8	COG0001	Coenzyme metabolism	
26991469	PP 4789		CBS domain containing protein		1.5	4.04E-01	7,5 g/l BuOH	4.7	31393	Cytoplasmic Membrane	5	COG4535	Inorganic ion transport and metabolism	
26991474	PP 4794	leuS	leucyl-tRNA synthetase		1.2	6.37E-02	7,5 g/l BuOH	5.6	96697	Cytoplasmic	28	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP 4795		rare lipoprotein B		2.2	3.98E-02	7,5 g/l BuOH	6.1	22414	Unknown	12	COG2980	Cell envelope biogenesis, outer membrane	
26991478	PP 4798		lytic murein transglycosylase		3.2	1.04E-02	7,5 g/l BuOH	7.7	48000	Cytoplasmic Membrane	9	COG2951	Cell envelope biogenesis, outer membrane	
26991481	PP 4801	lipB	lipoate-protein ligase B		1.1	8.55E-01	7,5 g/l BuOH	6.0	23689	Cytoplasmic	3	COG0321	Coenzyme metabolism	
26991483	PP 4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase		1.2	2.06E-01	7,5 g/l BuOH	6.6	42288	Cytoplasmic Membrane	9	COG1686	Cell envelope biogenesis, outer membrane	
26991490	PP 4810	nadD	nicotinic acid mononucleotide adenylyltransferase		1.2	9.75E-01	7,5 g/l BuOH	5.6	25291	Cytoplasmic	2	COG1057	Coenzyme metabolism	
26991491	PP 4811	proA	gamma-glutamyl phosphate reductase		1.2	3.36E-01	Control	6.1	45417	Cytoplasmic	11	COG0014	Amino acid transport and metabolism	
26991494	PP 4814		ATP-dependent protease La		1.0	8.99E-01	7,5 g/l BuOH	4.1	21846	Cytoplasmic	4	COG2802	General function prediction only	
26991502	PP 4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase		1.7	2.22E-01	Control	6.5	57695	Cytoplasmic	19	COG0138	Nucleotide transport and metabolism	
26991503	PP 4823	purD	phosphoribosylamine--glycine ligase		1.1	4.57E-01	7,5 g/l BuOH	4.7	45837	Cytoplasmic	7	COG0151	Nucleotide transport and metabolism	
26991504	PP 4824		integral membrane sensor hybrid histidine kinase		1.6	1.11E-01	Control	6.6	101587	Cytoplasmic Membrane	3	COG0642	Signal transduction mechanisms	
26991514	PP 4834		SPFH domain-containing protein/band 7 family protein		2.7	8.35E-03	Control	5.0	31015	Cytoplasmic	2	COG0330	Posttranslational modification, protein turnover, chaperones	
26991518	PP 4838	oprC	TonB-dependent copper receptor	Infinity		3.74E-01	7,5 g/l BuOH	6.2	74540	Outer Membrane	2	COG1629	Inorganic ion transport and metabolism	
26991528	PP 4848		DnaJ family curved-DNA-binding protein		1.5	3.34E-02	Control	9.8	34808	Cytoplasmic	15	COG0484	Posttranslational modification, protein turnover, chaperones	
26991536	PP 4856		bacterioferritin		107.3	2.15E-02	7,5 g/l BuOH	4.7	19202	Cytoplasmic	5	COG2193	Inorganic ion transport and metabolism	
26991542	PP 4862		short chain dehydrogenase/reductase family oxidoreductase		2.0	1.14E-01	Control	6.3	27400	Cytoplasmic	6	COG4221	General function prediction only	
26991543	PP 4863		branched chain amino acid ABC transporter ATP-binding protein		1.8	5.38E-02	Control	9.3	26312	Unknown	9	COG0410	Amino acid transport and metabolism	
26991544	PP 4864		branched chain amino acid ABC transporter ATP-binding protein		3.2	6.19E-02	Control	6.6	32427	Cytoplasmic Membrane	4	COG0411	Amino acid transport and metabolism	
26991547	PP 4867		extracellular ligand-binding receptor		1.2	1.53E-01	7,5 g/l BuOH	6.2	40270	Periplasmic	26	COG0683	Amino acid transport and metabolism	
26991549	PP 4869	nadE	NAD synthetase		1.8	1.71E-02	Control	5.6	29273	Cytoplasmic	12	COG0171	Coenzyme metabolism	
26991550	PP 4870		azurin		51.9	2.42E-03	7,5 g/l BuOH	6.9	16028	Periplasmic	7	COG3241	Energy production and conversion	
26991553	PP 4873	dnaB	replicative DNA helicase		1.8	6.65E-02	Control	4.7	51581	Cytoplasmic	4	COG0305	DNA replication, recombination, and repair	
26991557	PP 4877	rpsF	30S ribosomal protein S6		5.7	7.22E-02	7,5 g/l BuOH	4.7	16373	Cytoplasmic	3	COG0360	Translation, ribosomal structure and biogenesis	
26991558	PP 4879		RNA methyltransferase		1.7	1.70E-01	Control	6.8	27014	Cytoplasmic	8	COG0566	Translation, ribosomal structure and biogenesis	
26991559	PP 4880	vacB	ribonuclease R		1.8	9.01E-02	Control	7.9	96688	Cytoplasmic	21	COG0557	Transcription	
26991560	PP 4881		iron ABC transporter periplasmic iron-binding protein		2.4	8.99E-02	Control	5.0	36800	Periplasmic	8	COG1840	Inorganic ion transport and metabolism	
26991566	PP 4888		methyl-accepting chemotaxis sensory transducer		1.2	4.27E-01	Control	6.1	71958	Cytoplasmic Membrane	15	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP 4889	purA	adenylosuccinate synthetase		1.1	3.38E-01	Control	5.6	46833	Cytoplasmic	19	COG0104	Nucleotide transport and metabolism	
26991568	PP 4890	hisZ	ATP phosphoribosyltransferase regulatory subunit		1.8	2.22E-01	Control	4.7	42935	Cytoplasmic	3	COG3705	Amino acid transport and metabolism	
26991569	PP 4891	hflC	HflC protein		2.1	4.15E-02	Control	9.8	33001	Cytoplasmic	17	COG0330	Posttranslational modification, protein turnover, chaperones	
26991572	PP 4894	hfq	RNA-binding protein Hfq		114.4	1.76E-02	7,5 g/l BuOH	9.0	9462	Cytoplasmic	3	COG1923	General function prediction only	
26991580	PP 4902	orn	oligoribonuclease		1.5	4.21E-01	Control	5.8	20787	Cytoplasmic	3	COG1949	RNA processing and modification	
26991582	PP 4904	motB	flagellar motor protein MotB		1.2	7.92E-01	7,5 g/l BuOH	4.8	37802	Cytoplasmic Membrane	4	COG1360	Cell motility and secretion	
26991583	PP 4905		flagellar motor protein MotA		4.8	3.08E-02	Control	6.2	30312	Cytoplasmic Membrane	3	COG1291	Cell motility and secretion	
26991585	PP 4907	rhdA-2	rhodanese domain protein		1.2	5.67E-01	7,5 g/l BuOH	6.1	29517	Cytoplasmic	12	COG2897	Inorganic ion transport and metabolism	
26991586	PP 4908	psd	phosphatidylserine decarboxylase		1.7	2.22E-01	Control	8.6	31547	Cytoplasmic Membrane	5	COG0688	Lipid metabolism	
26991589	PP 4911		hypothetical protein		1.4	2.05E-02	7,5 g/l BuOH	8.5	27337	Periplasmic	5	COG3009	Function unknown	
26991590	PP 4912	parC	DNA topoisomerase IV subunit A		1.5	2.86E-01	Control	6.2	83181	Cytoplasmic	3	COG0188	DNA replication, recombination, and repair	
26991594	PP 4916		hypothetical protein		2.3	2.34E-01	Control	9.0	27390	Unknown	2	COG3150	General function prediction only	
26991597	PP 4919		NUDIX hydrolase		1.7	7.48E-02	Control	4.7	23607	Cytoplasmic	8			
26991600	PP 4922	thiC	thiamine biosynthesis protein ThiC		1.5	1.82E-01	7,5 g/l BuOH	5.7	69727	Cytoplasmic	10	COG0422	Coenzyme metabolism	
26991601	PP 4923		TolC family type I secretion outer membrane protein		3.6	2.08E-02	Control	5.2	52637	Outer Membrane	12	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991609	PP 4931		FAD dependent oxidoreductase		2.3	5.12E-02	Control	7.2	42015	Cytoplasmic	7	COG0578	Energy production and conversion	
26991610	PP 4932		aldo/keto reductase		2.9	1.62E-02	Control	6.4	29123	Cytoplasmic	2	COG0667	Energy production and conversion	
26991611	PP 4933		hypothetical protein		2.7	8.37E-02	Control	###	37000	Unknown	2			
26991612	PP 4934		bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenyltransferase		1.8	3.83E-02	Control	5.8	49970	Cytoplasmic	8	COG2870	Cell envelope biogenesis, outer membrane	
26991613	PP 4935		lipid ABC transporter ATPase/inner membrane protein		3.2	5.26E-02	Control	7.6	66279	Cytoplasmic Membrane	4	COG1132	Defense mechanisms	
26991615	PP 4937		toluene tolerance protein		2.6	6.54E-01	Control	###	25956	Cytoplasmic	4			
26991616	PP 4938		glycosyl transferase		1.4	4.72E-01	7,5 g/l BuOH	9.4	41783	Cytoplasmic	2	COG0438	Cell envelope biogenesis, outer membrane	
26991617	PP 4939		hypothetical protein		2.0	1.83E-01	Control	7.1	28978	Cytoplasmic	5			
26991622	PP 4944		carbamoyltransferase		1.2	7.61E-01	7,5 g/l BuOH	7.2	65646	Cytoplasmic	14	COG2192	Posttranslational modification, protein turnover, chaperones	
26991625	PP 4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase		2.5	1.56E-02	Control	6.3	142580	Cytoplasmic	33	COG4230	Energy production and conversion	
26991627	PP 4949		TldD/PmbA family protein		1.0	8.43E-01	7,5 g/l BuOH	6.6	55611	Unknown	3	COG0312	General function prediction only	
26991628	PP 4950		hypothetical protein		1.3	5.54E-01	Control	4.9	47741	Unknown	3	COG0312	General function prediction only	
26991637	PP 4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)		4.1	5.19E-02	Control	4.8	78896	Cytoplasmic Membrane	14	COG5001	Signal transduction mechanisms	
26991638	PP 4960	fda	fructose-1,6-bisphosphate aldolase		1.3	1.50E-01	7,5 g/l BuOH	5.6	38453	Cytoplasmic	22	COG0191	Carbohydrate transport and metabolism	
26991641	PP 4963	pgk	phosphoglycerate kinase		1.7	5.62E-02	7,5 g/l BuOH	4.9	40005	Cytoplasmic	18	COG0126	Carbohydrate transport and metabolism	
26991642	PP 4964	epd	D-erythrose-4-phosphate dehydrogenase		1.4	9.82E-02	7,5 g/l BuOH	6.4	38482	Cytoplasmic	2	COG0057	Carbohydrate transport and metabolism	
26991643	PP 4965	tktA	transketolase		1.1	9.05E-01	7,5 g/l BuOH	5.0	72463	Cytoplasmic	29	COG0021	Carbohydrate transport and metabolism	
26991644	PP 4966		ArsR family transcriptional regulator		1.6	3.61E-02	Control	6.4	36148	Cytoplasmic	6	COG2226	Coenzyme metabolism	
26991645	PP 4967	metK	S-adenosylmethionine synthetase		2.0	1.45E-02	Control	5.1	42779	Cytoplasmic	19	COG0192	Coenzyme metabolism	
26991654	PP 4977	metF	5,10-methylenetetrahydrofolate reductase		1.8	1.09E-01	Control	6.2	32979	Cytoplasmic	17	COG0685	Amino acid transport and metabolism	
26991657	PP 4980		DEAD-box ATP dependent DNA helicase		1.2	7.56E-01	7,5 g/l BuOH	###	68073	Cytoplasmic	12	COG0513	DNA replication, recombination, and repair	Transcription
26991658	PP 4981		hypothetical protein		1.7	4.09E-01	Control	8.8	22129	Unknown	10	COG2353	Function unknown	
26991661	PP 4984	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase		1.0	7.16E-01	Control	6.1	52453	Cytoplasmic	2	COG0161	Coenzyme metabolism	
26991665	PP 4988		chemotaxis protein CheA		1.5	1.28E-01	Control	4.7	180005	Unknown	5	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991666	PP 4989	pilJ	methyl-accepting chemotaxis sensory transducer		3.1	1.35E-01	7,5 g/l BuOH	4.6	73623	Outer Membrane	3	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991670	PP 4993	gshB	glutathione synthetase		1.1	6.90E-01	Control	5.1	35254	Cytoplasmic	4	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26991675	PP 4998	pyrB	aspartate carbamoyltransferase catalytic subunit		2.1	1.85E-01	Control	7.1	36344	Cytoplasmic	8	COG0540	Nucleotide transport and metabolism	
26991676	PP 4999	pyrC	dihydroorotase		1.6	2.78E-01	7,5 g/l BuOH	5.4	44116	Cytoplasmic	8	COG0044	Nucleotide transport and metabolism	
26991678	PP 5001	hslU	ATP-dependent protease ATP-binding subunit HslU		1.2	9.43E-01	7,5 g/l BuOH	5.7	49982	Cytoplasmic	16	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP 5003	phaA	poly(3-hydroxyalkanoate) polymerase 1		3.9	7.58E-03	Control	7.4	62241	Cytoplasmic	23	COG3243	Lipid metabolism	
26991682	PP 5005	phaC	poly(3-hydroxyalkanoate) polymerase 2		2.5	6.63E-02	Control	9.6	62722	Cytoplasmic	7	COG3243	Lipid metabolism	

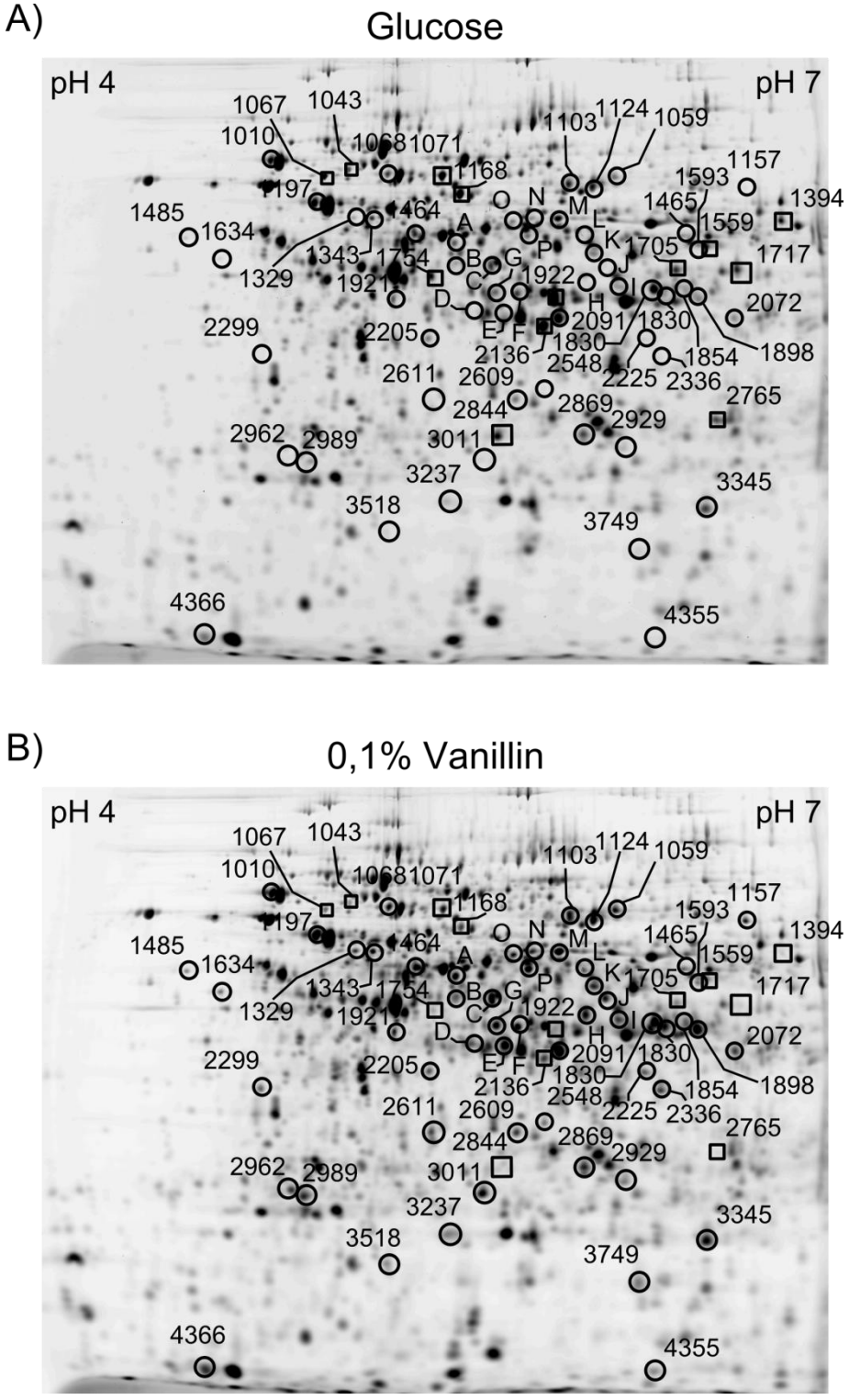
26991683	PP_5006		TetR family transcriptional regulator	1.5	7.80E-01	Control	5.3	23055	Cytoplasmic	5	COG1309	Transcription		
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	2.3	1.50E-02	Control	###	26214	Cytoplasmic	17	COG3937	Function unknown		
26991688	PP_5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.4	1.49E-01	Control	9.5	28397	Cytoplasmic	9	COG2226	Coenzyme metabolism		
26991689	PP_5012		hypothetical protein	1.9	1.90E-01	Control	5.4	22983	Unknown	4	COG3165	Function unknown		
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.1	7.85E-01	7,5 g/l BuOH	4.9	69017	Cytoplasmic Membrane	30	COG0840	Cell motility and secretion		Signal transduction mechanisms
26991698	PP_5022		amino acid ABC transporter ATP-binding protein	2.0	3.74E-01	Control	7.6	27004	Cytoplasmic Membrane	3	COG1126	Amino acid transport and metabolism		
26991700	PP_5024		amino acid ABC transporter periplasmic amino acid-binding protein	1.2	2.66E-01	Control	8.6	29848	Periplasmic	16	COG0834	Amino acid transport and metabolism		Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.4	6.57E-01	7,5 g/l BuOH	8.3	95875	Cytoplasmic Membrane	3	COG2943	Cell envelope biogenesis, outer membrane		
26991702	PP_5026	mdoG	glucan biosynthesis protein G	1.1	7.75E-01	7,5 g/l BuOH	6.5	62340	Periplasmic	9	COG3133	Inorganic ion transport and metabolism		
26991704	PP_5028	pip	proline iminopeptidase	1.4	2.25E-01	Control	6.2	36589	Cytoplasmic	16	COG0596	General function prediction only		
26991715	PP_5039		hypothetical protein	1.5	8.66E-01	Control	4.8	23220	Unknown	2	COG3803	Function unknown		
26991716	PP_5040	fbp	fructose-1,6-bisphosphatase	1.0	8.35E-01	Control	5.9	37246	Cytoplasmic	12	COG0158	Carbohydrate transport and metabolism		
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	1.8	1.09E-01	Control	6.4	92004	Cytoplasmic	19	COG0058	Carbohydrate transport and metabolism		
26991720	PP_5044		GTP-binding protein TypA	1.1	4.40E-02	7,5 g/l BuOH	5.3	67157	Cytoplasmic Membrane	17	COG1217	Signal transduction mechanisms		
26991722	PP_5046	glnA	glutamine synthetase, type I	1.0	8.12E-01	Control	5.1	51740	Cytoplasmic	23	COG0174	Amino acid transport and metabolism		
26991724	PP_5048	ntrC	nitrogen metabolism transcriptional regulator NtrC	1.9	1.89E-02	Control	6.0	53114	Cytoplasmic	3	COG2204	Signal transduction mechanisms		
26991732	PP_5056	pgm	phosphoglyceromutase	1.5	1.92E-03	Control	4.9	55180	Cytoplasmic	12	COG0696	Carbohydrate transport and metabolism		
26991734	PP_5058		carboxyl-terminal protease	2.1	7.17E-02	Control	5.6	46333	Cytoplasmic Membrane	10	COG0793	Cell envelope biogenesis, outer membrane		
26991739	PP_5063	betB	betaine aldehyde dehydrogenase	1.8	4.05E-01	7,5 g/l BuOH	4.8	52986	Cytoplasmic	6	COG1012	Energy production and conversion		
26991746	PP_5070		ParA family protein	1.6	4.16E-02	Control	4.7	28660	Cytoplasmic	4	COG1192	Cell division and chromosome partitioning		
26991750	PP_5074	hemE	uroporphyrinogen decarboxylase	1.7	1.93E-02	7,5 g/l BuOH	6.7	38883	Cytoplasmic	5	COG0407	Coenzyme metabolism		
26991751	PP_5075	gltD	glutamate synthase subunit beta	1.2	1.00E+00	7,5 g/l BuOH	6.3	51819	Cytoplasmic	8	COG0493	Amino acid transport and metabolism		General function prediction only
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.7	4.99E-02	Control	6.2	161772	Cytoplasmic	40	COG0069	Amino acid transport and metabolism		
26991753	PP_5077		sporulation domain protein	1.5	2.93E-01	7,5 g/l BuOH	7.1	55434	Unknown	8	COG3267	Intracellular trafficking and secretion		
26991754	PP_5078	aroB	3-dehydroquinate synthase	1.0	9.06E-01	7,5 g/l BuOH	6.0	39485	Cytoplasmic	6	COG0337	Amino acid transport and metabolism		
26991761	PP_5085	maeB	malic enzyme	1.1	2.96E-01	7,5 g/l BuOH	4.9	45127	Cytoplasmic	29	COG0281	Energy production and conversion		
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.0	9.93E-01	7,5 g/l BuOH	5.7	63668	Cytoplasmic	19	COG0018	Translation, ribosomal structure and biogenesis		
26991770	PP_5094		alanine racemase domain protein	1.2	9.24E-01	7,5 g/l BuOH	6.8	24192	Cytoplasmic	10	COG0325	General function prediction only		
26991771	PP_5095	proC-2	pyrroline-5-carboxylate reductase	1.6	1.17E-01	Control	4.7	28258	Cytoplasmic	10	COG0345	Amino acid transport and metabolism		
26991774	PP_5098	metW	methionine biosynthesis protein MetW	1.3	2.31E-02	Control	5.6	24002	Cytoplasmic	4	COG2226	Coenzyme metabolism		
26991779	PP_5103	trmB	tRNA (guanine-N(7)-)-methyltransferase	1.4	6.62E-01	7,5 g/l BuOH	7.3	27203	Cytoplasmic	3	COG0220	General function prediction only		
26991780	PP_5104	thiG	thiazole synthase	1.5	2.64E-01	7,5 g/l BuOH	5.8	28917	Cytoplasmic	9	COG2022	Nucleotide transport and metabolism		
26991786	PP_5110	ftsE	cell division ATP-binding protein FtsE	1.2	4.43E-01	Control	###	24830	Cytoplasmic Membrane	4	COG2884	Cell division and chromosome partitioning		
26991787	PP_5111	ftsY	signal recognition particle-docking protein FtsY	2.8	6.54E-01	7,5 g/l BuOH	4.9	51680	Cytoplasmic	5	COG0552	Intracellular trafficking and secretion		
26991788	PP_5112		peptidase M16 domain protein	1.6	2.94E-01	7,5 g/l BuOH	5.9	50095	Periplasmic	2	COG0612	General function prediction only		
26991789	PP_5113		peptidase M16 domain protein	1.3	2.65E-02	Control	8.0	52389	Unknown	3	COG0612	General function prediction only		
26991790	PP_5114		hypothetical protein	1.5	5.87E-02	7,5 g/l BuOH	8.2	22311	Unknown	4	COG0742	DNA replication, recombination, and repair		
26991794	PP_5118		rhodanese domain protein	1.2	1.86E-01	7,5 g/l BuOH	5.6	30750	Cytoplasmic	11	COG2897	Inorganic ion transport and metabolism		
26991796	PP_5120		conifer aldehyde dehydrogenase	2.2	1.74E-02	Control	9.2	52453	Cytoplasmic	7	COG1012	Energy production and conversion		
26991802	PP_5126		signal transduction protein	4.1	4.83E-02	7,5 g/l BuOH	5.6	28452	Unknown	3	COG1639	Signal transduction mechanisms		
26991803	PP_5127		hypothetical protein	1.3	4.95E-01	7,5 g/l BuOH	6.9	44126	Cytoplasmic	3	COG1092	General function prediction only		
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.8	8.51E-04	7,5 g/l BuOH	5.8	65671	Cytoplasmic	28	COG0129	Amino acid transport and metabolism		Carbohydrate transport and metabolism
26991820	PP_5144		hypothetical protein	1.0	7.69E-01	Control	5.3	26452	Unknown	4	COG3332	Function unknown		
26991821	PP_5145	ptsP	PTSNtr with GAF domain, PtsP	1.0	8.18E-01	Control	5.3	83337	Cytoplasmic	19	COG3605	Signal transduction mechanisms		
26991823	PP_5147		HAD superfamily hydrolase	1.3	3.37E-01	Control	4.7	24940	Cytoplasmic	2	COG0560	Amino acid transport and metabolism		
26991826	PP_5150	rpiA	ribose-5-phosphate isomerase A	1.1	8.68E-01	Control	4.9	23496	Unknown	7	COG0120	Carbohydrate transport and metabolism		
26991829	PP_5153		fumarylacetoacetate (FAA) hydrolase	2.2	1.59E-01	Control	4.7	23906	Cytoplasmic	4	COG0179	Secondary metabolites biosynthesis, transport, and catabolism		
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.1	4.78E-01	7,5 g/l BuOH	6.3	44339	Cytoplasmic	19	COG0111	Amino acid transport and metabolism		
26991836	PP_5160		hypothetical protein	1.0	7.78E-01	Control	8.9	27008	Cytoplasmic Membrane	5				
26991841	PP_5165		NLPA lipoprotein	3.6	1.05E-01	7,5 g/l BuOH	8.7	28159	Unknown	2	COG1464	Inorganic ion transport and metabolism		
26991849	PP_5173		acriflavin resistance protein	1.8	2.77E-03	Control	5.4	112277	Cytoplasmic Membrane	16	COG0841	Defense mechanisms		
26991850	PP_5174		RND efflux transporter	1.8	8.18E-02	Control	5.5	38032	Cytoplasmic Membrane	5	COG0845	Cell envelope biogenesis, outer membrane		
26991851	PP_5175		efflux transporter RND family, MFP subunit	3.2	1.21E-01	Control	6.5	38304	Cytoplasmic Membrane	6	COG0845	Cell envelope biogenesis, outer membrane		
26991853	PP_5177	potI	ornithine carbamoyltransferase	49.2	5.95E-02	Control	###	32247	Cytoplasmic Membrane	2	COG1177	Amino acid transport and metabolism		
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	2.4	7.76E-02	Control	6.5	42472	Cytoplasmic Membrane	8	COG3842	Amino acid transport and metabolism		
26991856	PP_5180	potF-1	putrescine ABC transporter periplasmic putrescine-binding protein	1.1	7.77E-01	7,5 g/l BuOH	8.0	39788	Periplasmic	10	COG0687	Amino acid transport and metabolism		
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.2	5.84E-01	7,5 g/l BuOH	6.4	40068	Periplasmic	24	COG0687	Amino acid transport and metabolism		
26991858	PP_5182		aminotransferase	1.1	2.71E-01	7,5 g/l BuOH	6.2	49871	Cytoplasmic	9	COG0161	Coenzyme metabolism		
26991859	PP_5183		glutamine synthetase	1.4	5.36E-02	Control	4.8	50877	Cytoplasmic	12	COG0174	Amino acid transport and metabolism		
26991860	PP_5184		glutamine synthetase	2.4	2.06E-02	Control	4.5	50974	Cytoplasmic	8	COG0174	Amino acid transport and metabolism		
26991861	PP_5185	argA	N-acetylglutamate synthase	1.7	2.02E-01	Control	5.9	47440	Cytoplasmic	2	COG0548	Amino acid transport and metabolism		
26991862	PP_5186	argE	acetylornithine deacetylase	1.6	3.89E-01	7,5 g/l BuOH	4.9	41425	Cytoplasmic	2	COG0624	Amino acid transport and metabolism		
26991863	PP_5187		adenylate cyclase	1.3	1.51E-01	7,5 g/l BuOH	5.6	52133	Cytoplasmic	7	COG3025	Function unknown		
26991868	PP_5192	gcvP-2	glycine dehydrogenase	1.3	4.36E-01	Control	6.3	104037	Cytoplasmic	14	COG1003	Amino acid transport and metabolism		
26991870	PP_5194	gcvT	glycine cleavage system aminomethyltransferase T	1.8	1.13E-01	Control	5.3	39379	Cytoplasmic	5	COG0404	Amino acid transport and metabolism		
26991877	PP_5201		hypothetical protein	1.3	8.60E-01	Control	3.9	19468	Unknown	3	COG3079	Function unknown		
26991882	PP_5206		secretion protein HlyD family protein	1.6	4.82E-02	Control	9.6	34522	Cytoplasmic Membrane	9	COG1566	Defense mechanisms		
26991883	PP_5207		ABC transporter ATP-binding protein/permease	1.9	2.89E-01	Control	7.8	98772	Cytoplasmic Membrane	2	COG1131	Defense mechanisms		
26991886	PP_5210		alcohol dehydrogenase, zinc-containing	4.8	7.30E-01	Control	7.6	33856	Cytoplasmic	6	COG0604	Energy production and conversion		General function prediction only
26991889	PP_5213		UbiD family decarboxylase	8.8	2.02E-01	7,5 g/l BuOH	7.8	61071	Cytoplasmic	2	COG0043	Coenzyme metabolism		
26991890	PP_5214	rho	transcription termination factor Rho	1.1	2.85E-01	7,5 g/l BuOH	8.2	47041	Cytoplasmic	27	COG1158	Transcription		
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.7	6.04E-02	Control	6.9	55958	Cytoplasmic	10	COG0248	Nucleotide transport and metabolism		Inorganic ion transport and metabolism
26991893	PP_5217	ppk	polyphosphate kinase	1.3	3.22E-01	Control	7.8	81732	Cytoplasmic Membrane	20	COG0855	Inorganic ion transport and metabolism		
26991896	PP_5220	elbB	isoprenoid biosynthesis protein with amidotransferase-like domain	1.1	8.32E-01	7,5 g/l BuOH	5.0	23891	Cytoplasmic	6	COG3155	Secondary metabolites biosynthesis, transport, and catabolism		
26991903	PP_5227	lysA-2	diaminopimelate decarboxylase	1.5	2.57E-01	Control	4.9	45213	Cytoplasmic	2	COG0019	Amino acid transport and metabolism		
26991905	PP_5229		hypothetical protein	1.0	9.10E-01	7,5 g/l BuOH	6.1	26395	Cytoplasmic	3	COG3159	Function unknown		
26991907	PP_5231		HAD superfamily hydrolase	1.1	7.22E-01	7,5 g/l BuOH	5.1	25611	Cytoplasmic	7	COG1011	General function prediction only		
26991928	PP_5252		amidohydrolase 3	1.2	2.39E-01	Control	6.4	72743	Unknown	23	COG1574	General function prediction only		
26991934	PP_5258		aldehyde dehydrogenase family protein	1.7	6.45E-03	Control	5.4	53106	Cytoplasmic	7	COG1012	Energy production and conversion		
26991940	PP_5264	rep	ATP-dependent DNA helicase Rep	1.4	3.67E-01	Control	5.6	76869	Cytoplasmic	2	COG0210	DNA replication, recombination, and repair		
26991941	PP_5265	xpt	xanthine phosphoribosyltransferase	2.4	5.40E-01	Control	6.1	20386	Cytoplasmic	3	COG0503	Nucleotide transport and metabolism		
26991954	PP_5278		aldehyde dehydrogenase family protein	1.2	3.83E-01	Control	5.5	53053	Cytoplasmic	12	COG1012	Energy production and conversion		
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.5	3.70E-01	7,5 g/l BuOH	###	8922	Cytoplasmic	2	COG0227	Translation, ribosomal structure and biogenesis		
26991959	PP_5283		periplasmic dipeptide-binding protein	2.5	1.10E-01	Control	8.5	57512	Periplasmic	5	COG0747	Amino acid transport and metabolism		
26991964	PP_5288		phosphomannomutase	4.3	3.47E-02	7,5 g/l BuOH	5.0	50271	Cytoplasmic	14	COG1109	Carbohydrate transport and metabolism		
26991965	PP_5289	argB	acetylglutamate kinase	2.2	1.27E-01	7,5 g/l BuOH	5.7	31953	Cytoplasmic	15	COG0548	Amino acid transport and metabolism		
26991967	PP_5291	pyrE	orotate phosphoribosyltransferase	1.0	9.02E-01	7,5 g/l BuOH	4.9	23079	Cytoplasmic	7	COG0461	Nucleotide transport and metabolism		
26991968	PP_5292	crc	exodeoxyribonuclease III Xth	1.8	1.67E-01	Control	4.9	29786	Cytoplasmic	4	COG0708	DNA replication, recombination, and repair		
26991970	PP_5294	rph	ribonuclease PH	5.1	1.14E-02	Control	5.9	25723	Cytoplasmic	2	COG0689	Translation, ribosomal structure and biogenesis		
26991972	PP_5296	gmk	guanylate kinase	1.4	2.92E-01	Control	6.4	23184	Cytoplasmic	4	COG0194	Nucleotide transport and metabolism		
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	1.6	2.08E-01	Control	9.2	78603	Cytoplasmic	14	COG0317	Signal transduction mechanisms		Transcription
26991979	PP_5303		endoribonuclease	66.6	1.73E-02	7,5 g/l BuOH	4.8	13508	Cytoplasmic	9	COG0251	Translation, ribosomal structure and biogenesis		
26991980	PP_5304		lipoprotein	1.5	3.12E-01	7,5 g/l BuOH	5.1	26284	Unknown	2				
26991985	PP_5309		LysR family transcriptional regulator	1.4	4.41E-02	Control	7.0	33763	Cytoplasmic	5	COG0583	Transcription		
26991989	PP_5313	hupA	histone family protein DNA-binding protein	77.5	5.13E-02	7,5 g/l BuOH	###	10551	Cytoplasmic	3	COG0776	DNA replication, recombination, and repair		
26991996	PP_5320	phoB	transcriptional regulator	1.0	9.85E-01	7,5 g/l BuOH	5.2	27080	Cytoplasmic	2	COG0745	Signal transduction mechanisms		Transcription
26992000	PP_5324		response regulator receiver protein	1.1	6.49E-01	7,5 g/l BuOH	8.9	31770	Cytoplasmic	8	COG2204	Signal transduction mechanisms		
26992001	PP_5325	phoU	phosphate transporter PhoU	1.3	3.01E-01	7,5 g/l BuOH	5.0	28893	Cytoplasmic	5	COG0704	Inorganic ion transport and metabolism		
26992005	PP_5329	pstS	phosphate ABC transporter phosphate-binding protein	1.1	4.92E-01	7,5 g/l BuOH	9.4	34955	Cytoplasmic Membrane	8	COG0226	Inorganic ion transport and metabolism		
26992008	PP_5332		aldose 1-epimerase	1.3	3.52E-01	Control	4.7	33226	Cytoplasmic	7	COG0676	Carbohydrate transport and metabolism		
26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.1	5.03E-01	Control	5.2	38702	Cytoplasmic Membrane	5	COG0026	Nucleotide transport and metabolism		
26992014	PP_5338	aspA	aspartate ammonia-lyase	2.9	3.08E-02	Control	5.9	51562	Cytoplasmic	7	COG1027	Amino acid transport and metabolism		
26992017	PP_5341		ABC transporter periplasmic polyamine-binding protein	1.4	1.38E-02	Control	8.8	40667	Periplasmic	5	COG0687	Amino acid transport and metabolism		
26992021	PP_5345		acetyltransferase	1.7	1.57E-01	Control	6.0	25042	Cytoplasmic	7	COG1670	Translation, ribosomal structure and biogenesis		
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	1.7	1.77E-01	Control	5.3	65626	Cytoplasmic	32	COG5016	Energy production and conversion		
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	2.5	4.52E-02	Control	6.5	51942	Cytoplasmic	19	COG0439	Lipid metabolism		
26992028	PP_5352	uvrD	DNA-dependent helicase II	1.9	2.36E-01	Control	6.2	81692	Cytoplasmic	2	COG0210	DNA replication, recombination, and repair		
26992029	PP_5353		hypothetical protein	1.1	7.82E-01	7,5 g/l BuOH	7.2	30672	Cytoplasmic Membrane	4	COG4395	Function unknown		
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	2.2	3.35E-02	Control	5.9	48114	Cytoplasmic	2	COG2230	Cell envelope biogenesis, outer membrane		
26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	11.8	1.09E-02	Control	6.0	49353	Cytoplasmic	2	COG1249	Energy production and conversion		
26992054	PP_5378		cytochrome c family protein	18.8	1.17E-03	Control	6.4	27551	Unknown	4				
26992055	PP_5379	copB	copper resistance B precursor	41.7	9.42E-03	Control	5.0	40230	Outer Membrane	3	COG3667	Inorganic ion transport and metabolism		
26992056	PP_5380	copA	copper resistance protein A	21.9	3.98E-03	Control	6.0	74225	Periplasmic	3	COG2132	Secondary metabolites biosynthesis, transport, and catabolism		
26992070	PP_5395		hypothetical protein	1.7	1.04E-02	Control	5.6	31623	Cytoplasmic	14	COG1568	General function prediction only		

26992076	PP_5401		hypothetical protein	4.5	9.11E-02	Control	6.2	22922	Unknown	3					
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.6	2.81E-01	Control	6.0	66312	Cytoplasmic	4	COG0449	Cell envelope biogenesis, outer membrane			
26992086	PP_5411	glmU	UDP-N-acetylglucosamine pyrophosphorylase	2.1	1.37E-01	Control	6.7	48471	Cytoplasmic	9	COG1207	Cell envelope biogenesis, outer membrane			
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.3	7.80E-02	7,5 g/l BuOH	4.6	49359	Cytoplasmic	49	COG0055	Energy production and conversion			
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.3	2.72E-01	7,5 g/l BuOH	9.2	31464	Cytoplasmic	15	COG0224	Energy production and conversion			
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.1	4.98E-01	Control	5.2	55352	Cytoplasmic	38	COG0056	Energy production and conversion			
26992091	PP_5416	atpH	F0F1 ATP synthase subunit delta	1.7	2.04E-01	7,5 g/l BuOH	5.7	19197	Cytoplasmic	5	COG0712	Energy production and conversion			
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	3.6	5.11E-02	7,5 g/l BuOH	5.3	16898	Cytoplasmic Membrane	4	COG0711	Energy production and conversion			
26992094	PP_5419	atpB	F0F1 ATP synthase subunit A	6.9	6.20E-02	Control	6.7	31712	Cytoplasmic Membrane	3	COG0356	Energy production and conversion			
148545375	Pput_0118		hypothetical protein	1.8	1.70E-01	Control	4.7	23815	Cytoplasmic	2					
148545524	Pput_0268		phosphoenolpyruvate carboxykinase	1.1	6.65E-01	7,5 g/l BuOH	5.0	55582	Cytoplasmic	20	COG1866	Energy production and conversion			
148545682	Pput_0430		hypothetical protein	2.8	1.20E-02	Control	7.0	48751	Cytoplasmic	7	COG2718	Function unknown			
148545801	Pput_0551		bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein	2.2	1.09E-01	Control	4.9	39219	Cytoplasmic	5	COG0108	Coenzyme metabolism			
148545966	Pput_0720	rplU	50S ribosomal protein L21	2.1	1.56E-01	7,5 g/l BuOH	###	11632	Cytoplasmic	2	COG0261	Translation, ribosomal structure and biogenesis			
148546138	Pput_0894		ornithine decarboxylase	1.9	2.23E-02	7,5 g/l BuOH	4.7	43509	Cytoplasmic	9	COG0019	Amino acid transport and metabolism			
148546201	Pput_0958		hypothetical protein	2.2	2.66E-01	7,5 g/l BuOH	6.3	30928	Unknown	2					
148546274	Pput_1031		RNA polymerase sigma factor	1.9	1.91E-01	7,5 g/l BuOH	9.0	21796	Cytoplasmic	2	COG1595	Transcription			
148546787	Pput_1548		TPR repeat-containing protein	12.7	1.86E-02	7,5 g/l BuOH	4.8	43184	Cytoplasmic Membrane	9	COG4235	Posttranslational modification, protein turnover, chaperones			
148547528	Pput_2307		hypothetical protein	6.7	1.12E-01	7,5 g/l BuOH	7.4	58966	Periplasmic	6					
148547837	Pput_2621		hypothetical protein	16.8	2.18E-02	7,5 g/l BuOH	5.2	28589	Cytoplasmic	2					
148548678	Pput_3470	tig	trigger factor	1.7	8.48E-02	7,5 g/l BuOH	4.5	48459	Cytoplasmic	25	COG0544	Posttranslational modification, protein turnover, chaperones			
148549148	Pput_3942	rpsA	30S ribosomal protein S1	1.1	6.26E-01	Control	4.6	61555	Cytoplasmic	33	COG0539	Translation, ribosomal structure and biogenesis			
148549381	Pput_4175	fabZ	(3R)-hydroxymyristoyl-ACP dehydratase	1.0	5.62E-01	Control	6.8	16583	Cytoplasmic	6	COG0764	Lipid metabolism			
148549632	Pput_4430		ATP-dependent RNA helicase RhlB	2.7	3.01E-01	Control	8.4	53170	Cytoplasmic	4	COG0513	DNA replication, recombination, and repair	Transcription		
148549970	Pput_4768		HflK protein	1.3	3.82E-01	7,5 g/l BuOH	5.2	43479	Unknown	19	COG0330	Posttranslational modification, protein turnover, chaperones			
148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	1.1	5.60E-01	Control	5.4	51447	Cytoplasmic	30	COG0499	Coenzyme metabolism			
170720128	PputW619_0942	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	1.6	3.16E-01	Control	5.7	47925	Cytoplasmic	3	COG0771	Cell envelope biogenesis, outer membrane			
24986476	not in database	Pseudomonas putida KT2440	carbamoyl-phosphate synthase, large subunit	1.8	1.63E-01	7,5 g/l BuOH				58					
24983268	not in database	Pseudomonas putida KT2440	ribosomal protein S1	1.0	8.03E-01	7,5 g/l BuOH				29					
313499732	not in database	Pseudomonas putida BIRD-1	Gap_2	1.4	8.89E-02	7,5 g/l BuOH				29					
313496770	not in database	Pseudomonas putida BIRD-1	LPS-assembly protein lptD	1.4	3.69E-01	7,5 g/l BuOH				22					
254521045	not in database	Stenotrophomonas sp. SKA14	TonB-dependent receptor domain protein	4.5	2.22E-01	7,5 g/l BuOH				15					
24987101	not in database	Pseudomonas putida KT2440	conserved hypothetical protein TIGR00255	2.4	6.41E-02	7,5 g/l BuOH				15					
190575345	not in database	Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	1.4	5.48E-01	7,5 g/l BuOH				14					
190572930	not in database	Stenotrophomonas maltophilia K279a	elongation factor Tu	6.1	5.89E-02	7,5 g/l BuOH				12					
254522278	not in database	Stenotrophomonas sp. SKA14	Oar protein	1.6	4.50E-01	7,5 g/l BuOH				11					
308070977	not in database	Paenibacillus polymyxa E681	Elongation factor Tu (EF-Tu)	28.7	9.02E-02	7,5 g/l BuOH				10					
334137473	not in database	Paenibacillus sp. HGF7	chaperonin GroL	40.9	5.56E-02	7,5 g/l BuOH				9					
190572988	not in database	Stenotrophomonas maltophilia K279a	outer membrane protein	2.3	3.22E-01	7,5 g/l BuOH				8					
254521740	not in database	Stenotrophomonas sp. SKA14	TonB-dependent outer membrane receptor	5.7	1.01E-01	7,5 g/l BuOH				8					
298682197	not in database	Pseudomonas putida DOT-T1E	hypothetical protein	129.0	8.45E-05	7,5 g/l BuOH				7					
377576294	not in database	Escherichia hermannii NBRC 105704	hypothetical protein YedS	4.2	7.14E-01	7,5 g/l BuOH				7					
10185848	not in database	Escherichia coli	malate dehydrogenase	24.4	6.78E-01	7,5 g/l BuOH				7					
261409551	not in database	Paenibacillus sp. Y412MC10	ATPase AAA-2 domain-containing protein	92.1	2.44E-01	7,5 g/l BuOH				7					
190572101	not in database	Stenotrophomonas maltophilia K279a	biopolymer transport exbB protein	2.2	2.54E-01	7,5 g/l BuOH				7					
377578145	not in database	Escherichia hermannii NBRC 105704	glutamate/aspartate ABC transporter substrate binding periplasmic protein	546.2	9.66E-02	7,5 g/l BuOH				6					
16804497	not in database	Listeria monocytogenes EGD-e	glyceraldehyde-3-phosphate dehydrogenase	38.2	2.38E-01	7,5 g/l BuOH				6					
344209060	not in database	Stenotrophomonas maltophilia JV3	60 kDa chaperonin	7.0	1.50E-01	7,5 g/l BuOH				6					
344206052	not in database	Stenotrophomonas maltophilia JV3	alpha/beta hydrolase fold domain-containing protein	79.7	1.27E-01	7,5 g/l BuOH				5					
377576439	not in database	Escherichia hermannii NBRC 105704	galactose/methyl-galactoside ABC transporter substrate binding periplasmic protein	40.9	1.87E-01	7,5 g/l BuOH				5					
157147228	not in database	Citrobacter koseri ATCC BAA-895	elongation factor Tu	33.0	2.85E-01	7,5 g/l BuOH				5					
190572301	not in database	Stenotrophomonas maltophilia K279a	peptidyl-dipeptidase Dcp	19.7	3.98E-02	7,5 g/l BuOH				5					
194366647	not in database	Stenotrophomonas maltophilia R551-3	endothelin-converting enzyme 1	8.9	8.48E-02	7,5 g/l BuOH				5					
344208107	not in database	Stenotrophomonas maltophilia JV3	TonB-dependent receptor	3.3	2.86E-01	7,5 g/l BuOH				5					
269200099	not in database	Pseudomonas putida DOT-T1E	hypothetical protein	1.0	8.03E-01	7,5 g/l BuOH				4					
190572956	not in database	Stenotrophomonas maltophilia K279a	50S ribosomal protein L5	6.2	2.70E-01	7,5 g/l BuOH				5					
253576477	not in database	Paenibacillus sp. oral taxon 786 str. D14	periplasmic binding protein/LacI transcriptional regulator	54.1	2.50E-02	7,5 g/l BuOH				4					
308068146	not in database	Paenibacillus polymyxa E681	ketol-acid reductoisomerase	48.3	4.99E-02	7,5 g/l BuOH				4					
16801615	not in database	Listeria innocua Clip11262	glyceraldehyde-3-phosphate dehydrogenase	74.7	1.79E-02	7,5 g/l BuOH				4					
261409071	not in database	Paenibacillus sp. Y412MC10	chaperonin GroEL	33.9	1.94E-01	7,5 g/l BuOH				4					
354586098	not in database	Paenibacillus lactis 154	enolase	11.5	2.25E-01	7,5 g/l BuOH				4					
190573698	not in database	Stenotrophomonas maltophilia K279a	phosphopyruvate hydratase	4.3	1.44E-01	7,5 g/l BuOH				3					
261406039	not in database	Paenibacillus sp. Y412MC10	stage IV sporulation protein A	45.0	3.40E-02	7,5 g/l BuOH				4					
190574492	not in database	Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	1.5	6.75E-01	7,5 g/l BuOH				4					
317401987	not in database	Achromobacter xylosoxidans C54	outer membrane porin protein	32.4	3.90E-01	7,5 g/l BuOH				5					
190572938	not in database	Stenotrophomonas maltophilia K279a	DNA-directed RNA polymerase subunit beta'	2.2	3.44E-01	7,5 g/l BuOH				4					
15599454	not in database	Pseudomonas aeruginosa PAO1	50S ribosomal protein L22	9.7	6.52E-02	7,5 g/l BuOH				3					
377577374	not in database	Escherichia hermannii NBRC 105704	glutamine ABC transporter substrate binding periplasmic protein	2.8	3.57E-01	7,5 g/l BuOH				3					
354581546	not in database	Paenibacillus lactis 154	ribosomal protein S2	43.1	8.57E-02	7,5 g/l BuOH				3					
315649715	not in database	Paenibacillus vortex V453	ribosomal protein L1	5.0	2.84E-01	7,5 g/l BuOH				4					
253576842	not in database	Paenibacillus sp. oral taxon 786 str. D14	cysteine synthase A	204.0	1.24E-01	7,5 g/l BuOH				3					
308068312	not in database	Paenibacillus polymyxa E681	Vegetative protein 296 (VEG296)	196.2	5.24E-01	7,5 g/l BuOH				3					
261407994	not in database	Paenibacillus sp. Y412MC10	succinyl-CoA synthetase subunit beta	389.7	2.70E-02	7,5 g/l BuOH				3					
16761724	not in database	Salmonella enterica subsp. enterica serovar Typhi str. CT18	phosphopyruvate hydratase	21.9	3.73E-01	7,5 g/l BuOH				3					
315646628	not in database	Paenibacillus vortex V453	catalytic domain of components of various dehydrogenase complexes	97.3	2.26E-01	7,5 g/l BuOH				3					
357011295	not in database	Paenibacillus elgii B69	family 1 extracellular solute-binding protein	16.5	9.25E-02	7,5 g/l BuOH				3					
261405767	not in database	Paenibacillus sp. Y412MC10	acetyl-CoA synthetase	78.9	7.56E-02	7,5 g/l BuOH				3					
251799648	not in database	Paenibacillus sp. JDR-2	translation elongation factor G	12332.6	8.55E-03	7,5 g/l BuOH				3					
152973457	not in database	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	ATPase with chaperone activity, ATP-binding subunit	31.3	3.99E-01	7,5 g/l BuOH				3					
261409529	not in database	Paenibacillus sp. Y412MC10	DNA-directed RNA polymerase subunit beta	268.7	3.08E-01	7,5 g/l BuOH				3					
190575561	not in database	Stenotrophomonas maltophilia K279a	peptidoglycan-associated lipoprotein	2.5	2.70E-01	7,5 g/l BuOH				2					
261407949	not in database	Paenibacillus sp. Y412MC10	translation elongation factor Ts	29.7	4.67E-02	7,5 g/l BuOH				2					
167464877	not in database	Paenibacillus larvae subsp. larvae BRL-230010	Thioredoxin peroxidase	201.0	7.55E-02	7,5 g/l BuOH				2					
190575124	not in database	Stenotrophomonas maltophilia K279a	superoxide dismutase	3.0	1.61E-01	7,5 g/l BuOH				2					
149181086	not in database	Bacillus sp. SG-1	30S ribosomal protein S4	1.5	3.81E-01	7,5 g/l BuOH				2					
24982932	not in database	Pseudomonas putida KT2440	ribosomal protein S16	11.3	1.27E-01	7,5 g/l BuOH				2					
260595953	not in database	Cronobacter turicensis z3032	superoxide dismutase	4.5	6.05E-01	7,5 g/l BuOH				2					
194364650	not in database	Stenotrophomonas maltophilia R551-3	3-ketoacyl-ACP reductase	1.5	6.56E-01	7,5 g/l BuOH				2					
190574022	not in database	Stenotrophomonas maltophilia K279a	transmembrane protein	4.4	3.68E-01	7,5 g/l BuOH				2					
190573688	not in database	Stenotrophomonas maltophilia K279a	pit accessory protein	7.1	5.71E-01	7,5 g/l BuOH				2					
190575505	not in database	Stenotrophomonas maltophilia K279a	TetR family transcriptional regulator	6.3	2.27E-01	7,5 g/l BuOH				2					
377576277	not in database	Escherichia hermannii NBRC 105704	outer membrane protein A	5.5	6.41E-01	7,5 g/l BuOH				2					
190572546	not in database	Stenotrophomonas maltophilia K279a	hypothetical protein Smlt0483	5.1	2.91E-01	7,5 g/l BuOH				2					
190572934	not in database	Stenotrophomonas maltophilia K279a	50S ribosomal protein L1	4.4	1.25E-01	7,5 g/l BuOH				2					
190573503	not in database	Stenotrophomonas maltophilia K279a	30S ribosomal protein S2	11.3	1.17E-01	7,5 g/l BuOH				2					
190576298	not in database	Stenotrophomonas maltophilia K279a	TonB dependent receptor protein	1.9	3.52E-01	7,5 g/l BuOH				1					
308070978	not in database	Paenibacillus polymyxa E681	elongation factor G	88.1	1.07E-01	7,5 g/l BuOH				2					
261405607	not in database	Paenibacillus sp. Y412MC10	hypothetical protein GYMC10_1758	119.1	5.88E-02	7,5 g/l BuOH				2					
194366390	not in database	Stenotrophomonas maltophilia R551-3	FKBP-type peptidylprolyl isomerase	5.1	1.51E-01	7,5 g/l BuOH				2					
260551344	not in database	Acinetobacter sp. RUH2624	membrane-bound ATP synthase F1 sector	7.5	7.22E-02	7,5 g/l BuOH				2					
190572978	not in database	Stenotrophomonas maltophilia K279a	malate dehydrogenase	6.7	2.13E-01	7,5 g/l BuOH				2					
308067147	not in database	Paenibacillus polymyxa E681	manganese-dependent inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase)	Infinity	1.17E-01	7,5 g/l BuOH				2					
15889243	not in database	Agrobacterium fabrum str. C58	elongation factor TU	86.3	5.20E-02	7,5 g/l BuOH				2					
190575684	not in database	Stenotrophomonas maltophilia K279a	type II citrate synthase	5.3	2.68E-01	7,5 g/l BuOH				2					
261409360	not in database	Paenibacillus sp. Y412MC10	O-acetylhomoserine aminocarboxypropyltransferase	108.4	2.93E-02	7,5 g/l BuOH				2					
261409688	not in database	Paenibacillus sp. Y412MC10	glycine hydroxymethyltransferase	42.4	1.05E-01	7,5 g/l BuOH				2					
337750195	not in database	Paenibacillus mucilaginosus KNP414	ABC transporter substrate-binding protein	26.6	2.65E-02	7,5 g/l BuOH				2					
261406205	not in database	Paenibacillus sp. Y412MC10	glutamine synthetase	13.9	2.60E-01	7,5 g/l BuOH				2					
251798795	not in database	Paenibacillus sp. JDR-2	family 5 extracellular solute-binding protein	432.6	6.59E-02	7,5 g/l BuOH				2					
158422048	not in database	Azorhizobium caulinodans ORS 571	chaperonin	Infinity	1.33E-01	7,5 g/l BuOH				2					
317405440	not in database	Achromobacter xylosoxidans C54	chaperonin	42.5	3.82E-01	7,5 g/l BuOH				2					
251794236	not in database	Paenibacillus sp. JDR-2	extracellular solute-binding protein	30.0	4.88E-02	7,5 g/l BuOH				2					
302870826	not in database	Caldicellulosiruptor obsidiansis OB47	ABC transporter-like protein	53.5	5.59E-01	7,5 g/l BuOH				2					
24981908	not in database	Pseudomonas putida KT2440	deoxyxylulose-5-phosphate synthase	1.8	3.59E-01	7,5 g/l BuOH				2					

251798736	not in database	Paenibacillus sp. JDR-2	serine protein kinase PrkA		617.5	1.61E-01	7,5 g/l BuOH	2
241207097	not in database	Rhizobium leguminosarum bv. trifolii WSM1325	molecular chaperone DnaK	Infinity		3.74E-01	7,5 g/l BuOH	1
190573963	not in database	Stenotrophomonas maltophilia K279a	molecular chaperone DnaK		31.2	2.03E-01	7,5 g/l BuOH	1
354585430	not in database	Paenibacillus lactis 154	translation elongation factor G		57.8	1.87E-01	7,5 g/l BuOH	2
167035954	not in database	Pseudomonas putida GB-1	DNA topoisomerase IV subunit A		4.0	5.64E-02	7,5 g/l BuOH	2
315649653	not in database	Paenibacillus vortex V453	Phosphoenolpyruvate carboxylase	Infinity		1.17E-01	7,5 g/l BuOH	2
190572528	not in database	Stenotrophomonas maltophilia K279a	TonB outer membrane protein oar family		5.8	2.38E-01	7,5 g/l BuOH	2
194363943	not in database	Stenotrophomonas maltophilia R551-3	peptidase M16 domain-containing protein		2.3	2.56E-01	7,5 g/l BuOH	2
24982083	not in database	Pseudomonas putida KT2440	ribosomal protein L21		2.6	9.67E-01	7,5 g/l BuOH	2
293604168	not in database	Achromobacter piechaudii ATCC 43553	outer membrane protein A		54.9	3.80E-01	7,5 g/l BuOH	2
190575057	not in database	Stenotrophomonas maltophilia K279a	NAD-dependent glutamate dehydrogenase		6.0	2.61E-01	7,5 g/l BuOH	2
313498081	not in database	Pseudomonas putida BIRD-1	D-hydantoinase/dihydropyrimidinase		1.2	3.71E-01	Control	31
24982804	not in database	Pseudomonas putida KT2440	preprotein translocase, SecA subunit		1.2	2.11E-01	Control	21
24981833	not in database	Pseudomonas putida KT2440	ribosomal protein L3		2.0	8.08E-02	Control	11
24981839	not in database	Pseudomonas putida KT2440	ribosomal protein S3		2.0	4.81E-02	Control	12
24982353	not in database	Pseudomonas putida KT2440	rod shape-determining protein MreB		1.1	3.80E-01	Control	9
313498324	not in database	Pseudomonas putida BIRD-1	Ribosyldihydronicotinamide dehydrogenase (quinone)		2.0	1.83E-01	Control	8
24986535	not in database	Pseudomonas putida KT2440	AMP nucleosidase		2.4	6.68E-02	Control	8
24986054	not in database	Pseudomonas putida KT2440	ParA family protein		2.2	1.04E-01	Control	6
24982449	not in database	Pseudomonas putida KT2440	transcriptional regulator HexR		2.9	2.89E-02	Control	6
24983623	not in database	Pseudomonas putida KT2440	conserved hypothetical protein		2.6	8.25E-02	Control	6
313496591	not in database	Pseudomonas putida BIRD-1	Serine O-acetyltransferase		1.6	2.75E-01	Control	5
228957652	not in database	Bacillus thuringiensis serovar pakistani str. T13001	Immune inhibitor A		6.2	7.83E-01	Control	5
118476855	not in database	Bacillus thuringiensis str. Al Hakam	camelysin		162.6	1.45E-01	Control	4
24985446	not in database	Pseudomonas putida KT2440	shikimate 5-dehydrogenase/quinate 5-dehydrogenase family protein		3.5	1.58E-02	Control	4
313501129	not in database	Pseudomonas putida BIRD-1	FAD linked oxidase domain-containing protein		2.3	1.14E-01	Control	3
326793551	not in database	Marinomonas mediterranea MMB-1	DNA-directed RNA polymerase subunit beta		2.6	9.13E-02	Control	3
313497959	not in database	Pseudomonas putida BIRD-1	Lipid-binding START domain-containing protein		3.3	2.45E-01	Control	2
206970137	not in database	Bacillus cereus AH1134	neutral protease B		49.4	7.05E-01	Control	2
104780459	not in database	Pseudomonas entomophila L48	peptide chain release factor 2		1.4	3.68E-01	Control	2
24986088	not in database	Pseudomonas putida KT2440	flagellum-specific ATP synthase FliI		20.6	6.44E-02	Control	2

5.3 Teilprojekt Vanillin

5.3.1 2D-DIGE-Analyse



Differenziell regulierte Spots zwischen auf 6,6 mM (0,1%) Vanillin und 10 mM Glucose kultiviertem *P. putida* KT2440 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in auf 6,6 mM (0,1%) Vanillin kultivierten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden. Aus Gründen der Übersichtlichkeit wurden folgende Proteine mit Buchstaben, statt der Spot-Nummer markiert:

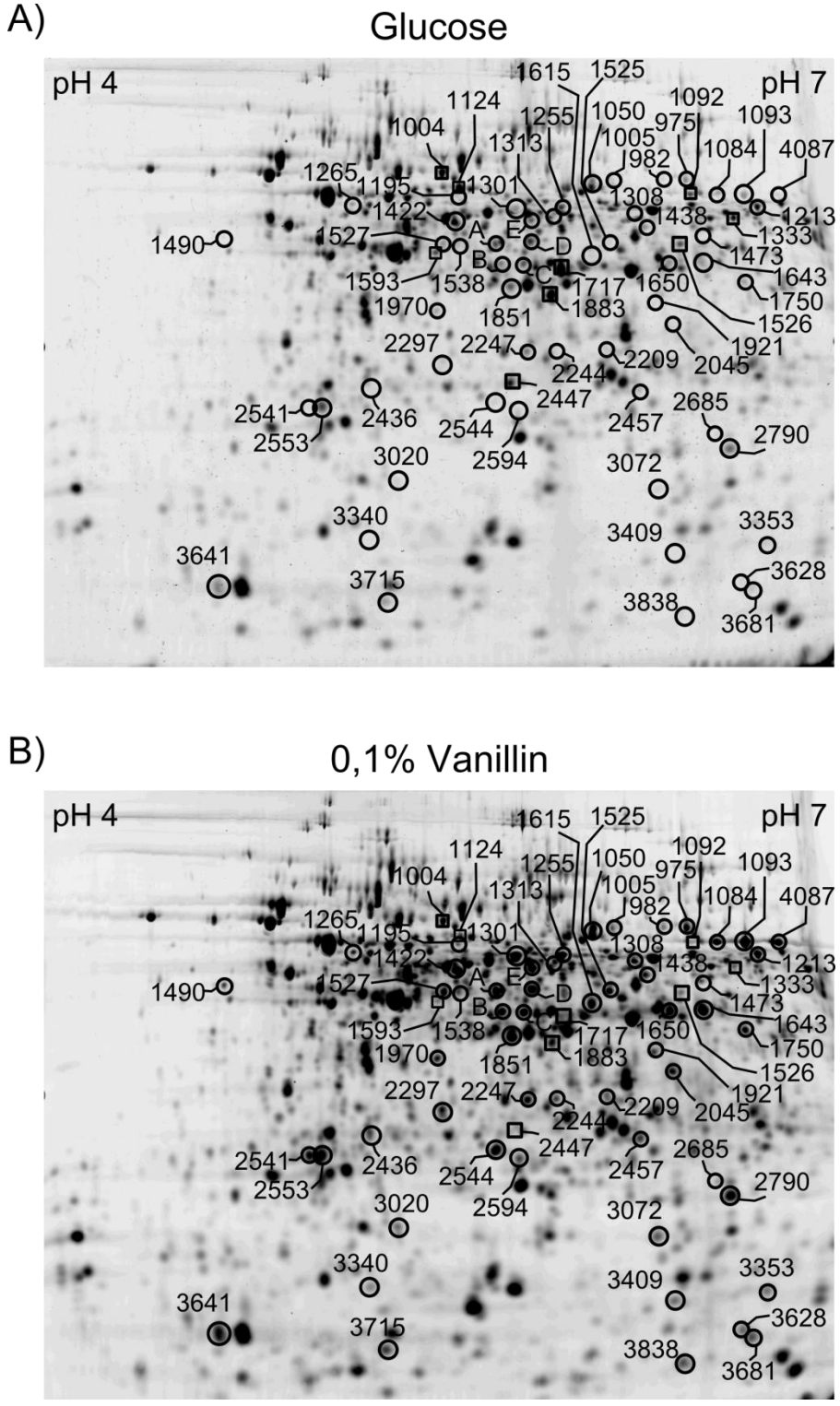
5.3.1.1 2D_DIGE_P_putida_KT2440_Vanillin_pH_4_7_Tabelle

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
1010	26991410	PP_4727	dnaK	molecular chaperone DnaK	2.2	3.24E-03	Vanillin	4.6	68800	41	59%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
1043	26988179	PP_1446		TonB-dependent receptor	2.4	4.91E-03	Control	4.9	74207	25	44%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1043	26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	2.4	4.91E-03	Control	5.5	150992	3	2%	Cytoplasmic	COG0085	Transcription	
1043	26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	2.4	4.91E-03	Control	4.9	75010	4	6%	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
1043	26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	2.4	4.91E-03	Control	4.9	75112	9	12%	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
1043	26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	2.4	4.91E-03	Control	4.8	68580	4	7%	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
1059	26991410	PP_4727	dnaK	molecular chaperone DnaK	2.7	5.08E-04	Vanillin	4.6	68800	2	3%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
1067	26990043	PP_3325		outer membrane ferric siderophore receptor	3.6	1.74E-03	Control	4.8	76226	44	73%	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
1067	26988095	PP_1361	groEL	chaperonin GroEL	3.6	1.74E-03	Control	4.7	56743	2	4%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1068	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.0	6.05E-03	Vanillin	5.3	55654	5	10%	Cytoplasmic	COG0508	Energy production and conversion	
1068	26990043	PP_3325		outer membrane ferric siderophore receptor	2.0	6.05E-03	Vanillin	4.8	76226	2	3%	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
1068	26991643	PP_4965	tktA	transketolase	2.0	6.05E-03	Vanillin	5.0	72463	7	11%	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
1068	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.0	6.05E-03	Vanillin	5.8	65671	3	6%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1068	26990871	PP_4179	htpG	heat shock protein 90	2.0	6.05E-03	Vanillin	5.0	71610	42	61%	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
1071	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.2	4.01E-03	Control	5.3	55654	2	4%	Cytoplasmic	COG0508	Energy production and conversion	
1071	26988179	PP_1446		TonB-dependent receptor	2.2	4.01E-03	Control	4.9	74207	3	5%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1103	26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.8	7.12E-03	Vanillin	6.0	66312	5	9%	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
1103	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.8	7.12E-03	Vanillin	5.8	65671	31	59%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1103	26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.8	7.12E-03	Vanillin	5.8	65541	7	14%	Cytoplasmic	COG1960	Lipid metabolism	
1103	26991518	PP_4838	oprC	TonB-dependent copper receptor	1.8	7.12E-03	Vanillin	6.2	74540	5	9%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1103	26987139	PP_0397		serine protein kinase, PrkA	1.8	7.12E-03	Vanillin	5.8	73782	24	40%	Cytoplasmic	COG2766	Signal transduction mechanisms	
1103	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.8	7.12E-03	Vanillin	6.2	63448	23	42%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
1124	26990043	PP_3325		outer membrane ferric siderophore receptor	1.9	1.41E-02	Vanillin	4.8	76226	7	11%	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
1124	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	1.9	1.41E-02	Vanillin	6.2	63448	36	61%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
1124	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.9	1.41E-02	Vanillin	5.8	65671	17	34%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1124	26987139	PP_0397		serine protein kinase, PrkA	1.9	1.41E-02	Vanillin	5.8	73782	39	60%	Cytoplasmic	COG2766	Signal transduction mechanisms	
1157	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	16.0	4.28E-03	Vanillin	7.0	69173	20	45%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1168	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	4.1	2.47E-04	Control	5.3	65626	39	72%	Cytoplasmic	COG5016	Energy production and conversion	
1168	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	4.1	2.47E-04	Control	6.2	63448	6	9%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
1197	26988095	PP_1361	groEL	chaperonin GroEL	2.2	4.08E-03	Vanillin	4.7	56743	25	41%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1197	26986986	PP_0243	gshA	glutamate--cysteine ligase	2.2	4.08E-03	Vanillin	4.8	59067	2	5%	Cytoplasmic	COG2918	Coenzyme metabolism	
1197	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.2	4.08E-03	Vanillin	5.3	65626	2	3%	Cytoplasmic	COG5016	Energy production and conversion	
1329	26987192	PP_0451	fusA	elongation factor G	5.2	1.06E-04	Vanillin	4.9	78817	4	6%	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
1329	26991410	PP_4727	dnaK	molecular chaperone DnaK	5.2	1.06E-04	Vanillin	4.6	68800	2	4%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
1329	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	5.2	1.06E-04	Vanillin	4.9	54767	19	50%	Cytoplasmic	COG1951	Energy production and conversion	
1329	26989818	PP_3099		hypothetical protein	5.2	1.06E-04	Vanillin	4.9	56072	7	13%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
1343	26989210	PP_2487		aldehyde dehydrogenase family protein	2.1	3.66E-03	Vanillin	5.0	54721	6	14%	Cytoplasmic	COG1012	Energy production and conversion	
1343	26986810	PP_0065	trkA	potassium transporter peripheral membrane component	2.1	3.66E-03	Vanillin	5.0	49812	9	16%	Cytoplasmic Membrane	COG0569	Inorganic ion transport and metabolism	
1343	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2.1	3.66E-03	Vanillin	4.9	54767	25	59%	Cytoplasmic	COG1951	Energy production and conversion	
1343	26989818	PP_3099		hypothetical protein	2.1	3.66E-03	Vanillin	4.9	56072	2	4%	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
1343	26987768	PP_1032	guaA	GMP synthase	2.1	3.66E-03	Vanillin	5.2	58204	5	11%	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
1350	26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	4.0	2.18E-05	Vanillin	6.0	49353	3	8%	Cytoplasmic	COG1249	Energy production and conversion	
1350	26991954	PP_5278		aldehyde dehydrogenase family protein	4.0	2.18E-05	Vanillin	5.5	53053	2	5%	Cytoplasmic	COG1012	Energy production and conversion	
1350	26987283	PP_0545		aldehyde dehydrogenase family protein	4.0	2.18E-05	Vanillin	5.9	55268	20	50%	Cytoplasmic	COG1012	Energy production and conversion	
1350	26988522	PP_1791		aldolase/synthase	4.0	2.18E-05	Vanillin	5.9	58534	2	4%	Cytoplasmic	COG0119	Amino acid transport and metabolism	
1350	26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	4.0	2.18E-05	Vanillin	5.8	62191	5	12%	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
1350	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	4.0	2.18E-05	Vanillin	6.3	49912	3	5%	Cytoplasmic	COG1249	Energy production and conversion	
1350	26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	4.0	2.18E-05	Vanillin	6.0	61223	3	7%	Cytoplasmic	COG0365	Lipid metabolism	
1350	26991765	PP_5089	argS	arginyl-tRNA synthetase	4.0	2.18E-05	Vanillin	5.7	63668	16	31%	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
1365	26988095	PP_1361	groEL	chaperonin GroEL	2.6	1.58E-03	Vanillin	4.7	56743	3	8%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1372	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	3.0	1.80E-04	Vanillin	6.3	49912	5	10%	Cytoplasmic	COG1249	Energy production and conversion	
1372	26987283	PP_0545		aldehyde dehydrogenase family protein	3.0	1.80E-04	Vanillin	5.9	55268	12	24%	Cytoplasmic	COG1012	Energy production and conversion	
1372	26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	3.0	1.80E-04	Vanillin	5.4	55551	3	6%	Cytoplasmic	COG2204	Signal transduction mechanisms	
1372	148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	3.0	1.80E-04	Vanillin	5.4	51447	4	10%	Cytoplasmic	COG0499	Coenzyme metabolism	
1372	26991954	PP_5278		aldehyde dehydrogenase family protein	3.0	1.80E-04	Vanillin	5.5	53053	2	4%	Cytoplasmic	COG1012	Energy production and conversion	
1372	26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	3.0	1.80E-04	Vanillin	5.6	51255	14	34%	Cytoplasmic	COG0065	Amino acid transport and metabolism	
1372	26989399	PP_2680		aldehyde dehydrogenase family protein	3.0	1.80E-04	Vanillin	5.5	54903	12	57%	Cytoplasmic	COG1012	Energy production and conversion	
1394	26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	6.3	3.45E-04	Control	6.8	55000	19	36%	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
1394	26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	6.3	3.45E-04	Control	7.0	51765	8	16%	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
1394	26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	6.3	3.45E-04	Control	7.7	53014	2	4%	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
1394	26989178	PP_2455	rbsA	ribose ABC transporter ATP-binding protein	6.3	3.45E-04	Control	6.5	56347	4	9%	Cytoplasmic Membrane	COG1129	Carbohydrate transport and metabolism	
1464	26987824	PP_1088	argG	argininosuccinate synthase	2.0	3.81E-03	Vanillin	5.1	45164	3	6%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
1464	26989272	PP_2552		aromatic-L-amino-acid decarboxylase	2.0	3.81E-03	Vanillin	5.2	51443	5	11%	Unknown	COG0076	Amino acid transport and metabolism	
1464	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.0	3.81E-03	Vanillin	5.2	55352	28	44%	Cytoplasmic	COG0056	Energy production and conversion	
1464	26991936	PP_5260		hypothetical protein	2.0	3.81E-03	Vanillin	5.1	51372	5	9%	Cytoplasmic	COG5383	Function unknown	
1464	26990740	PP_4038		dihydropyrimidine dehydrogenase	2.0	3.81E-03	Vanillin	5.1	46093	3	8%	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
1464	148550051	Pput_4849		S-adenosyl-L-homocysteine hydrolase	2.0	3.81E-03	Vanillin	5.4	51447	4	10%	Cytoplasmic	COG0499	Coenzyme metabolism	
1464	26989870	PP_3151		aldehyde dehydrogenase family protein	2.0	3.81E-03	Vanillin	5.0	49303	2	5%	Cytoplasmic	COG1012	Energy production and conversion	
1464	26990972	PP_4281	gad	guanine deaminase	2.0	3.81E-03	Vanillin	5.3	48084	3	7%	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
1464	26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	2.0	3.81E-03	Vanillin	5.2	52989	9	24%	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
1464	26990705	PP_4000	serS	seryl-tRNA synthetase	2.0	3.81E-03	Vanillin	5.1	46849	2	4%	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
1464	26989023	PP_2299	tig	trigger factor	2.0	3.81E-03	Vanillin	4.5	49190	4	9%	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
1464	26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	2.0	3.81E-03	Vanillin	5.2	51549	9	21%	Cytoplasmic	COG1012	Energy production and conversion	
1464	26991744	PP_5068		hypothetical protein	2.0	3.81E-03	Vanillin	6.2	60492	5	8%	Unknown	COG0397	Function unknown	
1464	26991319	PP_4635		trans-2-enoyl-CoA reductase	2.0	3.81E-03	Vanillin	5.0	44265	2	6%	Cytoplasmic	COG3007	Function unknown	
1464	26988391	PP_1659		hypothetical protein	2.0	3.81E-03	Vanillin	5.9	48336	2	5%	Periplasmic			
1465	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	2.0	3.69E-03	Vanillin	5.3	43264	3	7%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1465	26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	2.0	3.69E-03	Vanillin	6.2	51518	7	16%	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
1465	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.0	3.69E-03	Vanillin	5.2	55352	9	19%	Cytoplasmic	COG0056	Energy production and conversion	
1465	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	2.0	3.69E-03	Vanillin	6.5	49088	21	52%	Cytoplasmic	COG0439	Lipid metabolism	
1465	26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	2.0	3.69E-03	Vanillin	6.5	51942	5	12%	Cytoplasmic	COG0439	Lipid metabolism	
1465	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.0	3.69E-03	Vanillin	5.4	45695	11	26%	Unknown	COG0538	Energy production and conversion	
1465	26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.0	3.69E-03	Vanillin	6.5	106521	6	6%	Cytoplasmic	COG0567	Energy production and conversion	
1485	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	2.3	4.24E-03	Vanillin	5.2	55352	2	4%	Cytoplasmic	COG0056	Energy production and conversion	
1485	26987649	PP_0913		hypothetical protein	2.3	4.24E-03	Vanillin	4.4	47019	2	5%	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
1485	26989572	PP_2853		hypothetical protein	2.3	4.24E-03	Vanillin	4.5	46020	9	24%	Unknown			
1491	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	5.0	3.23E-05	Vanillin	5.2	55352	3	7%	Cytoplasmic	COG0056	Energy production and conversion	
1491	313498321	not in database			5.0	3.23E-05	Vanillin			4	8%				
1491	26987737	PP_1001	arcA	arginine deiminase	5.0	3.23E-05	Vanillin	5.7	46462	30	78%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1491	26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	5.0	3.23E-05	Vanillin	5.7	50918	12	31%	Unknown	COG1012	Energy production and conversion	
1491	26991567	PP_4889	purA	adenylosuccinate synthetase	5.0	3.23E-05	Vanillin	5.6	46833	12	39%	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
1510	26988204	PP_1471	thrC	threonine synthase	5.6	3.88E-05	Vanillin	6.2	51645	4	8%	Cytoplasmic	COG0498	Amino acid transport and metabolism	
1510	26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	5.6	3.88E-05	Vanillin	6.2	51518	18	41%	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
1510	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	5.6	3.88E-05	Vanillin	5.2	55352	8	17%	Cytoplasmic	COG0056	Energy production and conversion	

1510	26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	5.6	3.88E-05	Vanillin	5.9	53498	2	5%	Cytoplasmic	COG1012	Energy production and conversion	
1510	313498081	not in database			5.6	3.88E-05	Vanillin			10	30%				
1510	26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	5.6	3.88E-05	Vanillin	5.7	49982	5	10%	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
1510	26987824	PP_1088	argG	argininosuccinate synthase	5.6	3.88E-05	Vanillin	5.1	45164	2	5%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
1510	26987737	PP_1001	arcA	arginine deiminase	5.6	3.88E-05	Vanillin	5.7	46462	2	4%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1510	26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	5.6	3.88E-05	Vanillin	5.2	51549	2	5%	Cytoplasmic	COG1012	Energy production and conversion	
1536	26990810	PP_4116	aceA	isocitrate lyase	3.3	4.76E-04	Vanillin	5.3	48633	21	48%	Cytoplasmic	COG2224	Energy production and conversion	
1536	26987737	PP_1001	arcA	arginine deiminase	3.3	4.76E-04	Vanillin	5.7	46462	3	8%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1536	26988046	PP_1311		tryptophanyl-tRNA synthetase	3.3	4.76E-04	Vanillin	5.4	49297	7	17%	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis	
1536	26987824	PP_1088	argG	argininosuccinate synthase	3.3	4.76E-04	Vanillin	5.1	45164	8	22%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
1536	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	3.3	4.76E-04	Vanillin	5.4	50393	10	22%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1559	26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	2.2	6.87E-03	Control	5.4	50393	2	6%	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
1559	26990490	PP_3785		hypothetical protein	2.2	6.87E-03	Control	6.5	50495	16	50%	Cytoplasmic			
1559	26988596	PP_1866		phospho-2-dehydro-3-deoxyheptonate aldolase	2.2	6.87E-03	Control	6.4	49706	8	21%	Cytoplasmic	COG3200	Amino acid transport and metabolism	
1559	26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	2.2	6.87E-03	Control	6.5	48194	2	6%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
1559	26990501	PP_3796		L-ornithine N5-oxygenase	2.2	6.87E-03	Control	6.5	50047	9	21%	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
1559	26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	2.2	6.87E-03	Control	6.6	46750	3	8%	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
1559	26991109	PP_4421		hypothetical protein	2.2	6.87E-03	Control	6.5	50295	9	22%	Cytoplasmic	COG0161	Coenzyme metabolism	
1593	26990490	PP_3785		hypothetical protein	6.1	8.90E-05	Vanillin	6.5	50495	3	6%	Cytoplasmic			
1593	26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	6.1	8.90E-05	Vanillin	6.5	48194	8	21%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
1593	26991109	PP_4421		hypothetical protein	6.1	8.90E-05	Vanillin	6.5	50295	5	10%	Cytoplasmic	COG0161	Coenzyme metabolism	
1593	26990501	PP_3796		L-ornithine N5-oxygenase	6.1	8.90E-05	Vanillin	6.5	50047	3	7%	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
1632	26991661	PP_4984	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	1.9	3.51E-03	Vanillin	6.1	52453	2	4%	Cytoplasmic	COG0161	Coenzyme metabolism	
1632	26987680	PP_0944	fumC	fumarate hydratase	1.9	3.51E-03	Vanillin	5.9	48541	2	4%	Cytoplasmic	COG0114	Energy production and conversion	
1632	26990721	PP_4016	purB	adenylosuccinate lyase	1.9	3.51E-03	Vanillin	5.9	50555	7	13%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
1632	26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.9	3.51E-03	Vanillin	6.2	44897	16	42%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
1634	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	7.8	1.53E-05	Vanillin	5.3	55654	2	5%	Cytoplasmic	COG0508	Energy production and conversion	
1634	26990248	PP_3536		hypothetical protein	7.8	1.53E-05	Vanillin	4.4	41469	23	64%	Cytoplasmic			
1662	26987058	PP_0316		oxidoreductase FAD-binding domain protein	3.6	4.01E-05	Vanillin	5.1	40675	4	11%	Cytoplasmic	COG1018	Energy production and conversion	
1662	26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	3.6	4.01E-05	Vanillin	5.2	44973	2	4%	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
1662	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	3.6	4.01E-05	Vanillin	5.3	43264	2	5%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1662	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	3.6	4.01E-05	Vanillin	5.4	45695	10	22%	Unknown	COG0538	Energy production and conversion	
1662	26991676	PP_4999	pyrC	dihydroorotase	3.6	4.01E-05	Vanillin	5.4	44116	8	26%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
1679	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	2.8	1.68E-03	Vanillin	5.3	43264	8	23%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1679	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	2.8	1.68E-03	Vanillin	5.7	45178	2	5%	Cytoplasmic	COG0001	Coenzyme metabolism	
1679	26987515	PP_0779		methyl-accepting chemotaxis transducer/sensory box protein	2.8	1.68E-03	Vanillin	6.2	49856	4	9%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1679	26991676	PP_4999	pyrC	dihydroorotase	2.8	1.68E-03	Vanillin	5.4	44116	2	5%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
1679	26987468	PP_0732	hemA	glutamyl-tRNA reductase	2.8	1.68E-03	Vanillin	5.5	46305	2	5%	Cytoplasmic	COG0373	Coenzyme metabolism	
1679	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.8	1.68E-03	Vanillin	5.4	45695	25	56%	Unknown	COG0538	Energy production and conversion	
1679	26988462	PP_1730		aminopeptidase 2	2.8	1.68E-03	Vanillin	5.6	46996	3	6%	Cytoplasmic	COG1362	Amino acid transport and metabolism	
1684	26987407	PP_0671	glyA	serine hydroxymethyltransferase	11.0	2.05E-07	Vanillin	6.2	44897	3	6%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
1684	26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	11.0	2.05E-07	Vanillin	5.9	48114	6	15%	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
1684	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	11.0	2.05E-07	Vanillin	6.7	41895	2	5%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
1684	26988671	PP_1944		aminomethyltransferase	11.0	2.05E-07	Vanillin	6.0	48129	24	51%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1684	26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	11.0	2.05E-07	Vanillin	6.1	45417	14	37%	Cytoplasmic	COG0014	Amino acid transport and metabolism	
1705	26986828	PP_0083	trpB	tryptophan synthase subunit beta	2.2	4.36E-03	Control	6.4	44046	12	33%	Cytoplasmic	COG0133	Amino acid transport and metabolism	
1705	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	2.2	4.36E-03	Control	6.7	41895	5	14%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
1705	26987411	PP_0675	gdhA	glutamate dehydrogenase	2.2	4.36E-03	Control	6.5	48871	16	34%	Unknown	COG0334	Amino acid transport and metabolism	
1705	26988671	PP_1944		aminomethyltransferase	2.2	4.36E-03	Control	6.0	48129	2	4%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1705	26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	2.2	4.36E-03	Control	6.1	45417	5	11%	Cytoplasmic	COG0014	Amino acid transport and metabolism	
1717	26991409	PP_4726	dnaJ	chaperone protein DnaJ	7.7	1.30E-04	Control	6.7	40181	4	13%	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
1717	26987754	PP_1018		sugar ABC transporter ATP-binding subunit	7.7	1.30E-04	Control	6.7	41895	20	56%	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
1754	26987193	PP_0452	tuf	elongation factor Tu	5.4	2.16E-04	Control	5.0	43478	13	37%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1754	26987755	PP_1019	oprB-1	porin B	5.4	2.16E-04	Control	5.9	49646	21	52%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
1754	26988847	PP_2123	moeA	molybdopterin biosynthesis MoeA protein	5.4	2.16E-04	Control	5.1	43963	2	6%	Cytoplasmic	COG0303	Coenzyme metabolism	
1754	26991645	PP_4967	metK	S-adenosylmethionine synthetase	5.4	2.16E-04	Control	5.1	42779	9	25%	Cytoplasmic	COG0192	Coenzyme metabolism	
1812	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	7.2	1.89E-06	Vanillin	6.0	41851	18	42%	Cytoplasmic	COG0183	Lipid metabolism	
1812	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	7.2	1.89E-06	Vanillin	6.3	44339	5	10%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1812	26987578	PP_0842	iscS	cysteine desulfurase	7.2	1.89E-06	Vanillin	6.2	44468	9	22%	Cytoplasmic	COG1104	Amino acid transport and metabolism	
1812	26991645	PP_4967	metK	S-adenosylmethionine synthetase	7.2	1.89E-06	Vanillin	5.1	42779	4	12%	Cytoplasmic	COG0192	Coenzyme metabolism	
1812	26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	7.2	1.89E-06	Vanillin	6.1	44824	9	22%	Cytoplasmic	COG0160	Amino acid transport and metabolism	
1830	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	1.8	1.11E-02	Vanillin	6.0	41851	2	5%	Cytoplasmic	COG0183	Lipid metabolism	
1830	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.8	1.11E-02	Vanillin	6.3	44339	16	39%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1830	26990480	PP_3775		sarcosine oxidase	1.8	1.11E-02	Vanillin	6.4	41164	5	13%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1830	26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	1.8	1.11E-02	Vanillin	6.3	44262	7	17%	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
1830	26986902	PP_0158	gcdH	acyl-CoA dehydrogenase domain-containing protein	1.8	1.11E-02	Vanillin	6.2	43242	3	6%	Cytoplasmic	COG1960	Lipid metabolism	
1830	26991278	PP_4594		cystathionine gamma-lyase	1.8	1.11E-02	Vanillin	6.4	42503	3	6%	Cytoplasmic	COG0626	Amino acid transport and metabolism	
1830	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.8	1.11E-02	Vanillin	6.3	39364	3	7%	Cytoplasmic	COG1062	Energy production and conversion	
1836	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	3.4	1.63E-03	Vanillin	6.0	41851	7	19%	Cytoplasmic	COG0183	Lipid metabolism	
1836	26987578	PP_0842	iscS	cysteine desulfurase	3.4	1.63E-03	Vanillin	6.2	44468	13	44%	Cytoplasmic	COG1104	Amino acid transport and metabolism	
1836	26990480	PP_3775		sarcosine oxidase	3.4	1.63E-03	Vanillin	6.4	41164	8	23%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1836	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	3.4	1.63E-03	Vanillin	6.3	44339	17	50%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1836	26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	3.4	1.63E-03	Vanillin	6.3	44262	13	43%	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
1836	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	3.4	1.63E-03	Vanillin	6.3	39364	6	15%	Cytoplasmic	COG1062	Energy production and conversion	
1836	26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	3.4	1.63E-03	Vanillin	6.1	44824	20	58%	Cytoplasmic	COG0160	Amino acid transport and metabolism	
1854	26987877	PP_1141	braC	extracellular ligand-binding receptor	3.1	2.16E-03	Vanillin	6.4	39402	2	5%	Periplasmic	COG0683	Amino acid transport and metabolism	
1854	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	3.1	2.16E-03	Vanillin	6.3	39364	2	5%	Cytoplasmic	COG1062	Energy production and conversion	
1854	26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	3.1	2.16E-03	Vanillin	6.3	44262	4	13%	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
1854	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	3.1	2.16E-03	Vanillin	6.3	44339	3	8%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1854	26991844	PP_5168	cysA	sulfate ABC transporter ATPase subunit	3.1	2.16E-03	Vanillin	6.4	36972	4	14%	Cytoplasmic Membrane	COG1118	Inorganic ion transport and metabolism	
1854	26987722	PP_0986	gcvT-1	glycine cleavage system T protein	3.1	2.16E-03	Vanillin	6.4	40319	13	43%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1854	26990491	PP_3786		aminotransferase	3.1	2.16E-03	Vanillin	6.4	44067	9	30%	Cytoplasmic	COG0436	Amino acid transport and metabolism	
1863	26990480	PP_3775		sarcosine oxidase	5.4	9.27E-04	Vanillin	6.4	41164	2	5%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1863	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	5.4	9.27E-04	Vanillin	6.3	44339	5	13%	Cytoplasmic	COG0111	Amino acid transport and metabolism	
1863	26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	5.4	9.27E-04	Vanillin	6.3	44262	2	5%	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
1863	26987840	PP_1104		succinylglutamate desuccinylase/aspartoacylase	5.4	9.27E-04	Vanillin	6.3	40904	3	7%	Cytoplasmic	COG3608	General function prediction only	
1863	26987736	PP_1000	argI	ornithine carbamoyltransferase	5.4	9.27E-04	Vanillin	6.3	37911	16	39%	Cytoplasmic	COG0078	Amino acid transport and metabolism	
1863	26991548	PP_4868	pncB	nicotinate phosphoribosyltransferase	5.4	9.27E-04	Vanillin	6.4	46349	2	5%	Cytoplasmic	COG1488	Coenzyme metabolism	
1863	26991278	PP_4594		cystathionine gamma-lyase	5.4	9.27E-04	Vanillin	6.4	42503	2	5%	Cytoplasmic	COG0626	Amino acid transport and metabolism	
1863	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	5.4	9.27E-04	Vanillin	6.3	39364	4	9%	Cytoplasmic	COG1062	Energy production and conversion	
1874	26987877	PP_1141	braC	extracellular ligand-binding receptor	2.3	3.57E-04	Vanillin	6.4	39402	18	42%	Periplasmic	COG0683	Amino acid transport and metabolism	
1874	26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	2.3	3.57E-04	Vanillin	5.6	38453	10	33%	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
1874	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	2.3	3.57E-04	Vanillin	6.2	45449	6	19%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1874	26988458	PP_1726		ABC transporter periplasmic protein	2.3	3.57E-04	Vanillin	6.0	38636	17	61%	Unknown	COG1840	Inorganic ion transport and metabolism	
1874	26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	2.3	3.57E-04	Vanillin	6.1	41239	5	12%	Cytoplasmic	COG0045	Energy production and conversion	

1883	26990489	PP_3784		hypothetical protein	2.3	1.10E-03	Vanillin	5.4	41070	10	24%	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
1883	26990480	PP_3775		sarcosine oxidase	2.3	1.10E-03	Vanillin	6.4	41164	4	11%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1883	26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	2.3	1.10E-03	Vanillin	5.9	43631	6	18%	Cytoplasmic	COG1448	Amino acid transport and metabolism	
1883	26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	2.3	1.10E-03	Vanillin	5.6	38453	2	6%	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
1883	26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	2.3	1.10E-03	Vanillin	5.7	83310	3	4%	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
1883	26991547	PP_4867		extracellular ligand-binding receptor	2.3	1.10E-03	Vanillin	6.2	40270	16	39%	Periplasmic	COG0683	Amino acid transport and metabolism	
1898	26990480	PP_3775		sarcosine oxidase	4.8	1.99E-04	Vanillin	6.4	41164	6	18%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1898	26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	4.8	1.99E-04	Vanillin	6.3	44262	2	7%	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
1898	26987736	PP_1000	argI	ornithine carbamoyltransferase	4.8	1.99E-04	Vanillin	6.3	37911	3	7%	Cytoplasmic	COG0078	Amino acid transport and metabolism	
1898	26991278	PP_4594		cystathionine gamma-lyase	4.8	1.99E-04	Vanillin	6.4	42503	7	19%	Cytoplasmic	COG0626	Amino acid transport and metabolism	
1898	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	4.8	1.99E-04	Vanillin	6.3	39364	21	56%	Cytoplasmic	COG1062	Energy production and conversion	
1898	26987722	PP_0986	gcvT-1	glycine cleavage system T protein	4.8	1.99E-04	Vanillin	6.4	40319	7	20%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1921	26989192	PP_2469	pheS	phenylalanyl-tRNA synthetase subunit alpha	1.8	4.61E-03	Vanillin	5.2	38082	3	9%	Cytoplasmic	COG0016	Translation, ribosomal structure and biogenesis	
1921	26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	1.8	4.61E-03	Vanillin	5.0	35225	10	33%	Cytoplasmic	COG0113	Coenzyme metabolism	
1921	26988499	PP_1768	serC	phosphoserine aminotransferase	1.8	4.61E-03	Vanillin	5.1	39911	4	12%	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
1921	26987193	PP_0452	tuf	elongation factor Tu	1.8	4.61E-03	Vanillin	5.0	43478	16	40%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
1921	26991091	PP_4402	bkdA2	2-oxoisovalerate dehydrogenase, beta subunit	1.8	4.61E-03	Vanillin	5.2	37143	6	20%	Cytoplasmic	COG0022	Energy production and conversion	
1921	26988684	PP_1957		Pdr/VanB family oxidoreductase	1.8	4.61E-03	Vanillin	4.9	34943	6	23%	Cytoplasmic	COG1018	Energy production and conversion	
1921	26991641	PP_4963	pgk	phosphoglycerate kinase	1.8	4.61E-03	Vanillin	4.9	40005	5	17%	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
1921	26987153	PP_0412		polyamine ABC transporter periplasmic protein	1.8	4.61E-03	Vanillin	5.3	37801	12	36%	Periplasmic	COG0687	Amino acid transport and metabolism	
1921	26988075	PP_1341	ftsA	cell division protein FtsA	1.8	4.61E-03	Vanillin	4.9	47444	3	8%	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
1921	26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.8	4.61E-03	Vanillin	5.3	40672	2	6%	Cytoplasmic	COG0136	Amino acid transport and metabolism	
1922	26987877	PP_1141	braC	extracellular ligand-binding receptor	12.0	7.15E-05	Control	6.4	39402	5	14%	Periplasmic	COG0683	Amino acid transport and metabolism	
1922	26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	12.0	7.15E-05	Control	5.8	40626	5	14%	Cytoplasmic	COG1902	Energy production and conversion	
1922	26990480	PP_3775		sarcosine oxidase	12.0	7.15E-05	Control	6.4	41164	7	19%	Cytoplasmic	COG0665	Amino acid transport and metabolism	
1922	26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	12.0	7.15E-05	Control	5.6	38453	6	18%	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
1922	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	12.0	7.15E-05	Control	6.2	45449	33	66%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1922	26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	12.0	7.15E-05	Control	5.9	43631	4	12%	Cytoplasmic	COG1448	Amino acid transport and metabolism	
1922	26989149	PP_2426		D-isomer specific 2-hydroxyacid dehydrogenase family protein	12.0	7.15E-05	Control	6.0	37781	7	22%	Cytoplasmic	COG1064	General function prediction only	
1922	26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	12.0	7.15E-05	Control	6.1	40690	3	9%	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
1922	26987594	PP_0858		aminotransferase	12.0	7.15E-05	Control	5.9	42436	2	6%	Cytoplasmic	COG0436	Amino acid transport and metabolism	
1922	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	12.0	7.15E-05	Control	6.3	39364	6	15%	Cytoplasmic	COG1062	Energy production and conversion	
1922	26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	12.0	7.15E-05	Control	6.1	41239	6	15%	Cytoplasmic	COG0045	Energy production and conversion	
1998	26988499	PP_1768	serC	phosphoserine aminotransferase	7.6	1.77E-04	Vanillin	5.1	39911	5	13%	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
1998	26990489	PP_3784		hypothetical protein	7.6	1.77E-04	Vanillin	5.4	41070	3	7%	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
1998	26988489	PP_1758		hypothetical protein	7.6	1.77E-04	Vanillin	5.5	35163	5	17%	Cytoplasmic	COG1054	General function prediction only	
1998	26989546	PP_2827		alcohol dehydrogenase, zinc-containing	7.6	1.77E-04	Vanillin	5.4	36735	4	10%	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
1998	26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	7.6	1.77E-04	Vanillin	6.4	40124	5	12%	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
1998	26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	7.6	1.77E-04	Vanillin	5.9	43290	4	11%	Cytoplasmic	COG1448	Amino acid transport and metabolism	
1998	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	7.6	1.77E-04	Vanillin	6.2	45449	2	7%	Periplasmic	COG1653	Carbohydrate transport and metabolism	
1998	26991229	PP_4545		3-oxoacyl-[acyl carrier protein) synthase III	7.6	1.77E-04	Vanillin	5.7	42326	5	13%	Cytoplasmic	COG0332	acyl-carrier-protein	
1998	26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	7.6	1.77E-04	Vanillin	5.5	39542	7	23%	Cytoplasmic	COG4638	Inorganic ion transport and metabolism	General function prediction only
2021	26988489	PP_1758		hypothetical protein	4.8	9.39E-04	Vanillin	5.5	35163	7	29%	Cytoplasmic	COG1054	General function prediction only	
2021	26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	4.8	9.39E-04	Vanillin	5.9	43290	9	31%	Cytoplasmic	COG1448	Amino acid transport and metabolism	
2021	26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	4.8	9.39E-04	Vanillin	5.6	35858	2	6%	Unknown	COG2171	Amino acid transport and metabolism	
2021	26991362	PP_4678	ilvC	ketol-acid reductoisomerase	4.8	9.39E-04	Vanillin	5.4	36370	2	9%	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
2021	26987735	PP_0999	arcC	carbamate kinase	4.8	9.39E-04	Vanillin	5.5	33423	11	40%	Cytoplasmic	COG0549	Amino acid transport and metabolism	
2021	26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	4.8	9.39E-04	Vanillin	5.5	39542	13	49%	Cytoplasmic	COG4638	Inorganic ion transport and metabolism	General function prediction only
2021	26990397	PP_3689		serine/threonine protein phosphatase	4.8	9.39E-04	Vanillin	5.6	37041	5	21%	Cytoplasmic			
2021	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	4.8	9.39E-04	Vanillin	6.4	40068	11	35%	Periplasmic	COG0687	Amino acid transport and metabolism	
2021	26990544	PP_3839		alcohol dehydrogenase	4.8	9.39E-04	Vanillin	5.7	35397	5	20%	Cytoplasmic	COG1064	General function prediction only	
2072	26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2	2.9	1.07E-03	Vanillin	6.8	35284	3	10%	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
2072	26991343	PP_4659	ggt-2	gamma-glutamyltransferase	2.9	1.07E-03	Vanillin	6.0	59835	11	18%	Periplasmic	COG0405	Amino acid transport and metabolism	
2091	26991754	PP_5078	aroB	3-dehydroquinate synthase	1.8	1.52E-02	Vanillin	6.0	39485	8	23%	Cytoplasmic	COG0337	Amino acid transport and metabolism	
2091	26990414	PP_3706		hypothetical protein	1.8	1.52E-02	Vanillin	5.7	35856	6	17%	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
2091	26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.8	1.52E-02	Vanillin	5.9	43290	7	16%	Cytoplasmic	COG1448	Amino acid transport and metabolism	
2091	26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.8	1.52E-02	Vanillin	5.4	36370	6	18%	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
2091	26987735	PP_0999	arcC	carbamate kinase	1.8	1.52E-02	Vanillin	5.5	33423	3	9%	Cytoplasmic	COG0549	Amino acid transport and metabolism	
2091	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.8	1.52E-02	Vanillin	6.4	40068	15	38%	Periplasmic	COG0687	Amino acid transport and metabolism	
2136	26990488	PP_3783		hypothetical protein	4.2	8.14E-04	Control	5.8	34938	12	47%	Cytoplasmic			
2136	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	4.2	8.14E-04	Control	6.4	40068	3	7%	Periplasmic	COG0687	Amino acid transport and metabolism	
2205	26987755	PP_1019	oprB-1	porin B	1.8	3.01E-03	Vanillin	5.9	49646	12	29%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
2205	26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	1.8	3.01E-03	Vanillin	5.6	36424	16	43%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
2225	26988349	PP_1617		S-formylglutathione hydrolase	5.6	2.35E-05	Vanillin	6.4	31637	6	18%	Unknown	COG0627	General function prediction only	
2225	26987615	PP_0879	dppD	oligopeptide/dipeptide ABC transporter ATPase subunit	5.6	2.35E-05	Vanillin	6.3	34914	4	12%	Cytoplasmic Membrane	COG0444	Amino acid transport and metabolism	Inorganic ion transport and metabolism
2225	26989183	PP_2460		inosine/uridine-preferring nucleoside hydrolase	5.6	2.35E-05	Vanillin	6.2	34388	3	9%	Unknown	COG1957	Nucleotide transport and metabolism	
2299	26990444	PP_3737	vanB	ferredoxin	9.3	4.44E-04	Vanillin	4.6	34255	8	23%	Cytoplasmic	COG1018	Energy production and conversion	
2336	26989848	PP_3129	galE	UDP-glucose 4-epimerase	9.1	2.65E-04	Vanillin	6.3	34967	4	12%	Cytoplasmic	COG1087	Cell envelope biogenesis, outer membrane	
2336	26988670	PP_1943	purU	formyltetrahydrofolate deformylase	9.1	2.65E-04	Vanillin	6.4	32061	5	15%	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
2548	26989306	PP_2587		LuxR family transcriptional regulator	9.0	7.36E-05	Vanillin	5.8	31314	2	6%	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
2548	26988672	PP_1945	folD-1	5,10-methylene-tetrahydrofolate dehydrogenase/cyclohydrolase	9.0	7.36E-05	Vanillin	5.7	30531	3	8%	Cytoplasmic	COG0190	Coenzyme metabolism	
2548	26990382	PP_3671		aldo/keto reductase family oxidoreductase	9.0	7.36E-05	Vanillin	5.9	30068	5	17%	Cytoplasmic	COG0656	General function prediction only	
2609	26987810	PP_1074	glpR	DeoR family transcriptional regulator	2.0	3.06E-04	Vanillin	5.7	27749	2	7%	Cytoplasmic	COG1349	Transcription	Carbohydrate transport and metabolism
2609	26989721	PP_3002	aroE-2	shikimate 5-dehydrogenase	2.0	3.06E-04	Vanillin	5.5	29669	3	11%	Cytoplasmic	COG0169	Amino acid transport and metabolism	
2609	26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	2.0	3.06E-04	Vanillin	5.3	30957	3	10%	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
2609	26992070	PP_5395		hypothetical protein	2.0	3.06E-04	Vanillin	5.6	31623	13	46%	Cytoplasmic	COG1568	General function prediction only	
2611	26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	7.0	2.92E-06	Vanillin	5.3	27212	6	23%	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
2765	26991700	PP_5024		amino acid ABC transporter periplasmic amino acid-binding protein	14.0	1.46E-04	Control	8.6	29848	3	8%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
2765	26991558	PP_4879		RNA methyltransferase	14.0	1.46E-04	Control	6.8	27014	2	9%	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis	
2765	26987759	PP_1023	pgl	6-phosphogluconolactonase	14.0	1.46E-04	Control	6.7	25476	10	44%	Unknown	COG0363	Carbohydrate transport and metabolism	
2844	26991429	PP_4748		amino acid ABC transporter periplasmic amino acid-binding protein	7.0	1.43E-04	Control	5.4	28338	2	9%	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
2844	148546305	Pput_1062		keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	7.0	1.43E-04	Control	5.4	24085	9	45%	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
2869	26990958	PP_4267	recR	recombination protein RecR	1.8	8.82E-03	Vanillin	6.0	21613	3	20%	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
2869	26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.8	8.82E-03	Vanillin	7.5	26000	3	15%	Cytoplasmic Membrane	COG0479	Energy production and conversion	
2869	26986970	PP_0227		cystine transporter subunit	1.8	8.82E-03	Vanillin	8.7	28756	16	40%	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
2929	26989016	PP_2292		hypothetical protein	2.9	9.16E-05	Vanillin	5.8	28522	3	15%	Cytoplasmic			
2962	26991411	PP_4728	grpE	heat shock protein GrpE	13.0	1.46E-03	Vanillin	4.7	20531	3	12%	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
2962	26991829	PP_5153		fumarylacetoacetate (FAA) hydrolase	13.0	1.46E-03	Vanillin	4.7	23906	2	8%	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
2962	148549997	Pput_4795		NUDIX hydrolase	13.0	1.46E-03	Vanillin	4.6	23119	2	8%	Cytoplasmic			
2989	26991411	PP_4728	grpE	heat shock protein GrpE	4.1	4.61E-05	Vanillin	4.7	20531	5	27%	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
2989	26990657	PP_3952	pcaJ	3-oxoadipate CoA-transferase, subunit B	5.1	4.61E-05	Vanillin	4.7	22552	3	21%	Cytoplasmic	COG2057	Lipid metabolism	
3011	26991435	PP_4754		TetR family transcriptional regulator	14.0	8.20E-05	Vanillin	5.2	24816	2	5%	Unknown	COG1309	Transcription	
3011	26990656	PP_3951	pcaI	3-oxoadipate CoA-transferase, subunit A	14.0	8.20E-05	Vanillin	5.3	24319	7	29%	Cytoplasmic	COG1788	Lipid metabolism	
3237	26992091	PP_5416	atpH	F0F1 ATP synthase subunit delta	3.0	3.08E-05	Vanillin	5.7	19197	2	10%	Cytoplasmic	COG0712	Energy production and conversion	
3345	26991658	PP_4981		hypothetical protein	2.3	1.34E-03	Vanillin	8.8	22129	9	52%	Unknown	COG2353	Function unknown	

3749	26987256	PP_0518	nusB	transcription antitermination protein NusB	4.7	6.52E-06	Vanillin	6.5	18648	3	16%	Cytoplasmic	COG0781	Transcription
3749	26991516	PP_4836		hypothetical protein	4.7	6.52E-06	Vanillin	6.5	17387	2	12%	Periplasmic	COG2847	Inorganic ion transport and metabolism
3749	26989622	PP_2903	ppiB	peptidyl-prolyl cis-trans isomerase B	4.7	6.52E-06	Vanillin	6.5	18200	2	12%	Cytoplasmic	COG0652	Posttranslational modification, protein turnover, chaperones
4355	26988115	PP_1381	pcaC	4-carboxymuconolactone decarboxylase	4.9	7.60E-05	Vanillin	6.4	14802	2	15%	Unknown	COG0599	Function unknown



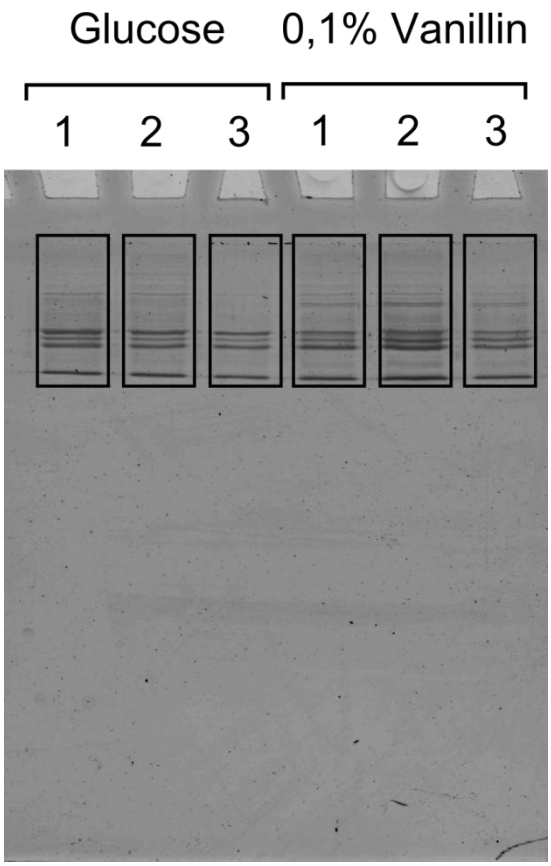
Differenziell regulierte Spots zwischen auf 6,6 mM (0,1%) Vanillin und 10 mM Glucose kultiviertem *P. putida* GN235 (pH 4-7). A) zeigt das Gelbild einer unbehandelten, B) das Gelbild einer behandelten Probe. Spots, welche durch einen Kreis markiert sind, waren in auf 6,6 mM (0,1%) Vanillin kultivierten Zellen nach oben, Spots, welche durch ein Rechteck gekennzeichnet sind, nach unten reguliert. Die in den einzelnen Spots identifizierten Proteine, sowie die Regulationsfaktoren der Spots sind in der zugehörigen Tabelle (siehe Excel-Datei) aufgeführt. Markierte Spots, welche im Gelbild, nicht jedoch in der Tabelle zu finden sind, konnten nicht identifiziert werden. Aus Platzgründen wurden einige Spots mit Buchstaben bezeichnet: A)1557, B)1684, C)1677, D)1528, E)1401

Spotnummer	gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Sequenzabdeckung	Lokalisation	COG ID	COG Funktion	COG Funktion 2
975	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.7	3.74E-06	Vanillin	6.4	71796	26	39%	Cytoplasmic	COG0365	Lipid metabolism	
982	26991173	PP_4487	acsA	acetyl-CoA synthetase	3.4	2.48E-04	Vanillin	6.4	71796	8	16%	Cytoplasmic	COG0365	Lipid metabolism	
982	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	3.4	2.48E-04	Vanillin	6.3	49912	2	7%	Cytoplasmic	COG1249	Energy production and conversion	
1004	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.9	4.22E-04	Control	5.4	79899	5	7%	Cytoplasmic	COG2838	Energy production and conversion	
1004	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.9	4.22E-04	Control	5.3	55654	29	49%	Cytoplasmic	COG0508	Energy production and conversion	
1005	26991518	PP_4838	oprC	TonB-dependent copper receptor	2.6	5.80E-04	Vanillin	6.2	74540	30	55%	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
1050	26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	2.2	1.43E-04	Vanillin	5.8	65671	2	3%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1050	26987139	PP_0397		serine protein kinase, PrkA	2.2	1.43E-04	Vanillin	5.8	73782	44	70%	Cytoplasmic	COG2766	Signal transduction mechanisms	
1050	26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	2.2	1.43E-04	Vanillin	6.2	63448	30	50%	Cytoplasmic Membrane	COG1053	Energy production and conversion	
1084	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	6.2	1.70E-06	Vanillin	7.0	69173	21	34%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1084	26990840	PP_4147		peptide ABC transporter periplamic peptide-binding protein	6.2	1.70E-06	Vanillin	7.2	69637	13	22%	Periplasmic	COG4166	Amino acid transport and metabolism	
1092	26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	3.8	3.73E-04	Control	6.5	67609	11	21%	Cytoplasmic	COG0649	Energy production and conversion	
1092	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	3.8	3.73E-04	Control	7.0	69173	7	13%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1092	26987746	PP_1010	edd	phosphogluconate dehydratase	3.8	3.73E-04	Control	6.4	65359	27	47%	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
1093	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	21	2.71E-06	Vanillin	7.0	69173	36	60%	Periplasmic	COG4993	Carbohydrate transport and metabolism	
1124	26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	4.9	2.27E-06	Control	5.4	79899	4	6%	Cytoplasmic	COG2838	Energy production and conversion	
1124	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	4.9	2.27E-06	Control	5.3	65626	27	41%	Cytoplasmic	COG5016	Energy production and conversion	
1124	26987410	PP_0674		ABC transporter ATP-binding protein	4.9	2.27E-06	Control	5.3	61860	5	8%	Cytoplasmic	COG0488	General function prediction only	
1196	26992022	PP_5346	oadA	pyruvate carboxylase subunit B	2.5	2.30E-04	Vanillin	5.3	65626	13	19%	Cytoplasmic	COG5016	Energy production and conversion	
1196	26987499	PP_0763		long-chain-fatty-acid--CoA ligase	2.5	2.30E-04	Vanillin	5.5	62125	2	3%	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1196	26987948	PP_1213	aspS	aspartyl-tRNA synthetase	2.5	2.30E-04	Vanillin	5.1	66568	11	21%	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
1196	26987137	PP_0395		SpoVR family protein	2.5	2.30E-04	Vanillin	5.4	61330	13	28%	Cytoplasmic	COG2719	Function unknown	
1213	26991385	PP_4701	pgi	Control-6-phosphate isomerase	1.9	3.42E-04	Vanillin	6.8	61455	16	27%	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
1213	26990704	PP_3999	cobA-2	uroporphyrin-III C-methyltransferase	1.9	3.42E-04	Vanillin	6.8	49494	3	6%	Cytoplasmic	COG0007	Coenzyme metabolism	
1213	24986535	not in database			1.9	3.42E-04	Vanillin			7	12%				
1213	26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	1.9	3.42E-04	Vanillin	7.1	60366	19	40%	Periplasmic	COG0747	Amino acid transport and metabolism	
1213	26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.9	3.42E-04	Vanillin	6.8	62781	5	9%	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
1255	26988095	PP_1361	groEL	chaperonin GroEL	2.4	4.92E-05	Vanillin	4.7	56743	2	8%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1255	26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	2.4	4.92E-05	Vanillin	5.8	51676	5	11%	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
1255	26987283	PP_0545		aldehyde dehydrogenase family protein	2.4	4.92E-05	Vanillin	5.9	55268	30	61%	Cytoplasmic	COG1012	Energy production and conversion	
1255	26990751	PP_4050	glgA	glycogen synthase	2.4	4.92E-05	Vanillin	6.0	57190	5	12%	Cytoplasmic	COG0297	Carbohydrate transport and metabolism	
1255	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	2.4	4.92E-05	Vanillin	6.3	49912	3	7%	Cytoplasmic	COG1249	Energy production and conversion	
1265	26991859	PP_5183		glutamine synthetase	2.5	3.94E-04	Vanillin	4.8	50877	3	6%	Cytoplasmic	COG0174	Amino acid transport and metabolism	
1265	26987192	PP_0451	fusA	elongation factor G	2.5	3.94E-04	Vanillin	4.9	78817	4	5%	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
1265	26990407	PP_3699		hypothetical protein	2.5	3.94E-04	Vanillin	6.1	63413	4	7%	Cytoplasmic	COG2849	Function unknown	
1265	26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2.5	3.94E-04	Vanillin	4.9	54767	12	18%	Cytoplasmic	COG1951	Energy production and conversion	
1265	26988095	PP_1361	groEL	chaperonin GroEL	2.5	3.94E-04	Vanillin	4.7	56743	6	11%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1265	26991410	PP_4727	dnaK	molecular chaperone DnaK	2.5	3.94E-04	Vanillin	4.6	68800	3	5%	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
1265	26987768	PP_1032	guaA	GMP synthase	2.5	3.94E-04	Vanillin	5.2	58204	3	6%	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
1301	26987283	PP_0545		aldehyde dehydrogenase family protein	6.1	1.74E-07	Vanillin	5.9	55268	15	24%	Cytoplasmic	COG1012	Energy production and conversion	
1301	26989399	PP_2680		aldehyde dehydrogenase family protein	6.1	1.74E-07	Vanillin	5.5	54903	19	80%	Cytoplasmic	COG1012	Energy production and conversion	
1308	26988072	PP_1338	murC	UDP-N-acetylmuramate--L-alanine ligase	2.8	6.73E-05	Vanillin	6.3	52166	3	6%	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
1308	26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	2.8	6.73E-05	Vanillin	6.3	49912	9	20%	Cytoplasmic	COG1249	Energy production and conversion	
1308	26991751	PP_5075	gltD	glutamate synthase subunit beta	2.8	6.73E-05	Vanillin	6.3	51819	5	11%	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
1308	26986899	PP_0154		acetyl-CoA hydrolase/transferase family protein	2.8	6.73E-05	Vanillin	6.1	53957	4	8%	Cytoplasmic	COG0427	Energy production and conversion	
1308	26988675	PP_1948		benzaldehyde dehydrogenase	2.8	6.73E-05	Vanillin	6.2	52881	20	47%	Cytoplasmic	COG1012	Energy production and conversion	
1313	26991987	PP_5311		signal transduction protein	2.1	3.99E-04	Vanillin	5.9	51775	3	6%	Cytoplasmic	COG1639	Signal transduction mechanisms	
1313	26991060	PP_4371	fleR	two component, sigma54 specific, transcriptional regulator, Fis family	2.1	3.99E-04	Vanillin	5.9	49058	2	7%	Cytoplasmic	COG2204	Signal transduction mechanisms	
1313	26988026	PP_1291		PhoH family protein	2.1	3.99E-04	Vanillin	5.7	51856	5	13%	Cytoplasmic	COG1875	General function prediction only	
1333	26990493	PP_3788		non-ribosomal peptide synthetase	3.3	3.76E-05	Control	6.7	56336	7	13%	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
1333	26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	3.3	3.76E-05	Control	6.5	51942	25	52%	Cytoplasmic	COG0439	Lipid metabolism	
1333	26988106	PP_1372		hypothetical protein	3.3	3.76E-05	Control	6.5	52321	6	13%	Unknown	COG0433	Replication, recombination, and repair	
1333	26990373	PP_3662		decarboxylase family protein	3.3	3.76E-05	Control	6.7	50729	5	11%	Cytoplasmic	COG1611	General function prediction only	
1333	26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	3.3	3.76E-05	Control	6.5	49088	8	18%	Cytoplasmic	COG0439	Lipid metabolism	
1401	26987737	PP_1001	arcA	arginine deiminase	4.1	9.14E-05	Vanillin	5.7	46462	23	60%	Cytoplasmic	COG2235	Amino acid transport and metabolism	
1401	26991567	PP_4889	purA	adenylosuccinate synthetase	4.1	9.14E-05	Vanillin	5.6	46833	6	17%	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
1401	26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	4.1	9.14E-05	Vanillin	5.7	50918	3	8%	Unknown	COG1012	Energy production and conversion	
1422	26987824	PP_1088	argG	argininosuccinate synthase	3.2	4.02E-05	Vanillin	5.1	45164	11	27%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
1422	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	3.2	4.02E-05	Vanillin	5.2	55352	10	21%	Cytoplasmic	COG0056	Energy production and conversion	
1422	26987948	PP_1213	aspS	aspartyl-tRNA synthetase	3.2	4.02E-05	Vanillin	5.1	66568	7	13%	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
1422	26990810	PP_4116	aceA	isocitrate lyase	3.2	4.02E-05	Vanillin	5.3	48633	21	49%	Cytoplasmic	COG2224	Energy production and conversion	
1438	26988204	PP_1471	thrC	threonine synthase	2.5	1.07E-04	Vanillin	6.2	51645	2	4%	Cytoplasmic	COG0498	Amino acid transport and metabolism	
1438	26990810	PP_4116	aceA	isocitrate lyase	2.5	1.07E-04	Vanillin	5.3	48633	3	7%	Cytoplasmic	COG2224	Energy production and conversion	
1438	26988486	PP_1755	fumC-2	fumarate hydratase	2.5	1.07E-04	Vanillin	6.4	49131	12	21%	Cytoplasmic	COG0114	Energy production and conversion	
1438	26990501	PP_3796		L-ornithine N5-oxygenase	2.5	1.07E-04	Vanillin	6.5	50047	5	10%	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
1438	26991858	PP_5182		aminotransferase	2.5	1.07E-04	Vanillin	6.2	49871	6	11%	Cytoplasmic	COG0161	Coenzyme metabolism	
1473	26990490	PP_3785		hypothetical protein	5.9	1.27E-04	Vanillin	6.5	50495	10	25%	Cytoplasmic			
1473	26990501	PP_3796		L-ornithine N5-oxygenase	5.9	1.27E-04	Vanillin	6.5	50047	5	11%	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
1473	26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	5.9	1.27E-04	Vanillin	6.5	48194	18	57%	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
1490	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	8.1	7.92E-06	Vanillin	5.3	55654	2	5%	Cytoplasmic	COG0508	Energy production and conversion	
1490	26990248	PP_3536		hypothetical protein	8.1	7.92E-06	Vanillin	4.4	41469	26	68%	Cytoplasmic			
1525	26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	8.4	4.13E-06	Vanillin	5.9	48114	4	9%	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
1525	26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	8.4	4.13E-06	Vanillin	6.1	45417	7	17%	Cytoplasmic	COG0014	Amino acid transport and metabolism	
1525	26988671	PP_1944		aminomethyltransferase	8.4	4.13E-06	Vanillin	6.0	48129	24	44%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1525	26987407	PP_0671	glyA	serine hydroxymethyltransferase	8.4	4.13E-06	Vanillin	6.2	44897	6	12%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
1526	26986828	PP_0083	trpB	tryptophan synthase subunit beta	2.4	1.34E-04	Control	6.4	44046	11	35%	Cytoplasmic	COG0133	Amino acid transport and metabolism	
1526	26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	2.4	1.34E-04	Control	6.1	45417	5	12%	Cytoplasmic	COG0014	Amino acid transport and metabolism	
1526	26987411	PP_0675	gdhA	glutamate dehydrogenase	2.4	1.34E-04	Control	6.5	48871	6	13%	Unknown	COG0334	Amino acid transport and metabolism	
1526	26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.4	1.34E-04	Control	6.2	44897	3	6%	Cytoplasmic	COG0112	Amino acid transport and metabolism	
1527	26991159	PP_4473		aspartate kinase	3.1	2.03E-04	Vanillin	5.0	44605	5	12%	Cytoplasmic	COG0527	Amino acid transport and metabolism	
1527	26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	3.1	2.03E-04	Vanillin	5.3	55654	2	3%	Cytoplasmic	COG0508	Energy production and conversion	
1527	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	3.1	2.03E-04	Vanillin	5.2	55352	15	27%	Cytoplasmic	COG0056	Energy production and conversion	
1527	26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	3.1	2.03E-04	Vanillin	5.2	44973	2	4%	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
1527	26990739	PP_4037		oxidoreductase	3.1	2.03E-04	Vanillin	5.5	48815	14	37%	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
1527	26987590	PP_0854	hisS	histidyl-tRNA synthetase	3.1	2.03E-04	Vanillin	5.1	47738	4	11%	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
1527	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	3.1	2.03E-04	Vanillin	5.4	45695	16	34%	Unknown	COG0538	Energy production and conversion	
1527	26988361	PP_1629	recA	recombinase A	3.1	2.03E-04	Vanillin	5.3	37545	5	16%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1527	26988095	PP_1361	groEL	chaperonin GroEL	3.1	2.03E-04	Vanillin	4.7	56743	5	12%	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
1528	26990415	PP_3707		hypothetical protein	1.8	1.57E-03	Vanillin	5.4	52925	10	22%	Cytoplasmic			
1528	26990737	PP_4034		allantoate amidohydrolase	1.8	1.57E-03	Vanillin	5.7	45010	16	43%	Cytoplasmic	COG0624	Amino acid transport and metabolism	
1528	26986928	PP_0184	argH	argininosuccinate lyase	1.8	1.57E-03	Vanillin	5.4	52061	5	8%	Cytoplasmic	COG0165	Amino acid transport and metabolism	
1528	26988361	PP_1629	recA	recombinase A	1.8	1.57E-03	Vanillin	5.3	37545	14	52%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1528	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.8	1.57E-03	Vanillin	5.7	45178	12	32%	Cytoplasmic	COG0001	Coenzyme metabolism	
1528	26988671	PP_1944		aminomethyltransferase	1.8	1.57E-03	Vanillin	6.0	48129	2	5%	Cytoplasmic	COG0404	Amino acid transport and metabolism	
1528	26991304	PP_4620		fumarylacetoacetase	1.8	1.57E-03	Vanillin	5.9	46325	2	5%	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
1538	26987824	PP_1088	argG	argininosuccinate synthase	2.2	1.93E-05	Vanillin	5.1	45164	7	17%	Cytoplasmic	COG0137	Amino acid transport and metabolism	
1538	26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	2.2	1.93E-05	Vanillin	5.2	44973	9	22%	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
1538	26990739	PP_4037		oxidoreductase	2.2	1.93E-05	Vanillin	5.5	48815	5	12%	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
1538	26991676	PP_4999	pyrC	dihydroorotase	2.2	1.93E-05	Vanillin	5.4	44116	12	29%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
1538	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	2.2	1.93E-05	Vanillin	5.4	45695	8	19%	Unknown	COG0538	Energy production and conversion	
1538	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	2.2	1.93E-05	Vanillin	6.3	39364	2	6%	Cytoplasmic	COG1062	Energy production and conversion	
1538	26987058	PP_0316		oxidoreductase FAD-binding domain protein	2.2	1.93E-05	Vanillin	5.1	40675	6	16%	Cytoplasmic	COG1018	Energy production and conversion	
1538	26987948	PP_1213	aspS	aspartyl-tRNA synthetase	2.2	1.93E-05	Vanillin	5.1	66568	6	10%	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
1538	26990810	PP_4116	aceA	isocitrate lyase	2.2	1.93E-05	Vanillin	5.3	48633	5	11%	Cytoplasmic	COG2224	Energy production and conversion	
1557	26987468	PP_0732	hemA	glutamyl-tRNA reductase	3.4	1.10E-05	Vanillin	5.5	46305	4	10%	Cytoplasmic	COG0373	Coenzyme metabolism	
1557	26987515	PP_0779		methyl-accepting chemotaxis transducer/sensory box protein	3.4	1.10E-05	Vanillin	6.2	49856	3	7%	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
1557	26990739	PP_4037		oxidoreductase	3.4	1.10E-05	Vanillin	5.5	48815	10	25%	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
1557	26991676	PP_4999	pyrC	dihydroorotase	3.4	1.10E-05	Vanillin	5.4	44116	3	8%	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
1557	26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	3.4	1.10E-05	Vanillin	5.7	45178	5	14%	Cytoplasmic	COG0001	Coenzyme metabolism	
1557	26988361	PP_1629	recA	recombinase A	3.4	1.10E-05	Vanillin	5.3	37545	2	6%	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
1557	26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	3.4	1.10E-05	Vanillin	5.4	45695	24	66%	Unknown	COG0538	Energy production and conversion	
1557	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	3.4	1.10E-05	Vanillin	5.3	43264	6	15%	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
1557	26988462	PP_1730		aminopeptidase 2	3.4	1.10E-05	Vanillin	5.6	46996	5	11%	Cytoplasmic	COG1362	Amino acid transport and metabolism	

1557	26991474	PP_4794	leuS	leucyl-tRNA synthetase	3.4	1.10E-05	Vanillin	5.6	96697	2	3%	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis
1593	148547246	Pput_2024		outer membrane porin	3.1	1.52E-03	Control	5.3	45897	4	16%	Outer Membrane		
1593	26988847	PP_2123	moeA	molybdopterin biosynthesis MoeA protein	3.1	1.52E-03	Control	5.1	43963	3	9%	Cytoplasmic	COG0303	Coenzyme metabolism
1593	26987181	PP_0440	tuf	elongation factor Tu	3.1	1.52E-03	Control	5.0	43495	12	34%	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis
1593	26987755	PP_1019	oprB-1	porin B	3.1	1.52E-03	Control	5.9	49646	17	37%	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane
1593	26989061	PP_2337		hypothetical protein	3.1	1.52E-03	Control	5.2	41312	6	19%	Cytoplasmic	COG2828	Function unknown
1593	26991645	PP_4967	metK	S-adenosylmethionine synthetase	3.1	1.52E-03	Control	5.1	42779	9	27%	Cytoplasmic	COG0192	Coenzyme metabolism
1615	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	6.6	9.85E-06	Vanillin	6.0	41851	17	33%	Cytoplasmic	COG0183	Lipid metabolism
1615	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	6.6	9.85E-06	Vanillin	6.3	44339	4	10%	Cytoplasmic	COG0111	Amino acid transport and metabolism
1615	26989029	PP_2305		patatin	6.6	9.85E-06	Vanillin	5.9	38234	2	6%	Cytoplasmic	COG1752	General function prediction only
1615	26987578	PP_0842	iscS	cysteine desulfurase	6.6	9.85E-06	Vanillin	6.2	44468	6	13%	Cytoplasmic	COG1104	Amino acid transport and metabolism
1615	26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	6.6	9.85E-06	Vanillin	6.1	44824	6	15%	Cytoplasmic	COG0160	Amino acid transport and metabolism
1643	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	4.3	2.55E-05	Vanillin	6.3	44339	4	11%	Cytoplasmic	COG0111	Amino acid transport and metabolism
1643	26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	4.3	2.55E-05	Vanillin	6.5	45235	17	66%	Cytoplasmic	COG2873	Amino acid transport and metabolism
1643	26987736	PP_1000	argI	ornithine carbamoyltransferase	4.3	2.55E-05	Vanillin	6.3	37911	5	14%	Cytoplasmic	COG0078	Amino acid transport and metabolism
1643	26991278	PP_4594		cystathionine gamma-lyase	4.3	2.55E-05	Vanillin	6.4	42503	8	19%	Cytoplasmic	COG0626	Amino acid transport and metabolism
1643	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	4.3	2.55E-05	Vanillin	6.3	39364	23	60%	Cytoplasmic	COG1062	Energy production and conversion
1650	26990491	PP_3786		aminotransferase	4.1	3.85E-07	Vanillin	6.4	44067	2	6%	Cytoplasmic	COG0436	Amino acid transport and metabolism
1650	26987722	PP_0986	gcvT-1	glycine cleavage system T protein	4.1	3.85E-07	Vanillin	6.4	40319	3	8%	Cytoplasmic	COG0404	Amino acid transport and metabolism
1650	148549948	Pput_4746		nicotinate phosphoribosyltransferase	4.1	3.85E-07	Vanillin	6.4	46205	8	19%	Cytoplasmic	COG1488	Coenzyme metabolism
1650	26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	4.1	3.85E-07	Vanillin	6.5	45235	5	11%	Cytoplasmic	COG2873	Amino acid transport and metabolism
1650	26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	4.1	3.85E-07	Vanillin	6.3	44339	6	16%	Cytoplasmic	COG0111	Amino acid transport and metabolism
1650	26987736	PP_1000	argI	ornithine carbamoyltransferase	4.1	3.85E-07	Vanillin	6.3	37911	24	55%	Cytoplasmic	COG0078	Amino acid transport and metabolism
1650	26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	4.1	3.85E-07	Vanillin	6.3	39364	5	13%	Cytoplasmic	COG1062	Energy production and conversion
1677	26990489	PP_3784		hypothetical protein	2.8	4.89E-05	Vanillin	5.4	41070	10	32%	Unknown	COG0251	Translation, ribosomal structure and biogenesis
1677	26987877	PP_1141	braC	extracellular ligand-binding receptor	2.8	4.89E-05	Vanillin	6.4	39402	2	5%	Periplasmic	COG0683	Amino acid transport and metabolism
1677	26990480	PP_3775		sarcosine oxidase	2.8	4.89E-05	Vanillin	6.4	41164	7	20%	Cytoplasmic	COG0665	Amino acid transport and metabolism
1677	26991120	PP_4432		peptidase, M24 family protein	2.8	4.89E-05	Vanillin	5.6	41581	2	5%	Cytoplasmic	COG0006	Amino acid transport and metabolism
1677	26991547	PP_4867		extracellular ligand-binding receptor	2.8	4.89E-05	Vanillin	6.2	40270	14	41%	Periplasmic	COG0683	Amino acid transport and metabolism
1684	26990489	PP_3784		hypothetical protein	2.9	3.63E-05	Vanillin	5.4	41070	2	5%	Unknown	COG0251	Translation, ribosomal structure and biogenesis
1684	26987877	PP_1141	braC	extracellular ligand-binding receptor	2.9	3.63E-05	Vanillin	6.4	39402	14	33%	Periplasmic	COG0683	Amino acid transport and metabolism
1684	26990480	PP_3775		sarcosine oxidase	2.9	3.63E-05	Vanillin	6.4	41164	2	6%	Cytoplasmic	COG0665	Amino acid transport and metabolism
1684	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	2.9	3.63E-05	Vanillin	6.2	45449	3	11%	Periplasmic	COG1653	Carbohydrate transport and metabolism
1684	26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	2.9	3.63E-05	Vanillin	6.0	41851	5	12%	Cytoplasmic	COG0183	Lipid metabolism
1684	26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	2.9	3.63E-05	Vanillin	5.6	38453	4	11%	Cytoplasmic	COG0191	Carbohydrate transport and metabolism
1684	26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	2.9	3.63E-05	Vanillin	5.3	43264	2	4%	Cytoplasmic	COG0304	Lipid metabolism
1684	26988458	PP_1726		ABC transporter periplasmic protein	2.9	3.63E-05	Vanillin	6.0	38636	12	38%	Unknown	COG1840	Inorganic ion transport and metabolism
1717	26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	5.4	3.92E-04	Control	5.8	40626	6	17%	Cytoplasmic	COG1902	Energy production and conversion
1717	26990480	PP_3775		sarcosine oxidase	5.4	3.92E-04	Control	6.4	41164	4	11%	Cytoplasmic	COG0665	Amino acid transport and metabolism
1717	26989778	PP_3059	gpFI	pyocin R2_PP, tail sheath protein	5.4	3.92E-04	Control	5.8	41702	2	4%	Unknown	COG3497	General function prediction only
1717	26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	5.4	3.92E-04	Control	6.2	45449	23	49%	Periplasmic	COG1653	Carbohydrate transport and metabolism
1717	26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	5.4	3.92E-04	Control	5.9	43631	3	8%	Cytoplasmic	COG1448	Amino acid transport and metabolism
1717	26989149	PP_2426		D-isomer specific 2-hydroxyacid dehydrogenase family protein	5.4	3.92E-04	Control	6.0	37781	5	17%	Cytoplasmic	COG1064	General function prediction only
1717	26988516	PP_1785	rmlB	dTDP-Control 4,6-dehydratase	5.4	3.92E-04	Control	6.1	40690	2	5%	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane
1717	26989228	PP_2505		GAF domain/GGDEF domain-containing protein	5.4	3.92E-04	Control	6.0	38522	2	6%	Cytoplasmic	COG3706	Signal transduction mechanisms
1717	26991338	PP_4654	trmA	tRNA (uracil-5-)-methyltransferase	5.4	3.92E-04	Control	5.7	40878	2	5%	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis
1717	26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	5.4	3.92E-04	Control	6.1	41239	6	17%	Cytoplasmic	COG0045	Energy production and conversion
1750	26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2	2.8	7.43E-04	Vanillin	6.8	35284	7	24%	Cytoplasmic	COG0175	Amino acid transport and metabolism
1750	26991343	PP_4659	ggt-2	gamma-glutamyltransferase	2.8	7.43E-04	Vanillin	6.0	59835	16	30%	Periplasmic	COG0405	Amino acid transport and metabolism
1750	26988560	PP_1830	aroC	chorismate synthase	2.8	7.43E-04	Vanillin	6.5	38987	2	6%	Cytoplasmic	COG0082	Amino acid transport and metabolism
1851	26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	3.6	3.55E-06	Vanillin	6.4	40068	11	36%	Periplasmic	COG0687	Amino acid transport and metabolism
1851	26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	3.6	3.55E-06	Vanillin	6.4	40124	3	8%	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane
1851	26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	3.6	3.55E-06	Vanillin	5.6	35858	12	38%	Unknown	COG2171	Amino acid transport and metabolism
1851	26991362	PP_4678	ilvC	ketol-acid reductoisomerase	3.6	3.55E-06	Vanillin	5.4	36370	4	13%	Cytoplasmic	COG0059	Amino acid transport and metabolism
1851	26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	3.6	3.55E-06	Vanillin	5.5	39542	15	60%	Cytoplasmic	COG4638	Inorganic ion transport and metabolism
1883	26987847	PP_1111		synthetase	3.9	4.37E-05	Control	6.0	29406	2	8%	Cytoplasmic	COG2872	General function prediction only
1883	26987498	PP_0762	hprA	glycerate dehydrogenase	3.9	4.37E-05	Control	6.1	34094	2	6%	Cytoplasmic	COG1052	Energy production and conversion
1883	26990488	PP_3783		hypothetical protein	3.9	4.37E-05	Control	5.8	34938	19	52%	Cytoplasmic		
1883	26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	3.9	4.37E-05	Control	5.5	39542	2	6%	Cytoplasmic	COG4638	Inorganic ion transport and metabolism
1921	26987615	PP_0879	dppD	oligopeptide/dipeptide ABC transporter ATPase subunit	5.6	1.44E-03	Vanillin	6.3	34914	12	43%	Cytoplasmic Membrane	COG0444	Amino acid transport and metabolism
1921	26989183	PP_2460		inosine/uridine-preferring nucleoside hydrolase	5.6	1.44E-03	Vanillin	6.2	34388	2	7%	Unknown	COG1957	Nucleotide transport and metabolism
1921	26988349	PP_1617		S-formylglutathione hydrolase	5.6	1.44E-03	Vanillin	6.4	31637	4	12%	Unknown	COG0627	General function prediction only
1921	26987478	PP_0742		hypothetical protein	5.6	1.44E-03	Vanillin	6.2	36114	4	14%	Unknown	COG3380	General function prediction only
1970	26991255	PP_4571	cysK	cysteine synthase A	2.4	7.86E-04	Vanillin	5.5	34357	3	10%	Cytoplasmic	COG0031	Amino acid transport and metabolism
1970	26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein	2.4	7.86E-04	Vanillin	5.6	36424	18	46%	Periplasmic	COG0834	Amino acid transport and metabolism
1970	26990907	PP_4215		hypothetical protein	2.4	7.86E-04	Vanillin	6.2	32723	2	6%	Unknown	COG1262	Function unknown
1970	26989058	PP_2334	prpB	2-methylisocitrate lyase	2.4	7.86E-04	Vanillin	5.4	31811	4	14%	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
1970	26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	2.4	7.86E-04	Vanillin	###	26214	3	12%	Cytoplasmic	COG3937	Function unknown
1970	26988892	PP_2168	tal	transaldolase B	2.4	7.86E-04	Vanillin	5.0	33615	2	7%	Unknown	COG0176	Carbohydrate transport and metabolism
2045	26989848	PP_3129	galE	UDP-Control 4-epimerase	6.1	9.94E-08	Vanillin	6.3	34967	9	31%	Cytoplasmic	COG1087	Cell envelope biogenesis, outer membrane
2045	26988670	PP_1943	purU	formyltetrahydrofolate deformylase	6.1	9.94E-08	Vanillin	6.4	32061	14	55%	Cytoplasmic	COG0788	Nucleotide transport and metabolism
2045	26987747	PP_1011	glk	glucokinase	6.1	9.94E-08	Vanillin	6.5	33904	10	30%	Cytoplasmic	COG0837	Carbohydrate transport and metabolism
2045	26987743	PP_1007		anti-FecI sigma factor, FecR	6.1	9.94E-08	Vanillin	7.4	39115	2	6%	Periplasmic	COG3712	Inorganic ion transport and metabolism
2209	26990495	PP_3790	dapF	diaminopimelate epimerase	2.7	1.12E-05	Vanillin	6.0	29286	5	20%	Cytoplasmic	COG0253	Amino acid transport and metabolism
2209	26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.7	1.12E-05	Vanillin	6.2	30111	7	31%	Cytoplasmic	COG0074	Energy production and conversion
2209	26987038	PP_0296		glycine betaine/L-proline ABC transporter periplasmic protein	2.7	1.12E-05	Vanillin	6.6	34568	12	41%	Unknown	COG2113	Amino acid transport and metabolism
2244	26989306	PP_2587		LuxR family transcriptional regulator	4.2	1.06E-03	Vanillin	5.8	31314	3	10%	Cytoplasmic	COG2197	Signal transduction mechanisms
2244	26988672	PP_1945	folD-1	5,10-methylene-tetrahydrofolate dehydrogenase/cyclohydrolase	4.2	1.06E-03	Vanillin	5.7	30531	5	15%	Cytoplasmic	COG0190	Coenzyme metabolism
2244	26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	4.2	1.06E-03	Vanillin	6.2	30111	2	7%	Cytoplasmic	COG0074	Energy production and conversion
2244	26990382	PP_3671		aldo/keto reductase family oxidoreductase	4.2	1.06E-03	Vanillin	5.9	30068	7	28%	Cytoplasmic	COG0656	General function prediction only
2247	26992070	PP_5395		hypothetical protein	2.2	7.79E-05	Vanillin	5.6	31623	13	45%	Cytoplasmic	COG1568	General function prediction only
2247	26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	2.2	7.79E-05	Vanillin	6.2	30111	5	17%	Cytoplasmic	COG0074	Energy production and conversion
2247	26989721	PP_3002	aroE-2	shikimate 5-dehydrogenase	2.2	7.79E-05	Vanillin	5.5	29669	2	7%	Cytoplasmic	COG0169	Amino acid transport and metabolism
2297	33807707	not in database			4.1	3.25E-06	Vanillin			2	7%			
2297	26988632	PP_1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	4.1	3.25E-06	Vanillin	5.2	27809	7	31%	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane
2297	26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	4.1	3.25E-06	Vanillin	5.3	27212	11	45%	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
2436	26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase	3.4	2.38E-05	Vanillin	5.1	28656	4	15%	Unknown	COG0596	General function prediction only
2436	26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	3.4	2.38E-05	Vanillin	5.2	55352	2	5%	Cytoplasmic	COG0056	Energy production and conversion
2436	26987034	PP_0292	hisA	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	3.4	2.38E-05	Vanillin	4.9	25907	9	42%	Cytoplasmic	COG0106	Amino acid transport and metabolism
2447	26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	6.3	7.04E-06	Control	5.4	25004	11	45%	Cytoplasmic	COG0800	Carbohydrate transport and metabolism
2447	26991429	PP_4748		amino acid ABC transporter periplasmic amino acid-binding protein	6.3	7.04E-06	Control	5.4	28338	3	13%	Unknown	COG0834	Amino acid transport and metabolism
2457	26987330	PP_0592		short chain dehydrogenase	2.6	3.39E-05	Vanillin	6.0	24627	2	8%	Extracellular	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
2457	26987360	PP_0624		hypothetical protein	2.6	3.39E-05	Vanillin	6.1	26401	4	20%	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism
2457	26989016	PP_2292		hypothetical protein	2.6	3.39E-05	Vanillin	5.8	28522	6	27%	Cytoplasmic		
2541	26991339	PP_4655	pcaG	protocatechuate 3,4-dioxygenase, alpha subunit	11	1.81E-05	Vanillin	4.7	22334	3	17%	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism
2541	148549997	Pput_4795		NUDIX hydrolase	11	1.81E-05	Vanillin	4.6	23119	2	9%	Cytoplasmic		
2544	26988712	PP_1986	leuD	isopropylmalate isomerase small subunit	10	1.09E-05	Vanillin	5.3	24284	3	14%	Cytoplasmic	COG0066	Amino acid transport and metabolism
2544	26988166	PP_1433	rnc	ribonuclease III	10	1.09E-05	Vanillin	5.2	25497	2	7%	Cytoplasmic	COG0571	Transcription
2544	26988406	PP_1674		cob(II)yrinic acid a,c-diamide reductase	10	1.09E-05	Vanillin	5.4	23976	2	9%	Unknown	COG0778	Energy production and conversion
2544	26991435	PP_4754		TetR family transcriptional regulator	10	1.09E-05	Vanillin	5.2	24816	2	8%	Unknown	COG1309	Transcription
2544	26990656	PP_3951	pcaI	3-oxoadipate CoA-transferase, subunit A	10	1.09E-05	Vanillin	5.3	24319	12	47%	Cytoplasmic	COG1788	Lipid metabolism
2553	26991411	PP_4728	grpE	heat shock protein GrpE	1.8	4.35E-05	Vanillin	4.7	20531	6	31%	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones
2553	26991829	PP_5153		fumarylacetoacetate (FAA) hydrolase	1.8	4.35E-05	Vanillin	4.7	23906	2	8%	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism
2553	26988600	PP_1870	tpm	thiopurine S-methyltransferase	1.8	4.35E-05	Vanillin	4.7	24365	7	27%	Cytoplasmic		
2553	26988502	PP_1771	cmk	cytidylate kinase	1.8	4.35E-05	Vanillin	4.9	24691	3	13%	Cytoplasmic	COG0283	Nucleotide transport and metabolism
2594	26987447	PP_0711		isochorismatase superfamily hydrolase	5	2.74E-06	Vanillin	5.3	23026	6	31%	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
2594	26992036	PP_5360		hypothetical protein	5	2.74E-06	Vanillin	5.6	23141	3	16%	Cytoplasmic		
2594	26988720	PP_1995	trpF	N-(5'-phosphoribosyl)anthranilate isomerase	5	2.74E-06	Vanillin	5.3	21886	2	9%	Cytoplasmic	COG0135	Amino acid transport and metabolism
2594	26991944	PP_5268		Cro/CI family transcriptional regulator	5	2.74E-06	Vanillin	5.3	20065	4	27%	Cytoplasmic	COG1396	Transcription
2594	26989024	PP_2300	clpP	ATP-dependent Clp protease proteolytic subunit	5	2.74E-06	Vanillin	5.6	23515	4	12%	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones
2790	26991658	PP_4981		hypothetical protein	2.3	2.33E-04	Vanillin	8.8	22129	5	19%	Unknown	COG2353	Function unknown
2790	26991658	PP_4981		hypothetical protein	2.3	2.33E-04	Vanillin	8.8	22129	10	36%	Unknown	COG2353	Function unknown
3020	26987945	PP_1210		DNA-binding stress protein	3.4	4.59E-06	Vanillin	5.0	17861	2	15%	Cytoplasmic	COG0783	Inorganic ion transport and metabolism
3340	26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	4.1	5.15E-05	Vanillin	5.3	16898	4	26%	Cytoplasmic Membrane	COG0711	Energy production and conversion

3340	26987686	PP_0950	ptsN	PTS IIA-like nitrogen-regulatory protein PtsN	4.1	5.15E-05	Vanillin	4.8	16772	4	28%	Cytoplasmic	COG1762	Carbohydrate transport and metabolism	Signal transduction mechanisms
3340	26991557	PP_4877	rpsF	30S ribosomal protein S6	4.1	5.15E-05	Vanillin	4.7	16373	2	12%	Cytoplasmic	COG0360	Translation, ribosomal structure and biogenesis	
3353	26987734	PP_0998		hypothetical protein	2.8	1.85E-05	Vanillin	6.6	16093	5	25%	Cytoplasmic			
3715	26991979	PP_5303		endoribonuclease	2	3.01E-05	Vanillin	4.8	13508	4	31%	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
3715	26991910	PP_5234		nitrogen regulatory protein P-II	2	3.01E-05	Vanillin	5.2	12330	2	18%	Cytoplasmic Membrane	COG0347	Amino acid transport and metabolism	
3715	26991910	PP_5234		nitrogen regulatory protein P-II	2	3.01E-05	Vanillin	5.2	12330	3	16%	Cytoplasmic Membrane	COG0347	Amino acid transport and metabolism	
4087	26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11	9.82E-04	Vanillin	7.0	69173	23	42%	Periplasmic	COG4993	Carbohydrate transport and metabolism	

5.3.2 Membranproteom-Analyse



1D-SDS-PAGE von auf 6,6 mM (0,1%) Vanillin und 10 mM Glucose kultiviertem *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.3.2.1 Membranfraktion_P_putida_KT440_Vanillin_Tabelle

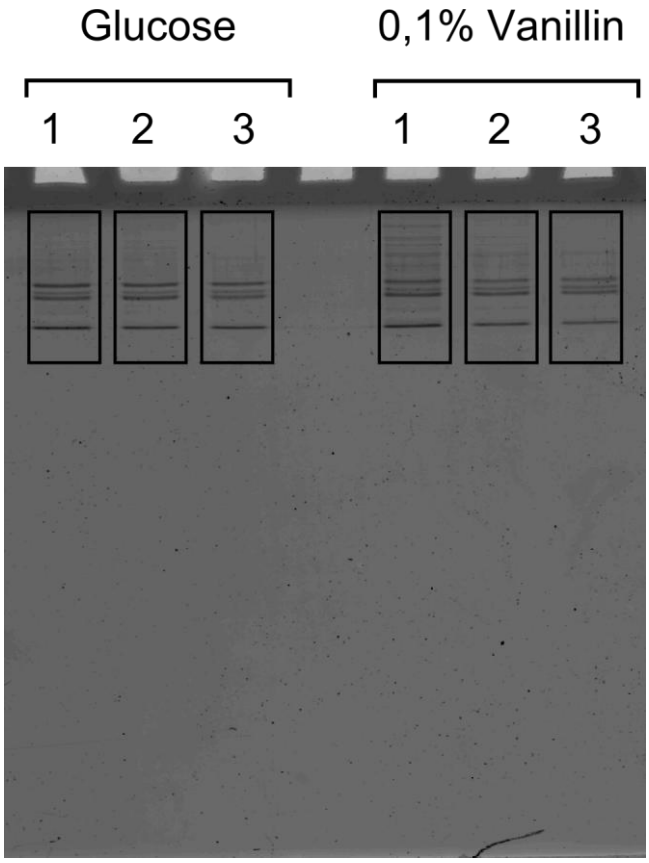
gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.0	7.64E-01	Control	9.1	61919	13	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.2	5.66E-01	Vanillin	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	1053.0	1.85E-01	Control	5.0	28482	2	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986856	PP_0111		electron transport protein SCO1/SenC	1.8	1.53E-01	Vanillin	8.2	22960	4	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	3.0	5.56E-02	Vanillin	7.4	25597	5	Unknown			
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.5	1.88E-01	Vanillin	9.6	29387	2	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	9.1	6.14E-03	Vanillin	7.3	50185	6	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.9	8.30E-03	Vanillin	6.3	71284	7	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.2	6.59E-01	Vanillin	7.8	51116	4	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.3	2.05E-01	Control	7.7	78583	12	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986920	PP_0176		fusaric acid resistance protein region	178.7	1.76E-02	Vanillin	7.2	76261	3	Cytoplasmic Membrane	COG1289	Function unknown	
26986922	PP_0178		secretion protein HlyD family protein	23.3	1.43E-04	Vanillin	9.4	32339	9	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986923	PP_0179		RND efflux transporter	29.2	8.01E-04	Vanillin	5.6	50813	10	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26986924	PP_0180		cytochrome c family protein	2.5	8.80E-04	Vanillin	4.9	68013	5	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	2.1	2.32E-02	Vanillin	9.6	46030	11	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	1.7	2.72E-01	Vanillin	11.3	32300	3	Cytoplasmic			
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.4	4.16E-01	Vanillin	5.2	51549	6	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.3	3.11E-01	Vanillin	6.1	44824	4	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	2.7	1.02E-02	Control	5.4	48317	29	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	14.6	1.15E-03	Vanillin	5.2	15616	7	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.5	1.09E-01	Vanillin	6.1	47787	12	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.7	3.06E-02	Vanillin	6.0	80277	9	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	7.4	2.44E-03	Control	5.3	55654	7	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	4.6	9.58E-03	Control	5.6	99332	13	Cytoplasmic	COG2609	Energy production and conversion	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.1	7.78E-01	Vanillin	4.6	69396	2	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.2	7.26E-01	Control	11.4	8370	6	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987139	PP_0397		serine protein kinase, PrkA	3.6	4.07E-01	Vanillin	5.8	73782	3	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987159	PP_0418		GDSL family lipase	2.6	1.97E-02	Vanillin	4.4	67175	9	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987181	PP_0440	tuf	elongation factor Tu	1.1	5.43E-01	Vanillin	5.0	43495	2	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	1.0	8.88E-01	Vanillin	10.5	14866	3	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.8	2.44E-01	Control	10.1	24251	3	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	1.4	2.73E-01	Control	10.2	17686	5	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.3	8.25E-01	Control	5.5	150992	25	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.3	9.23E-01	Control	7.2	154797	33	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	1.5	6.24E-01	Control	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	1.2	5.86E-01	Control	10.8	17578	12	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.7	2.63E-01	Control	4.9	78817	27	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.3	2.86E-01	Control	5.0	43478	28	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	1.2	6.72E-01	Vanillin	10.3	21811	7	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	2.1	1.63E-01	Control	10.7	10900	6	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.3	9.64E-01	Control	11.7	29669	13	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.0	7.42E-01	Vanillin	11.9	15373	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	1.1	8.59E-01	Control	11.6	13410	11	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	1.3	6.85E-01	Control	10.3	20329	11	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	1.0	9.46E-01	Control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	1.6	1.55E-01	Control	10.2	13975	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.6	3.08E-01	Control	10.4	19143	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.1	7.71E-01	Control	10.9	12628	5	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.1	8.87E-01	Control	10.6	17666	9	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987213	PP_0472	rpmD	50S ribosomal protein L30	1.6	3.79E-01	Control	10.6	6452	2	Cytoplasmic	COG1841	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	1.4	3.57E-01	Control	11.5	15189	9	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.4	1.69E-01	Control	10.4	47853	6	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	1.7	5.87E-01	Control	11.3	13256	6	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	2.3	3.24E-01	Control	11.5	13660	4	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.2	7.83E-01	Control	10.5	23056	14	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.5	8.50E-02	Control	4.7	36629	4	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	2.3	9.76E-02	Vanillin	11.3	14363	4	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	1.9	1.14E-01	Vanillin	4.6	17972	12	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987236	PP_0496		amino acid carrier protein	1.2	7.23E-01	Vanillin	9.0	51685	2	Cytoplasmic Membrane	COG1115	Amino acid transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	5.2	2.17E-02	Vanillin	4.8	24196	3	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	1.1	6.82E-01	Vanillin	9.7	45834	6	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987282	PP_0544		ethanolamine transproter	2.6	9.97E-02	Vanillin	8.0	50800	2	Cytoplasmic Membrane	COG0833	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	3.6	1.33E-02	Vanillin	5.9	55268	7	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.3	6.00E-01	Control	6.5	49088	4	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	2.0	1.63E-03	Vanillin	6.6	40223	6	Unknown	COG5345	Function unknown	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.5	2.09E-01	Vanillin	5.0	69953	16	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987336	PP_0599		hypothetical protein	3.6	7.28E-03	Vanillin	9.6	83247	4	Unknown	COG3008	General function prediction only	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.3	7.23E-01	Control	6.0	105800	5	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP_0622		competence lipoprotein ComL	1.7	1.42E-01	Vanillin	4.8	38410	6	Unknown	COG4105	General function prediction only	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.3	1.54E-01	Vanillin	6.2	44897	2	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987410	PP_0674		ABC transporter ATP-binding protein	1.6	3.78E-01	Control	5.3	61860	2	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.3	2.51E-01	Control	6.5	48871	3	Unknown	COG0334	Amino acid transport and metabolism	
26987414	PP_0678		hypothetical protein	17.4	1.88E-03	Vanillin	5.1	70138	3	Unknown			
26987425	PP_0689	rpmA	50S ribosomal protein L27	2.1	4.07E-01	Control	11.0	9341	2	Cytoplasmic	COG0211	Translation, ribosomal structure and biogenesis	
26987443	PP_0707		MscS mechanosensitive ion channel	1.3	1.96E-01	Vanillin	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	2.9	5.04E-02	Control	6.4	23242	5	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987460	PP_0724	lolB	outer membrane lipoprotein LolB	1.2	8.99E-01	Vanillin	8.2	22895	2	Unknown	COG3017	Cell envelope biogenesis, outer membrane	
26987461	PP_0725		hypothetical protein	1.2	9.68E-01	Vanillin	4.6	63994	2	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	2.2	1.30E-01	Control	8.4	54282	3	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.5	1.46E-01	Vanillin	9.5	20483	9	Unknown			
26987495	PP_0759		hypothetical protein	1.7	8.30E-02	Vanillin	7.0	29743	6	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987501	PP_0765		hypothetical protein	4.8	7.29E-04	Vanillin	5.0	67937	21	Outer Membrane			

26987502	PP_0766		hypothetical protein	6.6	7.42E-03	Vanillin	9.6	50572	2	Unknown			
26987509	PP_0773		OmpA/MotB domain protein	1.4	1.54E-01	Vanillin	9.5	24753	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987535	PP_0799		outer membrane porin	4.4	7.82E-02	Vanillin	5.0	49091	2	Outer Membrane			
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding protein	7.1	2.50E-01	Vanillin	9.2	79558	2	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	3.4	4.88E-03	Vanillin	6.7	34557	11	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	2.5	2.32E-03	Vanillin	7.8	74391	11	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	3.0	9.48E-02	Vanillin	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.0	9.75E-01	Vanillin	9.6	66913	18	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.9	4.17E-01	Vanillin	4.8	32758	3	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987585	PP_0849	ndk	nucleoside diphosphate kinase	1.8	2.40E-01	Control	5.3	15044	3	Extracellular	COG0105	Nucleotide transport and metabolism	
26987592	PP_0856		hypothetical protein	1.3	5.80E-01	Vanillin	4.7	40737	8	Outer Membrane	COG1520	Function unknown	
26987619	PP_0883		outer membrane porin	1.2	6.23E-01	Control	6.6	50256	7	Outer Membrane			
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	3.3	9.38E-03	Vanillin	4.9	54767	2	Cytoplasmic	COG1951	Energy production and conversion	
26987645	PP_0909		hypothetical protein	1.4	2.14E-02	Control	6.4	38380	10	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.2	6.53E-01	Vanillin	4.4	47019	11	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	3.0	6.39E-03	Vanillin	5.8	78578	7	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987680	PP_0944	fumC	fumarate hydratase	3.4	4.62E-03	Control	5.9	48541	4	Cytoplasmic	COG0114	Energy production and conversion	
26987695	PP_0959	ttg2B	hypothetical protein	1.0	9.16E-01	Vanillin	8.2	28489	2	Cytoplasmic Membrane	COG0767	Secondary metabolites biosynthesis, transport, and catabolism	
26987696	PP_0960	ttg2C	hypothetical protein	1.5	1.39E-01	Vanillin	4.6	16953	4	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.2	7.27E-01	Vanillin	5.1	107495	11	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.4	5.59E-01	Control	7.4	52433	4	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	21.8	9.05E-02	Vanillin	6.4	40319	3	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987724	PP_0988	gcvP-1	glycine dehydrogenase	5.6	1.19E-02	Vanillin	6.0	101991	8	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	14.4	6.81E-02	Vanillin	5.7	46462	5	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	28.4	1.08E-05	Vanillin	9.1	51061	2	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	3.1	1.05E-01	Control	5.6	84730	3	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	100.0	4.93E-05	Control	7.0	36057	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	176.4	5.96E-04	Control	6.4	65359	5	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	76.5	3.82E-02	Control	6.2	45449	4	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	253.0	2.33E-05	Control	10.1	33781	4	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane component	59.9	4.24E-02	Control	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	28.3	2.00E-04	Control	6.7	41895	7	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	74.5	3.93E-05	Control	5.9	49646	29	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	351.3	1.39E-02	Control	6.8	55000	2	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	65.0	3.84E-04	Control	6.7	25476	5	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	1257.9	6.95E-03	Control	5.4	25004	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.4	3.53E-01	Vanillin	5.1	61712	4	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.6	4.04E-01	Control	5.2	58204	4	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.0	8.88E-01	Control	4.7	140818	12	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987796	PP_1060		glutamate synthase, large subunit	1.3	4.37E-01	Control	8.1	59136	3	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26987806	PP_1070		polar amino acid ABC transporter inner membrane subunit	1.8	1.24E-01	Vanillin	8.2	27464	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
26987818	PP_1082	bfr	bacterioferritin	2.0	8.57E-02	Vanillin	4.4	17971	7	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.3	2.04E-01	Control	4.9	21730	6	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	1.6	4.97E-01	Control	5.1	45164	2	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987844	PP_1108		acylase	1.6	7.39E-02	Vanillin	8.7	88728	13	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	8.6	3.33E-04	Vanillin	5.0	24084	8	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	12.1	6.85E-03	Vanillin	4.7	27345	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987864	PP_1128		OmpA/MotB domain protein	2.7	1.67E-01	Vanillin	10.6	36308	3	Cytoplasmic Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	2.2	2.94E-02	Vanillin	9.3	15682	6	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987871	PP_1135		hypothetical protein	1.6	9.47E-01	Vanillin	6.9	26494	3	Unknown	COG3650	Function unknown	
26987888	PP_1152		secretion protein HlyD family protein	99.2	2.29E-04	Vanillin	6.4	32353	3	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26987893	PP_1157		acetolactate synthase	1.1	7.52E-01	Control	6.1	60059	2	Cytoplasmic	COG0028	Coenzyme metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	2.3	2.38E-01	Control	5.7	106948	11	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987923	PP_1188	dctA	C4-dicarboxylate transporter DctA	1.7	9.48E-01	Control	8.8	46298	2	Cytoplasmic Membrane	COG1301	Energy production and conversion	
26987936	PP_1201		virulence factor family protein	6.3	4.93E-03	Vanillin	5.0	46885	2	Unknown	COG3946	Intracellular trafficking and secretion	
26987941	PP_1206	oprD	outer membrane porin	1.0	9.14E-01	Control	4.6	46120	23	Outer Membrane			
26987944	PP_1209		cold-shock domain-contain protein	1.2	5.56E-01	Control	11.4	10246	2	Cytoplasmic	COG1278	Transcription	
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	1.5	6.43E-01	Control	5.1	66568	6	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.0	9.58E-01	Control	6.3	25310	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987957	PP_1222	tolB	translocation protein TolB	1.0	9.85E-01	Control	9.8	47431	4	Unknown	COG0823	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.0	7.93E-01	Vanillin	4.9	17833	15	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	2.1	2.06E-01	Control	4.8	40784	5	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987980	PP_1245		hypothetical protein	2.7	1.75E-03	Control	9.4	31144	16	Unknown			
26988008	PP_1273		RND efflux system, outer membrane lipoprotein, NodT family	118.8	3.57E-05	Vanillin	5.1	52832	14	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988050	PP_1315	rplM	50S ribosomal protein L13	3.8	2.10E-02	Control	10.3	15862	3	Unknown	COG0102	Translation, ribosomal structure and biogenesis	
26988051	PP_1316	rpsI	30S ribosomal protein S9	1.4	5.30E-01	Control	11.7	14592	6	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	12.0	2.16E-03	Vanillin	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	6.0	2.86E-03	Vanillin	7.1	29032	5	Unknown	COG2857	Energy production and conversion	
26988057	PP_1322		transport-associated protein	1.5	2.08E-01	Vanillin	9.8	20680	7	Periplasmic	COG2823	General function prediction only	
26988060	PP_1325		LppC family lipoprotein	1.5	1.22E-01	Vanillin	7.5	64637	18	Cytoplasmic Membrane	COG3107	General function prediction only	
26988093	PP_1359	fxsA	FxsA	1.4	5.98E-01	Vanillin	10.6	16958	2	Cytoplasmic Membrane	COG3030	General function prediction only	
26988095	PP_1361	groEL	chaperonin GroEL	1.8	8.02E-02	Control	4.7	56743	21	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.3	1.18E-01	Vanillin	4.8	67652	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	1.3	2.29E-01	Control	9.6	52425	2	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988110	PP_1376	pcaK	benzoate transport	211.8	1.38E-03	Vanillin	9.8	47128	5	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	22.8	1.79E-03	Vanillin	6.0	41851	6	Cytoplasmic	COG0183	Lipid metabolism	
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	117.0	2.52E-02	Vanillin	6.5	48194	3	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase	59.3	4.43E-03	Vanillin	5.1	28656	5	Unknown	COG0596	General function prediction only	
26988117	PP_1383		BenF-like porin	154.8	2.01E-06	Vanillin	6.8	46022	34	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	3.1	4.93E-03	Vanillin	5.1	52864	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	3.2	1.58E-02	Vanillin	5.3	112835	8	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	1.8	3.54E-01	Vanillin	6.0	41250	2	Unknown	COG0845	Cell envelope biogenesis, outer membrane	
26988134	PP_1400		metabolite/H+ symporter, major facilitator superfamily (MFS)	4.1	1.85E-03	Vanillin	9.4	47635	3	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	

26988152	PP_1419		outer membrane porin	7.2	5.90E-03	Vanillin	4.9	46644	3	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	1.2	2.39E-01	Vanillin	9.2	32060	5	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.9	5.56E-03	Vanillin	6.0	86581	10	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988179	PP_1446		TonB-dependent receptor	2.6	3.07E-02	Control	4.9	74207	16	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988198	PP_1465	rplS	50S ribosomal protein L19	1.7	2.91E-01	Control	11.0	13012	8	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	1.7	2.87E-02	Control	6.2	51645	4	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	2.5	2.52E-04	Vanillin	4.7	58605	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.0	9.38E-01	Vanillin	9.3	27023	15	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.6	4.78E-02	Control	4.9	30432	5	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988330	PP_1598		membrane-associated zinc metalloprotease	1.4	1.14E-01	Vanillin	9.3	48321	2	Cytoplasmic Membrane	COG0750	Cell envelope biogenesis, outer membrane	
26988331	PP_1599		surface antigen family outer membrane protein	1.8	4.24E-02	Vanillin	4.7	86513	15	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.5	1.92E-01	Control	4.7	45490	4	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	37.4	6.91E-04	Vanillin	6.3	39364	2	Cytoplasmic	COG1062	Energy production and conversion	
26988354	PP_1622	nlpD	peptidase M23B	1.5	3.12E-02	Vanillin	11.0	27506	9	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.5	1.96E-01	Vanillin	5.4	45693	9	Outer Membrane	COG2067	Lipid metabolism	
26988432	PP_1700		phospholipid/glycerol acyltransferase	1.8	2.17E-01	Vanillin	9.2	72239	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	2.5	2.25E-02	Control	4.8	26520	2	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988492	PP_1761		sensory box protein/GGDEF family protein	3.1	7.05E-02	Vanillin	6.8	108193	2	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26988511	PP_1780		mannosyltransferase	2.2	2.52E-01	Control	5.8	180042	2	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	3.1	1.38E-01	Control	6.1	40690	2	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	3.5	9.91E-02	Control	6.4	128499	7	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988535	PP_1805	wbpM	polysaccharide biosynthesis protein CapD	2.6	4.94E-01	Vanillin	9.2	76416	2	Cytoplasmic Membrane	COG1086	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26988568	PP_1838		hypothetical protein	1.0	8.26E-01	Vanillin	6.8	76615	8	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988588	PP_1858	efp	elongation factor P	1.7	9.61E-02	Control	4.5	21303	2	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988608	PP_1878		hypothetical protein	2.0	8.29E-02	Vanillin	7.3	29093	2	Cytoplasmic			
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	8.9	1.46E-04	Vanillin	6.9	89194	12	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	2.3	6.55E-01	Control	4.7	120904	2	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988670	PP_1943	purU	formyltetrahydrofolate deformylase	975.8	3.58E-03	Vanillin	6.4	32061	2	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
26988671	PP_1944		aminomethyltransferase	39.9	2.63E-02	Vanillin	6.0	48129	2	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	183.1	1.34E-02	Vanillin	5.3	27212	3	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.6	7.22E-02	Control	5.9	43290	7	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	3.6	9.43E-03	Control	5.6	56483	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	3.0	4.24E-02	Control	5.3	40672	3	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	2.2	4.23E-02	Vanillin	3.9	96918	22	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.8	1.05E-01	Vanillin	7.8	32510	3	Cytoplasmic	COG0777	Lipid metabolism	
26988742	PP_2017	pepN	aminopeptidase N	2.0	1.29E-01	Vanillin	4.8	99573	2	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988805	PP_2080		NAD-glutamate dehydrogenase	2.1	7.91E-02	Vanillin	5.8	187043	3	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.4	6.63E-01	Control	4.8	86015	8	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	1.1	2.91E-01	Vanillin	5.8	29111	3	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.5	5.92E-02	Vanillin	4.5	37012	35	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988845	PP_2121		lipoprotein	1.3	9.61E-01	Vanillin	5.0	8131	2	Unknown			
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.3	5.38E-01	Control	7.7	53014	12	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	2.6	6.62E-03	Vanillin	5.3	26061	8	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988973	PP_2249		methyl-accepting chemotaxis transducer	4.7	2.01E-03	Vanillin	5.1	68646	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989026	PP_2302	lon-2	ATP-dependent protease La	1.2	9.71E-01	Control	5.9	88722	2	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989030	PP_2306		lipoprotein	1.2	5.12E-01	Vanillin	9.3	9997	4	Unknown			
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	5.0	4.87E-03	Vanillin	5.3	52127	8	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	2.2	2.03E-04	Vanillin	8.5	8801	3	Outer Membrane			
26989055	PP_2331		hypothetical protein	1.4	2.13E-01	Vanillin	7.9	57064	7	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.1	5.02E-01	Vanillin	5.0	93609	10	Cytoplasmic	COG1049	Energy production and conversion	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.4	6.51E-01	Control	5.8	62191	2	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989170	PP_2447		hypothetical protein	2.0	3.35E-01	Control	10.2	26784	2	Unknown			
26989189	PP_2466	infC	translation initiation factor IF-3	1.0	9.11E-01	Control	10.0	20120	3	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	1.6	4.26E-01	Vanillin	12.1	13280	5	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989362	PP_2643		methyl-accepting chemotaxis sensory transducer	48.6	1.54E-04	Vanillin	5.3	59485	11	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989381	PP_2662		hypothetical protein	131.3	3.45E-02	Vanillin	4.3	42858	2	Outer Membrane			
26989572	PP_2853		hypothetical protein	13.5	7.13E-03	Vanillin	4.5	46020	4	Unknown			
26989663	PP_2944		sensor histidine kinase	18.3	1.77E-02	Vanillin	6.1	67470	2	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989810	PP_3091		hypothetical protein	1.4	1.52E-01	Control	6.8	138655	5	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	1.6	2.44E-02	Control	5.7	26868	2	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989818	PP_3099		hypothetical protein	10.3	4.01E-03	Control	4.9	56072	16	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989819	PP_3100		hypothetical protein	4.9	6.63E-02	Control	7.7	21741	2	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
26989825	PP_3106		hypothetical protein	1.2	6.00E-01	Vanillin	5.6	69529	3	Cytoplasmic	COG3501	Function unknown	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	28.9	1.52E-05	Vanillin	9.0	57141	4	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989859	PP_3140		glycosyl transferase, group 2 family protein	6.8	7.55E-03	Vanillin	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	6.6	1.45E-03	Vanillin	9.7	29885	7	Unknown			
26989874	PP_3155		outer membrane ferric siderophore receptor	38.5	1.15E-02	Control	4.9	78211	11	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990043	PP_3325		outer membrane ferric siderophore receptor	3.9	2.67E-02	Control	4.8	76226	32	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990047	PP_3330		TonB-dependent siderophore receptor	5.4	1.59E-02	Vanillin	5.8	80740	19	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	8.6	5.15E-03	Vanillin	4.8	77137	18	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990091	PP_3376	kguD	2-ketogluconate 6-phosphate reductase	45.3	2.01E-02	Control	6.3	34561	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26990092	PP_3377		major facilitator transporter	30.4	7.31E-05	Control	9.6	47449	3	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	257.2	1.30E-05	Control	8.9	47532	8	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990138	PP_3425	mexE	efflux transporter RND family, MFP subunit	32.4	1.82E-03	Vanillin	9.6	44603	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990139	PP_3426	mexF	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	17.4	5.76E-04	Vanillin	5.6	114759	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26990140	PP_3427	oprN	RND efflux system, outer membrane lipoprotein, NodT family	112.9	9.80E-05	Vanillin	4.9	50894	9	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	46.0	4.51E-04	Vanillin	6.3	44262	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	21.4	2.37E-04	Vanillin	6.9	85338	13	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	1.0	7.28E-01	Vanillin	5.2	53952	16	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.9	8.48E-02	Control	5.9	43631	2	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26990323	PP_3612		TonB-dependent siderophore receptor	15.1	1.76E-02	Control	5.2	85491	15	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990407	PP_3699		hypothetical protein	1.3	4.66E-01	Control	6.1	63413	3	Cytoplasmic	COG2849	Function unknown	
26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	482.2	5.76E-04	Vanillin	5.5	39542	7	Cytoplasmic	COG4638	Inorganic ion transport and metabolism	General function prediction only

26990444	PP_3737	vanB	ferredoxin		77.7	3.21E-03	Vanillin	4.6	34255	4	Cytoplasmic	COG1018	Energy production and conversion	
26990446	PP_3740		major facilitator family transporter		7894.5	1.81E-04	Vanillin	10.5	46421	4	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase		1.9	4.73E-02	Vanillin	4.9	129450	11	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase		3.2	5.07E-04	Control	6.4	41164	7	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990482	PP_3777		hypothetical protein		1.6	3.47E-02	Control	5.2	31324	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase		2.3	2.21E-05	Control	6.2	27714	6	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein		8.3	7.04E-04	Control	7.0	53071	11	Cytoplasmic	COG0635	Coenzyme metabolism	
26990488	PP_3783		hypothetical protein		9.6	4.99E-04	Control	5.8	34938	2	Cytoplasmic			
26990489	PP_3784		hypothetical protein		5.6	9.24E-04	Control	5.4	41070	7	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein		15.3	5.06E-03	Control	6.5	50495	7	Cytoplasmic			
26990491	PP_3786		aminotransferase		52.1	6.96E-04	Control	6.4	44067	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990493	PP_3788		non-ribosomal peptide synthetase		94.3	2.67E-02	Control	6.7	56336	3	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990501	PP_3796		L-ornithine N5-oxygenase		2.1	2.71E-02	Control	6.5	50047	4	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
26990502	PP_3797		hypothetical protein		4.2	3.67E-03	Control	9.5	44129	3	Cytoplasmic Membrane	COG3182	Function unknown	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase		1.3	3.11E-01	Vanillin	5.3	30957	3	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990627	PP_3922		periplasmic protease		2.1	3.66E-02	Vanillin	9.8	37502	6	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990656	PP_3951	pcaI	3-oxoadipate CoA-transferase, subunit A		549.0	8.68E-03	Vanillin	5.3	24319	3	Cytoplasmic	COG1788	Lipid metabolism	
26990657	PP_3952	pcaJ	3-oxoadipate CoA-transferase, subunit B	Infinity		3.93E-05	Vanillin	4.7	22552	2	Cytoplasmic	COG2057	Lipid metabolism	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE		1.1	6.32E-01	Control	6.4	91296	3	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent		2.6	6.64E-02	Control	5.4	79899	13	Cytoplasmic	COG2838	Energy production and conversion	
26990810	PP_4116	aceA	isocitrate lyase		9.5	1.92E-02	Vanillin	5.3	48633	2	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D		5.2	2.02E-02	Control	6.5	67609	2	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G		2.8	1.40E-01	Control	5.9	97582	5	Unknown	COG1034	Energy production and conversion	
26990838	PP_4145	mltD	lytic murein transglycosylase D		1.6	9.79E-01	Vanillin	10.5	52856	3	Outer Membrane	COG1388	Cell envelope biogenesis, outer membrane	
26990871	PP_4179	htpG	heat shock protein 90		3.1	1.68E-01	Control	5.0	71610	3	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha		3.0	2.82E-03	Control	6.2	30111	10	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta		2.5	1.49E-02	Control	6.1	41239	17	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase		1.7	9.81E-02	Control	6.3	49912	6	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase		1.0	9.48E-01	Vanillin	5.1	42434	6	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component		1.4	5.74E-01	Control	6.5	106521	8	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit		2.2	2.06E-02	Vanillin	7.5	26000	3	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit		1.7	1.01E-01	Vanillin	6.2	63448	8	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein		2.9	1.68E-03	Vanillin	9.0	13579	4	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit		3.2	4.69E-04	Vanillin	10.3	13813	3	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase		1.4	6.83E-01	Vanillin	7.0	47622	6	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit		1.1	8.83E-01	Vanillin	9.7	26361	4	Unknown	COG2086	Energy production and conversion	
26990903	PP_4211		RND efflux transporter		1.4	2.63E-01	Control	8.2	51199	20	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990908	PP_4216	pvdE	cyclic peptide transporter		1.6	1.43E-01	Control	7.4	61169	9	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor		1.5	3.98E-01	Control	5.5	89725	42	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990911	PP_4219	ppsD	non-ribosomal siderophore peptide synthetase		1.7	1.27E-01	Control	5.5	382081	45	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990912	PP_4220		non-ribosomal peptide synthetase		1.7	1.26E-01	Control	5.2	287552	52	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990913	PP_4221		non-ribosomal peptide synthetase		1.6	2.38E-01	Control	5.7	236392	27	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990934	PP_4243		peptide synthase		1.6	1.46E-01	Control	5.3	475264	70	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II		6.7	1.20E-03	Vanillin	9.0	22637	2	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III		7.8	7.78E-05	Vanillin	5.2	35613	7	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein		15.5	3.89E-03	Vanillin	8.5	53406	2	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA		2.0	2.20E-02	Vanillin	6.0	35312	11	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991058	PP_4369	fliF	flagellar MS-ring protein		1.3	5.43E-01	Vanillin	4.5	63090	2	Cytoplasmic Membrane	COG1766	Cell motility and secretion	
26991134	PP_4448		hypothetical protein		2.7	1.09E-01	Control	6.0	66331	2	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991160	PP_4474	alaS	alanyl-tRNA synthetase		1.1	9.26E-01	Control	5.1	94711	3	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein		1.3	5.22E-01	Control	6.5	43490	2	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase		2.2	1.16E-01	Vanillin	6.4	71796	3	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein		1.8	1.30E-01	Vanillin	5.4	50393	19	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor		13.6	2.73E-03	Vanillin	6.4	56605	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991226	PP_4542		ABC transporter ATP-binding protein/permease		1.2	2.81E-01	Vanillin	7.6	67748	3	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991254	PP_4570		hypothetical protein		1.9	2.04E-02	Vanillin	10.1	35846	2	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991325	PP_4641	cstA	carbon starvation protein CstA		1.7	2.04E-02	Vanillin	9.0	73763	11	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel		1.8	4.99E-02	Vanillin	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive		91.3	9.05E-05	Vanillin	9.1	53016	2	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit		1794.2	4.21E-03	Vanillin	9.4	26835	3	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer		1.0	8.70E-01	Vanillin	4.8	68764	4	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991353	PP_4669		OmpA/MotB domain protein		2.9	2.46E-02	Control	9.9	18241	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase		2.7	2.14E-02	Control	5.4	36370	7	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase		1.2	8.24E-01	Control	4.9	75010	5	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2		2.0	3.98E-01	Control	6.8	91460	4	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH		1.3	2.16E-01	Vanillin	5.4	69722	19	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK		1.4	1.62E-01	Control	4.6	68800	8	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991414	PP_4731	omlA	SmpA/OmlA domain protein		1.3	4.06E-01	Vanillin	4.4	19586	3	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991474	PP_4794	leuS	leucyl-tRNA synthetase		2.9	4.29E-01	Control	5.6	96697	2	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991475	PP_4795		rare lipoprotein B		1.1	5.49E-01	Vanillin	6.1	22414	10	Unknown	COG2980	Cell envelope biogenesis, outer membrane	
26991484	PP_4804		rare lipoprotein A family		1.5	6.11E-01	Control	10.0	35869	3	Unknown	COG0797	Cell envelope biogenesis, outer membrane	
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein		1.4	1.88E-02	Control	5.0	31015	4	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991518	PP_4838	oprC	TonB-dependent copper receptor		7.6	1.66E-03	Vanillin	6.2	74540	59	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991519	PP_4839		hypothetical protein		8.4	1.90E-04	Vanillin	9.6	50581	8	Cytoplasmic Membrane	COG3182	Function unknown	
26991556	PP_4876	rpsR	30S ribosomal protein S18		1.8	2.15E-01	Control	11.3	8927	4	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis	
26991567	PP_4889	purA	adenylosuccinate synthetase		1.7	2.36E-01	Control	5.6	46833	2	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991569	PP_4891	hflC	HflC protein		2.7	5.44E-03	Vanillin	9.8	33001	13	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein		2.3	3.52E-02	Vanillin	5.1	44762	5	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991586	PP_4908	psd	phosphatidylserine decarboxylase		2.7	9.94E-01	Vanillin	8.6	31547	3	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991588	PP_4910		hypothetical protein		1.3	4.81E-02	Vanillin	4.7	53632	9	Cytoplasmic	COG3726	General function prediction only	
26991589	PP_4911		hypothetical protein		2.5	4.56E-02	Vanillin	8.5	27337	3	Periplasmic	COG3009	Function unknown	
26991601	PP_4923		TolC family type I secretion outer membrane protein		4.0	7.01E-04	Vanillin	5.2	52637	17	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein		1.5	1.06E-01	Vanillin	7.6	66279	4	Cytoplasmic Membrane	COG1132	Defense mechanisms	

26991622	PP_4944		carbamoyltransferase	1.4	5.20E-01	Control	7.2	65646	2	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991643	PP_4965	tktA	transketolase	1.0	9.65E-01	Control	5.0	72463	5	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.9	3.45E-02	Control	5.1	42779	9	Cytoplasmic	COG0192	Coenzyme metabolism	
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	3.1	3.03E-01	Control	10.7	68073	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.2	7.71E-01	Control	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	5.6	7.15E-04	Vanillin	10.9	26214	8	Cytoplasmic	COG3937	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.2	1.42E-01	Vanillin	4.9	69017	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.5	1.11E-01	Vanillin	8.3	95875	7	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991720	PP_5044		GTP-binding protein TypA	2.0	7.20E-02	Control	5.3	67157	2	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.8	1.70E-01	Control	5.1	51740	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.9	3.33E-01	Control	6.2	161772	21	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP_5077		sporulation domain protein	2.7	6.77E-02	Vanillin	7.1	55434	2	Unknown	COG3267	Intracellular trafficking and secretion	
26991761	PP_5085	maeB	malic enzyme	1.2	4.16E-01	Control	4.9	45127	6	Cytoplasmic	COG0281	Energy production and conversion	
26991766	PP_5090		sporulation domain protein	1.8	1.28E-01	Vanillin	10.6	24964	3	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991772	PP_5096		hypothetical protein	1.4	2.54E-01	Control	9.9	21599	2	Cytoplasmic Membrane	COG0762	Function unknown	
26991785	PP_5109	ftsX	hypothetical protein	1.2	8.41E-01	Vanillin	6.5	36984	4	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.4	4.89E-01	Control	5.8	65671	2	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.1	6.48E-01	Vanillin	6.3	44339	7	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	9.6	2.09E-04	Vanillin	5.4	112277	3	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991958	PP_5282	rpmB	50S ribosomal protein L28	1.5	6.19E-01	Control	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991980	PP_5304		lipoprotein	1.5	6.61E-01	Control	5.1	26284	3	Unknown			
26991983	PP_5307	exbD	biopolymer transport protein ExbD	2.8	1.83E-04	Control	4.5	15269	3	Cytoplasmic Membrane	COG0848	Intracellular trafficking and secretion	
26991988	PP_5312		hypothetical protein	1.1	6.99E-01	Control	11.3	14000	2	Periplasmic			
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	5.9	1.68E-02	Control	5.3	65626	4	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	25.0	9.51E-04	Control	6.5	51942	7	Cytoplasmic	COG0439	Lipid metabolism	
26992029	PP_5353		hypothetical protein	2.2	8.24E-03	Vanillin	7.2	30672	3	Cytoplasmic Membrane	COG4395	Function unknown	
26992037	PP_5361		CobW/P47K family protein	1.3	8.61E-01	Control	4.6	45607	5	Cytoplasmic	COG0523	General function prediction only	
26992055	PP_5379	copB	copper resistance B precursor	4.0	1.02E-01	Vanillin	5.0	40230	2	Outer Membrane	COG3667	Inorganic ion transport and metabolism	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.1	6.22E-01	Control	4.6	49359	10	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.5	2.14E-01	Vanillin	9.2	31464	9	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.1	7.17E-01	Control	5.2	55352	15	Cytoplasmic	COG0056	Energy production and conversion	
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.3	5.55E-02	Vanillin	5.3	16898	8	Cytoplasmic Membrane	COG0711	Energy production and conversion	
313496770				2.2	9.52E-03	Vanillin			21				
313498866				1.1	6.40E-01	Vanillin			14				
24986476				1.1	8.75E-01	Control			14				
148550051				1.6	2.01E-01	Control			12				
24983268				2.0	4.78E-02	Control			10				
148547246				278.6	1.98E-04	Vanillin			10				
313497930				2.0	1.04E-01	Control			9				
24981839				1.9	1.76E-01	Control			9				
24981833				1.6	2.40E-01	Control			7				
109893221				1.5	7.04E-01	Control			6				
148545966				1.1	8.79E-01	Vanillin			5				
313500100				5.2	5.31E-03	Vanillin			4				
148545524				1.5	3.15E-01	Vanillin			4				
148549776				1.4	9.25E-01	Vanillin			3				
24982932				1.2	3.53E-01	Control			3				
148549576				1.5	2.34E-02	Vanillin			2				
148547137				1.1	9.52E-01	Control			2				
269200098				1.0	8.62E-01	Vanillin			2				
260222836				1.2	5.10E-01	Control			2				



1D-SDS-PAGE von auf 6,6 mM (0,1%) Vanillin und 10 mM Glucose kultiviertem *P. putida* GN235. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Proben bis zu einer Tiefe von ca. 1cm in das Trenngel migriert waren, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Die markierten Bereiche wurden aus dem Gel ausgeschnitten und mit Trypsin verdaut.

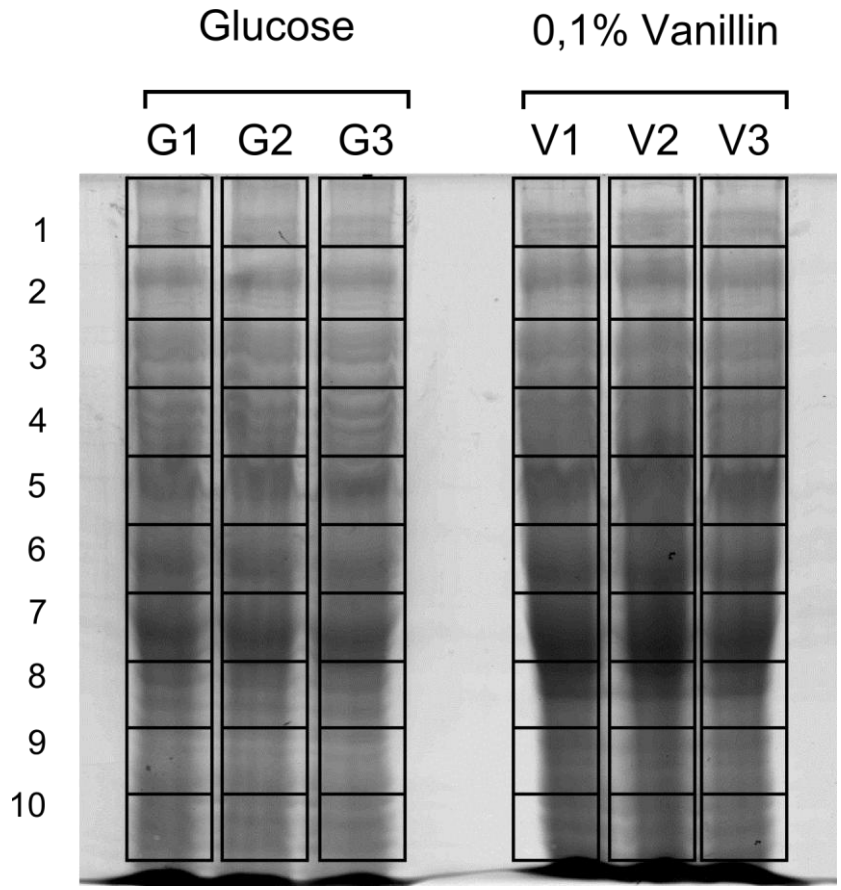
gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.5	4.62E-01	Control	9.1	61919	12	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986758	PP_0013	gyrB	DNA gyrase subunit B	5.3	5.89E-01	Vanillin	5.8	90030	2	Unknown	COG0187	DNA replication, recombination, and repair	
26986803	PP_0058		phospholipid/glycerol acyltransferase	1.3	5.72E-01	Control	10.0	29094	2	Cytoplasmic Membrane	COG0204	Lipid metabolism	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	2.7	7.34E-01	Vanillin	4.9	75112	6	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986841	PP_0096	prlC	oligopeptidase A	21.2	1.47E-01	Vanillin	5.0	75721	5	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986856	PP_0111		electron transport protein SCO1/SenC	1.2	9.44E-01	Control	8.2	22960	3	Cytoplasmic Membrane	COG1999	General function prediction only	
26986861	PP_0116		lipoprotein	1.2	6.37E-01	Vanillin	7.4	25597	5	Unknown			
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	3.1	2.97E-01	Vanillin	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986909	PP_0165		GGDEF domain-containing protein	1.0	6.47E-01	Control	6.3	71284	11	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986922	PP_0178		secretion protein HlyD family protein	30.6	2.60E-02	Vanillin	9.4	32339	8	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986923	PP_0179		RND efflux transporter	379.0	8.01E-04	Vanillin	5.6	50813	7	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26986924	PP_0180		cytochrome c family protein	1.1	6.53E-01	Vanillin	4.9	68013	4	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	2.3	9.23E-01	Vanillin	5.4	52061	3	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.2	4.08E-01	Vanillin	9.6	46030	12	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	2.4	7.52E-01	Control	11.3	32300	2	Cytoplasmic			
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	6.9	2.54E-01	Vanillin	5.2	51549	12	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	9.0	1.07E-01	Vanillin	6.1	44824	10	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	4.5	7.37E-02	Control	5.4	48317	25	Outer Membrane			
26987000	PP_0258		LysM domain/BON superfamily protein	8.1	1.56E-02	Vanillin	5.2	15616	4	Unknown	COG1652	Function unknown	
26987010	PP_0268	oprQ	outer membrane porin	1.4	5.19E-01	Control	6.1	47787	12	Outer Membrane			
26987029	PP_0287		AsmA family protein	1.3	6.21E-01	Control	6.0	80277	8	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	1.2	6.36E-01	Control	5.3	55654	5	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	1.8	2.23E-01	Control	5.6	99332	15	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase	9.1	8.31E-01	Vanillin	5.3	109432	2	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987098	PP_0356	glcB	malate synthase G	27.6	4.07E-01	Vanillin	5.8	78346	2	Cytoplasmic	COG2225	Energy production and conversion	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	17.7	1.64E-01	Vanillin	5.8	65541	8	Cytoplasmic	COG1960	Lipid metabolism	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.2	5.98E-01	Vanillin	4.6	69396	4	Cytoplasmic	COG0568	Transcription	
26987131	PP_0389	rpsU	30S ribosomal protein S21	1.9	5.21E-02	Control	11.4	8370	5	Cytoplasmic	COG0828	Translation, ribosomal structure and biogenesis	
26987139	PP_0397		serine protein kinase, PrkA	17.0	3.71E-02	Vanillin	5.8	73782	17	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987159	PP_0418		GDSL family lipase	2.1	3.28E-01	Vanillin	4.4	67175	8	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987181	PP_0440	tuf	elongation factor Tu	2.3	6.26E-01	Vanillin	5.0	43495	2	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987184	PP_0443	rplK	50S ribosomal protein L11	2.5	3.03E-02	Control	10.5	14866	4	Cytoplasmic	COG0080	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.9	2.35E-01	Control	10.1	24251	3	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987186	PP_0445	rplJ	50S ribosomal protein L10	3.2	1.61E-02	Control	10.2	17686	3	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	2.5	6.77E-01	Vanillin	5.5	150992	53	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	2.1	8.51E-01	Vanillin	7.2	154797	50	Cytoplasmic	COG0086	Transcription	
26987190	PP_0449	rpsL	30S ribosomal protein S12	4.2	1.72E-02	Control	11.7	13727	3	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
26987191	PP_0450	rpsG	30S ribosomal protein S7	4.3	5.08E-02	Control	10.8	17578	10	Cytoplasmic	COG0049	Translation, ribosomal structure and biogenesis	
26987192	PP_0451	fusA	elongation factor G	1.7	8.86E-01	Vanillin	4.9	78817	42	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.8	5.46E-01	Vanillin	5.0	43478	37	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987194	PP_0453	rpsJ	30S ribosomal protein S10	2.0	3.81E-01	Control	10.5	11753	2	Cytoplasmic	COG0051	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	2.0	1.69E-01	Control	10.3	21811	5	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987197	PP_0456	rplW	50S ribosomal protein L23	1.8	5.25E-01	Control	10.7	10900	5	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.3	5.29E-01	Control	11.7	29669	10	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987202	PP_0461	rplP	50S ribosomal protein L16	1.7	3.08E-01	Control	11.9	15373	3	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
26987204	PP_0463	rpsQ	30S ribosomal protein S17	2.8	4.32E-01	Control	10.5	10058	2	Cytoplasmic	COG0186	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	2.0	9.55E-02	Control	11.6	13410	11	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	2.7	2.66E-01	Control	10.3	20329	10	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	3.0	2.99E-02	Control	12.3	11403	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
26987209	PP_0468	rpsH	30S ribosomal protein S8	2.2	1.55E-02	Control	10.2	13975	4	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
26987210	PP_0469	rplF	50S ribosomal protein L6	1.6	3.93E-01	Control	10.4	19143	4	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	1.6	5.62E-01	Control	10.9	12628	5	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987212	PP_0471	rpsE	30S ribosomal protein S5	1.5	1.95E-01	Control	10.6	17666	11	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
26987213	PP_0472	rpmD	50S ribosomal protein L30	1.1	7.79E-01	Control	10.6	6452	2	Cytoplasmic	COG1841	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	2.8	3.96E-02	Control	11.5	15189	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.2	8.03E-01	Control	10.4	47853	4	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987217	PP_0476	rpsM	30S ribosomal protein S13	2.7	3.00E-02	Control	11.3	13256	5	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
26987218	PP_0477	rpsK	30S ribosomal protein S11	3.0	9.81E-02	Control	11.5	13660	3	Cytoplasmic	COG0100	Translation, ribosomal structure and biogenesis	
26987219	PP_0478	rpsD	30S ribosomal protein S4	1.7	2.64E-02	Control	10.5	23056	13	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	2.9	3.41E-01	Vanillin	4.7	36629	5	Cytoplasmic	COG0202	Transcription	
26987221	PP_0480	rplQ	50S ribosomal protein L17	2.0	2.72E-01	Control	11.3	14363	4	Cytoplasmic	COG0203	Translation, ribosomal structure and biogenesis	
26987223	PP_0482		bacterioferritin	2.6	1.20E-01	Control	4.6	17972	15	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987243	PP_0504	oprG	OmpW family protein	1.3	4.58E-01	Vanillin	4.8	24196	2	Outer Membrane	COG3047	Cell envelope biogenesis, outer membrane	
26987245	PP_0506		hypothetical protein	3.0	1.29E-01	Control	9.7	45834	6	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987283	PP_0545		aldehyde dehydrogenase family protein	31.8	2.53E-02	Vanillin	5.9	55268	15	Cytoplasmic	COG1012	Energy production and conversion	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	8.5	7.40E-02	Vanillin	6.5	49088	6	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	1.0	9.98E-01	Control	6.6	40223	4	Unknown	COG5345	Function unknown	
26987308	PP_0570		alpha-2-macroglobulin domain protein	17.7	1.65E-01	Vanillin	5.2	178472	4	Unknown	COG2373	General function prediction only	
26987322	PP_0584		methyl-accepting chemotaxis transducer	1.2	4.84E-01	Vanillin	5.0	69953	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	31.9	9.57E-01	Vanillin	5.9	53498	2	Cytoplasmic	COG1012	Energy production and conversion	
26987336	PP_0599		hypothetical protein	1.5	8.36E-01	Vanillin	9.6	83247	4	Unknown	COG3008	General function prediction only	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	4.7	5.81E-01	Vanillin	6.0	105800	11	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987359	PP_0622		competence lipoprotein ComL	5.6	1.16E-01	Control	4.8	38410	3	Unknown	COG4105	General function prediction only	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	4.3	3.64E-01	Vanillin	5.2	94861	3	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	2.6	1.28E-01	Vanillin	6.2	44897	4	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987408	PP_0672		sensory box protein	1.5	7.95E-01	Vanillin	5.7	144317	2	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987410	PP_0674		ABC transporter ATP-binding protein	1.6	5.06E-01	Vanillin	5.3	61860	5	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.4	9.43E-01	Vanillin	6.5	48871	3	Unknown	COG0334	Amino acid transport and metabolism	
26987443	PP_0707		MscS mechanosensitive ion channel	1.4	4.19E-04	Vanillin	9.9	92124	4	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.7	4.82E-01	Vanillin	5.9	34192	2	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987461	PP_0725		hypothetical protein	2.5	8.14E-02	Control	4.6	63994	2	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	2.7	1.17E-01	Control	8.4	54282	3	Cytoplasmic	COG0579	General function prediction only	
26987489	PP_0753		lipoprotein	1.9	6.37E-01	Control	9.5	20483	8	Unknown			
26987495	PP_0759		hypothetical protein	1.5	5.50E-01	Control	7.0	29743	4	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	80.3	3.65E-01	Vanillin	5.5	62125	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	2.8	1.70E-01	Vanillin	5.0	67937	21	Outer Membrane			
26987509	PP_0773		OmpA/MotB domain protein	4.0	1.79E-01	Control	9.5	24753	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding protein	7.2	9.30E-01	Vanillin	9.2	79558	3	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.2	7.25E-01	Vanillin	6.7	34557	12	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	1.3	5.63E-01	Control	7.8	74391	9	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987570	PP_0834	yajC	preprotein translocase subunit YajC	1.8	7.55E-01	Vanillin	9.6	11902	2	Cytoplasmic Membrane	COG1862	Intracellular trafficking and secretion	
26987571	PP_0835	secD	preprotein translocase subunit SecD	2.0	7.38E-02	Control	9.6	66913	16	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	1.4	9.72E-01	Control	4.8	32758	2	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987592	PP_0856		hypothetical protein	4.9	1.13E-01	Control	4.7	40737	5	Outer Membrane	COG1520	Function unknown	
26987619	PP_0883		outer membrane porin	1.2	6.08E-01	Control	6.6	50256	6	Outer Membrane			
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subunit	2.9	4.48E-01	Vanillin	4.9	54767	2	Cytoplasmic	COG1951	Energy production and conversion	
26987645	PP_0909		hypothetical protein	2.8	1.73E-01	Control	6.4	38380	9	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.0	9.25E-01	Control	4.4	47019	12	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	1.1	9.14E-01	Vanillin	5.8	78578	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987713	PP_0977	valS	valyl-tRNA synthetase	2.2	8.67E-01	Vanillin	5.1	107495	14	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	5.0	7.30E-01	Vanillin	7.4	52433	8	Cytoplasmic	COG0260	Amino acid transport and metabolism	

26987722	PP_0986	gcvT-1	glycine cleavage system T protein	42.3	4.44E-02	Vanillin	6.4	40319	4	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987724	PP_0988	gcvP-1	glycine dehydrogenase	48.0	3.53E-02	Vanillin	6.0	101991	15	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	1.9	3.69E-01	Vanillin	6.3	37911	4	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	21.2	1.07E-02	Vanillin	5.7	46462	13	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	54.0	8.31E-03	Control	7.0	36057	4	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane component	6210.3	1.81E-03	Control	10.1	33781	3	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	35.5	6.03E-03	Control	6.7	41895	3	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	109.3	5.56E-04	Control	5.9	49646	31	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987759	PP_1023	pgl	6-phosphogluconolactonase	35.8	1.44E-02	Control	6.7	25476	3	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	708.9	1.31E-02	Control	5.4	25004	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	5.2	8.92E-02	Vanillin	5.1	61712	6	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	4.9	5.13E-01	Vanillin	5.2	58204	7	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	4.6	5.55E-01	Vanillin	4.7	140818	22	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987794	PP_1058		hypothetical protein	23.0	8.68E-03	Vanillin	9.5	117041	3	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987818	PP_1082	bfr	bacterioferritin	2.5	1.33E-01	Control	4.4	17971	13	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	1.3	8.45E-01	Vanillin	4.9	21730	8	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987824	PP_1088	argG	argininosuccinate synthase	2.4	2.18E-01	Control	5.1	45164	2	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	9.4	3.08E-01	Vanillin	5.5	75186	3	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987844	PP_1108		acylase	1.6	4.90E-01	Control	8.7	88728	12	Periplasmic	COG2366	General function prediction only	
26987857	PP_1121		OmpA/MotB domain protein	8.9	1.44E-02	Vanillin	5.0	24084	7	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	18.8	1.56E-03	Vanillin	4.7	27345	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987867	PP_1131		17 kDa surface antigen	1.1	9.53E-01	Control	9.3	15682	4	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987888	PP_1152		secretion protein HlyD family protein	8.9	3.20E-02	Vanillin	6.4	32353	2	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26987893	PP_1157		acetolactate synthase	2.8	7.65E-01	Vanillin	6.1	60059	4	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta	1.7	9.88E-01	Vanillin	4.5	46989	3	Cytoplasmic	COG0208	Nucleotide transport and metabolism	
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha	4.5	4.59E-01	Vanillin	5.7	106948	15	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
26987923	PP_1188	dctA	C4-dicarboxylate transporter DctA	2.0	8.27E-01	Control	8.8	46298	3	Cytoplasmic Membrane	COG1301	Energy production and conversion	
26987936	PP_1201		virulence factor family protein	9.5	5.15E-03	Vanillin	5.0	46885	3	Unknown	COG3946	Intracellular trafficking and secretion	
26987941	PP_1206	oprD	outer membrane porin	1.3	6.35E-01	Control	4.6	46120	27	Outer Membrane			
26987948	PP_1213	aspS	aspartyl-tRNA synthetase	3.0	6.24E-01	Vanillin	5.1	66568	13	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis	
26987954	PP_1219	tolQ	biopolymer transport protein TolQ	1.6	2.99E-01	Control	6.3	25310	2	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26987958	PP_1223	oprL	peptidoglycan-associated lipoprotein OprL	1.7	4.00E-01	Control	4.9	17833	23	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987973	PP_1238		lipoprotein	4.4	5.69E-02	Control	4.8	40784	4	Unknown	COG3317	Cell envelope biogenesis, outer membrane	
26987980	PP_1245		hypothetical protein	7.8	3.15E-02	Control	9.4	31144	11	Unknown			
26988008	PP_1273		RND efflux system, outer membrane lipoprotein, NodT family	161.3	9.47E-05	Vanillin	5.1	52832	11	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	25.5	1.11E-01	Vanillin	5.6	69049	3	Cytoplasmic	COG2895	Inorganic ion transport and metabolism	
26988051	PP_1316	rpsI	30S ribosomal protein S9	4.1	1.23E-02	Control	11.7	14592	7	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis	
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b	3.3	9.41E-02	Vanillin	8.4	45901	3	Cytoplasmic Membrane	COG1290	Energy production and conversion	
26988054	PP_1319	petC	ubiquinol--cytochrome c reductase, cytochrome c1	2.5	1.65E-01	Vanillin	7.1	29032	5	Unknown	COG2857	Energy production and conversion	
26988057	PP_1322		transport-associated protein	1.3	9.25E-01	Control	9.8	20680	2	Periplasmic	COG2823	General function prediction only	
26988060	PP_1325		LppC family lipoprotein	2.2	2.11E-01	Control	7.5	64637	15	Cytoplasmic Membrane	COG3107	General function prediction only	
26988075	PP_1341	ftsA	cell division protein FtsA	2.2	7.13E-01	Vanillin	4.9	47444	2	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
26988095	PP_1361	groEL	chaperonin GroEL	1.2	7.62E-01	Control	4.7	56743	25	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
26988105	PP_1371		methyl-accepting chemotaxis transducer	1.4	3.15E-01	Vanillin	4.8	67652	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988107	PP_1373		phosphate transporter	2.9	7.54E-02	Control	9.6	52425	2	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism	
26988110	PP_1376	pcaK	benzoate transport	201.0	1.91E-04	Vanillin	9.8	47128	7	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase	17.2	9.49E-03	Vanillin	6.0	41851	14	Cytoplasmic	COG0183	Lipid metabolism	
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	22.8	1.45E-02	Vanillin	6.5	48194	5	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26988117	PP_1383		BenF-like porin	143.4	1.03E-03	Vanillin	6.8	46022	35	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	1.3	6.83E-01	Vanillin	5.1	52864	19	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	1.2	4.94E-01	Vanillin	5.3	112835	5	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	5.7	2.84E-01	Vanillin	6.0	41250	2	Unknown	COG0845	Cell envelope biogenesis, outer membrane	
26988134	PP_1400		metabolite/H+ symporter, major facilitator superfamily (MFS)	4.7	4.60E-03	Vanillin	9.4	47635	5	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26988152	PP_1419		outer membrane porin	4.5	1.62E-02	Vanillin	4.9	46644	2	Outer Membrane			
26988165	PP_1432	lepB	signal peptidase I	1.3	1.01E-01	Control	9.2	32060	4	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	1.7	9.07E-02	Vanillin	6.0	86581	6	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988179	PP_1446		TonB-dependent receptor	10.1	1.76E-02	Control	4.9	74207	15	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	1.2	6.29E-01	Control	9.0	45563	2	Cytoplasmic Membrane			
26988198	PP_1465	rplS	50S ribosomal protein L19	1.8	4.11E-01	Control	11.0	13012	8	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
26988204	PP_1471	thrC	threonine synthase	1.6	8.36E-01	Vanillin	6.2	51645	3	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	52.3	2.32E-03	Vanillin	5.7	50918	2	Unknown	COG1012	Energy production and conversion	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.7	1.65E-01	Vanillin	4.7	58605	15	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988323	PP_1591	rpsB	30S ribosomal protein S2	2.3	5.59E-02	Control	9.3	27023	15	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	2.0	7.42E-01	Control	4.9	30432	2	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988331	PP_1599		surface antigen family outer membrane protein	1.6	5.14E-01	Control	4.7	86513	14	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988342	PP_1610	pyrG	CTP synthetase	5.5	4.92E-01	Vanillin	5.8	59474	9	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.2	6.98E-01	Control	4.7	45490	5	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988354	PP_1622	nlpD	peptidase M23B	1.6	2.05E-01	Control	11.0	27506	5	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988421	PP_1689		aromatic hydrocarbon degradation protein	1.1	9.30E-01	Control	5.4	45693	9	Outer Membrane	COG2067	Lipid metabolism	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.0	9.16E-01	Control	4.8	26520	2	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988474	PP_1743	actP	acetate permease	3.5	4.69E-02	Vanillin	9.6	58972	2	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	Infinity	1.26E-01	Vanillin	8.2	57637	2	Cytoplasmic	COG2326	Function unknown	
26988498	PP_1767	gyrA	DNA gyrase subunit A	10.1	6.07E-01	Vanillin	4.7	102037	3	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanylyltransferase	3.6	6.78E-01	Vanillin	5.2	52989	2	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988511	PP_1780		mannosyltransferase	8.3	9.27E-01	Vanillin	5.8	180042	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	2.2	5.47E-01	Vanillin	6.4	128499	9	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	2.8	8.40E-01	Vanillin	5.9	58534	10	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988538	PP_1808	pgi	glucose-6-phosphate isomerase	1.9	1.92E-01	Vanillin	6.8	61383	4	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26988568	PP_1838		hypothetical protein	2.0	2.96E-01	Control	6.8	76615	7	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.1	5.29E-01	Control	9.2	60924	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	16.2	1.07E-04	Vanillin	6.9	89194	11	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.4	3.01E-01	Control	4.7	120904	2	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988670	PP_1943	purU	formyltetrahydrofolate deformylase	66.3	1.81E-02	Vanillin	6.4	32061	2	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
26988671	PP_1944		aminomethyltransferase	20.8	1.52E-02	Vanillin	6.0	48129	7	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26988675	PP_1948		benzaldehyde dehydrogenase	1.9	3.76E-01	Vanillin	6.2	52881	2	Cytoplasmic	COG1012	Energy production and conversion	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	2.2	6.28E-02	Control	5.9	43290	5	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	3.6	5.63E-01	Vanillin	5.6	56483	2	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	2.2	6.75E-01	Vanillin	5.6	51255	4	Cytoplasmic	COG0065	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	1.0	8.87E-01	Control	5.3	40672	3	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	1.4	5.38E-01	Vanillin	3.9	96918	21	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988725	PP_2000	purF	amidophosphoribosyltransferase	2.1	9.03E-01	Vanillin	6.5	55400	4	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988731	PP_2006		hypothetical protein	5.6	3.42E-02	Vanillin	5.1	63743	5	Unknown			
26988742	PP_2017	pepN	aminopeptidase N	7.7	3.62E-01	Vanillin	4.8	99573	8	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988805	PP_2080		NAD-glutamate dehydrogenase	6.5	3.40E-01	Vanillin	5.8	187043	21	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	2.1	9.54E-01	Vanillin	4.8	86015	10	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988812	PP_2087	cmpX	TM helix repeat-containing protein	2.0	1.39E-01	Control	5.8	29111	3	Cytoplasmic Membrane			
26988814	PP_2089	oprF	OmpF family protein	1.3	9.27E-01	Vanillin	4.5	37012	38	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988863	PP_2139	topA	DNA topoisomerase I	8.4	8.26E-01	Vanillin	8.0	97239	3	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.0	5.75E-01	Control	7.7	53014	13	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988887	PP_2163	vacJ	VacJ family lipoprotein	1.2	7.60E-01	Vanillin	5.3	26061	7	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988973	PP_2249		methyl-accepting chemotaxis transducer	4.4	1.79E-02	Vanillin	5.1	68646	8	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989026	PP_2302	lon-2	ATP-dependent protease La	4.1	6.21E-01	Vanillin	5.9	88722	8	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	

26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	2.0	8.55E-02	Vanillin	5.3	52127	10	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989046	PP_2322	oprI	outer membrane lipoprotein OprI	2.1	3.48E-01	Vanillin	8.5	8801	3	Outer Membrane			
26989055	PP_2331		hypothetical protein	1.3	4.22E-01	Control	7.9	57064	5	Cytoplasmic Membrane			
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	6.0	2.04E-01	Vanillin	5.0	93609	28	Cytoplasmic	COG1049	Energy production and conversion	
26989088	PP_2364		hypothetical protein	43.6	6.94E-02	Vanillin	5.2	42461	2	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	3.0	6.67E-01	Vanillin	5.8	62191	7	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP_2375	metH	B12-dependent methionine synthase	3.6	6.22E-01	Vanillin	4.7	135408	6	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989162	PP_2439	ahpC	alkyl hydroperoxide reductase, C subunit	2.2	9.48E-01	Vanillin	4.8	20507	2	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	8.9	6.33E-01	Vanillin	5.8	72697	5	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989189	PP_2466	infC	translation initiation factor IF-3	1.8	2.49E-01	Control	10.0	20120	2	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
26989362	PP_2643		methyl-accepting chemotaxis sensory transducer	47.9	7.96E-04	Vanillin	5.3	59485	13	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989381	PP_2662		hypothetical protein	99.0	1.68E-03	Vanillin	4.3	42858	5	Outer Membrane			
26989399	PP_2680		aldehyde dehydrogenase family protein	113.9	1.07E-03	Vanillin	5.5	54903	22	Cytoplasmic	COG1012	Energy production and conversion	
26989572	PP_2853		hypothetical protein	20.0	8.17E-04	Vanillin	4.5	46020	3	Unknown			
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	4.3	4.94E-01	Vanillin	6.1	64654	5	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989647	PP_2928		saccharopine dehydrogenase	1.2	8.95E-01	Vanillin	5.0	45363	4	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989825	PP_3106		hypothetical protein	5.3	8.90E-02	Vanillin	5.6	69529	7	Cytoplasmic	COG3501	Function unknown	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	15.0	8.70E-03	Vanillin	9.0	57141	8	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989859	PP_3140		glycosyl transferase, group 2 family protein	8.6	1.70E-04	Vanillin	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	4.1	1.50E-01	Vanillin	9.7	29885	6	Unknown			
26990043	PP_3325		outer membrane ferric siderophore receptor	3.4	1.73E-02	Control	4.8	76226	27	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990047	PP_3330		TonB-dependent siderophore receptor	45.4	1.15E-02	Vanillin	5.8	80740	3	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990055	PP_3340		TonB-dependent receptor	7.2	2.51E-01	Vanillin	4.8	77137	2	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26990092	PP_3377		major facilitator transporter	11937.0	1.01E-03	Control	9.6	47449	2	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990130	PP_3417	gntP	gluconate transporter	133.6	2.53E-04	Control	8.9	47532	10	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.9	7.02E-01	Vanillin	7.2	36863	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	64.5	2.15E-02	Vanillin	6.3	44262	6	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	12.1	6.25E-04	Vanillin	6.9	85338	14	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	2.5	8.83E-02	Control	5.2	53952	10	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990373	PP_3662		decarboxylase family protein	2.4	4.83E-01	Vanillin	6.7	50729	2	Cytoplasmic	COG1611	General function prediction only	
26990379	PP_3668		catalase/peroxidase HPI	117.2	2.49E-04	Vanillin	5.8	82061	3	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990399	PP_3691		DNA helicase-related protein	38.5	3.04E-01	Vanillin	5.0	245278	7	Unknown	COG1112	DNA replication, recombination, and repair	
26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	97.1	3.08E-03	Vanillin	5.5	39542	11	Cytoplasmic	COG4638	Inorganic ion transport and metabolism	General function prediction only
26990444	PP_3737	vanB	ferredoxin	39.8	1.20E-02	Vanillin	4.6	34255	9	Cytoplasmic	COG1018	Energy production and conversion	
26990446	PP_3740		major facilitator family transporter	402.5	1.28E-03	Vanillin	10.5	46421	4	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990466	PP_3761		multi-sensor hybrid histidine kinase	1.6	2.88E-01	Vanillin	4.9	129450	12	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	1.2	4.32E-01	Control	6.4	41164	6	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	2.0	2.42E-01	Control	6.2	27714	4	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family protein	6.2	3.60E-02	Control	7.0	53071	7	Cytoplasmic	COG0635	Coenzyme metabolism	
26990489	PP_3784		hypothetical protein	3.1	1.27E-01	Control	5.4	41070	6	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	1.4	5.65E-01	Vanillin	6.5	50495	4	Cytoplasmic			
26990491	PP_3786		aminotransferase	6.7	1.65E-01	Control	6.4	44067	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990501	PP_3796		L-ornithine N5-oxygenase	1.9	6.84E-01	Vanillin	6.5	50047	3	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.5	8.99E-01	Vanillin	5.3	30957	5	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990627	PP_3922		periplasmic protease	1.2	9.40E-01	Vanillin	9.8	37502	2	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	1.0	7.56E-01	Control	6.4	91296	4	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	12.2	4.78E-01	Vanillin	5.7	83310	3	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.2	5.32E-01	Control	5.4	79899	14	Cytoplasmic	COG2838	Energy production and conversion	
26990721	PP_4016	purB	adenylosuccinate lyase	1.9	2.52E-01	Control	5.9	50555	3	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990737	PP_4034		allantoate amidohydrolase	42.4	4.56E-02	Vanillin	5.7	45010	5	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990739	PP_4037		oxidoreductase	112.1	4.93E-02	Vanillin	5.5	48815	3	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038		dihydropyrimidine dehydrogenase	8.0	6.41E-02	Vanillin	5.1	46093	12	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990753	PP_4052	malQ	4-alpha-glucanotransferase	16.3	7.67E-01	Vanillin	5.5	76475	3	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	41.5	6.37E-01	Vanillin	6.6	103167	2	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	8.7	4.26E-01	Vanillin	5.1	81044	4	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990810	PP_4116	aceA	isocitrate lyase	29.5	5.50E-03	Vanillin	5.3	48633	7	Cytoplasmic	COG2224	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.4	7.09E-01	Vanillin	6.5	67609	3	Cytoplasmic	COG0649	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.1	9.32E-01	Control	5.9	97582	13	Unknown	COG1034	Energy production and conversion	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	3.2	2.81E-01	Vanillin	5.3	43264	4	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.1	9.38E-01	Vanillin	6.2	30111	10	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.5	5.39E-01	Vanillin	6.1	41239	20	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.4	6.43E-01	Control	6.3	49912	8	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.7	3.89E-01	Control	5.1	42434	5	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	2.7	7.07E-01	Vanillin	6.5	106521	20	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	2.6	3.20E-01	Vanillin	7.5	26000	5	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	13.4	2.20E-02	Vanillin	6.2	63448	16	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	2.0	9.74E-02	Vanillin	9.0	13579	3	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990885	PP_4193	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.7	4.53E-01	Control	10.3	13813	2	Cytoplasmic Membrane	COG2009	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	2.3	5.29E-01	Vanillin	7.0	47622	8	Cytoplasmic	COG0372	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	2.7	2.76E-01	Control	9.7	26361	2	Unknown	COG2086	Energy production and conversion	
26990903	PP_4211		RND efflux transporter	2.1	2.84E-01	Control	8.2	51199	16	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990908	PP_4216	pvdE	cyclic peptide transporter	2.3	6.86E-02	Control	7.4	61169	7	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.5	3.27E-01	Control	5.5	89725	31	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990911	PP_4219	ppsD	non-ribosomal siderophore peptide synthetase	1.6	2.52E-01	Control	5.5	382081	23	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990912	PP_4220		non-ribosomal peptide synthetase	1.2	7.42E-01	Vanillin	5.2	287552	39	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990913	PP_4221		non-ribosomal peptide synthetase	1.4	2.89E-01	Control	5.7	236392	15	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990914	PP_4222		syrP protein	1.5	7.70E-01	Vanillin	4.8	36904	2	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
26990934	PP_4243		peptide synthase	1.7	3.13E-01	Control	5.3	475264	30	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990947	PP_4256	ccoO-2	cbb3-type cytochrome c oxidase subunit II	8.7	2.76E-02	Vanillin	9.0	22637	2	Cytoplasmic	COG2993	Energy production and conversion	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	4.4	5.70E-02	Vanillin	5.2	35613	11	Unknown	COG2010	Energy production and conversion	
26990950	PP_4259		iron-sulfur cluster-binding protein	1.1	9.78E-01	Vanillin	8.5	53406	3	Cytoplasmic Membrane	COG0348	Energy production and conversion	
26990966	PP_4275	zipA	cell division protein ZipA	1.2	6.47E-01	Vanillin	6.0	35312	9	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26991134	PP_4448		hypothetical protein	2.4	7.48E-01	Vanillin	6.0	66331	4	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	3.9	5.70E-01	Vanillin	5.1	94711	7	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	3.5	3.16E-01	Vanillin	6.5	43490	4	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991173	PP_4487	acsA	acetyl-CoA synthetase	40.6	1.97E-02	Vanillin	6.4	71796	23	Cytoplasmic	COG0365	Lipid metabolism	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.2	9.05E-01	Vanillin	5.4	50393	18	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	16.5	2.12E-02	Vanillin	6.4	56605	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991226	PP_4542		ABC transporter ATP-binding protein/permease	2.3	5.18E-01	Vanillin	7.6	67748	2	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	7.4	4.60E-01	Vanillin	7.7	61812	5	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	Infinity	3.26E-03	Vanillin	7.8	61658	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991254	PP_4570		hypothetical protein	1.3	3.31E-01	Control	10.1	35846	3	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991325	PP_4641	cstA	carbon starvation protein CstA	2.0	7.53E-02	Vanillin	9.0	73763	10	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991329	PP_4645	mscL	large-conductance mechanosensitive channel	1.3	4.04E-01	Vanillin	4.8	14730	2	Cytoplasmic Membrane	COG1970	Cell envelope biogenesis, outer membrane	
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	299.0	3.75E-03	Vanillin	9.4	26835	4	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	1.4	5.22E-01	Vanillin	4.8	68764	4	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991353	PP_4669		OmpA/MotB domain protein	16.4	1.56E-02	Control	9.9	18241	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.1	9.80E-01	Vanillin	5.4	36370	8	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991368	PP_4684		hypothetical protein	4.8	8.35E-01	Vanillin	5.1	56095	2	Cytoplasmic	COG2187	Function unknown	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	2.7	8.18E-01	Vanillin	4.9	75010	10	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	4.4	8.07E-01	Vanillin	6.8	91460	15	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.4	4.25E-01	Control	5.4	69722	17	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	

26991410	PP_4727	dnaK	molecular chaperone DnaK	1.1	6.24E-01	Control	4.6	68800	13	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones		
26991414	PP_4731	omlA	SmpA/OmlA domain protein	1.7	2.25E-01	Control	4.4	19586	2	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane		
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	6.3	8.11E-01	Vanillin	5.7	45178	2	Cytoplasmic	COG0001	Coenzyme metabolism		
26991474	PP_4794	leuS	leucyl-tRNA synthetase	3.0	7.75E-01	Vanillin	5.6	96697	8	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis		
26991475	PP_4795		rare lipoprotein B	1.2	4.63E-01	Control	6.1	22414	9	Unknown	COG2980	Cell envelope biogenesis, outer membrane		
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	12.9	7.39E-01	Vanillin	6.1	45417	4	Cytoplasmic	COG0014	Amino acid transport and metabolism		
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	3.2	8.06E-01	Vanillin	6.5	57695	3	Cytoplasmic	COG0138	Nucleotide transport and metabolism		
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	3.4	6.09E-01	Vanillin	4.7	45837	3	Cytoplasmic	COG0151	Nucleotide transport and metabolism		
26991504	PP_4824		integral membrane sensor hybrid histidine kinase	1.3	4.96E-01	Vanillin	6.6	101587	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms		
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	2.0	3.87E-01	Control	5.0	31015	2	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones		
26991518	PP_4838	oprC	TonB-dependent copper receptor	13.7	4.79E-03	Vanillin	6.2	74540	38	Outer Membrane	COG1629	Inorganic ion transport and metabolism		
26991519	PP_4839		hypothetical protein	27.2	1.24E-04	Vanillin	9.6	50581	6	Cytoplasmic Membrane	COG3182	Function unknown		
26991556	PP_4876	rpsR	30S ribosomal protein S18	2.2	1.88E-01	Control	11.3	8927	5	Cytoplasmic	COG0238	Translation, ribosomal structure and biogenesis		
26991559	PP_4880	vacB	ribonuclease R	4.0	8.15E-01	Vanillin	7.9	96688	5	Cytoplasmic	COG0557	Transcription		
26991567	PP_4889	purA	adenylosuccinate synthetase	1.6	6.65E-01	Vanillin	5.6	46833	3	Cytoplasmic	COG0104	Nucleotide transport and metabolism		
26991569	PP_4891	hflC	HflC protein	2.2	2.22E-02	Vanillin	9.8	33001	12	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones		
26991570	PP_4892	hflK	HflK protein	1.1	7.77E-01	Vanillin	5.1	44762	5	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones		
26991588	PP_4910		hypothetical protein	1.3	5.42E-01	Control	4.7	53632	8	Cytoplasmic	COG3726	General function prediction only		
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	25.4	9.17E-01	Vanillin	6.2	83181	2	Cytoplasmic	COG0188	DNA replication, recombination, and repair		
26991601	PP_4923		TolC family type I secretion outer membrane protein	1.6	3.39E-01	Vanillin	5.2	52637	9	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	1.3	8.53E-01	Vanillin	7.6	66279	4	Cytoplasmic Membrane	COG1132	Defense mechanisms		
26991622	PP_4944		carbamoyltransferase	1.4	4.53E-01	Vanillin	7.2	65646	5	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones		
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	12.3	4.82E-01	Vanillin	6.3	142580	6	Cytoplasmic	COG4230	Energy production and conversion		
26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	42.3	2.69E-01	Vanillin	4.8	78896	2	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms		
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.0	7.38E-01	Vanillin	5.6	38453	3	Cytoplasmic	COG0191	Carbohydrate transport and metabolism		
26991641	PP_4963	pgk	phosphoglycerate kinase	1.2	7.92E-01	Vanillin	4.9	40005	2	Cytoplasmic	COG0126	Carbohydrate transport and metabolism		
26991643	PP_4965	tktA	transketolase	4.7	5.12E-01	Vanillin	5.0	72463	7	Cytoplasmic	COG0021	Carbohydrate transport and metabolism		
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.1	7.39E-01	Vanillin	5.1	42779	10	Cytoplasmic	COG0192	Coenzyme metabolism		
26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	1.1	3.70E-01	Vanillin	6.2	32979	2	Cytoplasmic	COG0685	Amino acid transport and metabolism		
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	1.7	2.32E-01	Control	10.7	68073	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.9	4.88E-01	Control	5.7	49982	3	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones		
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	1.4	4.13E-01	Vanillin	10.9	26214	4	Cytoplasmic	COG3937	Function unknown		
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.2	5.38E-01	Control	4.9	69017	13	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms	
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.2	2.90E-01	Control	8.3	95875	5	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane		
26991720	PP_5044		GTP-binding protein TypA	1.9	5.43E-01	Vanillin	5.3	67157	4	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms		
26991722	PP_5046	glnA	glutamine synthetase, type I	1.8	8.96E-01	Vanillin	5.1	51740	11	Cytoplasmic	COG0174	Amino acid transport and metabolism		
26991731	PP_5055		rhodanese domain-containing protein	4.5	8.02E-02	Control	9.9	14839	2	Cytoplasmic Membrane	COG0607	Inorganic ion transport and metabolism		
26991732	PP_5056	pgm	phosphoglyceromutase	6.1	2.67E-01	Vanillin	4.9	55180	4	Cytoplasmic	COG0696	Carbohydrate transport and metabolism		
26991752	PP_5076	gltB	glutamate synthase subunit alpha	3.9	5.21E-01	Vanillin	6.2	161772	28	Cytoplasmic	COG0069	Amino acid transport and metabolism		
26991761	PP_5085	maeB	malic enzyme	2.2	2.16E-01	Vanillin	4.9	45127	12	Cytoplasmic	COG0281	Energy production and conversion		
26991765	PP_5089	argS	arginyl-tRNA synthetase	6.3	7.05E-01	Vanillin	5.7	63668	4	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis		
26991766	PP_5090		sporulation domain protein	2.8	3.78E-01	Vanillin	10.6	24964	2	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning		
26991785	PP_5109	ftsX	hypothetical protein	1.3	7.23E-01	Control	6.5	36984	4	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning		
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	3.2	5.16E-01	Vanillin	5.8	65671	10	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.5	4.85E-01	Vanillin	6.3	44339	6	Cytoplasmic	COG0111	Amino acid transport and metabolism		
26991849	PP_5173		acriflavin resistance protein	11.6	1.81E-03	Vanillin	5.4	112277	4	Cytoplasmic Membrane	COG0841	Defense mechanisms		
26991851	PP_5175		efflux transporter RND family, MFP subunit	1.3	6.77E-01	Vanillin	6.5	38304	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane		
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding protein	1.3	9.19E-01	Vanillin	6.4	40068	2	Periplasmic	COG0687	Amino acid transport and metabolism		
26991893	PP_5217	ppk	polyphosphate kinase	1.5	4.84E-01	Vanillin	7.8	81732	3	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism		
26991958	PP_5282	rpmB	50S ribosomal protein L28	2.1	2.00E-01	Control	12.3	8922	4	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis		
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	19.6	7.91E-01	Vanillin	9.2	78603	2	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
26991980	PP_5304		lipoprotein	2.3	1.52E-01	Control	5.1	26284	2	Unknown				
26992029	PP_5353		hypothetical protein	1.9	8.60E-02	Vanillin	7.2	30672	3	Cytoplasmic Membrane	COG4395	Function unknown		
26992037	PP_5361		CobW/P47K family protein	5.6	5.88E-01	Vanillin	4.6	45607	6	Cytoplasmic	COG0523	General function prediction only		
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	2.2	2.06E-01	Control	4.6	49359	6	Cytoplasmic	COG0055	Energy production and conversion		
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	2.3	4.96E-02	Control	9.2	31464	4	Cytoplasmic	COG0224	Energy production and conversion		
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.1	7.05E-01	Vanillin	5.2	55352	13	Cytoplasmic	COG0056	Energy production and conversion		
26992092	PP_5417	atpF	F0F1 ATP synthase subunit B	1.0	1.00E+00	Vanillin	5.3	16898	7	Cytoplasmic Membrane	COG0711	Energy production and conversion		
148545524	Put_0268		phosphoenolpyruvate carboxykinase	6.4	2.20E-01	Vanillin	5.0	55582	9	Cytoplasmic	COG1866	Energy production and conversion		
148545966	Put_0720	rplU	50S ribosomal protein L21	2.3	3.02E-02	Control	10.7	11632	4	Cytoplasmic	COG0261	Translation, ribosomal structure and biogenesis		
148546787	Put_1548		TPR repeat-containing protein	3.2	4.11E-02	Vanillin	4.8	43184	3	Cytoplasmic Membrane	COG4235	Posttranslational modification, protein turnover, chaperones		
148547246	Put_2024		outer membrane porin	110.6	7.51E-04	Vanillin	5.3	45897	14	Outer Membrane				
148548654	Put_3446		phospho-2-dehydro-3-deoxyheptonate aldolase	1.1	4.06E-01	Control	6.4	39054	2	Cytoplasmic	COG0722	Amino acid transport and metabolism		
148549367	Put_4161		S-(hydroxymethyl)glutathione dehydrogenase	29.5	8.38E-03	Vanillin	6.3	39233	9	Cytoplasmic	COG1062	Energy production and conversion		
148550051	Put_4849		S-adenosyl-L-homocysteine hydrolase	2.1	6.09E-01	Vanillin	5.4	51447	13	Cytoplasmic	COG0499	Coenzyme metabolism		
24986476				3.5	4.90E-01	Vanillin			31					
313496770				1.5	4.34E-01	Vanillin			21					
24983268				1.4	9.64E-01	Vanillin			15					
313498866				1.7	4.15E-01	Control			13					
24981833				2.4	2.17E-02	Control			9					
24981839				1.2	5.96E-01	Vanillin			7					
313498081				36.8	2.19E-02	Vanillin			7					
313497930				1.5	2.64E-01	Control			6					
109893221				2.2	2.10E-01	Control			5					
269200090				1.6	5.39E-01	Control			4					
313500100				3.9	7.80E-02	Vanillin			3					
339485164				3.3	2.46E-01	Control			1					
24982932				1.9	2.01E-01	Control			2					
339485705				1.3	7.36E-01	Control			2					
260222836				2.7	2.92E-01	Vanillin			2					

5.3.3 GeLCMSMS



Gelbild der GeLCMSMS-Analyse von auf 6,6 mM (0,1%) Vanillin und 10 mM Glucose kultivierten Zellen von *P. putida* KT2440. Pro Zustand wurden die Proben dreier biologischer Replikate auf das Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Front den unteren Rand des Gels erreicht hatte, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Jede Spur wurde in 10 Fraktionen unterteilt und die markierten Bereiche aus dem Gel ausgeschnitten und mit Trypsin verdaut.

5.3.3 GeLCMSMS_P_putida_KT2440_Vanillin_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
26986746	PP_0001	parB	parB-like partition protein	1.2	2.08E-01	Vanillin	6.5	32390	13	Cytoplasmic	COG1475	Transcription	
26986747	PP_0002		ParA family protein	1.4	4.91E-02	Control	6.7	28919	4	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
26986748	PP_0003	gidB	16S rRNA methyltransferase GidB	3.2	2.41E-02	Control	7.1	24063	3	Unknown	COG0357	Cell envelope biogenesis, outer membrane	
26986750	PP_0005	trmE	tRNA modification GTPase TrmE	3.1	1.71E-01	Vanillin	5.0	48963	9	Cytoplasmic	COG0486	General function prediction only	
26986751	PP_0006	yidC	inner membrane protein translocase component YidC	1.3	5.82E-03	Control	9.1	61919	17	Cytoplasmic Membrane	COG0706	Intracellular trafficking and secretion	
26986755	PP_0010	dnaA	chromosomal replication initiation protein	1.1	4.04E-01	Vanillin	8.3	56473	10	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
26986756	PP_0011	dnaN	DNA polymerase III subunit beta	1.1	3.86E-01	Vanillin	4.9	40718	18	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
26986758	PP_0013	gyrB	DNA gyrase subunit B	1.0	9.82E-01	Vanillin	5.8	90030	25	Unknown	COG0187	DNA replication, recombination, and repair	
26986763	PP_0018		hypothetical protein	1.2	1.42E-01	Control	6.1	31236	14	Cytoplasmic			
26986764	PP_0019		hypothetical protein	1.2	6.27E-02	Control	4.8	24854	6	Unknown			
26986765	PP_0020		hypothetical protein	4.3	3.82E-02	Control	4.9	33146	2	Cytoplasmic			
26986775	PP_0030		sensor histidine kinase	2.7	3.36E-02	Vanillin	6.4	52113	4	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986797	PP_0052		beta-lactamase domain protein	14.6	2.86E-03	Vanillin	5.5	32706	4	Cytoplasmic	COG0491	General function prediction only	
26986805	PP_0060	glyS	glycyl-tRNA synthetase subunit beta	1.1	1.52E-01	Control	4.9	75112	27	Cytoplasmic	COG0751	Translation, ribosomal structure and biogenesis	
26986806	PP_0061	glyQ	glycyl-tRNA synthetase subunit alpha	1.2	3.14E-02	Control	4.8	36024	9	Cytoplasmic	COG0752	Translation, ribosomal structure and biogenesis	
26986810	PP_0065	trkA	potassium transporter peripheral membrane component	1.4	1.51E-02	Control	5.0	49812	6	Cytoplasmic Membrane	COG0569	Inorganic ion transport and metabolism	
26986811	PP_0066	sun	sun protein	1.2	2.27E-01	Control	7.0	47450	3	Cytoplasmic	COG0144	Translation, ribosomal structure and biogenesis	
26986812	PP_0067	fmt	methionyl-tRNA formyltransferase	1.0	8.09E-01	Vanillin	5.6	32822	7	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
26986817	PP_0072	qor-1	quinone oxidoreductase	2.5	5.53E-03	Vanillin	8.1	34224	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26986818	PP_0073	hemF	coproporphyrinogen III oxidase	1.7	2.09E-02	Control	5.6	34393	7	Cytoplasmic	COG0408	Coenzyme metabolism	
26986819	PP_0074	aroE	shikimate 5-dehydrogenase	1.0	7.43E-01	Control	5.0	29289	4	Cytoplasmic	COG0169	Amino acid transport and metabolism	
26986821	PP_0076		glycine/betaine-binding protein	5.6	1.10E-02	Vanillin	7.7	34182	3	Periplasmic	COG2113	Amino acid transport and metabolism	
26986827	PP_0082	trpA	tryptophan synthase subunit alpha	4.9	3.71E-05	Control	5.0	28482	10	Cytoplasmic	COG0159	Amino acid transport and metabolism	
26986828	PP_0083	trpB	tryptophan synthase subunit beta	4.9	2.57E-04	Control	6.4	44046	25	Cytoplasmic	COG0133	Amino acid transport and metabolism	
26986831	PP_0086		hypothetical protein	6.7	2.12E-02	Vanillin	7.9	7959	3	Unknown	COG3360	Function unknown	
26986833	PP_0088		luciferase family protein	1.2	3.11E-01	Control	6.4	36897	6	Cytoplasmic Membrane	COG2141	Energy production and conversion	
26986841	PP_0096	prlC	oligopeptidase A	1.1	5.22E-01	Vanillin	5.0	75721	34	Cytoplasmic	COG0339	Amino acid transport and metabolism	
26986845	PP_0100	cynT	carbonate dehydratase	1.5	1.27E-01	Control	6.8	26001	15	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
26986848	PP_0103		cytochrome c oxidase, subunit II	45.8	2.25E-03	Vanillin	6.8	42059	3	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26986857	PP_0112		metal ABC transporter periplasmic protein	1.2	1.44E-01	Vanillin	7.8	27711	12	Cytoplasmic Membrane	COG1464	Inorganic ion transport and metabolism	
26986859	PP_0114	metN	DL-methionine transporter ATP-binding subunit	1.1	9.82E-01	Control	6.1	36670	6	Cytoplasmic Membrane	COG1135	Inorganic ion transport and metabolism	
26986861	PP_0116		lipoprotein	1.3	2.92E-02	Vanillin	7.4	25597	6	Unknown			
26986863	PP_0118	znuC	zinc ABC transporter ATP-binding protein	1.2	2.16E-01	Control	7.3	27741	2	Cytoplasmic Membrane	COG1121	Inorganic ion transport and metabolism	
26986865	PP_0120		periplasmic solute binding protein	1.3	4.07E-02	Control	6.2	32810	3	Periplasmic	COG4531	Inorganic ion transport and metabolism	
26986866	PP_0121	thrB	homoserine kinase	1.3	8.09E-02	Control	4.8	35143	4	Cytoplasmic	COG2334	General function prediction only	
26986868	PP_0123	polA	DNA polymerase I	1.3	2.91E-02	Vanillin	5.1	99607	29	Cytoplasmic	COG0749	DNA replication, recombination, and repair	
26986874	PP_0129		GGDEF domain-containing protein	1.7	1.28E-02	Vanillin	4.8	71389	4	Cytoplasmic	COG2199	Signal transduction mechanisms	
26986875	PP_0130		N-acetylmuramoyl-L-alanine amidase family protein	1.1	4.58E-01	Vanillin	9.6	29387	5	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
26986878	PP_0133	algB	two component, sigma54 specific, transcriptional regulator, Fis f	1.0	7.08E-01	Vanillin	5.4	49604	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
26986884	PP_0139		lipoprotein	1.1	3.00E-01	Vanillin	9.5	23212	4	Unknown	COG3218	General function prediction only	
26986885	PP_0140		hypothetical protein	1.0	9.33E-01	Vanillin	5.4	33062	2	Unknown	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
26986886	PP_0141		ABC transporter ATP-binding protein	1.1	6.15E-01	Vanillin	6.7	28270	2	Cytoplasmic Membrane	COG1127	Secondary metabolites biosynthesis, transport, and catabolism	
26986899	PP_0154		acetyl-CoA hydrolase/transferase family protein	3.1	1.54E-02	Control	6.1	53957	2	Cytoplasmic	COG0427	Energy production and conversion	
26986900	PP_0155	pntB	NAD(P)(+) transhydrogenase (AB-specific)	1.1	3.00E-01	Vanillin	7.3	50185	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
26986902	PP_0158	gcdH	acyl-CoA dehydrogenase domain-containing protein	27.9	4.58E-03	Vanillin	6.2	43242	3	Cytoplasmic	COG1960	Lipid metabolism	
26986909	PP_0165		GGDEF domain-containing protein	1.6	3.52E-02	Vanillin	6.3	71284	16	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26986910	PP_0166		HlyD family type I secretion membrane fusion protein	1.9	3.13E-01	Control	7.8	51116	13	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986911	PP_0167		toxin secretion ATP-binding protein	1.5	3.82E-01	Control	7.7	78583	18	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26986912	PP_0168		surface adhesion protein	1.1	5.76E-01	Vanillin	3.9	888214	18	Extracellular	COG2931	Secondary metabolites biosynthesis, transport, and catabolism	
26986920	PP_0176		fusaric acid resistance protein region	49.1	1.51E-06	Vanillin	7.2	76261	5	Cytoplasmic Membrane	COG1289	Function unknown	
26986922	PP_0178		secretion protein HlyD family protein	72.3	1.44E-05	Vanillin	9.4	32339	13	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26986923	PP_0179		RND efflux transporter	51.1	4.01E-05	Vanillin	5.6	50813	12	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26986924	PP_0180		cytochrome c family protein	3.1	1.22E-02	Vanillin	4.9	68013	7	Cytoplasmic Membrane	COG0672	Inorganic ion transport and metabolism	
26986928	PP_0184	argH	argininosuccinate lyase	1.1	3.32E-01	Control	5.4	52061	26	Cytoplasmic	COG0165	Amino acid transport and metabolism	
26986929	PP_0185	pprA	LytTR family two component transcriptional regulator	8.3	1.78E-04	Vanillin	6.5	27422	10	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
26986930	PP_0186	hemC	porphobilinogen deaminase	1.4	1.24E-03	Control	5.1	33440	5	Cytoplasmic	COG0181	Coenzyme metabolism	
26986932	PP_0188		uroporphyrin-III C-methyltransferase	1.2	3.28E-01	Vanillin	4.8	40556	14	Cytoplasmic Membrane	COG2959	Coenzyme metabolism	
26986933	PP_0189	hemY	HemY domain protein	1.4	2.17E-01	Vanillin	9.6	46030	13	Cytoplasmic Membrane	COG3071	Coenzyme metabolism	
26986938	PP_0194	algP	alginate regulatory protein AlgP	2.5	3.35E-04	Vanillin	11.3	32300	3	Cytoplasmic			
26986940	PP_0196		ABC transporter ATP-binding protein	1.1	3.58E-01	Vanillin	5.7	70615	12	Cytoplasmic	COG0488	General function prediction only	
26986947	PP_0203		hypothetical protein	1.6	2.98E-02	Vanillin	5.9	62682	19	Unknown	COG0624	Amino acid transport and metabolism	
26986956	PP_0213	gabD	succinate-semialdehyde dehydrogenase I	1.7	5.93E-04	Vanillin	5.2	51549	28	Cytoplasmic	COG1012	Energy production and conversion	
26986957	PP_0214	gabT	4-aminobutyrate aminotransferase	1.6	1.36E-01	Vanillin	6.1	44824	30	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26986958	PP_0215		signal transduction protein	1.3	3.11E-01	Vanillin	7.0	45294	3	Cytoplasmic	COG1639	Signal transduction mechanisms	
26986968	PP_0225		amino-acid ABC transporter ATP-binding protein YecC	1.1	4.33E-01	Vanillin	10.2	27596	3	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26986970	PP_0227		cystine transporter subunit	1.3	1.91E-01	Vanillin	8.7	28756	17	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26986973	PP_0230	tauD	taurine dioxygenase	53.3	4.65E-02	Vanillin	6.0	31098	3	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
26986976	PP_0233	tauA	taurine ABC transporter periplasmic protein	37.2	2.29E-04	Vanillin	7.7	34324	4	Unknown	COG4521	Inorganic ion transport and metabolism	
26986977	PP_0234	oprE	outer membrane porin	5.2	1.18E-05	Control	5.4	48317	22	Outer Membrane			
26986978	PP_0235	lsfA	peroxidase	6.4	1.36E-04	Vanillin	6.0	23948	9	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26986980	PP_0237	ssuA	aliphatic sulfonate ABC transporter periplasmic ligand-binding p	12276.2	1.01E-02	Vanillin	9.1	34562	4	Unknown	COG0715	Inorganic ion transport and metabolism	
26986981	PP_0238	ssuD	alkanesulfonate monooxygenase	26.6	3.21E-02	Vanillin	5.6	41507	13	Cytoplasmic	COG2141	Energy production and conversion	
26986986	PP_0243	gshA	glutamate--cysteine ligase	1.2	9.93E-03	Control	4.8	59067	11	Cytoplasmic	COG2918	Coenzyme metabolism	
26986988	PP_0245		S1 RNA-binding domain-containing protein	1.1	5.81E-01	Vanillin	8.7	94304	28	Cytoplasmic	COG2183	Transcription	
26986989	PP_0246	ompR	osmolarity response regulator	2.2	5.60E-02	Vanillin	5.9	27492	13	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26986990	PP_0247	envZ	integral membrane sensor signal transduction histidine kinase	1.8	8.19E-02	Vanillin	6.1	48808	3	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26986991	PP_0248	rimK	alpha-L-glutamate ligase, RimK family	2.1	1.83E-02	Vanillin	10.1	32629	2	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis

26986995	PP_0252	hslO	Hsp33-like chaperonin	1.7	9.00E-03	Control	4.4	33472	12	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
26986998	PP_0256		molybdopterin oxidoreductase, alpha subunit	67.3	7.12E-05	Vanillin	7.0	86029	16	Cytoplasmic	COG0243	Energy production and conversion	
26986999	PP_0257		formate dehydrogenase family accessory protein FdhD	24.6	1.20E-03	Vanillin	6.5	29396	5	Cytoplasmic	COG1526	Energy production and conversion	
26987002	PP_0260	nudE	ADP-ribose diphosphatase NudE	1.5	4.07E-02	Vanillin	4.5	20947	5	Cytoplasmic			
26987005	PP_0263		two component, sigma54 specific, transcriptional regulator, Fis f	1.8	3.43E-02	Vanillin	5.9	50990	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
26987008	PP_0266		agmatine deiminase	5.8	1.36E-02	Vanillin	4.7	40837	10	Cytoplasmic	COG2957	Amino acid transport and metabolism	
26987010	PP_0268	oprQ	outer membrane porin	1.4	5.91E-02	Control	6.1	47787	12	Outer Membrane			
26987024	PP_0282		amino acid ABC transporter periplasmic amino acid-binding prot	2.3	2.37E-04	Vanillin	5.2	27869	20	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987025	PP_0283		amino acid ABC transporter ATP-binding protein	1.3	6.72E-02	Vanillin	7.7	28381	6	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism	
26987029	PP_0287		AsmA family protein	2.1	7.38E-03	Vanillin	6.0	80277	23	Unknown	COG2982	Cell envelope biogenesis, outer membrane	
26987030	PP_0288		major facilitator superfamily MFS_1	2.1	3.46E-01	Vanillin	8.5	58780	2	Cytoplasmic Membrane			
26987034	PP_0292	hisA	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneai	2.2	7.41E-03	Control	4.9	25907	13	Cytoplasmic	COG0106	Amino acid transport and metabolism	
26987035	PP_0293	hisF	imidazole glycerol phosphate synthase subunit HisF	4.2	1.56E-03	Control	5.0	27131	8	Cytoplasmic	COG0107	Amino acid transport and metabolism	
26987036	PP_0294		glycine betaine/L-proline ABC transporter ATP-binding subunit	15.4	3.77E-03	Vanillin	7.9	43724	7	Cytoplasmic Membrane	COG4175	Amino acid transport and metabolism	
26987038	PP_0296		glycine betaine/L-proline ABC transporter periplasmic protein	8.8	2.43E-05	Vanillin	6.6	34568	14	Unknown	COG2113	Amino acid transport and metabolism	
26987044	PP_0302		3-hydroxybutyryl-CoA dehydrogenase	16.3	3.59E-03	Vanillin	5.4	34618	2	Cytoplasmic	COG1250	Lipid metabolism	
26987050	PP_0308		membrane dipeptidase	14.3	7.04E-02	Vanillin	5.4	35978	1	Cytoplasmic	COG2355	Amino acid transport and metabolism	
26987063	PP_0321		threonine aldolase	1.7	1.44E-03	Vanillin	5.4	38068	11	Cytoplasmic	COG2008	Amino acid transport and metabolism	
26987064	PP_0322	glyA-1	serine hydroxymethyltransferase	2.8	4.12E-02	Vanillin	6.4	44555	4	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987067	PP_0325	soxA	sarcosine oxidase, alpha subunit family	3.8	3.05E-03	Vanillin	7.6	109175	9	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987078	PP_0336	msrA	methionine sulfoxide reductase A	2.6	3.48E-03	Control	4.7	24565	6	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
26987080	PP_0338	aceF	dihydrolipoamide acetyltransferase	2.7	3.83E-04	Control	5.3	55654	19	Cytoplasmic	COG0508	Energy production and conversion	
26987081	PP_0339	aceE	pyruvate dehydrogenase subunit E1	2.6	8.16E-04	Control	5.6	99332	70	Cytoplasmic	COG2609	Energy production and conversion	
26987082	PP_0340	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadeny	1.4	6.04E-03	Vanillin	5.3	109432	19	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
26987083	PP_0341	waaF	lipopolysaccharide heptosyltransferase II	1.6	3.35E-02	Vanillin	6.7	38423	4	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane	
26987084	PP_0342	waaC	lipopolysaccharide heptosyltransferase I	2.1	4.47E-03	Vanillin	9.8	39419	4	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane	
26987085	PP_0343	waaG	lipopolysaccharide core biosynthesis protein WaaG	1.2	5.41E-01	Control	8.4	42067	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26987086	PP_0344	waaP	lipopolysaccharide kinase	1.1	6.53E-01	Vanillin	10.2	30807	2	Cytoplasmic			
26987087	PP_0345		lipopolysaccharide kinase	1.6	2.64E-01	Vanillin	10.4	28715	2	Cytoplasmic			
26987089	PP_0347		hypothetical protein	1.2	2.35E-01	Vanillin	7.4	53779	8	Cytoplasmic			
26987098	PP_0356	glcB	malate synthase G	3.8	2.71E-03	Vanillin	5.8	78346	30	Cytoplasmic	COG2225	Energy production and conversion	
26987108	PP_0366	bioD	dithiobiotin synthetase	1.9	1.85E-01	Vanillin	5.3	23871	3	Cytoplasmic	COG0132	Coenzyme metabolism	
26987110	PP_0368		acyl-CoA dehydrogenase domain-containing protein	1.1	7.19E-01	Vanillin	5.8	65541	24	Cytoplasmic	COG1960	Lipid metabolism	
26987112	PP_0370		acyl-CoA dehydrogenase domain-containing protein	1.3	5.14E-03	Vanillin	4.9	63592	7	Cytoplasmic	COG1960	Lipid metabolism	
26987117	PP_0375		prolyl oligopeptidase family protein	7.4	5.79E-02	Vanillin	6.0	67549	7	Cytoplasmic	COG1506	Amino acid transport and metabolism	
26987118	PP_0376	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	10.9	4.08E-02	Vanillin	6.5	42507	6	Cytoplasmic	COG0535	General function prediction only	
26987120	PP_0378	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	5.0	9.63E-03	Vanillin	6.8	29075	13	Cytoplasmic	COG5424	Coenzyme metabolism	
26987124	PP_0382		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferas	4.0	7.40E-03	Vanillin	4.9	29311	5	Cytoplasmic	COG0388	General function prediction only	
26987128	PP_0386		sensory box protein	18.6	1.53E-03	Vanillin	5.6	139392	4	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987129	PP_0387	rpoD	RNA polymerase sigma factor RpoD	1.3	3.37E-01	Vanillin	4.6	69396	23	Cytoplasmic	COG0568	Transcription	
26987130	PP_0388	dnaG	DNA primase	1.4	5.72E-01	Vanillin	6.8	73829	3	Cytoplasmic	COG0358	DNA replication, recombination, and repair	
26987132	PP_0390	gcp	DNA-binding/iron metalloprotein/AP endonuclease	1.2	5.75E-02	Control	4.8	36606	7	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
26987137	PP_0395		SpoVR family protein	5.7	4.61E-04	Vanillin	5.4	61330	12	Cytoplasmic	COG2719	Function unknown	
26987138	PP_0396		hypothetical protein	8.4	3.57E-04	Vanillin	7.0	50488	12	Cytoplasmic	COG2718	Function unknown	
26987139	PP_0397		serine protein kinase, PrkA	6.9	4.86E-06	Vanillin	5.8	73782	32	Cytoplasmic	COG2766	Signal transduction mechanisms	
26987141	PP_0399	apaH	diadenosine tetraphosphatase	1.1	5.84E-01	Control	6.6	32603	4	Cytoplasmic			
26987143	PP_0401	ksgA	dimethyladenosine transferase	1.5	7.67E-03	Control	8.5	29666	3	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
26987144	PP_0402	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	1.2	1.66E-01	Vanillin	6.3	34953	7	Cytoplasmic	COG1995	Coenzyme metabolism	
26987145	PP_0403	surA	survival protein SurA	1.2	6.17E-02	Control	5.2	49082	21	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
26987146	PP_0405		aminoglycoside phosphotransferase	1.1	4.35E-01	Control	4.8	38238	9	Cytoplasmic	COG3178	General function prediction only	
26987149	PP_0408		hypothetical protein	1.4	2.47E-01	Control	4.8	35332	3	Periplasmic			
26987150	PP_0409		PAS/PAC sensor signal transduction histidine kinase	5.7	1.02E-02	Vanillin	5.4	89442	2	Cytoplasmic Membrane	COG4585	Signal transduction mechanisms	
26987152	PP_0411		spermidine/putrescine ABC transporter ATPase	5.0	5.97E-02	Vanillin	6.6	41197	2	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26987153	PP_0412		polyamine ABC transporter periplasmic protein	3.2	1.98E-03	Vanillin	5.3	37801	10	Periplasmic	COG0687	Amino acid transport and metabolism	
26987154	PP_0413		binding-protein-dependent transport systems inner membrane c	3.0	4.61E-02	Vanillin	9.5	45808	3	Cytoplasmic Membrane	COG1176	Amino acid transport and metabolism	
26987157	PP_0416	gph	phosphoglycolate phosphatase	1.2	1.04E-01	Vanillin	5.4	29604	2	Cytoplasmic	COG0546	General function prediction only	
26987158	PP_0417	trpE	anthranilate synthase component I	1.5	1.28E-03	Control	4.8	54406	18	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
26987159	PP_0418		GDSL family lipase	2.9	2.04E-02	Vanillin	4.4	67175	6	Outer Membrane	COG3240	Lipid metabolism	General function prediction only
26987162	PP_0421	trpD	anthranilate phosphoribosyltransferase	1.0	7.06E-01	Vanillin	5.6	37245	9	Cytoplasmic	COG0547	Amino acid transport and metabolism	
26987163	PP_0422	trpC	indole-3-glycerol-phosphate synthase	1.5	5.55E-03	Control	4.7	30433	14	Cytoplasmic	COG0134	Amino acid transport and metabolism	
26987164	PP_0423		hypothetical protein	1.5	6.00E-03	Vanillin	5.9	25784	4	Cytoplasmic	COG0095	Coenzyme metabolism	
26987168	PP_0427		hypothetical protein	3.0	1.22E-04	Vanillin	6.1	24001	8	Cytoplasmic	COG2941	Coenzyme metabolism	
26987171	PP_0430		hypothetical protein	4.2	4.99E-05	Vanillin	6.7	33680	3	Unknown	COG2070	General function prediction only	
26987173	PP_0432	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.0	8.37E-01	Vanillin	6.8	36277	19	Cytoplasmic	COG0002	Amino acid transport and metabolism	
26987175	PP_0434	anmK	anhydro-N-acetylmuramic acid kinase	2.9	8.18E-03	Vanillin	5.8	38235	5	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
26987177	PP_0436	tyrS	tyrosyl-tRNA synthetase	2.0	3.06E-04	Control	5.5	44287	20	Cytoplasmic	COG0162	Translation, ribosomal structure and biogenesis	
26987178	PP_0437	birA	biotin--protein ligase	1.1	1.28E-01	Vanillin	7.0	35019	6	Cytoplasmic	COG0340	Coenzyme metabolism	
26987181	PP_0440	tuf	elongation factor Tu	1.1	6.19E-01	Vanillin	5.0	43495	22	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987185	PP_0444	rplA	50S ribosomal protein L1	1.7	8.93E-04	Control	10.1	24251	24	Cytoplasmic	COG0081	Translation, ribosomal structure and biogenesis	
26987188	PP_0447	rpoB	DNA-directed RNA polymerase subunit beta	1.5	8.71E-03	Vanillin	5.5	150992	105	Cytoplasmic	COG0085	Transcription	
26987189	PP_0448	rpoC	DNA-directed RNA polymerase subunit beta'	1.4	2.24E-02	Vanillin	7.2	154797	89	Cytoplasmic	COG0086	Transcription	
26987192	PP_0451	fusA	elongation factor G	1.0	7.56E-01	Control	4.9	78817	64	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26987193	PP_0452	tuf	elongation factor Tu	1.5	2.69E-02	Control	5.0	43478	44	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
26987196	PP_0455	rplD	50S ribosomal protein L4	11.0	2.39E-02	Control	10.3	21811	6	Cytoplasmic	COG0088	Translation, ribosomal structure and biogenesis	
26987198	PP_0457	rplB	50S ribosomal protein L2	1.9	2.44E-03	Control	11.7	29669	22	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
26987205	PP_0464	rplN	50S ribosomal protein L14	22.8	8.64E-03	Control	11.6	13410	2	Cytoplasmic	COG0093	Translation, ribosomal structure and biogenesis	
26987207	PP_0466	rplE	50S ribosomal protein L5	19.4	1.80E-02	Control	10.3	20329	3	Cytoplasmic	COG0094	Translation, ribosomal structure and biogenesis	
26987208	PP_0467	rpsN	30S ribosomal protein S14	64.4	5.16E-05	Control	12.3	11403	2	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	

26987210	PP_0469	rplF	50S ribosomal protein L6	6.0	1.92E-02	Control	10.4	19143	6	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
26987211	PP_0470	rplR	50S ribosomal protein L18	16.6	1.08E-03	Control	10.9	12628	4	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
26987214	PP_0473	rplO	50S ribosomal protein L15	27.7	6.90E-03	Control	11.5	15189	3	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
26987215	PP_0474	secY	preprotein translocase subunit SecY	1.7	6.89E-03	Control	10.4	47853	12	Cytoplasmic Membrane	COG0201	Intracellular trafficking and secretion	
26987219	PP_0478	rpsD	30S ribosomal protein S4	3.3	1.42E-02	Control	10.5	23056	14	Cytoplasmic	COG0522	Translation, ribosomal structure and biogenesis	
26987220	PP_0479	rpoA	DNA-directed RNA polymerase subunit alpha	1.1	4.11E-01	Control	4.7	36629	25	Cytoplasmic	COG0202	Transcription	
26987222	PP_0481	katA	catalase	28.5	3.46E-03	Vanillin	6.6	53589	3	Periplasmic	COG0753	Inorganic ion transport and metabolism	
26987224	PP_0483	uvrA	excinuclease ABC subunit A	1.2	4.23E-01	Control	7.0	104378	15	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
26987233	PP_0493	selA	selenocysteine synthase	2.2	1.06E-02	Vanillin	7.7	51723	6	Cytoplasmic	COG1921	Amino acid transport and metabolism	
26987234	PP_0494	selB	selenocysteine-specific translation elongation factor	7.2	1.39E-02	Vanillin	7.4	70141	4	Cytoplasmic	COG3276	Translation, ribosomal structure and biogenesis	
26987235	PP_0495	ansB	asparaginase	1.2	2.14E-01	Control	5.1	34799	2	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
26987239	PP_0500		dTDP-4-dehydrorhamnose reductase	1.0	7.78E-01	Vanillin	6.6	32700	3	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26987240	PP_0501		NAD-dependent epimerase/dehydratase	1.8	3.70E-03	Control	5.2	33325	5	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987245	PP_0506		hypothetical protein	1.3	4.80E-02	Vanillin	9.7	45834	10	Cytoplasmic Membrane	COG0577	Defense mechanisms	
26987246	PP_0507		efflux ABC transporter ATP-binding protein	2.3	1.35E-01	Control	7.2	25648	6	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26987247	PP_0508		hypothetical protein	1.7	3.70E-01	Control	5.0	20628	4	Unknown			
26987249	PP_0510	trx-1	thioredoxin	1.1	5.58E-01	Control	4.6	31822	14	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
26987257	PP_0519	thiL	thiamine monophosphate kinase	1.4	2.80E-01	Control	4.7	32955	2	Unknown	COG0611	Coenzyme metabolism	
26987259	PP_0521		hypothetical protein	1.6	1.92E-01	Vanillin	6.4	28523	3	Unknown			
26987266	PP_0528	ispA	polyprenyl synthetase	1.3	7.24E-02	Vanillin	4.9	31352	10	Cytoplasmic	COG0142	Coenzyme metabolism	
26987273	PP_0535		TonB-dependent siderophore receptor	2.5	4.38E-02	Control	4.7	79268	2	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26987280	PP_0542		ethanolamine ammonia-lyase small subunit	7.5	3.05E-04	Vanillin	6.9	29573	5	Cytoplasmic	COG4302	Amino acid transport and metabolism	
26987281	PP_0543	eutB	ethanolamine ammonia lyase large subunit	14.0	1.13E-03	Vanillin	5.0	49939	6	Cytoplasmic	COG4303	Amino acid transport and metabolism	
26987283	PP_0545		aldehyde dehydrogenase family protein	5.5	1.57E-04	Vanillin	5.9	55268	33	Cytoplasmic	COG1012	Energy production and conversion	
26987285	PP_0547	mpl	UDP-N-acetylmuramate	1.4	1.73E-03	Vanillin	6.1	48202	8	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
26987296	PP_0558	accC-1	acetyl-CoA carboxylase biotin carboxylase subunit	1.1	7.19E-02	Control	6.5	49088	26	Cytoplasmic	COG0439	Lipid metabolism	
26987302	PP_0564		hypothetical protein	1.1	2.31E-01	Vanillin	6.6	40223	12	Unknown	COG5345	Function unknown	
26987305	PP_0567	speA	arginine decarboxylase	1.6	4.89E-02	Vanillin	5.3	71043	19	Unknown	COG1166	Amino acid transport and metabolism	
26987308	PP_0570		alpha-2-macroglobulin domain protein	3.5	1.45E-03	Vanillin	5.2	178472	38	Unknown	COG2373	General function prediction only	
26987312	PP_0574		LuxR family DNA-binding response regulator	1.7	7.23E-02	Vanillin	5.1	29040	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
26987318	PP_0580		MaoC domain-containing protein	9.1	1.20E-04	Vanillin	7.5	31356	2	Cytoplasmic	COG2030	Lipid metabolism	
26987319	PP_0581	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	5.0	4.91E-04	Vanillin	7.5	47782	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26987320	PP_0582		acetyl-CoA acetyltransferase	2.3	4.26E-02	Vanillin	8.3	45543	4	Cytoplasmic	COG0183	Lipid metabolism	
26987322	PP_0584		methyl-accepting chemotaxis transducer	2.2	8.09E-03	Vanillin	5.0	69953	18	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26987324	PP_0586		heavy metal translocating P-type ATPase	6.3	3.96E-03	Vanillin	6.6	83475	7	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26987329	PP_0591	add	adenosine deaminase	1.9	6.55E-03	Vanillin	4.8	35845	6	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
26987334	PP_0596		beta alanine--pyruvate transaminase	1.8	3.05E-02	Vanillin	6.8	48529	13	Cytoplasmic	COG0161	Coenzyme metabolism	
26987335	PP_0597	mmsA-1	methylmalonate-semialdehyde dehydrogenase	1.0	9.52E-01	Control	5.9	53498	18	Cytoplasmic	COG1012	Energy production and conversion	
26987336	PP_0599		hypothetical protein	2.1	3.17E-02	Vanillin	9.6	83247	16	Unknown	COG3008	General function prediction only	
26987339	PP_0602	ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	1.2	1.38E-01	Control	9.7	34827	14	Cytoplasmic	COG0196	Coenzyme metabolism	
26987340	PP_0603	ileS	isoleucyl-tRNA synthetase	1.2	1.08E-02	Control	6.0	105800	36	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
26987343	PP_0606	ispH	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1.0	8.50E-01	Control	4.7	34543	10	Cytoplasmic	COG0761	Lipid metabolism	
26987349	PP_0612		FAD dependent oxidoreductase	2.8	4.24E-02	Control	5.1	38679	4	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26987350	PP_0613		amidase	85.0	3.47E-03	Vanillin	6.3	50420	5	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987351	PP_0614		allantoate amidohydrolase	5.3	5.96E-03	Vanillin	5.6	45279	2	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26987359	PP_0622		competence lipoprotein ComL	1.2	4.35E-02	Vanillin	4.8	38410	9	Unknown	COG4105	General function prediction only	
26987360	PP_0624		hypothetical protein	1.1	9.12E-01	Control	6.1	26401	2	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
26987361	PP_0625	clpB	ATP-dependent Clp protease, ATP-binding subunit ClpB	1.7	6.41E-03	Vanillin	5.2	94861	56	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26987362	PP_0626	ndh	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	5.8	1.39E-01	Control	9.0	47080	3	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26987376	PP_0640		hypothetical protein	1.0	8.51E-01	Vanillin	6.6	44093	9	Cytoplasmic Membrane			
26987393	PP_0657		amino acid ABC transporter periplasmic amino acid-binding prot	1.6	1.93E-01	Control	4.6	30384	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987394	PP_0658		homocysteine S-methyltransferase family protein	1.1	5.17E-01	Vanillin	5.0	33406	3	Cytoplasmic	COG2040	Amino acid transport and metabolism	
26987407	PP_0671	glyA	serine hydroxymethyltransferase	1.1	2.30E-01	Control	6.2	44897	22	Cytoplasmic	COG0112	Amino acid transport and metabolism	
26987408	PP_0672		sensory box protein	1.7	1.26E-01	Vanillin	5.7	144317	10	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987410	PP_0674		ABC transporter ATP-binding protein	1.2	7.53E-03	Control	5.3	61860	31	Cytoplasmic	COG0488	General function prediction only	
26987411	PP_0675	gdhA	glutamate dehydrogenase	1.2	5.25E-01	Vanillin	6.5	48871	20	Unknown	COG0334	Amino acid transport and metabolism	
26987414	PP_0678		hypothetical protein	1.3	6.87E-01	Vanillin	5.1	70138	1	Unknown			
26987416	PP_0680		ATP-dependent protease	1.1	6.52E-01	Vanillin	4.5	89677	38	Cytoplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
26987420	PP_0684	fklB-1	peptidyl-prolyl cis-trans isomerase, FKBP-type	14.3	4.39E-02	Control	4.4	21678	2	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26987423	PP_0687	ispB	polyprenyl synthetase	1.1	6.50E-02	Control	4.8	35269	15	Cytoplasmic	COG0142	Coenzyme metabolism	
26987426	PP_0690	obgE	GTPase ObgE	1.2	3.66E-01	Vanillin	4.5	44825	9	Cytoplasmic	COG0536	General function prediction only	
26987427	PP_0691	proB	gamma-glutamyl kinase	1.7	2.28E-02	Control	7.8	39661	14	Cytoplasmic	COG0263	Amino acid transport and metabolism	
26987429	PP_0693		hypothetical protein	1.1	3.03E-01	Control	5.1	106556	31	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26987430	PP_0694		hypothetical protein	1.4	1.64E-01	Control	4.3	26935	4	Cytoplasmic			
26987431	PP_0695		hypothetical protein	1.7	1.89E-02	Control	7.8	51069	6	Cytoplasmic			
26987443	PP_0707		MscS mechanosensitive ion channel	2.1	1.63E-02	Vanillin	9.9	92124	9	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26987447	PP_0711		isochorismatase superfamily hydrolase	9.5	1.72E-01	Vanillin	5.3	23026	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
26987448	PP_0712		hypothetical protein	7.8	5.00E-05	Vanillin	10.5	31284	8	Cytoplasmic	COG2326	Function unknown	
26987455	PP_0719		GTP-dependent nucleic acid-binding protein EngD	1.7	2.79E-03	Control	4.7	39962	14	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
26987457	PP_0721		50S ribosomal protein L25/general stress protein Ctc	1.6	3.09E-02	Control	6.4	23242	12	Cytoplasmic	COG1825	Translation, ribosomal structure and biogenesis	
26987458	PP_0722	prsA	ribose-phosphate pyrophosphokinase	1.2	3.53E-01	Control	5.9	34192	24	Cytoplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
26987461	PP_0725		hypothetical protein	1.2	2.29E-01	Vanillin	4.6	63994	8	Cytoplasmic	COG5010	Intracellular trafficking and secretion	
26987468	PP_0732	hemA	glutamyl-tRNA reductase	1.0	8.45E-01	Control	5.5	46305	7	Cytoplasmic	COG0373	Coenzyme metabolism	
26987469	PP_0733	prfA	peptide chain release factor 1	1.2	2.24E-01	Vanillin	4.7	40319	5	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis	
26987471	PP_0735		molybdopterin biosynthesis protein MoeB	1.1	5.94E-01	Vanillin	5.1	26584	3	Cytoplasmic	COG0476	Coenzyme metabolism	
26987475	PP_0739	phrB	deoxyribodipyrimidine photo-lyase	1.9	1.92E-02	Vanillin	8.4	54977	3	Cytoplasmic	COG0415	DNA replication, recombination, and repair	
26987478	PP_0742		hypothetical protein	3.1	1.02E-04	Vanillin	6.2	36114	5	Unknown	COG3380	General function prediction only	
26987480	PP_0744	hemH	ferrochelatase	1.4	9.88E-02	Vanillin	6.8	37758	7	Cytoplasmic	COG0276	Coenzyme metabolism	

26987487	PP_0751	mqo-1	malate:quinone oxidoreductase	2.2	1.18E-03	Control	8.4	54282	25	Cytoplasmic	COG0579	General function prediction only	
26987492	PP_0756		phospholipid/glycerol acyltransferase	1.4	2.92E-01	Vanillin	8.3	47784	6	Cytoplasmic			
26987495	PP_0759		hypothetical protein	1.2	1.88E-03	Vanillin	7.0	29743	10	Unknown	COG0501	Posttranslational modification, protein turnover, chaperones	
26987497	PP_0761		rRNA (guanine-N(2)-)-methyltransferase	1.3	2.72E-01	Vanillin	6.8	35787	3	Cytoplasmic	COG2813	Translation, ribosomal structure and biogenesis	
26987498	PP_0762	hprA	glycerate dehydrogenase	1.6	7.26E-02	Vanillin	6.1	34094	15	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26987499	PP_0763		long-chain-fatty-acid--CoA ligase	3.3	7.60E-04	Vanillin	5.5	62125	13	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26987501	PP_0765		hypothetical protein	4.5	4.30E-05	Vanillin	5.0	67937	16	Outer Membrane			
26987502	PP_0766		hypothetical protein	4.6	1.76E-05	Vanillin	9.6	50572	29	Unknown			
26987504	PP_0768		response regulator/hypothetical protein	1.7	1.40E-01	Vanillin	8.4	59272	11	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26987505	PP_0769		histidine kinase	1.3	2.44E-01	Vanillin	4.6	25229	6	Cytoplasmic	COG0642	Signal transduction mechanisms	
26987508	PP_0772		beta-lactamase domain protein	1.2	2.24E-01	Control	6.3	23621	2	Cytoplasmic	COG0491	General function prediction only	
26987510	PP_0774	pta	phosphate acetyltransferase	1.4	9.67E-02	Vanillin	5.2	74642	15	Cytoplasmic Membrane	COG0280	Energy production and conversion	
26987522	PP_0786	trxB	thioredoxin reductase	1.2	4.60E-01	Vanillin	5.1	33841	12	Unknown	COG0492	Posttranslational modification, protein turnover, chaperones	
26987523	PP_0787	nadC	nicotinate-nucleotide pyrophosphorylase	1.3	1.09E-01	Vanillin	5.2	30163	8	Cytoplasmic	COG0157	Coenzyme metabolism	
26987528	PP_0792	fruR	DNA-binding transcriptional regulator FruR	1.1	1.99E-01	Control	6.7	36210	8	Cytoplasmic	COG1609	Transcription	
26987529	PP_0793	fruB	phosphoenolpyruvate-protein phosphotransferase	5.4	2.35E-04	Control	4.8	101497	17	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
26987530	PP_0794	fruK	1-phosphofructokinase	24.6	1.89E-05	Control	6.0	33188	6	Cytoplasmic	COG1105	Carbohydrate transport and metabolism	
26987531	PP_0795	fruA	PTS system, fructose subfamily, IIC subunit	774.6	1.51E-02	Control	8.7	59235	2	Cytoplasmic Membrane	COG1299	Carbohydrate transport and metabolism	
26987535	PP_0799		outer membrane porin	5.2	1.15E-01	Vanillin	5.0	49091	6	Outer Membrane			
26987540	PP_0804		protein secretion ABC efflux system, permease and ATP-binding	8.2	3.36E-03	Vanillin	9.2	79558	10	Cytoplasmic Membrane	COG2274	Defense mechanisms	
26987541	PP_0805		TolC family type I secretion outer membrane protein	3.8	1.66E-03	Vanillin	5.8	51839	5	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26987542	PP_0806		surface adhesion protein	37.6	1.11E-04	Vanillin	3.5	615675	14	Extracellular			
26987548	PP_0812	cyoA	ubiquinol oxidase subunit 2	1.5	1.80E-02	Vanillin	6.7	34557	9	Cytoplasmic Membrane	COG1622	Energy production and conversion	
26987549	PP_0813	cyoB	cytochrome o ubiquinol oxidase, subunit I	1.1	3.16E-01	Control	7.8	74391	12	Cytoplasmic Membrane	COG0843	Energy production and conversion	
26987553	PP_0817		aminotransferase	1.4	1.41E-01	Vanillin	8.1	44996	9	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26987558	PP_0822		tRNA 2-selenouridine synthase	1.6	1.95E-01	Vanillin	7.6	41897	2	Cytoplasmic	COG2603	General function prediction only	
26987559	PP_0823	selD	selenophosphate synthetase	2.2	1.27E-02	Vanillin	5.4	36245	6	Unknown	COG0709	Amino acid transport and metabolism	
26987560	PP_0824		phosphonate ABC transporter periplasmic phosphonate-binding	1.9	5.24E-03	Vanillin	8.6	31104	16	Periplasmic	COG3221	Inorganic ion transport and metabolism	
26987561	PP_0825		phosphate ABC transporter ATP-binding protein	2.8	7.24E-02	Vanillin	10.0	28635	2	Cytoplasmic Membrane	COG3638	Inorganic ion transport and metabolism	
26987568	PP_0832	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1.6	2.51E-03	Control	6.2	38364	7	Cytoplasmic	COG0809	Translation, ribosomal structure and biogenesis	
26987569	PP_0833	tgt	queuine tRNA-ribosyltransferase	1.3	6.78E-02	Control	6.8	41335	12	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis	
26987571	PP_0835	secD	preprotein translocase subunit SecD	1.7	3.35E-02	Control	9.6	66913	20	Cytoplasmic Membrane	COG0342	Intracellular trafficking and secretion	
26987572	PP_0836	secF	preprotein translocase subunit SecF	4.6	4.20E-03	Control	4.8	32758	4	Cytoplasmic Membrane	COG0341	Intracellular trafficking and secretion	
26987574	PP_0838	suhB	inositol-phosphate phosphatase	1.2	1.57E-03	Control	6.6	29753	17	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26987575	PP_0839		RNA methyltransferase	1.2	4.37E-01	Control	6.6	27468	4	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis	
26987576	PP_0840	cysE	serine O-acetyltransferase	1.2	6.30E-01	Control	6.7	28206	4	Cytoplasmic	COG1045	Amino acid transport and metabolism	
26987578	PP_0842	iscS	cysteine desulfurase	1.4	1.30E-02	Control	6.2	44468	29	Cytoplasmic	COG1104	Amino acid transport and metabolism	
26987582	PP_0846	hscA	chaperone protein HscA	1.9	1.03E-03	Control	4.7	65888	15	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26987586	PP_0850		radical SAM enzyme, Cfr family	1.3	3.45E-01	Control	7.0	41914	4	Cytoplasmic	COG0820	General function prediction only	
26987588	PP_0852		Cro/CI family transcriptional regulator	1.8	5.93E-02	Control	5.6	34931	12	Unknown	COG1426	Function unknown	
26987589	PP_0853	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1.3	1.04E-01	Control	6.2	39687	19	Cytoplasmic	COG0821	Lipid metabolism	
26987590	PP_0854	hisS	histidyl-tRNA synthetase	1.5	4.08E-02	Control	5.1	47738	20	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
26987592	PP_0856		hypothetical protein	1.3	3.58E-02	Control	4.7	40737	16	Outer Membrane	COG1520	Function unknown	
26987593	PP_0857	engA	GTP-binding protein EngA	1.2	2.93E-01	Vanillin	9.2	54154	16	Cytoplasmic Membrane	COG1160	General function prediction only	
26987594	PP_0858		aminotransferase	1.1	7.24E-01	Vanillin	5.9	42436	6	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26987595	PP_0859		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferas	1.8	1.31E-01	Vanillin	6.5	29780	3	Cytoplasmic	COG0388	General function prediction only	
26987608	PP_0872	prfC	peptide chain release factor 3	1.4	1.04E-02	Control	6.2	59713	12	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
26987614	PP_0878	dppF	dipeptide transporter ATP-binding subunit	10.0	9.97E-04	Vanillin	9.7	35754	4	Cytoplasmic Membrane	COG4608	Amino acid transport and metabolism	
26987615	PP_0879	dppD	oligopeptide/dipeptide ABC transporter ATPase subunit	4.1	2.19E-03	Vanillin	6.3	34914	8	Cytoplasmic Membrane	COG0444	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987617	PP_0881	dppB	alkaline phosphatase	2.0	2.97E-02	Vanillin	8.4	36980	3	Cytoplasmic Membrane	COG0601	Amino acid transport and metabolism	Inorganic ion transport and metabolism
26987618	PP_0882	dppA	dipeptide ABC transporter periplasmic dipeptide-binding proteir	2.4	3.54E-04	Vanillin	7.4	60974	8	Periplasmic	COG0747	Amino acid transport and metabolism	
26987619	PP_0883		outer membrane porin	2.4	1.58E-02	Vanillin	6.6	50256	7	Outer Membrane			
26987620	PP_0884		dipeptide ABC transporter periplasmic peptide-binding protein	7.2	7.63E-05	Vanillin	7.3	59564	5	Periplasmic	COG0747	Amino acid transport and metabolism	
26987621	PP_0885		dipeptide ABC transporter periplasmic peptide-binding protein	7.9	3.35E-04	Vanillin	7.1	60366	28	Periplasmic	COG0747	Amino acid transport and metabolism	
26987622	PP_0886		hypothetical protein	1.8	3.29E-02	Vanillin	8.4	25634	6	Periplasmic	COG3471	Function unknown	
26987629	PP_0893		intracellular protease, PfpI family	2.4	1.49E-01	Vanillin	5.5	21071	2	Cytoplasmic	COG0693	General function prediction only	
26987633	PP_0897		hydro-lyase, Fe-S type, tartrate/fumarate subfamily, alpha subur	2.2	5.99E-05	Vanillin	4.9	54767	21	Cytoplasmic	COG1951	Energy production and conversion	
26987637	PP_0901	colR	winged helix family two component transcriptional regulator	1.8	5.35E-02	Control	6.2	25489	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987642	PP_0906		multidrug efflux protein	60.3	4.62E-02	Vanillin	4.8	110352	2	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26987643	PP_0907		RND efflux membrane fusion protein-related protein	5.1	8.85E-04	Vanillin	9.7	43537	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26987644	PP_0908		hypothetical protein	1.7	1.41E-02	Control	6.8	39944	5	Cytoplasmic Membrane	COG3490	Function unknown	
26987645	PP_0909		hypothetical protein	1.5	7.05E-04	Control	6.4	38380	20	Unknown	COG3489	General function prediction only	
26987649	PP_0913		hypothetical protein	1.1	4.84E-01	Control	4.4	47019	30	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
26987650	PP_0914		GGDEF domain-containing protein	4.0	5.20E-03	Vanillin	5.8	78578	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987654	PP_0918		NAD-dependent epimerase/dehydratase	1.9	1.46E-01	Control	9.3	37056	2	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26987655	PP_0919		hypothetical protein	1.2	4.97E-01	Vanillin	10.2	18933	7	Unknown			
26987656	PP_0920	xenB	NADH:flavin oxidoreductase/NADH oxidase	1.5	4.26E-01	Vanillin	5.3	37805	21	Cytoplasmic	COG1902	Energy production and conversion	
26987661	PP_0925		hypothetical protein	3.0	3.10E-02	Vanillin	5.8	31410	3	Unknown			
26987666	PP_0930	gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	1.2	2.37E-01	Control	4.8	52678	24	Cytoplasmic	COG0064	Translation, ribosomal structure and biogenesis	
26987667	PP_0931	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A	1.3	1.37E-01	Control	6.2	51518	22	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26987670	PP_0934	mreC	rod shape-determining protein MreC	1.1	7.34E-01	Vanillin	7.8	35514	6	Unknown	COG1792	Cell envelope biogenesis, outer membrane	
26987673	PP_0937	cafA	ribonuclease, Rne/Rng family	1.2	1.84E-01	Vanillin	5.2	54840	7	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26987675	PP_0939		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferas	1.7	1.77E-02	Vanillin	6.5	30410	7	Cytoplasmic	COG0388	General function prediction only	
26987676	PP_0940	tldD	tldD protein	1.2	1.81E-01	Vanillin	4.9	50161	9	Cytoplasmic	COG0312	General function prediction only	
26987680	PP_0944	fumC	fumarate hydratase	2.7	1.07E-03	Control	5.9	48541	24	Cytoplasmic	COG0114	Energy production and conversion	
26987685	PP_0949		hypothetical protein	1.5	3.19E-02	Vanillin	6.2	32097	7	Cytoplasmic	COG1660	General function prediction only	
26987688	PP_0952	rpoN	RNA polymerase factor sigma-54	1.3	2.14E-01	Vanillin	4.4	56215	8	Cytoplasmic	COG1508	Transcription	
26987689	PP_0953		ABC transporter ATP-binding protein	1.5	9.79E-02	Control	7.0	26579	5	Cytoplasmic	COG1137	General function prediction only	

26987693	PP_0957		KpsF/GutQ family protein	1.0	9.78E-01	Control	5.6	34397	12	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
26987694	PP_0958	ttg2A	toluene tolerance ABC efflux transporter ATP-binding protein	1.1	2.51E-01	Control	5.4	29144	4	Cytoplasmic Membrane	COG1127	Secondary metabolites biosynthesis, transport, and catabolism	
26987700	PP_0964	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.2	1.73E-01	Control	5.2	44973	19	Cytoplasmic	COG0766	Cell envelope biogenesis, outer membrane	
26987701	PP_0965	hisG	ATP phosphoribosyltransferase catalytic subunit	4.3	1.20E-01	Control	8.4	22938	3	Cytoplasmic	COG0040	Amino acid transport and metabolism	
26987702	PP_0966	hisD	histidinol dehydrogenase	1.7	1.46E-03	Control	5.1	47605	21	Cytoplasmic	COG0141	Amino acid transport and metabolism	
26987703	PP_0967	hisC	histidinol-phosphate aminotransferase	1.4	1.29E-03	Control	4.9	38768	11	Cytoplasmic	COG0079	Amino acid transport and metabolism	
26987709	PP_0973	ndpA	nucleoid-associated protein NdpA	1.6	8.20E-02	Vanillin	5.6	37617	9	Cytoplasmic	COG3081	General function prediction only	
26987712	PP_0976		SAM-dependent methyltransferase	3.2	5.66E-04	Vanillin	10.0	35187	2	Cytoplasmic	COG3129	General function prediction only	
26987713	PP_0977	valS	valyl-tRNA synthetase	1.0	8.41E-01	Control	5.1	107495	42	Cytoplasmic	COG0525	Translation, ribosomal structure and biogenesis	
26987716	PP_0980	pepA	leucyl aminopeptidase	1.2	5.02E-02	Vanillin	7.4	52433	31	Cytoplasmic	COG0260	Amino acid transport and metabolism	
26987718	PP_0982		permease YjgP/YjgQ family protein	1.2	1.64E-01	Control	9.7	41323	6	Cytoplasmic Membrane	COG0795	General function prediction only	
26987719	PP_0983		permease YjgP/YjgQ family protein	1.2	4.47E-01	Control	7.1	38733	3	Cytoplasmic Membrane	COG0795	General function prediction only	
26987722	PP_0986	gcvT-1	glycine cleavage system T protein	2.8	2.79E-03	Vanillin	6.4	40319	20	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26987723	PP_0987	sda-2	L-serine dehydratase 1	19.6	4.35E-04	Vanillin	6.7	48814	5	Cytoplasmic	COG1760	Amino acid transport and metabolism	
26987724	PP_0988	gcvP-1	glycine dehydrogenase	4.4	1.06E-03	Vanillin	6.0	101991	32	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26987735	PP_0999	arcC	carbamate kinase	9.9	5.43E-06	Vanillin	5.5	33423	11	Cytoplasmic	COG0549	Amino acid transport and metabolism	
26987736	PP_1000	argI	ornithine carbamoyltransferase	7.6	1.57E-04	Vanillin	6.3	37911	23	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987737	PP_1001	arcA	arginine deiminase	8.2	2.81E-06	Vanillin	5.7	46462	32	Cytoplasmic	COG2235	Amino acid transport and metabolism	
26987738	PP_1002	arcD	arginine/ornithine antiporter	173.0	4.15E-06	Vanillin	9.1	51061	3	Cytoplasmic Membrane	COG0531	Amino acid transport and metabolism	
26987742	PP_1006		TonB-dependent hemoglobin/transferrin/lactoferrin family rece	3.4	9.63E-03	Control	5.6	84730	10	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26987745	PP_1009	gap-1	glyceraldehyde-3-phosphate dehydrogenase, type I	39.6	1.22E-05	Control	7.0	36057	19	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26987746	PP_1010	edd	phosphogluconate dehydratase	38.8	6.40E-06	Control	6.4	65359	34	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26987747	PP_1011	glk	glucokinase	27.8	3.82E-05	Control	6.5	33904	13	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
26987748	PP_1012	gltR-2	winged helix family two component transcriptional regulator	12.9	3.77E-05	Control	6.4	27124	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26987750	PP_1014		hypothetical protein	121.0	3.17E-03	Control	6.4	45472	6	Unknown	COG2942	Carbohydrate transport and metabolism	
26987751	PP_1015		sugar ABC transporter periplasmic sugar-binding protein	67.3	1.62E-05	Control	6.2	45449	34	Periplasmic	COG1653	Carbohydrate transport and metabolism	
26987752	PP_1016		binding-protein-dependent transport systems inner membrane c	178.5	3.24E-05	Control	10.1	33781	6	Cytoplasmic Membrane	COG1175	Carbohydrate transport and metabolism	
26987753	PP_1017		binding-protein-dependent transport systems inner membrane c	2406.1	1.58E-02	Control	9.9	30428	2	Cytoplasmic Membrane	COG0395	Carbohydrate transport and metabolism	
26987754	PP_1018		sugar ABC transporter ATP-binding subunit	337.3	9.02E-05	Control	6.7	41895	14	Cytoplasmic Membrane	COG3839	Carbohydrate transport and metabolism	
26987755	PP_1019	oprB-1	porin B	95.6	9.34E-07	Control	5.9	49646	22	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
26987758	PP_1022	zwf-1	glucose-6-phosphate 1-dehydrogenase	46.4	8.31E-07	Control	6.8	55000	23	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26987759	PP_1023	pgl	6-phosphogluconolactonase	84.7	4.30E-06	Control	6.7	25476	12	Unknown	COG0363	Carbohydrate transport and metabolism	
26987760	PP_1024	eda	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate	158.5	3.13E-07	Control	5.4	25004	10	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
26987761	PP_1025	leuA	2-isopropylmalate synthase	1.6	1.42E-02	Vanillin	5.1	61712	34	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26987763	PP_1027	xseA	exodeoxyribonuclease VII large subunit	1.0	8.11E-01	Vanillin	11.3	51388	3	Cytoplasmic	COG1570	DNA replication, recombination, and repair	
26987767	PP_1031	guaB	inosine 5'-monophosphate dehydrogenase	1.1	2.00E-01	Control	7.0	51765	30	Cytoplasmic	COG0516	Nucleotide transport and metabolism	
26987768	PP_1032	guaA	GMP synthase	1.6	1.05E-02	Control	5.2	58204	29	Cytoplasmic	COG0519	Nucleotide transport and metabolism	
26987770	PP_1034	cumA	multicopper oxidase	1.3	1.40E-01	Control	6.4	52374	6	Unknown	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
26987773	PP_1037	purL	phosphoribosylformylglycinamidine synthase	1.3	2.26E-02	Vanillin	4.7	140818	63	Cytoplasmic	COG0046	Nucleotide transport and metabolism	
26987792	PP_1056		iron-chelator utilization protein	1.7	4.37E-03	Vanillin	5.2	28123	6	Cytoplasmic	COG2375	Inorganic ion transport and metabolism	
26987794	PP_1058		hypothetical protein	16.0	4.08E-04	Vanillin	9.5	117041	8	Unknown	COG0744	Cell envelope biogenesis, outer membrane	
26987799	PP_1063	metR-1	transcriptional activator MetR	1.1	7.02E-01	Control	6.2	33975	4	Cytoplasmic	COG0583	Transcription	
26987802	PP_1066		two component, sigma54 specific, transcriptional regulator, Fis f	1.0	8.37E-01	Vanillin	5.4	48717	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
26987804	PP_1068		amino acid ABC transporter ATP-binding protein	1.4	1.89E-01	Control	8.2	28149	5	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26987807	PP_1071		amino acid ABC transporter periplasmic amino acid-binding prot	1.9	3.59E-03	Vanillin	8.9	33428	32	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26987810	PP_1074	glpR	DeoR family transcriptional regulator	1.2	3.18E-01	Control	5.7	27749	5	Cytoplasmic	COG1349	Transcription	Carbohydrate transport and metabolism
26987811	PP_1075	glpK	glycerol kinase	2.3	5.69E-02	Vanillin	4.9	55282	9	Cytoplasmic	COG0554	Energy production and conversion	
26987814	PP_1078		ABC transporter ATP-binding protein	2.6	2.49E-03	Control	6.4	40244	6	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26987815	PP_1079	argF	ornithine carbamoyltransferase	1.6	7.20E-02	Control	5.7	34433	13	Cytoplasmic	COG0078	Amino acid transport and metabolism	
26987820	PP_1084		anti-oxidant AhpCTSA family protein	3.2	8.30E-02	Control	4.9	21730	4	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
26987821	PP_1085	rnt	ribonuclease T	2.5	3.59E-02	Control	5.3	22457	3	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
26987822	PP_1086	pyrC	dihydroorotase	1.9	8.40E-03	Control	6.9	38414	14	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
26987823	PP_1087		OmpA family outer membrane protein	1.1	4.38E-01	Vanillin	10.0	34341	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987824	PP_1088	argG	argininosuccinate synthase	1.8	1.60E-02	Control	5.1	45164	33	Cytoplasmic	COG0137	Amino acid transport and metabolism	
26987833	PP_1097	metG	methionyl-tRNA synthetase	1.3	9.48E-02	Control	5.5	75186	25	Cytoplasmic	COG0143	Translation, ribosomal structure and biogenesis	
26987834	PP_1098		ATP-binding Mrp/Nbp35 family protein	1.3	2.72E-01	Control	4.8	38207	9	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
26987840	PP_1104		succinylglutamate desuccinylase/aspartoacylase	2.3	2.56E-03	Vanillin	6.3	40904	7	Cytoplasmic	COG3608	General function prediction only	
26987844	PP_1108		acylase	1.5	4.32E-02	Vanillin	8.7	88728	20	Periplasmic	COG2366	General function prediction only	
26987846	PP_1110		serine O-acetyltransferase	3.2	2.21E-02	Control	8.8	19246	2	Cytoplasmic	COG1045	Amino acid transport and metabolism	
26987847	PP_1111		synthetase	1.2	2.37E-01	Control	6.0	29406	9	Cytoplasmic	COG2872	General function prediction only	
26987849	PP_1113		pyridoxal-phosphate dependent enzyme family protein	1.2	3.27E-02	Vanillin	7.6	32597	15	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26987857	PP_1121		OmpA/MotB domain protein	6.7	6.35E-04	Vanillin	5.0	24084	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987858	PP_1122		OmpA/MotB domain protein	9.1	2.84E-04	Vanillin	4.7	27345	3	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987861	PP_1125	dinG	ATP-dependent DNA helicase DinG	1.2	6.89E-01	Control	5.7	79041	7	Cytoplasmic	COG1199	Transcription	DNA replication, recombination, and repair
26987862	PP_1126		Beta-agarase	3.2	2.70E-02	Vanillin	6.6	86407	6	Periplasmic			
26987863	PP_1127	estC	beta-lactamase	1.1	6.34E-01	Vanillin	5.2	41131	4	Periplasmic	COG1680	Defense mechanisms	
26987864	PP_1128		OmpA/MotB domain protein	1.3	1.26E-01	Vanillin	10.6	36308	9	Cytoplasmic Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26987865	PP_1129	pdxH	pyridoxamine 5'-phosphate oxidase	1.8	6.58E-02	Control	6.4	24581	4	Cytoplasmic	COG0259	Coenzyme metabolism	
26987867	PP_1131		17 kDa surface antigen	3.2	7.00E-02	Vanillin	9.3	15682	4	Outer Membrane	COG3133	Cell envelope biogenesis, outer membrane	
26987870	PP_1134		FAD dependent oxidoreductase	1.6	3.39E-02	Control	6.9	58398	11	Cytoplasmic	COG2509	General function prediction only	
26987871	PP_1135		hypothetical protein	3.6	1.67E-03	Control	6.9	26494	4	Unknown	COG3650	Function unknown	
26987874	PP_1138	livG	leucine/isoleucine/valine transporter ATP-binding subunit	1.4	6.98E-02	Vanillin	9.7	28280	5	Cytoplasmic	COG0411	Amino acid transport and metabolism	
26987877	PP_1141	braC	extracellular ligand-binding receptor	1.9	9.59E-03	Vanillin	6.4	39402	24	Periplasmic	COG0683	Amino acid transport and metabolism	
26987879	PP_1143		3-hydroxyisobutyrate dehydrogenase	1.1	4.88E-01	Vanillin	5.8	30664	9	Unknown	COG2084	Lipid metabolism	
26987880	PP_1144		GGDEF domain-containing protein	265.4	3.03E-02	Vanillin	6.8	82754	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26987881	PP_1145	hepA	ATP-dependent helicase HepA	1.3	9.47E-02	Control	4.8	105994	14	Cytoplasmic	COG0553	Transcription	DNA replication, recombination, and repair
26987882	PP_1146		hypothetical protein	4.0	4.98E-03	Vanillin	4.1	25115	3	Cytoplasmic			
26987888	PP_1152		secretion protein HlyD family protein	32.3	2.78E-05	Vanillin	6.4	32353	2	Cytoplasmic Membrane	COG1566	Defense mechanisms	

26987893	PP_1157		acetolactate synthase		1.2	4.76E-01	Vanillin	6.1	60059	20	Cytoplasmic	COG0028	Coenzyme metabolism
26987904	PP_1169	dctP	TRAP dicarboxylate transporter DctP subunit		19.7	2.22E-03	Vanillin	6.3	35583	3	Periplasmic	COG1638	Carbohydrate transport and metabolism
26987912	PP_1177	nrdB	ribonucleotide-diphosphate reductase subunit beta		1.2	2.40E-01	Control	4.5	46989	21	Cytoplasmic	COG0208	Nucleotide transport and metabolism
26987914	PP_1179	nrdA	ribonucleotide-diphosphate reductase subunit alpha		1.3	1.39E-02	Control	5.7	106948	36	Cytoplasmic	COG0209	Nucleotide transport and metabolism
26987919	PP_1184		dienelactone hydrolase		3.5	5.89E-04	Vanillin	6.8	28722	13	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism
26987923	PP_1188	dctA	C4-dicarboxylate transporter DctA		71.2	1.10E-01	Vanillin	8.8	46298	2	Cytoplasmic Membrane	COG1301	Energy production and conversion
26987926	PP_1191		S4 domain-containing protein		1.0	9.02E-01	Vanillin	8.9	26724	7	Cytoplasmic	COG1187	Translation, ribosomal structure and biogenesis
26987932	PP_1197	rimO	ribosomal protein S12 methylthiotransferase		1.4	7.54E-02	Vanillin	5.1	52418	7	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis
26987936	PP_1201		virulence factor family protein		2.8	5.58E-06	Vanillin	5.0	46885	4	Unknown	COG3946	Intracellular trafficking and secretion
26987937	PP_1202		hypothetical protein		8.0	2.88E-04	Vanillin	9.7	95622	8	Cytoplasmic Membrane	COG2898	Function unknown
26987939	PP_1204		lipoprotein		1.3	6.98E-02	Control	5.0	35969	3	Cytoplasmic		
26987940	PP_1205	proS	prolyl-tRNA synthetase		1.2	1.43E-01	Control	5.0	63623	26	Cytoplasmic	COG0442	Translation, ribosomal structure and biogenesis
26987941	PP_1206	oprD	outer membrane porin		1.4	4.91E-02	Vanillin	4.6	46120	17	Outer Membrane		
26987945	PP_1210		DNA-binding stress protein		4.5	2.11E-03	Vanillin	5.0	17861	5	Cytoplasmic	COG0783	Inorganic ion transport and metabolism
26987948	PP_1213	aspS	aspartyl-tRNA synthetase		1.1	1.96E-01	Control	5.1	66568	39	Cytoplasmic	COG0173	Translation, ribosomal structure and biogenesis
26987949	PP_1214		hypothetical protein		1.1	4.72E-01	Control	4.4	26842	4	Cytoplasmic	COG0217	Function unknown
26987952	PP_1217	ruvB	Holliday junction DNA helicase RuvB		1.9	4.40E-02	Vanillin	5.1	38536	2	Cytoplasmic	COG2255	DNA replication, recombination, and repair
26987956	PP_1221	tolA	biopolymer transport protein TolA		2.7	2.47E-01	Vanillin	9.8	40133	2	Outer Membrane	COG1196	Cell division and chromosome partitioning
26987957	PP_1222	tolB	translocation protein TolB		1.6	1.55E-02	Control	9.8	47431	20	Unknown	COG0823	Intracellular trafficking and secretion
26987959	PP_1224		hypothetical protein		1.9	8.86E-02	Control	8.3	28730	3	Unknown	COG1729	Function unknown
26987961	PP_1226	exsB	exsB protein		1.8	4.62E-02	Control	4.7	23961	6	Cytoplasmic	COG0603	General function prediction only
26987965	PP_1230		hypothetical protein		1.3	6.99E-02	Control	5.1	53328	11	Cytoplasmic Membrane	COG5339	Function unknown
26987966	PP_1231	nadA	quinolinate synthetase		1.5	3.49E-02	Control	4.8	38417	2	Cytoplasmic	COG0379	Coenzyme metabolism
26987967	PP_1232		hypothetical protein		1.4	8.02E-01	Control	6.9	53219	9	Unknown	COG4783	General function prediction only
26987972	PP_1237	dapA	dihydrodipicolinate synthase		1.2	1.19E-01	Control	6.0	31654	19	Cytoplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
26987973	PP_1238		lipoprotein		1.1	2.07E-01	Control	4.8	40784	20	Unknown	COG3317	Cell envelope biogenesis, outer membrane
26987975	PP_1240	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase		1.9	3.98E-03	Control	5.1	26916	18	Cytoplasmic	COG0152	Nucleotide transport and metabolism
26987980	PP_1245		hypothetical protein		4.1	4.43E-04	Control	9.4	31144	10	Unknown		
26987981	PP_1246		hypothetical protein		2.5	9.17E-04	Control	6.0	65952	24	Unknown	COG5373	Function unknown
26987984	PP_1249		hypothetical protein		31.4	2.21E-04	Control	9.3	6714	3	Unknown		
26987989	PP_1254	xenA	xenobiotic reductase A		1.9	1.57E-01	Control	6.2	39835	6	Cytoplasmic	COG1902	Energy production and conversion
26987996	PP_1261		2-hydroxyacid dehydrogenase		5.2	4.49E-05	Vanillin	7.7	34919	17	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26987997	PP_1262		LysR family transcriptional regulator		1.4	2.73E-01	Vanillin	6.4	34783	5	Unknown	COG0583	Transcription
26988007	PP_1272		secretion protein HlyD family protein		8.4	6.91E-03	Vanillin	7.8	39273	11	Cytoplasmic Membrane	COG1566	Defense mechanisms
26988008	PP_1273		RND efflux system, outer membrane lipoprotein, NodT family		31.0	4.06E-04	Vanillin	5.1	52832	12	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988024	PP_1289		hypothetical protein		1.4	5.55E-02	Vanillin	6.5	29332	4	Unknown	COG3022	Function unknown
26988026	PP_1291		PhoH family protein		6.2	2.10E-04	Vanillin	5.7	51856	12	Cytoplasmic	COG1875	General function prediction only
26988032	PP_1297	aapJ	general amino acid ABC transporter periplasmic protein		4.1	3.85E-03	Vanillin	5.6	36424	17	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26988036	PP_1301	algW	2-alkenal reductase		1.3	2.47E-01	Control	7.2	42971	6	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones
26988037	PP_1302		hypothetical protein		1.1	2.31E-01	Vanillin	5.8	27492	6	Cytoplasmic	COG0327	Function unknown
26988038	PP_1303	cysD	sulfate adenylyltransferase subunit 2		1.0	7.04E-01	Vanillin	6.8	35284	16	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26988039	PP_1304	cysNC	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfat		1.2	1.73E-01	Vanillin	5.6	69049	28	Cytoplasmic	COG2895	Inorganic ion transport and metabolism
26988046	PP_1311		tryptophanyl-tRNA synthetase		1.6	2.06E-02	Control	5.4	49297	15	Cytoplasmic	COG0180	Translation, ribosomal structure and biogenesis
26988047	PP_1312		AFG1-family ATPase		1.4	9.81E-02	Control	6.8	42094	15	Cytoplasmic	COG1485	General function prediction only
26988048	PP_1313		AraC family transcriptional regulator		1.8	5.39E-02	Vanillin	6.8	35325	3	Cytoplasmic	COG4977	Transcription
26988049	PP_1314		aldo/keto reductase family oxidoreductase		2.1	1.86E-04	Vanillin	6.5	38777	16	Cytoplasmic	COG0667	Energy production and conversion
26988051	PP_1316	rpsI	30S ribosomal protein S9	Infinity		2.21E-07	Control	11.7	14592	3	Cytoplasmic	COG0103	Translation, ribosomal structure and biogenesis
26988052	PP_1317	petA	ubiquinol-cytochrome c reductase, iron-sulfur subunit		2.2	7.32E-02	Vanillin	7.5	20855	4	Cytoplasmic Membrane	COG0723	Energy production and conversion
26988053	PP_1318	petB	ubiquinol--cytochrome c reductase, cytochrome b		59.9	4.78E-04	Vanillin	8.4	45901	5	Cytoplasmic Membrane	COG1290	Energy production and conversion
26988060	PP_1325		LppC family lipoprotein		1.0	9.80E-01	Control	7.5	64637	25	Cytoplasmic Membrane	COG3107	General function prediction only
26988061	PP_1326		uroporphyrin-III C/tetrapyrrole methyltransferase		1.3	1.66E-01	Vanillin	5.4	31389	4	Cytoplasmic	COG0313	General function prediction only
26988063	PP_1329	mraW	S-adenosyl-methyltransferase MraW		1.3	1.07E-01	Vanillin	7.2	34314	9	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane
26988065	PP_1331	ftsI	peptidoglycan glycosyltransferase		2.7	3.67E-02	Vanillin	10.0	63453	6	Cytoplasmic Membrane	COG0768	Cell envelope biogenesis, outer membrane
26988066	PP_1332	murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelat		1.3	9.02E-02	Vanillin	5.3	53602	22	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane
26988067	PP_1333	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-		1.8	8.79E-03	Vanillin	6.6	46750	14	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane
26988069	PP_1335	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase		1.4	1.93E-02	Vanillin	5.7	48300	7	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane
26988071	PP_1337	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylg		1.8	3.86E-02	Vanillin	9.9	38127	12	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane
26988072	PP_1338	murC	UDP-N-acetylmuramate--L-alanine ligase		1.4	1.01E-01	Control	6.3	52166	9	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane
26988073	PP_1339	ddl	D-alanine--D-alanine ligase		1.2	1.12E-01	Control	4.7	34131	12	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane
26988075	PP_1341	ftsA	cell division protein FtsA		1.1	5.78E-01	Vanillin	4.9	47444	22	Cytoplasmic	COG0849	Cell division and chromosome partitioning
26988076	PP_1342	ftsZ	cell division protein FtsZ		1.7	2.40E-02	Control	4.7	41830	20	Cytoplasmic	COG0206	Cell division and chromosome partitioning
26988077	PP_1343	lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		1.0	5.47E-01	Vanillin	4.8	33269	11	Cytoplasmic	COG0774	Cell envelope biogenesis, outer membrane
161378135	PP_1345	secA	preprotein translocase subunit SecA		1.2	7.09E-03	Control	5.7	102867	27	Cytoplasmic	COG0653	Intracellular trafficking and secretion
26988080	PP_1346	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synt		3.5	8.45E-03	Control	5.0	42236	6	Cytoplasmic	COG1364	Amino acid transport and metabolism
26988082	PP_1348		hypothetical protein		1.1	4.20E-01	Control	5.5	34390	9	Cytoplasmic	COG0352	Coenzyme metabolism
26988087	PP_1353		MscS mechanosensitive ion channel		1.8	2.42E-01	Control	7.5	30804	2	Cytoplasmic Membrane	COG0668	Cell envelope biogenesis, outer membrane
26988092	PP_1358		hypothetical protein		1.3	1.60E-01	Vanillin	7.8	32006	9	Unknown	COG0748	Inorganic ion transport and metabolism
26988095	PP_1361	groEL	chaperonin GroEL		1.8	1.39E-03	Control	4.7	56743	62	Cytoplasmic	COG0459	Posttranslational modification, protein turnover, chaperones
26988096	PP_1362	pykA	pyruvate kinase		2.0	1.41E-05	Control	6.7	52057	29	Cytoplasmic	COG0469	Carbohydrate transport and metabolism
26988101	PP_1367	purU	formyltetrahydrofolate deformylase		1.2	4.06E-02	Control	6.6	32376	12	Cytoplasmic	COG0788	Nucleotide transport and metabolism
26988105	PP_1371		methyl-accepting chemotaxis transducer		1.1	8.51E-01	Vanillin	4.8	67652	9	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988106	PP_1372		hypothetical protein		3.1	4.33E-03	Vanillin	6.5	52321	10	Unknown	COG0433	Replication, recombination, and repair
26988107	PP_1373		phosphate transporter		1.2	3.32E-01	Control	9.6	52425	5	Cytoplasmic Membrane	COG0306	Inorganic ion transport and metabolism
26988109	PP_1375	pcaR	pca regulon regulatory protein		2.2	3.21E-03	Vanillin	7.2	31741	7	Cytoplasmic	COG1414	Transcription
26988110	PP_1376	pcaK	benzoate transport		41.9	2.58E-05	Vanillin	9.8	47128	6	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism
26988111	PP_1377	pcaF	beta-ketoadipyl CoA thiolase		219.0	3.07E-06	Vanillin	6.0	41851	36	Cytoplasmic	COG0183	Lipid metabolism
26988113	PP_1379	pcaB	3-carboxy-cis,cis-muconate cycloisomerase		92.7	1.10E-05	Vanillin	6.5	48194	25	Cytoplasmic	COG0015	Nucleotide transport and metabolism
26988114	PP_1380	pcaD	3-oxoadipate enol-lactonase		35.1	1.13E-04	Vanillin	5.1	28656	12	Unknown	COG0596	General function prediction only

26988117	PP_1383		BenF-like porin	223.3	2.52E-06	Vanillin	6.8	46022	29	Outer Membrane			
26988118	PP_1384	ttgC	RND efflux system, outer membrane lipoprotein, NodT family	2.6	3.42E-03	Vanillin	5.1	52864	14	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26988119	PP_1385	ttgB	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	2.7	9.11E-04	Vanillin	5.3	112835	17	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988120	PP_1386	ttgA	efflux transporter RND family, MFP subunit	2.3	2.36E-02	Vanillin	6.0	41250	10	Unknown	COG0845	Cell envelope biogenesis, outer membrane	
26988123	PP_1389		carboxyphosphonoenolpyruvate phosphonomutase	1.3	1.44E-01	Vanillin	4.9	31783	12	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26988129	PP_1395		AraC family transcriptional regulator	5.7	3.41E-03	Vanillin	7.6	34370	8	Cytoplasmic	COG4977	Transcription	
26988134	PP_1400		metabolite/H+ symporter, major facilitator superfamily (MFS)	1.9	4.16E-01	Vanillin	9.4	47635	2	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26988137	PP_1403	bglX	periplasmic beta-glucosidase	1.5	1.16E-01	Control	6.1	83414	12	Periplasmic	COG1472	Carbohydrate transport and metabolism	
26988140	PP_1406		hypothetical protein	1.3	3.70E-01	Control	7.8	37042	3	Unknown			
26988145	PP_1412		enoyl-CoA hydratase/isomerase	11.2	5.12E-04	Vanillin	6.5	40490	5	Cytoplasmic	COG1024	Lipid metabolism	
26988151	PP_1418		tricarboxylate transport protein TctC	49.5	7.23E-04	Vanillin	6.6	34981	8	Periplasmic	COG3181	Function unknown	
26988152	PP_1419		outer membrane porin	148.6	5.76E-02	Vanillin	4.9	46644	2	Outer Membrane			
26988156	PP_1423		hypothetical protein	1.2	4.57E-01	Vanillin	6.0	33350	8	Unknown	COG0354	General function prediction only	
26988159	PP_1426	nadB	L-aspartate oxidase	1.5	2.17E-02	Vanillin	5.8	59215	11	Cytoplasmic	COG0029	Coenzyme metabolism	
26988160	PP_1427	algU	RNA polymerase sigma factor AlgU	1.2	1.28E-01	Control	5.2	22282	8	Cytoplasmic	COG1595	Transcription	
26988162	PP_1429	algN	sigma E regulatory protein, MucB/RseB	4.7	1.67E-02	Vanillin	6.6	34982	4	Periplasmic	COG3026	Signal transduction mechanisms	
26988163	PP_1430	algY	protease Do	1.4	9.50E-02	Vanillin	6.6	52617	14	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
26988164	PP_1431	lepA	GTP-binding protein LepA	1.2	2.45E-01	Vanillin	5.5	66116	17	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
26988165	PP_1432	lepB	signal peptidase I	1.2	2.63E-01	Control	9.2	32060	11	Cytoplasmic Membrane	COG0681	Intracellular trafficking and secretion	
26988166	PP_1433	rnc	ribonuclease III	6.1	7.49E-03	Control	5.2	25497	2	Cytoplasmic	COG0571	Transcription	
26988167	PP_1434	era	GTP-binding protein Era	1.1	7.71E-01	Control	6.9	34243	13	Cytoplasmic Membrane	COG1159	General function prediction only	
26988169	PP_1436	pdxJ	pyridoxine 5'-phosphate synthase	1.2	1.93E-01	Vanillin	6.2	26737	6	Cytoplasmic	COG0854	Coenzyme metabolism	
26988173	PP_1440		methyltransferase	1.1	3.00E-01	Control	5.2	36056	3	Cytoplasmic	COG2227	Coenzyme metabolism	
26988176	PP_1443	lon-1	ATP-dependent protease La	1.5	6.23E-02	Control	6.4	89794	26	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26988177	PP_1444	gcd	glucose dehydrogenase (pyrroloquinoline-quinone)	3.0	4.76E-03	Vanillin	6.0	86581	17	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26988179	PP_1446		TonB-dependent receptor	2.9	8.79E-03	Control	4.9	74207	26	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26988190	PP_1457	purT	phosphoribosylglycinamide formyltransferase 2	1.0	9.57E-01	Vanillin	5.7	42575	21	Cytoplasmic Membrane	COG0027	Nucleotide transport and metabolism	
26988191	PP_1458		metabolite-proton symporter	2.6	1.27E-02	Control	9.0	45563	4	Cytoplasmic Membrane			
26988192	PP_1459		CBS domain-containing protein	4.3	2.43E-01	Vanillin	4.7	44174	2	Cytoplasmic Membrane	COG4536	Inorganic ion transport and metabolism	
26988197	PP_1464	trmD	tRNA (guanine-N(1)-)-methyltransferase	1.3	2.03E-01	Vanillin	5.1	27994	2	Cytoplasmic	COG0336	Translation, ribosomal structure and biogenesis	
26988202	PP_1469	dsbC	thiol:disulfide interchange protein DsbC	1.7	1.52E-02	Control	7.9	27601	5	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
26988203	PP_1470	hom	homoserine dehydrogenase	1.5	2.03E-02	Control	5.1	46194	14	Cytoplasmic	COG0460	Amino acid transport and metabolism	
26988204	PP_1471	thrC	threonine synthase	1.4	2.95E-03	Control	6.2	51645	30	Cytoplasmic	COG0498	Amino acid transport and metabolism	
26988208	PP_1475		L-carnitine dehydratase/bile acid-inducible protein F	1.5	3.16E-01	Vanillin	5.5	43320	8	Cytoplasmic	COG1804	Energy production and conversion	
26988211	PP_1478		NADH:flavin oxidoreductase/NADH oxidase	7.0	9.91E-05	Vanillin	5.8	40626	17	Cytoplasmic	COG1902	Energy production and conversion	
26988214	PP_1481		gamma-aminobutyraldehyde dehydrogenase	13.0	1.77E-04	Vanillin	5.7	50918	18	Unknown	COG1012	Energy production and conversion	
26988217	PP_1484		spermidine/putrescine ABC transporter ATPase	530.7	1.85E-02	Vanillin	8.9	37966	2	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26988219	PP_1486		polyamine ABC transporter periplasmic polyamine-binding prote	12.5	1.57E-04	Vanillin	6.4	41728	9	Periplasmic	COG0687	Amino acid transport and metabolism	
26988221	PP_1488		methyl-accepting chemotaxis sensory transducer	1.6	1.19E-02	Vanillin	4.7	58605	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988223	PP_1490		methyltransferase, CheR-like	4.1	1.20E-02	Vanillin	8.6	46889	2	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
26988225	PP_1492		chemotaxis protein CheA	5.0	4.57E-03	Vanillin	5.0	83257	9	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
26988226	PP_1493		chemotaxis-specific methylesterase	6.3	6.30E-02	Vanillin	6.8	35823	2	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
26988227	PP_1494		response regulator/GGDEF domain-containing protein	2.3	1.19E-02	Vanillin	5.7	37046	8	Cytoplasmic	COG3706	Signal transduction mechanisms	
26988228	PP_1496	lysS	lysyl-tRNA synthetase	1.1	6.18E-01	Control	5.0	57137	38	Cytoplasmic	COG1190	Translation, ribosomal structure and biogenesis	
26988231	PP_1499		hypothetical protein	1.6	2.78E-01	Vanillin	6.3	49645	5	Cytoplasmic	COG3930	Function unknown	
26988234	PP_1502		OmpA/MotB domain protein	1.2	5.02E-01	Vanillin	9.5	28964	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988237	PP_1505	ppc	phosphoenolpyruvate carboxylase	4.5	3.13E-03	Vanillin	6.6	96963	19	Cytoplasmic	COG2352	Energy production and conversion	
26988238	PP_1506	adk	adenylate kinase	1.0	7.74E-01	Vanillin	5.7	23222	16	Cytoplasmic	COG0563	Nucleotide transport and metabolism	
26988242	PP_1510		carboxyvinyl-carboxyphosphonate phosphorylmutase	9.2	1.03E-03	Vanillin	4.2	29130	7	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26988248	PP_1516		efflux transporter RND family, MFP subunit	1.2	6.11E-01	Control	8.4	39409	4	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26988249	PP_1517		acriflavin resistance protein	1.4	2.67E-02	Vanillin	7.3	112935	12	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26988252	PP_1520	plsB	glycerol-3-phosphate acyltransferase	2.2	3.71E-02	Vanillin	9.9	93692	6	Cytoplasmic Membrane	COG2937	Lipid metabolism	
26988256	PP_1524		rRNA (guanine-N(1)-)-methyltransferase	1.1	5.99E-01	Vanillin	7.2	29822	2	Cytoplasmic	COG2226	Coenzyme metabolism	
26988257	PP_1525	dapE	succinyl-diaminopimelate desuccinylase	1.3	7.97E-02	Control	4.8	41238	5	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26988258	PP_1526		beta-(1-3)-glucosyl transferase	10.0	5.34E-03	Vanillin	8.1	97324	10	Cytoplasmic Membrane	COG5309	Carbohydrate transport and metabolism	
26988261	PP_1529	csdA	cysteine sulfinate desulfinase	1.3	1.53E-01	Control	6.7	43287	3	Cytoplasmic	COG0520	Posttranslational modification, protein turnover, chaperones	
26988262	PP_1530		2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1.5	9.45E-03	Control	5.6	35858	16	Unknown	COG2171	Amino acid transport and metabolism	
26988281	PP_1549		Cro/CI family transcriptional regulator	1.0	8.07E-01	Vanillin	6.9	31438	4	Cytoplasmic	COG2932	Transcription	
26988320	PP_1588		succinyldiaminopimelate transaminase	1.0	8.57E-01	Control	5.4	43759	15	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988321	PP_1589	glnD	PII uridylyl-transferase	3.8	1.87E-03	Vanillin	5.9	102620	15	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones	
26988322	PP_1590	map	methionine aminopeptidase	1.1	4.07E-01	Control	6.6	28956	11	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis	
26988323	PP_1591	rpsB	30S ribosomal protein S2	1.9	3.26E-04	Control	9.3	27023	19	Cytoplasmic	COG0052	Translation, ribosomal structure and biogenesis	
26988324	PP_1592	tsf	elongation factor Ts	1.4	1.48E-03	Control	4.9	30432	26	Cytoplasmic	COG0264	Translation, ribosomal structure and biogenesis	
26988325	PP_1593	pyrH	uridylate kinase	1.2	2.55E-01	Control	6.2	26484	6	Cytoplasmic	COG0528	Nucleotide transport and metabolism	
26988326	PP_1594	frr	ribosome recycling factor	3.9	2.32E-01	Control	8.9	20152	2	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis	
26988327	PP_1595	uppS	undecaprenyl diphosphate synthase	1.3	3.38E-01	Vanillin	8.5	27951	5	Cytoplasmic	COG0020	Lipid metabolism	
26988329	PP_1597	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1.8	4.73E-02	Vanillin	5.7	43236	4	Cytoplasmic	COG0743	Lipid metabolism	
26988331	PP_1599		surface antigen family outer membrane protein	1.0	7.54E-01	Control	4.7	86513	25	Outer Membrane	COG4775	Cell envelope biogenesis, outer membrane	
26988333	PP_1601	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	1.9	7.85E-02	Control	6.4	36484	4	Cytoplasmic	COG1044	3-hydroxymyristoyl	
26988335	PP_1603	lpxA	UDP-N-acetylglucosamine acyltransferase	1.0	8.86E-01	Control	6.9	28107	7	Cytoplasmic	COG1043	acyl carrier protein	
26988336	PP_1604	lpxB	lipid-A-disaccharide synthase	1.0	7.23E-01	Vanillin	8.3	41194	6	Cytoplasmic	COG0763	Cell envelope biogenesis, outer membrane	
26988338	PP_1606	dnaE	DNA polymerase III subunit alpha	1.1	3.22E-01	Control	5.3	130923	12	Cytoplasmic	COG0587	DNA replication, recombination, and repair	
26988339	PP_1607	accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.2	1.19E-01	Control	6.0	35135	18	Cytoplasmic	COG0825	Lipid metabolism	
26988342	PP_1610	pyrG	CTP synthetase	1.2	8.44E-02	Vanillin	5.8	59474	31	Cytoplasmic	COG0504	Nucleotide transport and metabolism	
26988343	PP_1611	kdsA-1	2-dehydro-3-deoxyphosphooctonate aldolase	1.4	4.46E-02	Vanillin	5.8	31034	12	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
26988344	PP_1612	eno	phosphopyruvate hydratase	1.1	5.32E-01	Control	4.7	45490	23	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
26988348	PP_1616		D-isomer specific 2-hydroxyacid dehydrogenase family protein	32.1	8.96E-05	Vanillin	6.3	39364	28	Cytoplasmic	COG1062	Energy production and conversion	
26988349	PP_1617		S-formylglutathione hydrolase	47.8	9.73E-06	Vanillin	6.4	31637	10	Unknown	COG0627	General function prediction only	

26988351	PP_1619	truD	tRNA pseudouridine synthase D	1.3	2.04E-01	Control	6.9	38439	5	Cytoplasmic	COG0585	Function unknown	
26988354	PP_1622	nlpD	peptidase M23B	1.0	9.81E-01	Control	11.0	27506	7	Outer Membrane	COG0739	Cell envelope biogenesis, outer membrane	
26988355	PP_1623	rpoS	RNA polymerase sigma factor RpoS	2.1	1.77E-01	Vanillin	4.9	38175	8	Cytoplasmic	COG0568	Transcription	
26988358	PP_1626	mutS	DNA mismatch repair protein MutS	2.0	2.56E-02	Control	6.3	95111	14	Cytoplasmic	COG0249	DNA replication, recombination, and repair	
26988361	PP_1629	recA	recombinase A	1.3	1.29E-01	Vanillin	5.3	37545	15	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
26988363	PP_1631		hypothetical protein	7.3	2.07E-01	Vanillin	6.7	42143	2	Cytoplasmic	COG1611	General function prediction only	
26988370	PP_1638	fpr	oxidoreductase FAD/NAD(P)-binding domain protein	2.7	2.32E-03	Control	5.1	29710	11	Cytoplasmic	COG1018	Energy production and conversion	
26988373	PP_1641		C32 tRNA thiolase	1.6	6.69E-03	Control	6.8	31043	5	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
26988381	PP_1649	ldhA	D-lactate dehydrogenase	1.5	1.18E-02	Vanillin	6.6	37126	7	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26988382	PP_1650	gacS	multi-sensor hybrid histidine kinase	2.6	1.65E-03	Vanillin	5.4	100653	5	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26988386	PP_1654	cysM	cysteine synthase B	1.3	4.15E-02	Control	4.9	32305	8	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26988388	PP_1656	relA	(p)ppGpp synthetase I, SpoT/RelA	1.0	9.15E-01	Vanillin	7.9	83609	27	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26988391	PP_1659		hypothetical protein	16.2	2.46E-04	Vanillin	5.9	48336	10	Periplasmic			
26988393	PP_1661		dehydrogenase subunit	16.0	2.07E-04	Vanillin	5.5	81020	27	Extracellular	COG2303	Amino acid transport and metabolism	
26988395	PP_1663		hypothetical protein	1.2	2.06E-01	Control	9.2	26313	12	Periplasmic			
26988396	PP_1664	purN	phosphoribosylglycinamide formyltransferase	1.2	1.50E-01	Control	6.7	23338	5	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
26988397	PP_1665	purM	phosphoribosylaminoimidazole synthetase	1.0	7.65E-01	Control	4.6	36942	15	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
26988398	PP_1666		hypothetical protein	1.5	3.51E-02	Vanillin	5.5	37790	4	Unknown	COG3249	Function unknown	
26988408	PP_1676	cobC	threonine-phosphate decarboxylase	1.6	4.50E-02	Vanillin	7.2	35825	3	Cytoplasmic	COG0079	Amino acid transport and metabolism	
26988411	PP_1679	cobT	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltr	2.7	5.08E-06	Vanillin	5.3	36067	3	Cytoplasmic	COG2038	Coenzyme metabolism	
26988434	PP_1702	rdgC	recombination associated protein	1.3	5.57E-02	Control	4.6	34283	23	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
26988446	PP_1714	fklB-2	peptidyl-prolyl cis-trans isomerase, FKBP-type	1.0	7.93E-01	Control	4.8	26520	13	Cytoplasmic	COG0545	Posttranslational modification, protein turnover, chaperones	
26988451	PP_1719	prc	carboxyl-terminal protease	2.0	1.18E-02	Vanillin	7.1	79096	28	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26988452	PP_1720		alcohol dehydrogenase, zinc-containing	1.7	2.39E-03	Vanillin	4.7	33921	10	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26988454	PP_1722		ABC transporter ATP-binding protein	8.9	1.33E-02	Vanillin	8.0	36445	5	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	
26988458	PP_1726		ABC transporter periplasmic protein	12.3	2.29E-06	Vanillin	6.0	38636	19	Unknown	COG1840	Inorganic ion transport and metabolism	
26988462	PP_1730		aminopeptidase 2	1.0	7.99E-01	Vanillin	5.6	46996	8	Cytoplasmic	COG1362	Amino acid transport and metabolism	
26988464	PP_1733	minD	septum site-determining protein MinD	1.2	3.09E-01	Vanillin	6.2	29650	14	Cytoplasmic	COG2894	Cell division and chromosome partitioning	
26988465	PP_1734	minC	septum formation inhibitor	1.1	5.36E-01	Vanillin	8.9	29680	3	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
26988466	PP_1735	htrB	lipid A biosynthesis lauroyl acyltransferase	1.5	2.13E-02	Control	10.2	35743	2	Cytoplasmic Membrane	COG1560	Cell envelope biogenesis, outer membrane	
26988474	PP_1743	actP	acetate permease	171.3	3.38E-02	Vanillin	9.6	58972	2	Cytoplasmic Membrane	COG4147	General function prediction only	
26988483	PP_1752		hypothetical protein	1.4	7.42E-03	Vanillin	8.2	57637	17	Cytoplasmic	COG2326	Function unknown	
26988486	PP_1755	fumC-2	fumarate hydratase	5.6	2.82E-04	Vanillin	6.4	49131	19	Cytoplasmic	COG0114	Energy production and conversion	
26988489	PP_1758		hypothetical protein	3.6	2.08E-02	Control	5.5	35163	7	Cytoplasmic	COG1054	General function prediction only	
26988492	PP_1761		sensory box protein/GGDEF family protein	8.6	4.43E-04	Vanillin	6.8	108193	11	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
26988494	PP_1763		short chain dehydrogenase	1.0	6.71E-01	Vanillin	4.7	26253	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988496	PP_1765	ubiG	3-demethylubiquinone-9 3-methyltransferase	1.1	4.73E-02	Control	5.7	26084	6	Cytoplasmic	COG2227	Coenzyme metabolism	
26988497	PP_1766	mtnA	methylthioribose-1-phosphate isomerase	1.8	4.74E-02	Control	4.5	38652	4	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis	
26988498	PP_1767	gyrA	DNA gyrase subunit A	1.0	9.13E-01	Vanillin	4.7	102037	36	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26988499	PP_1768	serC	phosphoserine aminotransferase	1.6	4.88E-03	Control	5.1	39911	22	Cytoplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
26988500	PP_1769	pheA	chorismate mutase	1.9	1.11E-02	Control	6.4	40816	20	Cytoplasmic	COG0077	Amino acid transport and metabolism	
26988501	PP_1770		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikima	1.6	1.02E-02	Control	6.4	79133	22	Cytoplasmic	COG0128	Amino acid transport and metabolism	
26988502	PP_1771	cmk	cytidylate kinase	8.8	3.38E-02	Control	4.9	24691	2	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
26988506	PP_1775		beta-lactamase domain protein	2.6	3.82E-02	Vanillin	6.5	52195	3	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
26988507	PP_1776		mannose-6-phosphate isomerase/mannose-1-phosphate guanyl	1.2	1.24E-02	Control	5.2	52989	8	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
26988508	PP_1777	xanA	phosphomannomutase	1.9	6.71E-03	Control	5.2	49615	16	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26988510	PP_1779		lipopolysaccharide ABC export system, ATP-binding protein	2.4	2.42E-03	Control	5.4	44481	6	Cytoplasmic	COG1134	Carbohydrate transport and metabolism	Cell envelope biogenesis, outer membrane
26988511	PP_1780		mannosyltransferase	1.3	1.05E-01	Control	5.8	180042	33	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988514	PP_1783	rmlA	glucose-1-phosphate thymidylyltransferase	3.0	9.06E-04	Control	4.9	32517	9	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
26988515	PP_1784	rmlD	dTDP-4-dehydrorhamnose reductase	2.7	1.45E-05	Control	6.7	32131	12	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
26988516	PP_1785	rmlB	dTDP-glucose 4,6-dehydratase	2.2	7.21E-03	Control	6.1	40690	22	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
26988517	PP_1786		glycosyl transferase	2.0	1.36E-03	Control	6.4	128499	37	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988518	PP_1787		hypothetical protein	1.2	8.33E-02	Control	5.3	37903	10	Unknown			
26988519	PP_1788		hypothetical protein	8.4	6.40E-03	Control	8.7	42109	9	Cytoplasmic			
26988521	PP_1790		acylneuraminate cytidylyltransferase	2.8	8.89E-03	Control	6.4	26350	4	Cytoplasmic	COG1083	Cell envelope biogenesis, outer membrane	
26988522	PP_1791		aldolase/synthase	1.3	7.72E-02	Control	5.9	58534	22	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26988523	PP_1792		glycosyl transferase, group 2 family protein	1.2	6.66E-02	Control	6.5	88305	19	Cytoplasmic	COG1216	General function prediction only	
26988524	PP_1793		glycosyl transferase, group 2 family protein	1.1	4.87E-01	Vanillin	8.3	94732	10	Cytoplasmic Membrane	COG1216	General function prediction only	
26988525	PP_1794		hypothetical protein	2.9	1.58E-02	Control	3.5	48714	3	Extracellular			
26988526	PP_1795		hypothetical protein	2.5	1.66E-03	Control	6.4	31450	10	Unknown			
26988529	PP_1799	gmd	GDP-mannose 4,6 dehydratase	1.2	5.58E-02	Control	6.4	40124	26	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
26988530	PP_1800	rmd	oxidoreductase Rmd	1.0	8.53E-01	Control	7.2	32310	9	Unknown	COG1089	Cell envelope biogenesis, outer membrane	
26988531	PP_1801	wbpY	glycosyl transferase WbpY	1.4	2.01E-01	Control	9.0	42654	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988532	PP_1802	wbpZ	glycosyl transferase WbpZ	1.3	4.46E-03	Vanillin	8.4	44831	4	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26988535	PP_1805	wbpM	polysaccharide biosynthesis protein CapD	2.0	2.15E-02	Vanillin	9.2	76416	5	Cytoplasmic Membrane	COG1086	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26988537	PP_1807	kdsA-2	2-dehydro-3-deoxyphosphooctonate aldolase	1.4	3.22E-02	Vanillin	6.0	30469	10	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
26988538	PP_1808	pgi	glucose-6-phosphate isomerase	1.3	7.76E-03	Control	6.8	61383	26	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26988546	PP_1816		alcohol dehydrogenase, zinc-containing	6.4	2.31E-03	Vanillin	7.4	35802	13	Cytoplasmic	COG2130	General function prediction only	
26988549	PP_1819		methyl-accepting chemotaxis sensory transducer	25.2	1.74E-02	Vanillin	4.7	68069	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988557	PP_1827		N5-glutamine S-adenosyl-L-methionine-dependent methyltransf	1.1	7.11E-01	Vanillin	4.4	34094	5	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26988560	PP_1830	aroC	chorismate synthase	1.1	2.41E-01	Control	6.5	38987	12	Cytoplasmic	COG0082	Amino acid transport and metabolism	
26988568	PP_1838		hypothetical protein	1.1	4.58E-01	Vanillin	6.8	76615	9	Cytoplasmic Membrane	COG1368	Cell envelope biogenesis, outer membrane	
26988572	PP_1842		amidotransferase	1.2	1.64E-03	Vanillin	4.9	27317	7	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
26988575	PP_1845		enoyl-CoA hydratase	1.3	4.08E-01	Control	7.7	24641	4	Cytoplasmic	COG1024	Lipid metabolism	
26988588	PP_1858	efp	elongation factor P	1.8	1.38E-02	Control	4.5	21303	10	Cytoplasmic	COG0231	Translation, ribosomal structure and biogenesis	
26988595	PP_1865		ISPpu8, transposase	1.2	3.51E-01	Control	8.2	48506	6	Cytoplasmic			
26988596	PP_1866		phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	4.54E-01	Vanillin	6.4	49706	4	Cytoplasmic	COG3200	Amino acid transport and metabolism	
26988598	PP_1868		DEAD-box ATP dependent DNA helicase	1.3	2.05E-01	Control	9.2	60924	26	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription

26988602	PP_1872		aminotransferase AlaT	1.2	4.84E-02	Control	5.8	44705	16	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26988606	PP_1876		hypothetical protein	1.5	4.38E-02	Control	8.8	38962	12	Cytoplasmic	COG2607	General function prediction only	
26988608	PP_1878		hypothetical protein	1.9	6.68E-02	Vanillin	7.3	29093	6	Cytoplasmic			
26988623	PP_1893	fadE	acyl-CoA dehydrogenase	17.6	2.82E-04	Vanillin	6.9	89194	26	Cytoplasmic Membrane	COG1960	Lipid metabolism	
26988625	PP_1895		ABC transporter ATP-binding protein	1.7	3.61E-02	Vanillin	7.1	34488	5	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26988632	PP_1902	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.0	8.12E-01	Vanillin	5.2	27809	8	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
26988634	PP_1904	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	1.4	1.85E-02	Vanillin	6.6	38526	9	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
26988635	PP_1905	rne	ribonuclease, Rne/Rng family	1.5	2.63E-03	Control	4.7	120904	34	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
26988637	PP_1908		signal peptide peptidase SppA, 36K type	1.1	1.83E-01	Control	6.4	36497	9	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26988639	PP_1910		hypothetical protein	1.2	1.75E-01	Control	4.2	19332	3	Cytoplasmic	COG1399	General function prediction only	
26988641	PP_1912	plsX	glycerol-3-phosphate acyltransferase PlsX	1.3	1.58E-02	Vanillin	7.9	35093	2	Cytoplasmic	COG0416	Lipid metabolism	
26988642	PP_1913	fabD	malonyl CoA-acyl carrier protein transacylase	1.1	2.67E-01	Vanillin	4.7	32614	8	Cytoplasmic	COG0331	Lipid metabolism	
26988643	PP_1914	fabG	3-ketoacyl-(acyl-carrier-protein) reductase	1.8	6.80E-01	Control	6.0	25470	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988645	PP_1916	fabF	3-oxoacyl-(acyl carrier protein) synthase II	1.1	5.25E-01	Vanillin	5.8	43152	6	Cytoplasmic Membrane	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26988646	PP_1917	pabC	4-amino-4-deoxychorismate lyase	1.5	3.02E-01	Vanillin	7.2	29486	3	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26988647	PP_1918		aminodeoxychorismate lyase	3.5	1.31E-01	Vanillin	5.1	47420	3	Cytoplasmic	COG1559	Coenzyme transport and metabolism	
26988655	PP_1927		arsenical resistance protein ArsH	1.4	1.27E-01	Vanillin	6.1	27717	3	Cytoplasmic	COG0431	General function prediction only	
26988670	PP_1943	purU	formyltetrahydrofolate deformylase	107.9	8.22E-05	Vanillin	6.4	32061	15	Cytoplasmic	COG0788	Nucleotide transport and metabolism	
26988671	PP_1944		aminomethyltransferase	283.7	7.98E-06	Vanillin	6.0	48129	26	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26988672	PP_1945	folD-1	5,10-methylene-tetrahydrofolate dehydrogenase/cyclohydrolas	Infinity	6.70E-10	Vanillin	5.7	30531	5	Cytoplasmic	COG0190	Coenzyme metabolism	
26988673	PP_1946		short chain dehydrogenase/reductase family oxidoreductase	175.9	2.90E-05	Vanillin	5.3	27212	18	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988674	PP_1947		hypothetical protein	180.3	7.97E-02	Vanillin	5.4	34865	5	Unknown	COG2309	Amino acid transport and metabolism	
26988675	PP_1948		benzaldehyde dehydrogenase	57.2	1.06E-03	Vanillin	6.2	52881	19	Cytoplasmic	COG1012	Energy production and conversion	
26988676	PP_1949		GMC family oxidoreductase	41.1	1.24E-04	Vanillin	8.3	59605	15	Cytoplasmic Membrane	COG2303	Amino acid transport and metabolism	
26988677	PP_1950		hypothetical protein	225.7	2.64E-04	Vanillin	5.7	43504	15	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
26988678	PP_1951		short chain dehydrogenase/reductase family oxidoreductase	41.6	6.51E-04	Vanillin	6.1	28629	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988679	PP_1952		metallo-beta-lactamase family protein	63.6	8.74E-02	Vanillin	5.5	34578	5	Cytoplasmic	COG0491	General function prediction only	
26988680	PP_1953		short chain dehydrogenase/reductase family oxidoreductase	191.1	2.87E-04	Vanillin	5.3	28569	11	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988681	PP_1954		hypothetical protein	86.3	5.42E-05	Vanillin	5.4	41904	11	Unknown	COG1680	Defense mechanisms	
26988682	PP_1955		cytochrome P450 family protein	49.1	1.69E-02	Vanillin	5.2	46465	7	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
26988684	PP_1957		Pdr/VanB family oxidoreductase	89.0	1.71E-03	Vanillin	4.9	34943	3	Cytoplasmic	COG1018	Energy production and conversion	
26988685	PP_1958		hypothetical protein	2.0	4.26E-02	Vanillin	8.0	30813	2	Cytoplasmic			
26988686	PP_1959		hypothetical protein	1.4	2.49E-01	Control	6.4	43578	5	Unknown			
26988691	PP_1964		deoxynucleotide monophosphate kinase	1.5	2.66E-02	Vanillin	5.9	30146	5	Unknown			
26988692	PP_1966	holB	DNA polymerase III subunit delta'	2.4	6.51E-03	Vanillin	7.8	36281	3	Cytoplasmic	COG0470	DNA replication, recombination, and repair	
26988693	PP_1967		TatD family deoxyribonuclease	1.9	3.14E-01	Control	5.7	28469	2	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
26988698	PP_1972	tyrB-1	aromatic amino acid aminotransferase	1.4	2.61E-03	Control	5.9	43290	33	Cytoplasmic	COG1448	Amino acid transport and metabolism	
26988700	PP_1974	uvrB	excinuclease ABC subunit B	4.5	7.29E-03	Vanillin	4.9	76034	8	Cytoplasmic	COG0556	DNA replication, recombination, and repair	
26988703	PP_1977	gltX	glutamyl-tRNA synthetase	1.7	1.45E-02	Control	5.6	56483	27	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26988709	PP_1983		sensory box protein	2.7	1.24E-01	Vanillin	5.7	128000	8	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26988710	PP_1984		LysR family transcriptional regulator	2.1	5.75E-02	Vanillin	6.7	31995	2	Cytoplasmic	COG0583	Transcription	
26988711	PP_1985	leuC	isopropylmalate isomerase large subunit	2.6	1.26E-03	Control	5.6	51255	21	Cytoplasmic	COG0065	Amino acid transport and metabolism	
26988712	PP_1986	leuD	isopropylmalate isomerase small subunit	5.6	2.82E-04	Control	5.3	24284	7	Cytoplasmic	COG0066	Amino acid transport and metabolism	
26988713	PP_1987		UbiE/COQ5 family methlytransferase	20.5	3.54E-04	Control	5.8	28181	5	Cytoplasmic	COG2226	Coenzyme metabolism	
26988714	PP_1988	leuB	3-isopropylmalate dehydrogenase	2.9	1.78E-03	Control	4.8	38824	17	Cytoplasmic	COG0473	Amino acid transport and metabolism	
26988715	PP_1989	asd	aspartate-semialdehyde dehydrogenase	2.0	3.90E-03	Control	5.3	40672	29	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988718	PP_1992		aspartate-semialdehyde dehydrogenase	1.2	2.28E-01	Control	4.8	35304	7	Cytoplasmic	COG0136	Amino acid transport and metabolism	
26988719	PP_1993		peptidoglycan-binding LysM	4.4	3.82E-04	Vanillin	3.9	96918	24	Unknown	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
26988721	PP_1996	accD	acetyl-CoA carboxylase subunit beta	1.5	4.30E-02	Control	7.8	32510	12	Cytoplasmic	COG0777	Lipid metabolism	
26988722	PP_1997	folC	FolC bifunctional protein	1.6	1.47E-01	Vanillin	4.8	46895	9	Cytoplasmic	COG0285	Coenzyme metabolism	
26988723	PP_1998		sporulation domain protein	1.1	7.13E-01	Vanillin	10.1	22947	3	Cytoplasmic Membrane	COG3147	Function unknown	
26988725	PP_2000	purF	amidophosphoribosyltransferase	1.5	2.62E-02	Control	6.5	55400	22	Cytoplasmic	COG0034	Nucleotide transport and metabolism	
26988726	PP_2001	metZ	O-succinylhomoserine sulfhydrylase	1.0	7.74E-01	Vanillin	5.4	43284	10	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26988727	PP_2002		oxidoreductase	1.0	8.19E-01	Vanillin	6.6	27212	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26988730	PP_2005		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferas	8.4	2.02E-01	Vanillin	7.9	41069	2	Unknown	COG0388	General function prediction only	
26988731	PP_2006		hypothetical protein	1.5	1.72E-01	Control	5.1	63743	27	Unknown			
26988732	PP_2007		P-47-related protein	3.6	1.30E-03	Control	5.8	44707	5	Unknown			
26988733	PP_2008	fadH	NADH:flavin oxidoreductase/NADH oxidase	6.2	4.76E-03	Vanillin	7.0	73935	7	Cytoplasmic	COG1902	Energy production and conversion	
26988737	PP_2012	ppnK	inorganic polyphosphate/ATP-NAD kinase	1.2	9.97E-02	Vanillin	7.0	34318	5	Cytoplasmic	COG0061	Coenzyme metabolism	
26988741	PP_2016		hypothetical protein	2.7	3.65E-02	Control	7.6	30748	3	Cytoplasmic			
26988742	PP_2017	pepN	aminopeptidase N	2.4	2.55E-03	Vanillin	4.8	99573	32	Cytoplasmic	COG0308	Amino acid transport and metabolism	
26988744	PP_2019		hypothetical protein	7.5	5.69E-03	Vanillin	6.6	87732	2	Cytoplasmic Membrane	COG1033	General function prediction only	
26988746	PP_2021		hypothetical protein	4.5	7.97E-02	Vanillin	7.2	40684	4	Periplasmic	COG2706	Carbohydrate transport and metabolism	
26988749	PP_2024	sbcC	SMC domain protein	1.0	9.49E-01	Vanillin	5.5	136091	19	Cytoplasmic	COG0419	DNA replication, recombination, and repair	
26988750	PP_2025	sbcD	nuclease SbcCD, D subunit	1.2	5.10E-01	Control	4.9	46051	2	Cytoplasmic	COG0420	DNA replication, recombination, and repair	
26988757	PP_2032		ATPase	1.2	2.05E-01	Vanillin	5.0	35347	4	Cytoplasmic	COG0714	General function prediction only	
26988761	PP_2036		dihydrodipicolinate synthetase	1.6	7.06E-03	Vanillin	5.3	31332	4	Cytoplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
26988802	PP_2077	lysA-1	diaminopimelate decarboxylase	3.4	3.16E-04	Control	6.1	44869	4	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26988805	PP_2080		NAD-glutamate dehydrogenase	3.2	9.89E-04	Vanillin	5.8	187043	65	Cytoplasmic Membrane	COG2902	Amino acid transport and metabolism	
26988806	PP_2081		hypothetical protein	1.2	3.01E-01	Control	6.6	30824	9	Cytoplasmic	COG1806	Function unknown	
26988807	PP_2082	ppsA	phosphoenolpyruvate synthase	1.2	1.42E-01	Vanillin	4.8	86015	46	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
26988810	PP_2085	cmaX	cmaX protein	1.1	3.25E-01	Control	4.8	38094	4	Cytoplasmic Membrane	COG0598	Inorganic ion transport and metabolism	
26988814	PP_2089	oprF	OmpF family protein	1.0	1.65E-01	Vanillin	4.5	37012	22	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26988820	PP_2095	pyrD	dihydroorotate dehydrogenase 2	1.2	8.03E-02	Control	8.2	35545	12	Cytoplasmic Membrane	COG0167	Nucleotide transport and metabolism	
26988823	PP_2098	dacB	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endope	1.3	9.17E-02	Vanillin	9.9	50799	9	Periplasmic	COG2027	Cell envelope biogenesis, outer membrane	
26988835	PP_2111	aer-2	aerotaxis receptor Aer-2	1.1	3.57E-01	Vanillin	6.0	57068	10	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988836	PP_2112	acnA	aconitate hydratase	7.1	1.44E-04	Vanillin	5.7	99147	14	Cytoplasmic	COG1048	Energy production and conversion	
26988837	PP_2113		RNA 2'-O-ribose methyltransferase	3.5	1.41E-01	Control	8.4	40142	2	Cytoplasmic	COG2933	General function prediction only	

26988841	PP_2117	pdxB	erythronate-4-phosphate dehydrogenase	1.2	2.44E-01	Control	5.1	41614	6	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26988847	PP_2123	moeA	molybdopterin biosynthesis MoeA protein	1.4	2.36E-01	Control	5.1	43963	4	Cytoplasmic	COG0303	Coenzyme metabolism	
26988852	PP_2128	chev-2	chemotaxis protein CheV	1.2	2.93E-01	Vanillin	6.5	34556	15	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26988853	PP_2129		MOSC domain containing protein	1.0	9.48E-01	Vanillin	5.5	29621	7	Cytoplasmic	COG3217	General function prediction only	
26988854	PP_2130		soluble lytic transglycosylase	1.3	1.42E-01	Vanillin	9.9	75337	17	Periplasmic	COG0741	Cell envelope biogenesis, outer membrane	
26988855	PP_2131		ABC transporter ATP-binding protein	1.0	8.75E-01	Control	5.1	71398	23	Cytoplasmic	COG0488	General function prediction only	
26988860	PP_2136	fadB	multifunctional fatty acid oxidation complex subunit alpha	1.9	1.25E-02	Vanillin	5.9	77449	17	Cytoplasmic	COG1250	Lipid metabolism	
26988861	PP_2137	fadA	3-ketoacyl-CoA thiolase	1.5	2.93E-01	Vanillin	7.0	41556	7	Cytoplasmic	COG0183	Lipid metabolism	
26988863	PP_2139	topA	DNA topoisomerase I	1.1	3.21E-02	Vanillin	8.0	97239	37	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
26988869	PP_2145	nagZ	beta-hexosaminidase	1.4	8.23E-04	Vanillin	6.3	36513	6	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
26988872	PP_2148	mfd	transcription-repair coupling factor	1.1	4.57E-01	Vanillin	5.7	128301	22	Unknown	COG1197	DNA replication, recombination, and repair	Transcription
26988873	PP_2149	gap-2	glyceraldehyde-3-phosphate dehydrogenase	1.3	4.85E-02	Control	7.7	53014	39	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26988875	PP_2151	sthA	soluble pyridine nucleotide transhydrogenase	1.6	2.06E-03	Control	7.7	50905	17	Cytoplasmic	COG1249	Energy production and conversion	
26988876	PP_2152		glycerophosphoryl diester phosphodiesterase	1.9	7.11E-02	Control	7.5	26252	6	Cytoplasmic	COG0584	Energy production and conversion	
26988879	PP_2155	lolD	lipoprotein releasing system, ATP-binding protein	3.2	1.45E-02	Control	7.3	25304	3	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26988880	PP_2156	lolE	lipoprotein releasing system, transmembrane protein, LolC/E far	1.4	3.81E-01	Vanillin	9.5	44220	3	Cytoplasmic Membrane	COG4591	Cell envelope biogenesis, outer membrane	
26988884	PP_2160	queF	7-cyano-7-deazaguanine reductase	1.3	2.12E-01	Vanillin	6.5	30686	2	Cytoplasmic	COG2904	Function unknown	
26988887	PP_2163	vacJ	VacJ family lipoprotein	2.4	3.60E-02	Control	5.3	26061	3	Outer Membrane	COG2853	Cell envelope biogenesis, outer membrane	
26988889	PP_2165		response regulator	1.1	9.47E-01	Vanillin	4.7	43436	3	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription
26988892	PP_2168	tal	transaldolase B	1.6	1.24E-03	Vanillin	5.0	33615	16	Unknown	COG0176	Carbohydrate transport and metabolism	
26988893	PP_2169		tRNA-dihydrouridine synthase A	3.5	5.85E-02	Control	6.7	37130	2	Cytoplasmic	COG0042	Translation, ribosomal structure and biogenesis	
26988905	PP_2181		Cro/CI family transcriptional regulator	1.9	1.28E-02	Control	5.3	20453	3	Cytoplasmic	COG1396	Transcription	
26988911	PP_2187		universal stress protein	8.0	4.23E-04	Vanillin	6.3	31384	10	Cytoplasmic	COG0589	Signal transduction mechanisms	
26988919	PP_2195		periplasmic polyamine-binding protein	45.4	1.41E-04	Vanillin	5.5	39788	6	Periplasmic	COG0687	Amino acid transport and metabolism	
26988930	PP_2206		U32 family peptidase	4.7	5.16E-03	Vanillin	6.8	47941	2	Cytoplasmic	COG0826	Posttranslational modification, protein turnover, chaperones	
26988935	PP_2211		AraC family transcriptional regulator	2.2	1.60E-01	Vanillin	7.9	38658	2	Cytoplasmic	COG2207	Transcription	
26988937	PP_2213	fadDx	AMP-dependent synthetase and ligase	6.0	2.20E-03	Vanillin	6.0	61223	4	Cytoplasmic	COG0365	Lipid metabolism	
26988939	PP_2215	fadAx	acetyl-CoA acetyltransferase	3.5	4.48E-03	Vanillin	6.9	41382	7	Cytoplasmic	COG0183	Lipid metabolism	
26988941	PP_2217	fadB1x	enoyl-CoA hydratase/isomerase	1.1	4.52E-01	Control	5.2	27668	12	Cytoplasmic	COG1024	Lipid metabolism	
26988962	PP_2238		peptidase M24	1.7	2.15E-03	Vanillin	5.4	68915	10	Unknown	COG0006	Amino acid transport and metabolism	
26988973	PP_2249		methyl-accepting chemotaxis transducer	1.8	5.16E-02	Vanillin	5.1	68646	12	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988981	PP_2257	aer-1	aerotaxis receptor Aer-1	2.8	1.56E-01	Control	6.8	55029	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26988982	PP_2258		sensory box protein	2.0	5.12E-02	Control	6.1	62891	2	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26988988	PP_2264		extracellular solute-binding protein, family 1	2.5	4.83E-03	Vanillin	5.6	65243	4	Unknown	COG1653	Carbohydrate transport and metabolism	
26988989	PP_2265	folD-2	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5	1.7	1.51E-03	Control	6.4	30623	10	Cytoplasmic	COG0190	Coenzyme metabolism	
26989001	PP_2277		hypothetical protein	1.5	3.62E-01	Control	9.1	51877	5	Cytoplasmic			
26989016	PP_2292		hypothetical protein	3.2	9.38E-03	Vanillin	5.8	28522	6	Cytoplasmic			
26989023	PP_2299	tig	trigger factor	1.8	6.07E-03	Control	4.5	49190	43	Cytoplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
26989025	PP_2301	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.3	7.56E-03	Control	4.8	48526	25	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
26989026	PP_2302	lon-2	ATP-dependent protease La	1.1	1.64E-02	Vanillin	5.9	88722	48	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
26989028	PP_2304		PpiC-type peptidyl-prolyl cis-trans isomerase	1.2	2.43E-01	Control	4.8	68580	27	Cytoplasmic Membrane	COG0760	Posttranslational modification, protein turnover, chaperones	
26989029	PP_2305		patatin	3.1	8.03E-02	Vanillin	5.9	38234	2	Cytoplasmic	COG1752	General function prediction only	
26989031	PP_2307		CHAD domain containing protein	5.6	3.77E-04	Vanillin	10.8	29498	8	Cytoplasmic	COG5607	Function unknown	
26989032	PP_2308		acyl-CoA thioesterase II	2.4	8.76E-04	Vanillin	6.1	28745	5	Unknown	COG1946	Lipid metabolism	
26989034	PP_2310		methyl-accepting chemotaxis sensory transducer	4.3	3.48E-03	Vanillin	5.3	52127	7	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989035	PP_2311		TatD family hydrolase	1.0	9.51E-01	Vanillin	5.9	29409	4	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
26989040	PP_2316		hypothetical protein	6.9	4.59E-03	Vanillin	9.5	88411	4	Cytoplasmic Membrane	COG3127	Secondary metabolites biosynthesis, transport, and catabolism	
26989044	PP_2320		ErfK/YbiS/YcfS/YnhG family protein	1.0	7.11E-01	Control	5.4	35051	15	Unknown	COG1376	Function unknown	
26989049	PP_2325		2-dehydropantoate 2-reductase	5.0	2.99E-02	Vanillin	6.7	33694	4	Cytoplasmic	COG1893	Coenzyme metabolism	
26989051	PP_2327	cysB	transcriptional regulator CysB	1.4	2.13E-02	Vanillin	6.7	35955	13	Cytoplasmic	COG0583	Transcription	
26989052	PP_2328	cysH	phosphoadenosine phosphosulfate reductase	1.2	2.12E-01	Vanillin	6.5	27896	11	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
26989054	PP_2330		alpha-L-glutamate ligase-like protein	1.2	5.69E-01	Control	6.8	35904	4	Cytoplasmic			
26989055	PP_2331		hypothetical protein	1.2	9.98E-02	Vanillin	7.9	57064	6	Cytoplasmic Membrane			
26989058	PP_2334	prpB	2-methylisocitrate lyase	1.6	5.85E-03	Vanillin	5.4	31811	9	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
26989059	PP_2335		methylcitrate synthase	1.7	8.57E-03	Vanillin	6.7	41995	17	Cytoplasmic	COG0372	Energy production and conversion	
26989060	PP_2336		aconitate hydratase	2.8	4.10E-04	Vanillin	5.3	93961	19	Cytoplasmic	COG1048	Energy production and conversion	
26989061	PP_2337		hypothetical protein	2.1	8.71E-03	Vanillin	5.2	41312	8	Cytoplasmic	COG2828	Function unknown	
26989062	PP_2338	prpD	2-methylcitrate dehydratase	6.5	1.30E-04	Vanillin	7.1	54860	5	Cytoplasmic	COG2079	General function prediction only	
26989063	PP_2339	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydrata	1.4	4.51E-03	Vanillin	5.0	93609	61	Cytoplasmic	COG1049	Energy production and conversion	
26989075	PP_2351		acetyl-CoA synthetase	19.3	4.62E-05	Vanillin	6.1	68868	7	Cytoplasmic	COG0365	Lipid metabolism	
26989076	PP_2352		AFG1-family ATPase	2.1	3.27E-02	Vanillin	7.0	42007	6	Cytoplasmic	COG1485	General function prediction only	
26989078	PP_2354		multi-sensor hybrid histidine kinase	3.9	4.26E-03	Vanillin	5.0	88511	9	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989085	PP_2361	csuC	type 1 pili usher pathway chaperone CsuC	14.6	7.15E-04	Vanillin	10.3	28448	8	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
26989088	PP_2364		hypothetical protein	2.2	2.73E-04	Vanillin	5.2	42461	9	Unknown	COG2866	Amino acid transport and metabolism	
26989095	PP_2371	cysI	sulphite reductase hemoprotein, beta subunit	1.0	7.81E-01	Vanillin	5.8	62191	31	Cytoplasmic	COG0155	Inorganic ion transport and metabolism	
26989099	PP_2375	metH	B12-dependent methionine synthase	1.1	3.85E-01	Vanillin	4.7	135408	29	Cytoplasmic	COG1410	Amino acid transport and metabolism	
26989100	PP_2376	cti	fatty acid cistrans isomerase	1.8	3.03E-02	Vanillin	7.7	87107	6	Unknown			
26989111	PP_2387		hypothetical protein	1.8	2.33E-02	Vanillin	8.7	39427	4	Unknown			
26989113	PP_2389		hypothetical protein	1.5	1.16E-01	Vanillin	6.6	29586	2	Cytoplasmic	COG3403	Function unknown	
26989114	PP_2390		LysR family transcriptional regulator	5.5	9.73E-02	Vanillin	6.7	34592	2	Cytoplasmic	COG0583	Transcription	
26989129	PP_2406	aroE	shikimate 5-dehydrogenase	407.5	4.24E-04	Vanillin	5.6	30092	9	Cytoplasmic	COG0169	Amino acid transport and metabolism	
26989139	PP_2416		iron ABC transporter ATP-binding protein	1.1	7.37E-01	Vanillin	8.0	28148	2	Cytoplasmic Membrane	COG1120	Inorganic ion transport and metabolism	Coenzyme metabolism
26989141	PP_2418		periplasmic protein	1.1	3.01E-01	Vanillin	5.5	39626	11	Unknown	COG0614	Inorganic ion transport and metabolism	
26989142	PP_2419		hypothetical protein	5.4	2.20E-03	Control	10.2	47269	2	Cytoplasmic Membrane	COG3503	Function unknown	
26989155	PP_2432		dihydropteridine reductase	2.7	3.82E-02	Control	7.0	24212	6	Cytoplasmic	COG0778	Energy production and conversion	
26989159	PP_2436		LysR family transcriptional regulator	3.9	7.19E-03	Vanillin	9.4	35025	3	Cytoplasmic	COG0583	Transcription	
26989166	PP_2443		serine/threonine transporter SstT	2.2	9.28E-02	Vanillin	7.3	42012	2	Cytoplasmic Membrane	COG3633	Amino acid transport and metabolism	
26989171	PP_2448		FAD dependent oxidoreductase	3.3	1.24E-04	Vanillin	8.3	46589	4	Cytoplasmic	COG0665	Amino acid transport and metabolism	

26989176	PP_2453	ansA	L-asparaginase, type II	1.1	5.87E-01	Control	7.9	38608	6	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
26989177	PP_2454	rbsB	monosaccharide-transporting ATPase	5.6	2.31E-05	Vanillin	5.9	33763	13	Periplasmic	COG1879	Carbohydrate transport and metabolism	
26989180	PP_2457	rbsR	ribose operon repressor	4.9	9.72E-05	Vanillin	6.3	36652	9	Cytoplasmic	COG1609	Transcription	
26989181	PP_2458	rbsK	ribokinase	2.4	9.79E-03	Vanillin	5.1	31151	2	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
26989183	PP_2460		inosine/uridine-preferring nucleoside hydrolase	4.1	8.05E-04	Vanillin	6.2	34388	4	Unknown	COG1957	Nucleotide transport and metabolism	
26989188	PP_2465	thrS	threonyl-tRNA synthetase	1.4	6.83E-02	Control	5.8	72697	30	Cytoplasmic	COG0441	Translation, ribosomal structure and biogenesis	
26989191	PP_2468	rplT	50S ribosomal protein L20	4.2	3.62E-03	Control	12.1	13280	6	Cytoplasmic	COG0292	Translation, ribosomal structure and biogenesis	
26989192	PP_2469	pheS	phenylalanyl-tRNA synthetase subunit alpha	1.7	2.46E-02	Control	5.2	38082	17	Cytoplasmic	COG0016	Translation, ribosomal structure and biogenesis	
26989193	PP_2470	pheT	phenylalanyl-tRNA synthetase subunit beta	1.2	2.66E-01	Vanillin	4.8	86617	28	Cytoplasmic	COG0072	Translation, ribosomal structure and biogenesis	
26989199	PP_2476		alcohol dehydrogenase, zinc-containing	2.0	2.35E-01	Vanillin	6.5	37013	7	Cytoplasmic	COG2130	General function prediction only	
26989201	PP_2478		isoquinoline 1-oxidoreductase, beta subunit	1.4	5.29E-01	Vanillin	6.4	78674	5	Cytoplasmic Membrane	COG1529	Energy production and conversion	
26989209	PP_2486		Oye family NADH-dependent flavin oxidoreductase	1.3	1.25E-01	Control	6.4	41089	14	Cytoplasmic	COG1902	Energy production and conversion	
26989210	PP_2487		aldehyde dehydrogenase family protein	1.5	1.89E-01	Control	5.0	54721	9	Cytoplasmic	COG1012	Energy production and conversion	
26989211	PP_2488		succinic-semialdehyde dehydrogenase	1.3	1.15E-01	Vanillin	5.1	50254	10	Cytoplasmic	COG1012	Energy production and conversion	
26989214	PP_2491		ThiJ/PfpI family protein	1.1	9.47E-01	Vanillin	4.6	23692	3	Unknown	COG0693	General function prediction only	
26989215	PP_2492		butanol dehydrogenase, NADH-dependent	1.0	7.14E-01	Control	5.6	42414	5	Cytoplasmic	COG1979	Energy production and conversion	
26989228	PP_2505		GAF domain/GGDEF domain-containing protein	4.0	2.85E-03	Vanillin	6.0	38522	6	Cytoplasmic	COG3706	Signal transduction mechanisms	
26989248	PP_2528	metY	O-acetylhomoserine aminocarboxypropyltransferase	1.7	1.74E-01	Vanillin	6.5	45235	19	Cytoplasmic	COG2873	Amino acid transport and metabolism	
26989253	PP_2533		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.4	3.98E-01	Control	6.4	35784	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26989260	PP_2540		short chain dehydrogenase/reductase family oxidoreductase	1.9	4.19E-02	Vanillin	7.7	26775	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989262	PP_2542		GntR family transcriptional regulator	1.8	1.24E-01	Vanillin	7.3	53097	2	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
26989265	PP_2545		trans-aconitate 2-methyltransferase	1.6	1.15E-02	Vanillin	6.8	30767	3	Cytoplasmic	COG4106	General function prediction only	
26989270	PP_2550		hypothetical protein	1.4	4.06E-01	Control	4.6	25315	2	Cytoplasmic	COG0217	Function unknown	
26989272	PP_2552		aromatic-L-amino-acid decarboxylase	21.1	3.76E-05	Vanillin	5.2	51443	9	Unknown	COG0076	Amino acid transport and metabolism	
26989273	PP_2553		major facilitator family transporter	7.3	2.09E-02	Vanillin	8.9	49555	7	Cytoplasmic Membrane	COG2814	Carbohydrate transport and metabolism	
26989274	PP_2554		4-hydroxyphenylpyruvate dioxygenase	51.5	4.96E-05	Vanillin	5.0	70406	12	Cytoplasmic	COG3185	Amino acid transport and metabolism	General function prediction only
26989319	PP_2600		FAD-binding dehydrogenase	1106.2	1.20E-03	Vanillin	9.1	60515	11	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26989320	PP_2601		IclR family transcriptional regulator	14.5	8.17E-04	Vanillin	5.4	27864	4	Cytoplasmic Membrane	COG1414	Transcription	
26989321	PP_2602		oxidoreductase domain protein	70.3	7.15E-04	Vanillin	6.7	37747	6	Unknown	COG0673	General function prediction only	
26989322	PP_2603		xylose isomerase	15.6	2.74E-05	Vanillin	4.9	29670	7	Cytoplasmic	COG1082	Carbohydrate transport and metabolism	
26989362	PP_2643		methyl-accepting chemotaxis sensory transducer	14.0	2.22E-05	Vanillin	5.3	59485	16	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989367	PP_2648		universal stress protein	16.6	1.59E-05	Vanillin	7.4	33804	10	Cytoplasmic	COG0589	Signal transduction mechanisms	
26989371	PP_2652		hydratase/decarboxylase	11.3	1.29E-04	Vanillin	6.6	27774	7	Unknown	COG3971	Secondary metabolites biosynthesis, transport, and catabolism	
26989375	PP_2656		phosphate ABC transporter periplasmic phosphate-binding prote	2.2	3.37E-02	Control	8.8	37133	5	Periplasmic	COG0226	Inorganic ion transport and metabolism	
26989381	PP_2662		hypothetical protein	7.5	6.56E-02	Vanillin	4.3	42858	7	Outer Membrane			
26989382	PP_2663		hypothetical protein	8.2	1.39E-01	Vanillin	6.3	42469	6	Cytoplasmic	COG3287	Function unknown	
26989383	PP_2664		PAS/PAC sensor hybrid histidine kinase	314.0	4.28E-03	Vanillin	6.6	73094	8	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26989387	PP_2668		efflux ABC transporter ATP-binding protein	23.5	1.16E-02	Vanillin	9.8	27178	6	Cytoplasmic Membrane	COG1131	Defense mechanisms	
26989388	PP_2669		YVTN family beta-propeller repeat-containing protein	40.2	1.00E-02	Vanillin	6.2	36051	8	Unknown	COG3391	Function unknown	
26989393	PP_2674	qedH	quinoprotein ethanol dehydrogenase	11.1	5.63E-02	Vanillin	7.0	69173	40	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989395	PP_2676		periplasmic protein	21.8	1.35E-02	Vanillin	6.5	34540	5	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26989396	PP_2677		hypothetical protein	5.7	6.49E-02	Vanillin	5.3	28059	6	Unknown			
26989397	PP_2678		beta-lactamase domain protein	8.0	2.73E-01	Vanillin	6.4	33711	4	Unknown	COG0491	General function prediction only	
26989398	PP_2679		quinoprotein ethanol dehydrogenase	2.0	1.35E-01	Vanillin	9.1	64883	23	Periplasmic	COG4993	Carbohydrate transport and metabolism	
26989399	PP_2680		aldehyde dehydrogenase family protein	9.3	1.90E-02	Vanillin	5.5	54903	32	Cytoplasmic	COG1012	Energy production and conversion	
26989417	PP_2698	metE	5-methyltetrahydropteroyltriglutamate-- homocysteine methylt	1.4	3.93E-01	Control	6.3	38659	3	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26989420	PP_2701		LysR family transcriptional regulator	1.1	6.48E-01	Control	8.4	34726	3	Cytoplasmic	COG0583	Transcription	
26989545	PP_2826	mexT	transcriptional regulator MexT	2.2	2.61E-02	Vanillin	6.7	33299	2	Cytoplasmic Membrane	COG0583	Transcription	
26989546	PP_2827		alcohol dehydrogenase, zinc-containing	5.0	1.77E-03	Vanillin	5.4	36735	8	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26989572	PP_2853		hypothetical protein	11.1	4.68E-04	Vanillin	4.5	46020	4	Unknown			
26989580	PP_2861		methyl-accepting chemotaxis sensory transducer	32.1	1.26E-01	Vanillin	5.7	58659	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26989586	PP_2867		pyridine nucleotide-disulphide oxidoreductase family protein	1.3	4.29E-03	Vanillin	5.6	42483	5	Cytoplasmic Membrane	COG1252	Energy production and conversion	
26989595	PP_2876	ampC	beta-lactamase	1.5	2.34E-02	Control	8.2	40787	6	Periplasmic	COG1680	Defense mechanisms	
26989609	PP_2890	xthA	exonuclease III	1.1	4.79E-01	Vanillin	6.7	30951	6	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
26989612	PP_2893		hypothetical protein	1.6	8.61E-02	Vanillin	5.7	131100	3	Unknown	COG2911	Function unknown	
26989620	PP_2901		penicillin amidase family protein	3.4	3.12E-03	Control	8.0	83333	22	Periplasmic	COG2366	General function prediction only	
26989623	PP_2904	glnS	glutaminyl-tRNA synthetase	1.4	2.85E-03	Control	6.1	64654	28	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26989624	PP_2905	cysS	cysteinyl-tRNA synthetase	1.9	1.31E-03	Control	5.8	51676	24	Cytoplasmic	COG0215	Translation, ribosomal structure and biogenesis	
26989631	PP_2912		hypothetical protein	1.0	9.99E-01	Control	5.0	33023	2	Cytoplasmic	COG1718	Signal transduction mechanisms	Cell division and chromosome partitioning
26989632	PP_2913	hemB-1	delta-aminolevulinic acid dehydratase	1.1	5.60E-01	Vanillin	5.0	35225	8	Cytoplasmic	COG0113	Coenzyme metabolism	
26989644	PP_2925	mqo-3	malate:quinone oxidoreductase	338.1	2.40E-02	Vanillin	8.0	59671	4	Unknown	COG0579	General function prediction only	
26989647	PP_2928		saccharopine dehydrogenase	1.8	2.25E-02	Control	5.0	45363	19	Cytoplasmic	COG1748	Amino acid transport and metabolism	
26989648	PP_2929	nspC	carboxynorspermidine decarboxylase	2.2	1.34E-02	Control	4.9	41026	10	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26989649	PP_2930		L-serine dehydratase	1.2	1.76E-01	Control	6.6	31890	5	Cytoplasmic	COG1171	Amino acid transport and metabolism	
26989651	PP_2932		amidase	1.7	2.95E-02	Vanillin	4.5	60346	8	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
26989652	PP_2933		glutathione S-transferase YghU	1.7	2.41E-03	Vanillin	6.0	31202	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26989655	PP_2936		ABC transporter ATP-binding protein	4.0	2.46E-02	Control	4.8	58859	10	Cytoplasmic	COG0488	General function prediction only	
26989661	PP_2942		response regulator	10.5	6.05E-04	Vanillin	5.6	51291	4	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
26989662	PP_2943		cytochrome c551 peroxidase	14.2	2.76E-04	Vanillin	5.4	37072	3	Periplasmic	COG1858	Inorganic ion transport and metabolism	
26989663	PP_2944		sensor histidine kinase	13.0	2.70E-04	Vanillin	6.1	67470	5	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26989708	PP_2989		short chain dehydrogenase/reductase family oxidoreductase	2.1	4.33E-03	Vanillin	5.1	28161	3	Cytoplasmic	COG0300	General function prediction only	
26989738	PP_3019		Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferas	1.0	9.03E-01	Vanillin	5.1	26214	5	Cytoplasmic	COG0388	General function prediction only	
26989743	PP_3024		hypothetical protein	1.2	5.33E-01	Control	10.3	45171	7	Cytoplasmic			
26989752	PP_3033		transcriptional repressor pyocin R2_PP	1.1	7.64E-01	Vanillin	6.4	26740	2	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
26989786	PP_3067		hypothetical protein	6.1	1.59E-02	Control	6.6	48836	3	Cytoplasmic			
26989792	PP_3073	bdhA	3-hydroxybutyrate dehydrogenase	2.6	4.75E-02	Vanillin	6.9	26852	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26989807	PP_3088		hypothetical protein	6.8	1.95E-02	Control	4.4	39853	2	Unknown	COG3515	Intracellular trafficking, secretion, and vesicular transport	
26989808	PP_3089		hypothetical protein	28.9	5.03E-03	Control	5.3	19453	2	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	

26989809	PP_3090		OmpA domain-containing protein	1.9	2.21E-01	Control	9.0	93143	3	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989810	PP_3091		hypothetical protein	2.4	1.28E-01	Control	6.8	138655	14	Cytoplasmic Membrane	COG3523	Intracellular trafficking, secretion, and vesicular transport	
26989811	PP_3092		hypothetical protein	3.0	8.63E-02	Control	5.7	26868	4	Cytoplasmic	COG3455	Intracellular trafficking, secretion, and vesicular transport	
26989813	PP_3094		hypothetical protein	3.4	2.97E-02	Control	4.7	25945	3	Unknown	COG3521	Intracellular trafficking, secretion, and vesicular transport	
26989814	PP_3095		chaperone-associated ATPase	1.6	2.53E-01	Control	6.1	96474	17	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26989818	PP_3099		hypothetical protein	3.4	5.31E-02	Control	4.9	56072	20	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
26989823	PP_3104		hypothetical protein	2.6	5.01E-03	Vanillin	9.5	35101	4	Unknown			
26989825	PP_3106		hypothetical protein	1.1	9.38E-01	Control	5.6	69529	18	Cytoplasmic	COG3501	Function unknown	
26989827	PP_3108		rhs-related protein	2.2	1.88E-03	Vanillin	6.0	155811	27	Unknown	COG3209	Cell envelope biogenesis, outer membrane	
26989839	PP_3120		aldo/keto reductase family oxidoreductase	1.2	2.70E-01	Vanillin	6.4	27746	4	Cytoplasmic	COG0656	General function prediction only	
26989846	PP_3127		lipopolysaccharide biosynthesis protein	8.1	1.16E-03	Vanillin	9.0	57141	16	Cytoplasmic Membrane	COG3206	Cell envelope biogenesis, outer membrane	
26989847	PP_3128		protein-tyrosine kinase	6.7	5.64E-04	Vanillin	7.1	29623	7	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
26989848	PP_3129	galE	UDP-glucose 4-epimerase	7.2	9.29E-05	Vanillin	6.3	34967	4	Cytoplasmic	COG1087	Cell envelope biogenesis, outer membrane	
26989849	PP_3130		hypothetical protein	13.2	1.39E-03	Vanillin	6.4	96618	3	Unknown			
26989852	PP_3133		GMC oxidoreductase	43.9	8.48E-04	Vanillin	5.2	52611	3	Cytoplasmic	COG2303	Amino acid transport and metabolism	
26989854	PP_3135		glycosyl transferase	10.8	6.41E-04	Vanillin	8.6	35887	13	Cytoplasmic	COG1216	General function prediction only	
26989857	PP_3138		VirK domain-containing protein	8.1	2.32E-03	Vanillin	8.6	37023	4	Unknown	COG2990	Function unknown	
26989858	PP_3139		glycosyl transferase, group 1 family protein	5.9	3.06E-03	Vanillin	7.9	44606	5	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26989859	PP_3140		glycosyl transferase, group 2 family protein	20.5	1.76E-03	Vanillin	9.4	43092	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26989864	PP_3145		hypothetical protein	2.3	7.00E-02	Vanillin	9.7	29885	10	Unknown			
26989866	PP_3147		periplasmic polyamine-binding protein	4.6	4.24E-02	Vanillin	6.1	40025	4	Periplasmic	COG0687	Amino acid transport and metabolism	
26989869	PP_3150		hypothetical protein	1.1	3.61E-01	Vanillin	7.2	75137	3	Cytoplasmic Membrane			
26989870	PP_3151		aldehyde dehydrogenase family protein	42.0	6.74E-06	Vanillin	5.0	49303	10	Cytoplasmic	COG1012	Energy production and conversion	
26989874	PP_3155		outer membrane ferric siderophore receptor	12.7	2.92E-03	Control	4.9	78211	27	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26989876	PP_3157		inositol monophosphatase family protein	2.9	8.25E-03	Control	4.3	27793	6	Cytoplasmic	COG0483	Carbohydrate transport and metabolism	
26989908	PP_3189	codA	N-isopropylammelide isopropylaminohydrolase	3.9	2.17E-03	Vanillin	6.1	45821	5	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
26989910	PP_3191		hypothetical protein	1.3	1.95E-01	Vanillin	5.4	36931	3	Cytoplasmic	COG1171	Amino acid transport and metabolism	
26989937	PP_3219		alkansulfonate monooxygenase	1.4	3.46E-01	Vanillin	6.8	40195	2	Cytoplasmic	COG2141	Energy production and conversion	
26989966	PP_3248		Dyp-type peroxidase family	1.7	1.65E-02	Control	4.6	31295	11	Unknown	COG2837	Inorganic ion transport and metabolism	
26989988	PP_3270	phaL	bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	6.9	3.30E-03	Vanillin	6.8	72880	3	Cytoplasmic	COG1012	Energy production and conversion	
26990042	PP_3324		GTP cyclohydrolase	2.5	1.02E-02	Control	6.6	35587	8	Unknown	COG1469	Function unknown	
26990043	PP_3325		outer membrane ferric siderophore receptor	2.4	1.45E-03	Control	4.8	76226	34	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990044	PP_3326		hypothetical protein	2.5	3.77E-02	Control	8.9	25930	7	Unknown	COG5266	Inorganic ion transport and metabolism	
26990047	PP_3330		TonB-dependent siderophore receptor	18.5	1.42E-01	Vanillin	5.8	80740	4	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990067	PP_3352		arylsulfatase	133.4	4.77E-04	Vanillin	6.6	61071	8	Unknown	COG3119	Inorganic ion transport and metabolism	
26990072	PP_3357	vdh	vanillin dehydrogenase	11.1	4.38E-01	Vanillin	5.5	49959	2	Unknown	COG1012	Energy production and conversion	
26990076	PP_3361		hypothetical protein	3.5	3.47E-03	Vanillin	6.3	110896	9	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26990079	PP_3364		response regulator	7.0	1.95E-03	Vanillin	6.4	91750	9	Cytoplasmic	COG4251	Signal transduction mechanisms	
26990085	PP_3370		aldo/keto reductase family oxidoreductase	4.0	4.92E-02	Vanillin	6.3	36759	2	Cytoplasmic	COG0667	Energy production and conversion	
26990091	PP_3376	kguD	2-ketogluconate 6-phosphate reductase	226.0	6.41E-08	Control	6.3	34561	20	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26990092	PP_3377		major facilitator transporter	2081.3	1.40E-02	Control	9.6	47449	4	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990093	PP_3378	kguK	PfkB domain protein	1334.7	2.51E-05	Control	5.7	33615	16	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
26990094	PP_3379		xylose isomerase	78.0	3.28E-05	Control	5.3	28095	10	Cytoplasmic			
26990095	PP_3380	ptxS	PtxS family transcriptional regulator	3.8	2.48E-05	Control	6.9	36789	7	Cytoplasmic	COG1609	Transcription	
26990097	PP_3382		gluconate 2-dehydrogenase acceptor subunit	544.1	2.34E-06	Control	6.2	44276	5	Cytoplasmic Membrane	COG2010	Energy production and conversion	
26990098	PP_3383		gluconate 2-dehydrogenase acceptor subunit	100.4	1.55E-05	Control	8.0	65163	15	Unknown	COG2303	Amino acid transport and metabolism	
26990118	PP_3404		alpha/beta hydrolase fold	1.8	5.89E-02	Vanillin	8.3	31909	3	Cytoplasmic	COG0596	General function prediction only	
26990128	PP_3415		LacI family transcription regulator	13.4	1.99E-04	Control	7.6	36204	5	Unknown	COG1609	Transcription	
26990130	PP_3417	gntP	gluconate transporter	40.5	3.24E-06	Control	8.9	47532	8	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
26990138	PP_3425	mexE	efflux transporter RND family, MFP subunit	8.4	3.89E-01	Vanillin	9.6	44603	8	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990139	PP_3426	mexF	transporter hydrophobe/amphiphile efflux-1 (HAE1) family	9.7	5.41E-03	Vanillin	5.6	114759	11	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26990140	PP_3427	oprN	RND efflux system, outer membrane lipoprotein, NodT family	72.0	1.92E-03	Vanillin	4.9	50894	9	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990144	PP_3431		ThiJ/PfpI domain protein	2.4	8.23E-02	Vanillin	6.5	25246	6	Unknown	COG0693	General function prediction only	
26990154	PP_3441		hypothetical protein	36.3	1.10E-04	Vanillin	9.3	43139	5	Cytoplasmic			
26990156	PP_3443		glyceraldehyde-3-phosphate dehydrogenase	5.5	2.28E-04	Control	6.2	59980	22	Cytoplasmic	COG1012	Energy production and conversion	
26990161	PP_3448	nfrB	bacteriophage N4 adsorption protein B	23.0	1.78E-02	Vanillin	7.4	82370	4	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
26990203	PP_3491		enoly-coenzyme A hydratase/isomerase family protein	2.5	9.55E-03	Vanillin	4.9	39382	8	Cytoplasmic	COG1024	Lipid metabolism	
26990204	PP_3492	acdA	acyl-CoA dehydrogenase domain-containing protein	1.1	5.47E-01	Vanillin	5.7	41553	11	Cytoplasmic	COG1960	Lipid metabolism	
26990209	PP_3497		U32 family peptidase	1.4	1.83E-01	Vanillin	7.0	74339	6	Cytoplasmic	COG0826	Posttranslational modification, protein turnover, chaperones	
26990218	PP_3506		magnesium chelatase	2.1	6.86E-02	Vanillin	5.0	36032	2	Cytoplasmic	COG1239	Coenzyme metabolism	
26990220	PP_3508	cobW	cobalamin biosynthesis protein CobW	1.1	6.57E-01	Vanillin	4.6	38579	8	Cytoplasmic	COG0523	General function prediction only	
26990223	PP_3511	ilvE	branched-chain amino acid aminotransferase	1.1	5.27E-01	Vanillin	7.2	36863	24	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
26990239	PP_3527		TetR family transcriptional regulator	1.2	5.03E-01	Control	6.5	26116	2	Cytoplasmic	COG1309	Transcription	
26990240	PP_3528		aliphatic sulfonate ABC transporter periplasmic ligand-binding p	5.8	4.64E-05	Vanillin	9.6	34793	2	Unknown	COG0715	Inorganic ion transport and metabolism	
26990242	PP_3530		hypothetical protein	1.8	5.17E-03	Vanillin	6.2	31546	11	Cytoplasmic	COG3257	General function prediction only	
26990248	PP_3536		hypothetical protein	86.8	1.76E-06	Vanillin	4.4	41469	15	Cytoplasmic			
26990249	PP_3537	pobA	4-hydroxybenzoate 3-monooxygenase	545.6	1.27E-06	Vanillin	6.3	44262	28	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
26990252	PP_3540	mvaB	hydroxymethylglutaryl-CoA lyase	1.3	1.27E-01	Vanillin	5.4	31341	9	Cytoplasmic	COG0119	Amino acid transport and metabolism	
26990259	PP_3547		short chain dehydrogenase/reductase family oxidoreductase	2.0	1.01E-01	Control	6.0	26030	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990261	PP_3549	emrA	secretion protein HlyD family protein	Infinity	1.31E-06	Vanillin	6.0	42851	3	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26990269	PP_3557		methyl-accepting chemotaxis transducer	1.2	5.77E-01	Vanillin	4.7	76982	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26990270	PP_3558		substrate-binding region of ABC-type glycine betaine transport s	12.5	5.84E-04	Vanillin	5.5	36928	14	Periplasmic	COG2113	Amino acid transport and metabolism	
26990275	PP_3563		hypothetical protein	1.1	4.26E-01	Vanillin	5.1	30285	2	Unknown	COG2340	Function unknown	
26990281	PP_3569		quinate dehydrogenase (pyrroloquinoline-quinone)	36.4	1.32E-04	Vanillin	6.9	85338	17	Cytoplasmic Membrane	COG4993	Carbohydrate transport and metabolism	
26990290	PP_3578		phosphoglucomutase	1.5	2.57E-02	Control	5.6	58620	22	Unknown	COG0033	Carbohydrate transport and metabolism	
26990294	PP_3582		RND efflux transporter	2.8	3.94E-03	Control	5.2	53952	7	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990296	PP_3585		efflux transporter RND family, MFP subunit	3.9	8.90E-03	Control	9.4	46468	6	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990301	PP_3590	tyrB-2	aromatic amino acid aminotransferase	1.6	1.52E-02	Control	5.9	43631	15	Cytoplasmic	COG1448	Amino acid transport and metabolism	

26990304	PP_3593		amino acid ABC transporter periplasmic amino acid-binding prot	2.5	1.05E-02	Vanillin	4.8	27259	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26990313	PP_3602		ketoglutarate semialdehyde dehydrogenase	5.8	2.67E-03	Vanillin	5.2	55538	7	Cytoplasmic	COG1012	Energy production and conversion	
26990314	PP_3603		GntR family transcriptional regulator	1.3	3.68E-01	Vanillin	9.0	28149	4	Cytoplasmic	COG2186	Transcription	
26990323	PP_3612		TonB-dependent siderophore receptor	7.7	5.46E-04	Control	5.2	85491	20	Outer Membrane	COG4774	Inorganic ion transport and metabolism	
26990331	PP_3620		hypothetical protein	1.4	1.35E-02	Control	4.3	81519	10	Cytoplasmic	COG1944	Function unknown	
26990333	PP_3622		isoquinoline 1-oxidoreductase, beta subunit	150.3	7.13E-06	Vanillin	7.0	80889	32	Cytoplasmic Membrane	COG1529	Energy production and conversion	
26990334	PP_3623		gluconate 2-dehydrogenase acceptor subunit	41.6	5.57E-05	Vanillin	7.2	47849	12	Cytoplasmic Membrane	COG2010	Energy production and conversion	
26990347	PP_3636		sulfonate ABC transporter periplasmic sulfonate-binding protein	7.3	3.19E-03	Vanillin	7.3	43742	13	Cytoplasmic Membrane	COG0715	Inorganic ion transport and metabolism	
26990348	PP_3637		sulfonate ABC transporter ATP-binding protein	3.4	1.51E-03	Vanillin	7.1	29618	3	Cytoplasmic Membrane	COG1116	Inorganic ion transport and metabolism	
26990349	PP_3638		acyl-CoA dehydrogenase	4.3	1.44E-03	Vanillin	6.1	38476	24	Cytoplasmic	COG1960	Lipid metabolism	
26990355	PP_3644		luciferase family protein	2.8	6.32E-03	Vanillin	5.4	38951	7	Cytoplasmic	COG2141	Energy production and conversion	
26990360	PP_3649		GntR family transcriptional regulator	1.2	4.04E-01	Vanillin	7.0	28178	9	Cytoplasmic	COG1802	Transcription	
26990362	PP_3651		GAF sensor hybrid histidine kinase	3.9	3.37E-03	Vanillin	4.9	79274	6	Cytoplasmic Membrane	COG4191	Signal transduction mechanisms	
26990373	PP_3662		decarboxylase family protein	1.4	8.62E-02	Control	6.7	50729	23	Cytoplasmic	COG1611	General function prediction only	
26990375	PP_3664	pssA	phosphatidylserine synthase	1.2	4.34E-01	Control	10.1	49526	2	Cytoplasmic	COG1502	Lipid metabolism	
26990379	PP_3668		catalase/peroxidase HPI	11.8	1.82E-04	Vanillin	5.8	82061	38	Cytoplasmic	COG0376	Inorganic ion transport and metabolism	
26990382	PP_3671		aldo/keto reductase family oxidoreductase	234.2	6.55E-07	Vanillin	5.9	30068	14	Cytoplasmic	COG0656	General function prediction only	
26990389	PP_3680		hypothetical protein	1.7	1.15E-02	Vanillin	6.3	75093	14	Unknown	COG3593	DNA replication, recombination, and repair	
26990390	PP_3681		helicase	2.1	2.47E-02	Vanillin	8.6	62371	2	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
26990399	PP_3691		DNA helicase-related protein	1.3	1.98E-01	Vanillin	5.0	245278	61	Unknown	COG1112	DNA replication, recombination, and repair	
26990400	PP_3692		hypothetical protein	3.7	1.52E-02	Vanillin	8.0	98331	10	Cytoplasmic	COG4988	Energy production and conversion	Posttranslational modification, protein turnover, chaperones
26990407	PP_3699		hypothetical protein	2.4	4.04E-03	Control	6.1	63413	15	Cytoplasmic	COG2849	Function unknown	
26990413	PP_3705		hypothetical protein	3.6	4.59E-03	Control	9.0	43629	3	Cytoplasmic Membrane			
26990414	PP_3706		hypothetical protein	1.2	4.78E-01	Control	5.7	35856	8	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26990415	PP_3707		hypothetical protein	1.2	2.19E-01	Vanillin	5.4	52925	6	Cytoplasmic			
26990426	PP_3718		hypothetical protein	15.8	1.96E-03	Vanillin	5.5	52206	9	Cytoplasmic	COG0161	Coenzyme metabolism	
26990427	PP_3719		periplasmic polyamine-binding protein	73.8	1.78E-04	Vanillin	7.0	40452	5	Periplasmic	COG0687	Amino acid transport and metabolism	
26990428	PP_3720		ribosyldihydronicotinamide dehydrogenase (quinone)	4.5	6.92E-01	Control	5.3	26500	2	Cytoplasmic	COG2249	General function prediction only	
26990429	PP_3721	aspC	aspartate aminotransferase	5.5	2.68E-05	Vanillin	5.1	42461	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990443	PP_3736	vanA	Rieske (2Fe-2S) domain protein	126.1	4.88E-07	Vanillin	5.5	39542	27	Cytoplasmic	COG4638	Inorganic ion transport and metabolism	General function prediction only
26990444	PP_3737	vanB	ferredoxin	412.9	2.11E-07	Vanillin	4.6	34255	11	Cytoplasmic	COG1018	Energy production and conversion	
26990446	PP_3740		major facilitator family transporter	2078.3	1.07E-07	Vanillin	10.5	46421	4	Cytoplasmic Membrane	COG2271	Carbohydrate transport and metabolism	
26990459	PP_3754		beta-ketothiolase	4.2	1.33E-03	Vanillin	6.9	40988	18	Cytoplasmic	COG0183	Lipid metabolism	
26990460	PP_3755	paaH	3-hydroxybutyryl-CoA dehydrogenase	18.3	2.76E-03	Vanillin	6.3	30088	3	Cytoplasmic	COG1250	Lipid metabolism	
26990463	PP_3758		response regulator receiver sensor signal transduction histidine	1.1	6.26E-01	Vanillin	5.5	45788	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990466	PP_3761		multi-sensor hybrid histidine kinase	2.1	3.39E-03	Vanillin	4.9	129450	31	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990480	PP_3775		sarcosine oxidase	2.4	3.97E-02	Control	6.4	41164	19	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26990481	PP_3776	rarD-3	rarD protein	1.3	6.55E-01	Control	9.5	32267	2	Cytoplasmic Membrane	COG2962	General function prediction only	
26990482	PP_3777		hypothetical protein	2.6	5.77E-02	Control	5.2	31324	11	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
26990483	PP_3778	proC-1	pyrroline-5-carboxylate reductase	2.4	2.35E-02	Control	6.2	27714	18	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26990484	PP_3779		LysR family transcriptional regulator	7.5	5.51E-03	Control	6.9	33862	7	Cytoplasmic	COG0583	Transcription	
26990486	PP_3781		oxygen-independent coproporphyrinogen III oxidase family prot	14.6	3.22E-03	Control	7.0	53071	19	Cytoplasmic	COG0635	Coenzyme metabolism	
26990488	PP_3783		hypothetical protein	12.2	4.21E-03	Control	5.8	34938	20	Cytoplasmic			
26990489	PP_3784		hypothetical protein	6.4	1.75E-02	Control	5.4	41070	24	Unknown	COG0251	Translation, ribosomal structure and biogenesis	
26990490	PP_3785		hypothetical protein	3.3	5.25E-02	Control	6.5	50495	27	Cytoplasmic			
26990491	PP_3786		aminotransferase	20.4	3.44E-03	Control	6.4	44067	16	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26990492	PP_3787		hypothetical protein	5.8	2.45E-02	Control	6.8	33215	9	Unknown	COG0332	acyl-carrier-protein	
26990493	PP_3788		non-ribosomal peptide synthetase	56.9	4.66E-05	Control	6.7	56336	16	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990494	PP_3789		efflux transporter	36.7	2.60E-03	Control	9.2	43505	2	Cytoplasmic Membrane			
26990495	PP_3790	dapF	diaminopimelate epimerase	7.6	8.90E-03	Control	6.0	29286	12	Cytoplasmic	COG0253	Amino acid transport and metabolism	
26990499	PP_3794	pbpG	D-alanyl-D-alanine endopeptidase	1.4	4.52E-02	Control	10.5	33802	5	Unknown	COG1686	Cell envelope biogenesis, outer membrane	
26990501	PP_3796		L-ornithine N5-oxygenase	2.1	1.83E-02	Control	6.5	50047	26	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
26990502	PP_3797		hypothetical protein	6.3	2.20E-03	Control	9.5	44129	6	Cytoplasmic Membrane	COG3182	Function unknown	
26990507	PP_3802		cation ABC transporter ATP-binding protein	2.4	1.29E-03	Control	7.6	26939	3	Cytoplasmic Membrane	COG1121	Inorganic ion transport and metabolism	
26990509	PP_3804		hypothetical protein	1.8	3.39E-02	Control	5.4	30144	9	Unknown	COG0803	Inorganic ion transport and metabolism	
26990512	PP_3807		thioesterase	4.1	1.57E-02	Control	6.5	26350	4	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	
26990519	PP_3814		polyamine ABC transporter periplasmic polyamine-binding prote	12.7	4.68E-04	Vanillin	5.2	37113	7	Periplasmic	COG0687	Amino acid transport and metabolism	
26990524	PP_3819	gor	glutathione reductase	1.7	6.45E-03	Vanillin	5.2	49180	9	Cytoplasmic	COG1249	Energy production and conversion	
26990526	PP_3821	galU	UTP-glucose-1-phosphate uridylyltransferase	1.1	4.33E-01	Vanillin	5.3	30957	14	Cytoplasmic	COG1210	Cell envelope biogenesis, outer membrane	
26990537	PP_3832		carbon storage regulator	1.6	4.72E-01	Control	7.8	7271	4	Unknown	COG1551	Signal transduction mechanisms	
26990539	PP_3834		non-specific serine/threonine protein kinase	9.9	1.27E-02	Vanillin	6.6	51271	3	Cytoplasmic	COG0467	Signal transduction mechanisms	
26990544	PP_3839		alcohol dehydrogenase	13.9	4.60E-05	Vanillin	5.7	35397	15	Cytoplasmic	COG1064	General function prediction only	
26990627	PP_3922		periplasmic protease	1.1	3.51E-01	Vanillin	9.8	37502	9	Cytoplasmic Membrane	COG0616	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
26990631	PP_3926		short chain dehydrogenase	3.5	1.37E-04	Vanillin	7.4	26721	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
26990656	PP_3951	pcaI	3-oxoadipate CoA-transferase, subunit A	1349.9	3.20E-05	Vanillin	5.3	24319	7	Cytoplasmic	COG1788	Lipid metabolism	
26990657	PP_3952	pcaJ	3-oxoadipate CoA-transferase, subunit B	4442.0	9.70E-03	Vanillin	4.7	22552	5	Cytoplasmic	COG2057	Lipid metabolism	
26990659	PP_3954		periplasmic protein	14.0	1.11E-05	Vanillin	9.3	33239	12	Unknown	COG2358	General function prediction only	
26990693	PP_3988		hypothetical protein	1.4	2.16E-01	Vanillin	6.3	76259	24	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
26990702	PP_3997		hypothetical protein	1.1	2.71E-01	Vanillin	7.1	37157	8	Cytoplasmic	COG0547	Amino acid transport and metabolism	
26990703	PP_3998		glutathione S-transferase domain-containing protein	39.7	4.96E-04	Vanillin	6.6	37715	9	Cytoplasmic	COG0435	Posttranslational modification, protein turnover, chaperones	
26990704	PP_3999	cobA-2	uroporphyrin-III C-methyltransferase	1.2	6.09E-02	Control	6.8	49494	11	Cytoplasmic	COG0007	Coenzyme metabolism	
26990705	PP_4000	serS	seryl-tRNA synthetase	1.2	5.26E-02	Control	5.1	46849	18	Cytoplasmic	COG0172	Translation, ribosomal structure and biogenesis	
26990707	PP_4002		recombination factor protein RarA	1.2	9.16E-01	Control	6.1	49147	2	Cytoplasmic	COG2256	DNA replication, recombination, and repair	
26990709	PP_4004	ftsK	cell divisionFtsK/SpoIIIE	1.1	9.32E-02	Vanillin	6.4	91296	9	Cytoplasmic Membrane	COG1674	Cell division and chromosome partitioning	
26990713	PP_4008	clpA	ATP-dependent Clp protease, ATP-binding subunit clpA	1.2	2.90E-02	Vanillin	5.7	83310	30	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
26990716	PP_4011	icd	isocitrate dehydrogenase, NADP-dependent	5.7	2.64E-04	Vanillin	5.4	45695	34	Unknown	COG0538	Energy production and conversion	
26990717	PP_4012		isocitrate dehydrogenase, NADP-dependent	1.4	4.42E-02	Control	5.4	79899	53	Cytoplasmic	COG2838	Energy production and conversion	
26990719	PP_4014	mnmA	tRNA-specific 2-thiouridylase MnmA	1.3	3.44E-02	Control	5.5	41489	9	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	

26990721	PP_4016	purB	adenylosuccinate lyase	1.6	6.79E-03	Control	5.9	50555	28	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
26990722	PP_4017		cupin 4 family protein	1.5	5.54E-02	Control	4.2	44137	3	Cytoplasmic	COG2850	Function unknown	
26990726	PP_4021	est	alpha/beta hydrolase fold	18.0	7.30E-04	Vanillin	6.1	30206	5	Cytoplasmic	COG0596	General function prediction only	
26990732	PP_4029	nudC	NADH pyrophosphatase	1.6	1.25E-01	Vanillin	5.0	30868	3	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
26990733	PP_4030		enoyl-CoA hydratase	1.8	4.50E-03	Vanillin	5.2	30613	5	Cytoplasmic	COG1024	Lipid metabolism	
26990734	PP_4031	nhaB	sodium/proton antiporter	3.1	1.27E-01	Vanillin	6.7	54559	2	Cytoplasmic Membrane	COG3067	Inorganic ion transport and metabolism	
26990737	PP_4034		allantoate amidohydrolase	39.4	1.59E-04	Vanillin	5.7	45010	22	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26990738	PP_4035		NCS1 nucleoside transporter	98.0	5.83E-04	Vanillin	7.9	53519	2	Cytoplasmic Membrane	COG1953	Nucleotide transport and metabolism	Coenzyme metabolism
26990739	PP_4037		oxidoreductase	20.3	6.26E-04	Vanillin	5.5	48815	23	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26990740	PP_4038		dihydropyrimidine dehydrogenase	23.8	8.47E-05	Vanillin	5.1	46093	18	Cytoplasmic	COG0167	Nucleotide transport and metabolism	
26990742	PP_4041		glycoside hydrolase 15-related	17.9	1.27E-02	Vanillin	6.4	69769	4	Cytoplasmic	COG3387	Carbohydrate transport and metabolism	
26990744	PP_4043	gnd	6-phosphogluconate dehydrogenase	3.1	2.42E-04	Vanillin	6.4	35366	9	Cytoplasmic	COG1023	Carbohydrate transport and metabolism	
26990751	PP_4050	glgA	glycogen synthase	6.1	1.63E-04	Vanillin	6.0	57190	13	Cytoplasmic	COG0297	Carbohydrate transport and metabolism	
26990752	PP_4051		malto-oligosyltrehalose trehalohydrolase	17.6	8.21E-05	Vanillin	6.0	64544	10	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990753	PP_4052	malQ	4-alpha-glucanotransferase	31.5	5.37E-06	Vanillin	5.5	76475	24	Cytoplasmic	COG1640	Carbohydrate transport and metabolism	
26990754	PP_4053		maltooligosyl trehalose synthase	11.3	7.61E-06	Vanillin	6.6	103167	24	Cytoplasmic	COG3280	Carbohydrate transport and metabolism	
26990756	PP_4055	glgX	glycogen debranching protein GlgX	22.2	2.07E-05	Vanillin	5.1	81044	18	Cytoplasmic	COG1523	Carbohydrate transport and metabolism	
26990759	PP_4058	glgB	glycogen branching enzyme	4.6	5.32E-06	Vanillin	5.9	82877	17	Cytoplasmic	COG0296	Carbohydrate transport and metabolism	
26990760	PP_4059		trehalose synthase	19.0	1.58E-04	Vanillin	5.4	125589	4	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990761	PP_4060		alpha-amylase family protein	28.1	2.92E-05	Vanillin	6.1	75542	4	Cytoplasmic	COG0366	Carbohydrate transport and metabolism	
26990765	PP_4064	ivd	acyl-CoA dehydrogenase domain-containing protein	2.6	2.43E-03	Vanillin	7.2	46572	11	Cytoplasmic	COG1960	Lipid metabolism	
26990766	PP_4065		propionyl-CoA carboxylase	3.0	1.11E-02	Vanillin	6.9	57504	8	Cytoplasmic	COG4799	Lipid metabolism	
26990767	PP_4066		gamma-carboxygeranoyl-CoA hydratase	3.2	1.85E-03	Vanillin	5.5	30015	6	Cytoplasmic	COG1024	Lipid metabolism	
26990768	PP_4067		acetyl-CoA carboxylase, biotin carboxylase	3.5	1.81E-04	Vanillin	5.8	69729	10	Cytoplasmic	COG4770	Lipid metabolism	
26990793	PP_4098	uvrC	excinuclease ABC subunit C	1.3	3.28E-01	Vanillin	8.4	67458	3	Cytoplasmic	COG0322	DNA replication, recombination, and repair	
26990799	PP_4104		glutathione S-transferase family protein	3.5	1.84E-03	Control	7.8	26354	6	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
26990806	PP_4111	fusA	elongation factor G	9.9	7.59E-06	Vanillin	5.0	77832	21	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
26990809	PP_4115		NolW domain protein	1.4	1.82E-01	Vanillin	6.7	29306	4	Unknown			
26990810	PP_4116	aceA	isocitrate lyase	5.2	9.29E-04	Vanillin	5.3	48633	22	Cytoplasmic	COG2224	Energy production and conversion	
26990814	PP_4120	nuoB	NADH dehydrogenase subunit B	1.0	9.31E-01	Control	4.9	25523	7	Cytoplasmic Membrane	COG0377	Energy production and conversion	
26990815	PP_4121	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	1.2	2.52E-03	Control	6.5	67609	30	Cytoplasmic	COG0649	Energy production and conversion	
26990817	PP_4123	nuoF	NADH dehydrogenase I subunit F	1.3	9.07E-02	Vanillin	7.1	49135	23	Cytoplasmic	COG1894	Energy production and conversion	
26990818	PP_4124	nuoG	NADH dehydrogenase subunit G	1.2	2.60E-02	Vanillin	5.9	97582	27	Unknown	COG1034	Energy production and conversion	
26990819	PP_4125	nuoH	NADH dehydrogenase subunit H	1.1	7.22E-01	Vanillin	6.1	37637	2	Cytoplasmic Membrane	COG1005	Energy production and conversion	
26990823	PP_4129	nuoL	NADH dehydrogenase subunit L	3.6	4.42E-03	Control	9.2	66178	2	Cytoplasmic Membrane	COG1009	Energy production and conversion	Inorganic ion transport and metabolism
26990824	PP_4130	nuoM	NADH dehydrogenase subunit M	6.5	1.00E-02	Control	8.2	55614	3	Cytoplasmic Membrane	COG1008	Energy production and conversion	
26990834	PP_4141	dnaQ	DNA polymerase III subunit epsilon	1.3	4.44E-01	Vanillin	4.7	27215	2	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
26990837	PP_4144	gloB	hydroxyacylglutathione hydrolase	1.0	7.89E-01	Control	6.3	28767	5	Cytoplasmic	COG0491	General function prediction only	
26990839	PP_4146		peptide ABC transporter periplamic peptide-binding protein	1.4	2.18E-01	Control	9.9	69712	2	Periplasmic	COG4166	Amino acid transport and metabolism	
26990840	PP_4147		peptide ABC transporter periplamic peptide-binding protein	1.2	2.79E-01	Control	7.2	69637	8	Periplasmic	COG4166	Amino acid transport and metabolism	
26990842	PP_4149		binding-protein-dependent transport systems inner membrane c	1.7	2.18E-02	Vanillin	10.0	37951	2	Cytoplasmic Membrane	COG4239	General function prediction only	
26990843	PP_4150		peptide ABC transporter ATP-binding protein	1.7	4.99E-01	Control	8.4	59159	3	Cytoplasmic Membrane	COG4172	General function prediction only	
26990847	PP_4154		hypothetical protein	1.1	4.65E-01	Vanillin	5.1	99530	7	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26990851	PP_4158	kdpD	osmosensitive K+ channel signal transduction histidine kinase	8.6	2.09E-02	Vanillin	7.2	96700	3	Cytoplasmic Membrane	COG2205	Signal transduction mechanisms	
26990855	PP_4163		hypothetical protein	1.5	1.36E-01	Vanillin	5.5	28880	4	Unknown			
26990861	PP_4169	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1.0	9.67E-01	Control	6.6	36520	10	Cytoplasmic	COG0240	Energy production and conversion	
26990863	PP_4171		hypothetical protein	1.7	9.91E-02	Vanillin	4.9	79685	4	Outer Membrane	COG4771	Inorganic ion transport and metabolism	
26990865	PP_4173		integral membrane sensor hybrid histidine kinase	1.3	2.75E-01	Vanillin	5.4	70995	8	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26990867	PP_4175	fabB	3-oxoacyl-(acyl carrier protein) synthase I	1.0	8.29E-01	Vanillin	5.3	43264	17	Cytoplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26990870	PP_4178		dienelactone hydrolase	1.2	1.09E-01	Control	7.1	26269	21	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
26990871	PP_4179	htpG	heat shock protein 90	1.4	1.03E-01	Control	5.0	71610	61	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
26990877	PP_4185	sucD	succinyl-CoA synthetase subunit alpha	1.5	2.83E-03	Control	6.2	30111	23	Cytoplasmic	COG0074	Energy production and conversion	
26990878	PP_4186	sucC	succinyl-CoA synthetase subunit beta	1.6	1.03E-02	Control	6.1	41239	32	Cytoplasmic	COG0045	Energy production and conversion	
26990879	PP_4187	lpdG	dihydrolipoamide dehydrogenase	1.3	2.44E-04	Control	6.3	49912	27	Cytoplasmic	COG1249	Energy production and conversion	
26990880	PP_4188	kgdB	dihydrolipoamide succinyltransferase	1.2	5.14E-02	Control	5.1	42434	26	Cytoplasmic	COG0508	Energy production and conversion	
26990881	PP_4189	sucA	2-oxoglutarate dehydrogenase E1 component	1.2	2.95E-02	Vanillin	6.5	106521	52	Cytoplasmic	COG0567	Energy production and conversion	
26990882	PP_4190	sdhB	succinate dehydrogenase iron-sulfur subunit	1.6	5.34E-02	Vanillin	7.5	26000	17	Cytoplasmic Membrane	COG0479	Energy production and conversion	
26990883	PP_4191	sdhA	succinate dehydrogenase flavoprotein subunit	2.1	9.59E-04	Vanillin	6.2	63448	27	Cytoplasmic Membrane	COG1053	Energy production and conversion	
26990884	PP_4192	sdhD	succinate dehydrogenase, hydrophobic membrane anchor prote	1.0	9.20E-01	Vanillin	9.0	13579	3	Cytoplasmic Membrane	COG2142	Energy production and conversion	
26990886	PP_4194	gltA	type II citrate synthase	1.0	9.64E-01	Vanillin	7.0	47622	30	Cytoplasmic	COG0372	Energy production and conversion	
26990889	PP_4197		GntR family transcriptional regulator	1.4	2.43E-01	Vanillin	8.8	59302	6	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
26990890	PP_4198		OmpA/MotB domain protein	1.3	8.47E-02	Control	8.9	29694	6	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
26990892	PP_4200		hypothetical protein	1.3	1.71E-01	Control	8.1	29611	6	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26990893	PP_4201		electron transfer flavoprotein, alpha subunit	1.2	1.50E-01	Control	4.9	31237	16	Unknown	COG2025	Energy production and conversion	
26990894	PP_4202		electron transfer flavoprotein, beta subunit	1.5	2.36E-02	Control	9.7	26361	17	Unknown	COG2086	Energy production and conversion	
26990895	PP_4203		electron-transferring-flavoprotein dehydrogenase	2.6	1.97E-02	Vanillin	5.7	61082	19	Cytoplasmic	COG0644	Energy production and conversion	
26990901	PP_4209		efflux transporter RND family, MFP subunit	6.0	4.97E-04	Control	9.4	41974	9	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26990902	PP_4210		efflux ABC transporter ATP-binding protein	3.0	5.48E-03	Control	7.3	69687	4	Cytoplasmic Membrane	COG1136	Defense mechanisms	
26990903	PP_4211		RND efflux transporter	2.4	1.18E-02	Control	8.2	51199	14	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26990904	PP_4212		hypothetical protein	3.0	3.69E-03	Control	7.1	62081	12	Cytoplasmic			
26990905	PP_4213		dipeptidase	1.7	9.58E-03	Control	5.0	50104	15	Unknown	COG2355	Amino acid transport and metabolism	
26990906	PP_4214		aminotransferase, class V	3.0	1.13E-03	Control	7.6	47747	18	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
26990907	PP_4215		hypothetical protein	2.1	2.00E-03	Control	6.2	32723	7	Unknown	COG1262	Function unknown	
26990908	PP_4216	pvdE	cyclic peptide transporter	2.0	2.30E-03	Control	7.4	61169	18	Cytoplasmic Membrane	COG4615	Secondary metabolites biosynthesis, transport, and catabolism	Inorganic ion transport and metabolism
26990909	PP_4217	fpvA	outer membrane ferripyoverdine receptor	1.4	4.66E-02	Control	5.5	89725	45	Outer Membrane	COG4773	Inorganic ion transport and metabolism	
26990910	PP_4218		lipase/esterase family protein	1.2	3.67E-01	Control	4.6	34239	10	Cytoplasmic	COG0657	Lipid metabolism	
26990911	PP_4219	ppsD	non-ribosomal siderophore peptide synthetase	2.5	2.13E-03	Control	5.5	382081	107	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990912	PP_4220		non-ribosomal peptide synthetase	1.9	5.32E-03	Control	5.2	287552	101	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	

26990913	PP_4221		non-ribosomal peptide synthetase	2.2	1.82E-03	Control	5.7	236392	65	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990914	PP_4222		syrP protein	1.6	5.35E-02	Control	4.8	36904	13	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
26990915	PP_4223		diaminobutyrate--2-oxoglutarate aminotransferase	2.2	1.42E-02	Control	7.0	48859	32	Cytoplasmic	COG0160	Amino acid transport and metabolism	
26990934	PP_4243		peptide synthase	2.2	1.71E-03	Control	5.3	475264	142	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
26990946	PP_4255	ccoN-2	cbb3-type cytochrome c oxidase subunit I	4.0	1.92E-03	Vanillin	9.6	53567	3	Cytoplasmic Membrane	COG3278	Posttranslational modification, protein turnover, chaperones	
26990949	PP_4258	ccoP-2	cytochrome c oxidase, cbb3-type, subunit III	13.2	3.43E-04	Vanillin	5.2	35613	12	Unknown	COG2010	Energy production and conversion	
26990952	PP_4261		heavy metal translocating P-type ATPase	23.4	2.93E-03	Vanillin	7.2	94969	3	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
26990955	PP_4264	hemN	coproporphyrinogen III oxidase	23.4	1.89E-02	Vanillin	6.0	52607	7	Cytoplasmic	COG0635	Coenzyme metabolism	
26990956	PP_4265	anr	transcriptional regulator Anr	1.1	3.99E-01	Control	6.5	27221	6	Cytoplasmic	COG0664	Signal transduction mechanisms	
26990957	PP_4266	apt	adenine phosphoribosyltransferase	3.1	5.36E-03	Control	4.6	20018	4	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
26990958	PP_4267	recR	recombination protein RecR	1.2	5.40E-01	Control	6.0	21613	2	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
26990960	PP_4269	dnaX	DNA polymerase III subunits gamma and tau	1.1	4.05E-01	Vanillin	4.4	74471	5	Cytoplasmic	COG2812	DNA replication, recombination, and repair	
26990965	PP_4274	ligA	NAD-dependent DNA ligase LigA	1.3	2.88E-01	Vanillin	5.3	84112	20	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
26990966	PP_4275	zipA	cell division protein ZipA	1.3	2.38E-01	Vanillin	6.0	35312	12	Cytoplasmic Membrane	COG3115	Cell division and chromosome partitioning	
26990967	PP_4276		chromosome segregation protein SMC	83.1	4.89E-04	Vanillin	4.7	131729	6	Cytoplasmic	COG1196	Cell division and chromosome partitioning	
26990969	PP_4278	xdhA	xanthine dehydrogenase, XdhA subunit	45.3	2.12E-04	Vanillin	6.1	53174	3	Cytoplasmic	COG4630	Nucleotide transport and metabolism	
26990970	PP_4279	xdhB	xanthine dehydrogenase, XdhB subunit	37.2	8.05E-04	Vanillin	6.4	88031	4	Cytoplasmic	COG4631	Nucleotide transport and metabolism	
26990972	PP_4281	gad	guanine deaminase	3.7	1.30E-03	Vanillin	5.3	48084	4	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
26990974	PP_4283		GntR family transcriptional regulator	1.2	3.68E-02	Control	6.8	27912	8	Cytoplasmic	COG1802	Transcription	
26990977	PP_4286		polysaccharide deacetylase family protein	2.8	1.23E-02	Vanillin	5.9	35315	4	Cytoplasmic	COG0726	Carbohydrate transport and metabolism	
26990989	PP_4298	hyi	hydroxypyruvate isomerase	1.9	1.92E-02	Vanillin	5.0	29057	5	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
26990990	PP_4299	glxR	2-hydroxy-3-oxopropionate reductase	2.2	4.63E-03	Vanillin	6.6	30864	14	Cytoplasmic	COG2084	Lipid metabolism	
26990996	PP_4305		sulfate ABC transporter periplasmic sulfate-binding protein	1.5	8.30E-04	Vanillin	6.3	36692	13	Periplasmic	COG1613	Inorganic ion transport and metabolism	
26990997	PP_4306		hypothetical protein	1.4	1.07E-02	Control	6.3	35472	4	Cytoplasmic	COG1092	General function prediction only	
26991006	PP_4315		PhzF family phenazine biosynthesis protein	1.3	1.06E-01	Vanillin	4.5	28437	10	Cytoplasmic	COG0384	General function prediction only	
26991007	PP_4316		2-hydroxyacid dehydrogenase	2.0	1.54E-03	Vanillin	6.3	32995	7	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
26991027	PP_4337	cheB	chemotaxis-specific methylesterase	1.4	5.50E-03	Control	9.0	39451	9	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
26991028	PP_4338	cheA	chemotaxis protein CheA	1.5	1.65E-03	Vanillin	4.4	79674	16	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991029	PP_4339	cheZ	chemotaxis phosphatase, CheZ	1.1	5.15E-01	Vanillin	4.8	29533	9	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
26991031	PP_4341	fliA	flagellar biosynthesis sigma factor	1.2	5.80E-01	Control	5.1	27595	3	Cytoplasmic	COG1191	Transcription	
26991032	PP_4342	fleN	flagellar number regulator FleN	1.2	2.38E-01	Vanillin	8.0	29670	7	Cytoplasmic Membrane	COG0455	Cell motility	
26991033	PP_4343	flhF	flagellar biosynthesis regulator FlhF	1.1	6.78E-01	Control	6.1	47446	4	Unknown	COG1419	Cell motility and secretion	
26991034	PP_4344	flhA	flagellar biosynthesis protein FlhA	1.6	1.85E-01	Control	6.9	76003	2	Cytoplasmic Membrane	COG1298	Cell motility and secretion	Intracellular trafficking and secretion
26991035	PP_4345		GntR family transcriptional regulator	1.8	4.34E-02	Control	6.5	26216	6	Cytoplasmic	COG1802	Transcription	
26991047	PP_4358	fliM	flagellar motor switch protein FliM	1.3	1.48E-01	Control	5.1	36011	8	Cytoplasmic	COG1868	Cell motility and secretion	
26991050	PP_4361	fliK	flagellar hook-length control protein	1.3	3.94E-01	Vanillin	4.4	43396	2	Extracellular	COG3144	Cell motility and secretion	
26991058	PP_4369	fliF	flagellar MS-ring protein	1.1	7.31E-01	Vanillin	4.5	63090	12	Cytoplasmic Membrane	COG1766	Cell motility and secretion	
26991062	PP_4373	fleQ	sigma54 specific transcriptional regulator, Fis family	1.2	1.39E-01	Vanillin	5.4	55551	10	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991065	PP_4376	fliD	flagellar cap protein FliD	1.1	6.02E-01	Vanillin	5.2	46522	10	Extracellular	COG1345	Cell motility and secretion	
26991067	PP_4378	fliC	flagellin FliC	1.3	1.07E-01	Control	4.2	67846	23	Extracellular	COG1344	Cell motility and secretion	
26991068	PP_4379		beta-ketoacyl-acyl-carrier-protein synthase I	1.1	2.61E-01	Vanillin	4.8	33207	14	Cytoplasmic	COG0332	acyl-carrier-protein	
26991069	PP_4380	flgL	flagellar hook-associated protein FlgL	1.1	4.72E-01	Control	4.3	54938	6	Extracellular	COG1344	Cell motility and secretion	
26991070	PP_4381	flgK	flagellar hook-associated protein FlgK	1.2	3.42E-01	Vanillin	4.5	69628	11	Extracellular	COG1256	Cell motility and secretion	
26991077	PP_4388	flgE	flagellar hook protein FlgE	2.0	1.45E-02	Control	4.3	45796	6	Extracellular	COG1749	Cell motility and secretion	
26991081	PP_4392	cheR	chemotaxis protein methyltransferase CheR	1.4	5.22E-02	Control	9.3	31084	11	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
26991082	PP_4393	cheV-3	chemotaxis protein CheV	1.2	1.28E-01	Control	6.2	34498	12	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
26991086	PP_4397		type IV pilus assembly PilZ	1.2	2.52E-01	Control	6.7	28449	19	Cytoplasmic	COG5581	Signal transduction mechanisms	
26991088	PP_4399		glutamine synthetase	5.0	1.70E-02	Vanillin	6.2	45023	4	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991109	PP_4421		hypothetical protein	2.3	4.85E-03	Control	6.5	50295	12	Cytoplasmic	COG0161	Coenzyme metabolism	
26991116	PP_4428		amino acid ABC transporter periplasmic amino acid-binding prot	26.9	6.45E-04	Vanillin	5.8	30355	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991120	PP_4432		peptidase, M24 family protein	1.3	5.34E-01	Vanillin	5.6	41581	3	Cytoplasmic	COG0006	Amino acid transport and metabolism	
26991133	PP_4447		hypothetical protein	1.4	5.94E-02	Control	8.5	47496	7	Cytoplasmic			
26991134	PP_4448		hypothetical protein	1.1	5.76E-01	Control	6.0	66331	30	Cytoplasmic	COG0433	Replication, recombination, and repair	
26991146	PP_4460		LysR family transcriptional regulator	1.2	4.16E-01	Control	10.3	34163	3	Cytoplasmic	COG0583	Transcription	
26991159	PP_4473		aspartate kinase	1.6	8.84E-03	Control	5.0	44605	22	Cytoplasmic	COG0527	Amino acid transport and metabolism	
26991160	PP_4474	alaS	alanyl-tRNA synthetase	1.1	2.23E-01	Vanillin	5.1	94711	42	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
26991161	PP_4475	astE	succinylglutamate desuccinylase	3.0	1.60E-05	Vanillin	6.2	37580	11	Cytoplasmic	COG2988	Amino acid transport and metabolism	
26991163	PP_4477	astB	succinylarginine dihydrolase	1.6	3.92E-03	Vanillin	6.4	48862	13	Cytoplasmic	COG3724	Amino acid transport and metabolism	
26991164	PP_4478	astD	succinylglutamic semialdehyde dehydrogenase	1.5	1.88E-02	Vanillin	5.4	51330	7	Cytoplasmic	COG1012	Energy production and conversion	
26991165	PP_4479	aruG	arginine N-succinyltransferase, beta subunit	1.4	5.77E-02	Vanillin	7.0	37782	8	Cytoplasmic	COG3138	Amino acid transport and metabolism	
26991166	PP_4480	aruF	arginine N-succinyltransferase, alpha subunit	1.0	8.33E-01	Control	4.6	37061	3	Cytoplasmic	COG3138	Amino acid transport and metabolism	
26991167	PP_4481	argD	bifunctional N-succinyldiaminopimelate-aminotransferase/acety	1.3	1.31E-01	Control	6.5	43490	22	Cytoplasmic	COG4992	Amino acid transport and metabolism	
26991168	PP_4482		AraC family transcriptional regulator	1.5	8.85E-02	Vanillin	7.6	36306	5	Cytoplasmic Membrane	COG4977	Transcription	
26991169	PP_4483		basic amino acid ABC transporter ATP-binding protein	1.3	1.86E-01	Vanillin	7.8	28000	10	Cytoplasmic Membrane	COG4598	Amino acid transport and metabolism	
26991172	PP_4486		cationic amino acid ABC transporter periplasmic protein	2.0	1.02E-02	Vanillin	8.1	28302	10	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991173	PP_4487	acsA	acetyl-CoA synthetase	4.8	1.57E-03	Vanillin	6.4	71796	36	Cytoplasmic	COG0365	Lipid metabolism	
26991179	PP_4493		FAD linked oxidase domain protein	1.3	1.44E-01	Vanillin	7.2	110944	22	Cytoplasmic	COG0277	Energy production and conversion	
26991182	PP_4497		hypothetical protein	1.9	4.29E-02	Vanillin	4.4	31510	2	Cytoplasmic	COG1386	DNA replication, recombination and repair	
26991193	PP_4508		AraC family transcriptional regulator	3.5	9.60E-03	Vanillin	6.8	39367	6	Cytoplasmic	COG2207	Transcription	
26991201	PP_4516	recQ	ATP-dependent DNA helicase RecQ	1.3	5.89E-01	Vanillin	5.5	79266	5	Cytoplasmic	COG0514	DNA replication, recombination, and repair	
26991204	PP_4519	tolC	TolC family type I secretion outer membrane protein	1.4	3.56E-02	Vanillin	5.4	50393	31	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991206	PP_4521		aerotaxis receptor	5.0	3.75E-04	Vanillin	6.4	56605	11	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991217	PP_4532		DEAD-box ATP dependent DNA helicase	1.3	6.06E-02	Control	10.3	48478	16	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991218	PP_4533		MscS mechanosensitive ion channel	7.4	8.54E-03	Control	8.1	48784	2	Cytoplasmic Membrane	COG0668	Cell envelope biogenesis, outer membrane	
26991220	PP_4535		hypothetical protein	1.0	8.74E-01	Vanillin	6.4	75326	11	Cytoplasmic			
26991222	PP_4538		NAD(P)H dehydrogenase (quinone)	111.1	7.97E-02	Vanillin	6.5	21716	5	Cytoplasmic	COG1182	Lipid metabolism	
26991223	PP_4539		LysR family transcriptional regulator	1.8	3.84E-02	Control	7.1	33901	6	Cytoplasmic	COG0583	Transcription	
26991226	PP_4542		ABC transporter ATP-binding protein/permease	1.9	4.78E-02	Control	7.6	67748	2	Cytoplasmic Membrane	COG1132	Defense mechanisms	

26991229	PP_4545		3-oxoacyl-(acyl carrier protein) synthase III	1.2	2.15E-01	Vanillin	5.7	42326	15	Cytoplasmic	COG0332	acyl-carrier-protein	
26991230	PP_4546	hrpA	ATP-dependent helicase HrpA	1.2	1.21E-01	Vanillin	8.3	146950	16	Cytoplasmic	COG1643	DNA replication, recombination, and repair	
26991233	PP_4549	fadD	long-chain-fatty-acid--CoA ligase	2.3	6.64E-03	Vanillin	7.7	61812	17	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991234	PP_4550	fadD2	long-chain-fatty-acid--CoA ligase	7.8	2.63E-03	Vanillin	7.8	61658	10	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
26991247	PP_4563		RNA binding S1 domain protein	1.5	3.39E-02	Control	6.8	30959	3	Cytoplasmic	COG2996	General function prediction only	
26991249	PP_4565	aceK	bifunctional isocitrate dehydrogenase kinase/phosphatase prote	34.4	5.63E-02	Vanillin	5.3	65954	2	Cytoplasmic	COG4579	Signal transduction mechanisms	
26991254	PP_4570		hypothetical protein	1.3	8.74E-02	Vanillin	10.1	35846	15	Cytoplasmic Membrane	COG3555	Posttranslational modification, protein turnover, chaperones	
26991255	PP_4571	cysK	cysteine synthase A	1.4	8.36E-02	Vanillin	5.5	34357	16	Cytoplasmic	COG0031	Amino acid transport and metabolism	
26991257	PP_4573		ATPase AAA	1.2	1.51E-01	Vanillin	5.8	32146	16	Cytoplasmic	COG0714	General function prediction only	
26991258	PP_4574		hypothetical protein	10.5	7.40E-03	Vanillin	6.8	45721	3	Cytoplasmic	COG3825	Function unknown	
26991259	PP_4575		urea amidolyase related protein	2.3	5.52E-03	Vanillin	5.3	32471	2	Cytoplasmic	COG1984	Amino acid transport and metabolism	
26991265	PP_4581		hypothetical protein	2.0	1.10E-03	Vanillin	6.2	28647	3	Cytoplasmic	COG0121	General function prediction only	
26991267	PP_4583		oligopeptidase B	1.6	2.56E-02	Vanillin	4.7	75818	14	Unknown	COG1770	Amino acid transport and metabolism	
26991270	PP_4586		hypothetical protein	1.0	8.48E-01	Vanillin	10.4	44637	3	Unknown	COG3975	General function prediction only	
26991275	PP_4591	rnd	ribonuclease D	1.4	2.26E-01	Control	5.5	42668	7	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
26991278	PP_4594		cystathionine gamma-lyase	1.4	4.05E-01	Control	6.4	42503	6	Cytoplasmic	COG0626	Amino acid transport and metabolism	
26991280	PP_4596		molybdopterin oxidoreductase, alpha subunit	120.9	4.99E-03	Vanillin	6.4	85593	8	Cytoplasmic	COG0243	Energy production and conversion	
26991286	PP_4602		AraC family transcriptional regulator	2.8	7.86E-03	Vanillin	8.9	31224	4	Cytoplasmic	COG2207	Transcription	
26991304	PP_4620		fumarylacetoacetase	3.0	2.91E-04	Vanillin	5.9	46325	6	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
26991306	PP_4622		IclR family transcriptional regulator	1.0	9.96E-01	Control	6.9	29036	4	Cytoplasmic	COG1414	Transcription	
26991319	PP_4635		trans-2-enoyl-CoA reductase	1.1	4.21E-01	Control	5.0	44265	23	Cytoplasmic	COG3007	Function unknown	
26991321	PP_4637		5-methyltetrahydropteroyltriglutamate-- homocysteine S-methy	6.5	2.85E-04	Control	4.9	30363	4	Cytoplasmic	COG0620	Amino acid transport and metabolism	
26991323	PP_4639		CobW/P47K family protein	1.2	8.79E-02	Vanillin	4.6	35444	10	Cytoplasmic	COG0523	General function prediction only	
26991325	PP_4641	cstA	carbon starvation protein CstA	2.2	2.43E-03	Vanillin	9.0	73763	10	Cytoplasmic Membrane	COG1966	Signal transduction mechanisms	
26991328	PP_4644	radA	DNA repair protein RadA	1.1	6.52E-01	Vanillin	6.9	48741	6	Unknown	COG1066	Posttranslational modification, protein turnover, chaperones	
26991330	PP_4646		oxidoreductase FAD/NAD(P)-binding domain protein	1.4	1.67E-02	Control	5.2	28960	9	Cytoplasmic	COG1018	Energy production and conversion	
26991335	PP_4651	cioA	ubiquinol oxidase subunit I, cyanide insensitive	2.8	1.69E-02	Vanillin	9.1	53016	2	Cytoplasmic Membrane	COG1271	Energy production and conversion	
26991338	PP_4654	trmA	tRNA (uracil-5-)-methyltransferase	1.3	3.19E-01	Control	5.7	40878	7	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis	
26991340	PP_4656	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	105.7	2.17E-05	Vanillin	9.4	26835	15	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
26991341	PP_4657		metallopeptidase, zinc binding	11.0	4.05E-03	Vanillin	6.7	34400	4	Unknown	COG2321	General function prediction only	
26991342	PP_4658		methyl-accepting chemotaxis sensory transducer	3.5	5.24E-03	Control	4.8	68764	12	Unknown	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991343	PP_4659	ggt-2	gamma-glutamyltransferase	14.8	1.14E-05	Vanillin	6.0	59835	14	Periplasmic	COG0405	Amino acid transport and metabolism	
26991350	PP_4666	mmsB	3-hydroxyisobutyrate dehydrogenase	11.3	5.30E-04	Vanillin	6.1	30321	6	Cytoplasmic	COG2084	Lipid metabolism	
26991351	PP_4667	mmsA-2	methylmalonate-semialdehyde dehydrogenase	8.1	1.30E-03	Vanillin	6.0	54367	9	Cytoplasmic	COG1012	Energy production and conversion	
26991356	PP_4672	recD	exodeoxyribonuclease V, alpha subunit	6.1	2.15E-02	Vanillin	7.2	75545	6	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
26991361	PP_4677	pssA-2	CDP-diacylglycerol--serine O-phosphatidyltransferase	1.0	9.71E-01	Control	9.2	30359	2	Cytoplasmic Membrane	COG1183	Lipid metabolism	
26991362	PP_4678	ilvC	ketol-acid reductoisomerase	1.6	1.95E-03	Control	5.4	36370	27	Cytoplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
26991364	PP_4680	ilvB	acetolactate synthase 3 catalytic subunit	1.3	2.55E-01	Control	6.8	62781	38	Cytoplasmic	COG0028	Amino acid transport and metabolism	Coenzyme metabolism
26991366	PP_4682		hypothetical protein	1.2	4.62E-01	Control	8.2	27215	5	Unknown	COG4783	General function prediction only	
26991367	PP_4683	mrcB	penicillin-binding protein 1B	2.6	1.90E-02	Vanillin	9.5	85156	9	Cytoplasmic Membrane	COG0744	Cell envelope biogenesis, outer membrane	
26991368	PP_4684		hypothetical protein	1.4	1.41E-02	Control	5.1	56095	15	Cytoplasmic	COG2187	Function unknown	
26991373	PP_4689		periplasmic protein	1.1	4.06E-01	Control	7.1	30685	9	Periplasmic	COG4558	Inorganic ion transport and metabolism	
26991376	PP_4692		hypothetical protein	1.1	2.48E-01	Vanillin	6.5	42505	7	Cytoplasmic	COG0436	Amino acid transport and metabolism	
26991378	PP_4694		glutamyl-Q tRNA(Asp) synthetase	1.1	8.04E-01	Control	6.7	33736	5	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
26991380	PP_4696		two component, sigma54 specific, transcriptional regulator, Fis f	1.1	5.61E-01	Vanillin	5.3	52585	10	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991381	PP_4697	pcnB	poly(A) polymerase	1.6	8.75E-02	Vanillin	9.6	52721	8	Cytoplasmic	COG0617	Translation, ribosomal structure and biogenesis	
26991383	PP_4699	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.7	3.42E-04	Vanillin	5.8	27762	7	Unknown	COG0413	Coenzyme metabolism	
26991384	PP_4700	panC	pantoate--beta-alanine ligase	1.6	2.06E-02	Vanillin	7.7	31189	12	Cytoplasmic	COG0414	Coenzyme metabolism	
26991385	PP_4701	pgi	glucose-6-phosphate isomerase	1.6	4.10E-02	Vanillin	6.8	61455	14	Cytoplasmic	COG0166	Carbohydrate transport and metabolism	
26991386	PP_4702	acsB	acetyl-CoA synthetase	33.4	1.24E-04	Vanillin	6.5	71251	9	Cytoplasmic	COG0365	Lipid metabolism	
26991388	PP_4704		hypothetical protein	3.3	1.79E-03	Vanillin	5.6	107252	18	Outer Membrane	COG2982	Cell envelope biogenesis, outer membrane	
26991392	PP_4708	pnp	polynucleotide phosphorylase/polyadenylase	1.1	4.55E-01	Vanillin	4.9	75010	37	Cytoplasmic	COG1185	Translation, ribosomal structure and biogenesis	
26991395	PP_4712	infB	translation initiation factor IF-2	1.1	4.70E-02	Vanillin	6.8	91460	46	Cytoplasmic	COG0532	Translation, ribosomal structure and biogenesis	
26991396	PP_4713	nusA	transcription elongation factor NusA	1.2	2.51E-02	Control	4.3	54673	22	Cytoplasmic	COG0195	Transcription	
26991398	PP_4715	tpiA	triosephosphate isomerase	1.3	7.88E-02	Control	4.7	25991	7	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
26991399	PP_4716	glmM	phosphoglucosamine mutase	1.6	9.64E-03	Control	6.0	47744	18	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991400	PP_4717	folP	dihydropteroate synthase	1.5	3.23E-02	Control	5.4	30274	7	Cytoplasmic	COG0294	Coenzyme metabolism	
26991401	PP_4718	ftsH	ATP-dependent metalloprotease FtsH	1.0	8.53E-01	Vanillin	5.4	69722	23	Cytoplasmic Membrane	COG0465	Posttranslational modification, protein turnover, chaperones	
26991407	PP_4724	carA	carbamoyl phosphate synthase small subunit	1.3	1.01E-01	Control	5.8	40574	9	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
26991408	PP_4725	dapB	dihydrodipicolinate reductase	1.4	2.68E-02	Control	5.9	28423	17	Cytoplasmic	COG0289	Amino acid transport and metabolism	
26991409	PP_4726	dnaJ	chaperone protein DnaJ	1.9	8.14E-03	Control	6.7	40181	16	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
26991410	PP_4727	dnaK	molecular chaperone DnaK	1.3	1.83E-01	Control	4.6	68800	56	Cytoplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
26991411	PP_4728	grpE	heat shock protein GrpE	2.3	2.86E-01	Control	4.7	20531	3	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
26991412	PP_4729	recN	DNA repair protein RecN	13.1	1.32E-02	Vanillin	5.3	60898	9	Cytoplasmic	COG0497	DNA replication, recombination, and repair	
26991414	PP_4731	omlA	SmpA/OmlA domain protein	1.6	1.06E-01	Control	4.4	19586	7	Outer Membrane	COG2913	Cell envelope biogenesis, outer membrane	
26991419	PP_4736	lldD	L-lactate dehydrogenase	1.2	2.12E-01	Vanillin	8.9	41391	2	Cytoplasmic	COG1304	Coenzyme transport and metabolism	
26991423	PP_4740	hsdR	type I restriction-modification system, R subunit	2.0	4.06E-02	Vanillin	5.2	89615	17	Cytoplasmic	COG4096	Defense mechanisms	
26991424	PP_4741	hsdM	type I restriction-modification system, M subunit	2.0	1.23E-02	Control	5.4	55775	12	Cytoplasmic	COG0286	Defense mechanisms	
26991425	PP_4742	hsdS	type I restriction-modification system, S subunit	1.4	3.69E-01	Control	6.5	62995	6	Cytoplasmic	COG0732	Defense mechanisms	
26991429	PP_4748		amino acid ABC transporter periplasmic amino acid-binding prot	7.4	1.55E-04	Vanillin	5.4	28338	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991434	PP_4753		N-methylproline demethylase	11.6	7.22E-05	Vanillin	6.5	75215	13	Cytoplasmic	COG1902	Energy production and conversion	
26991441	PP_4760		alcohol dehydrogenase, zinc-containing	3.7	2.34E-03	Vanillin	6.2	35615	8	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
26991443	PP_4762	tesB	acyl-CoA thioesterase II	5.3	4.53E-02	Vanillin	6.1	32319	3	Cytoplasmic	COG1946	Lipid metabolism	
26991447	PP_4766		DEAD-box ATP dependent DNA helicase	1.4	2.51E-01	Control	10.4	48823	4	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991460	PP_4780		acyl-CoA dehydrogenase domain-containing protein	7.8	1.64E-04	Vanillin	6.6	59803	3	Cytoplasmic	COG1960	Lipid metabolism	
26991462	PP_4782	thiD	phosphomethylpyrimidine kinase	1.2	4.53E-02	Control	5.1	28338	6	Cytoplasmic	COG0351	Coenzyme metabolism	
26991464	PP_4784	hemL	glutamate-1-semialdehyde aminotransferase	1.4	5.00E-03	Control	5.7	45178	16	Cytoplasmic	COG0001	Coenzyme metabolism	
26991467	PP_4787		PhoH family protein	1.6	8.42E-03	Control	7.0	37501	11	Cytoplasmic	COG1702	Signal transduction mechanisms	

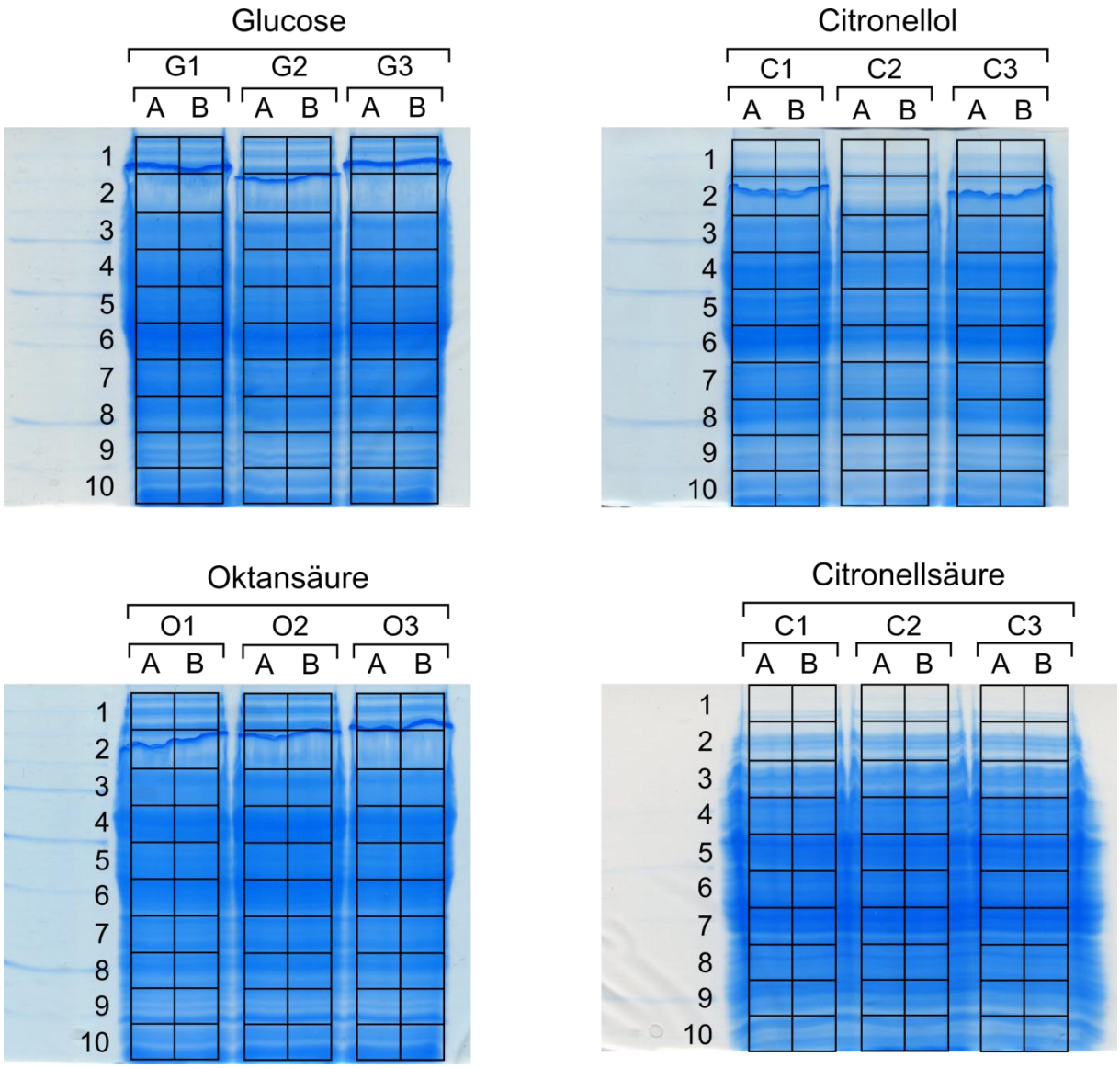
26991469	PP_4789		CBS domain containing protein	1.4	9.63E-03	Control	4.7	31393	9	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism	
26991470	PP_4790	lnt	apolipoprotein N-acyltransferase	4.7	4.18E-02	Control	8.5	56126	2	Cytoplasmic Membrane	COG0815	Cell envelope biogenesis, outer membrane	
26991474	PP_4794	leuS	leucyl-tRNA synthetase	1.2	3.50E-01	Control	5.6	96697	40	Cytoplasmic	COG0495	Translation, ribosomal structure and biogenesis	
26991476	PP_4796	holA	DNA polymerase III subunit delta	1.0	8.37E-01	Vanillin	6.9	37518	2	Unknown	COG1466	DNA replication, recombination, and repair	
26991478	PP_4798		lytic murein transglycosylase	1.4	6.79E-02	Control	7.7	48000	8	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991479	PP_4799		muramoyltetrapeptide carboxypeptidase	1.1	9.29E-02	Control	6.5	33219	3	Cytoplasmic	COG1619	Defense mechanisms	
26991480	PP_4800	lipA	lipoyl synthase	1.7	4.93E-03	Control	7.1	37956	13	Cytoplasmic	COG0320	Coenzyme metabolism	
26991483	PP_4803	dacA	serine-type D-Ala-D-Ala carboxypeptidase	1.4	8.27E-02	Control	6.6	42288	20	Cytoplasmic Membrane	COG1686	Cell envelope biogenesis, outer membrane	
26991484	PP_4804		rare lipoprotein A family	1.6	5.94E-02	Control	10.0	35869	7	Unknown	COG0797	Cell envelope biogenesis, outer membrane	
26991485	PP_4805	mltB	lytic murein transglycosylase B	1.7	2.21E-02	Control	6.0	39145	3	Cytoplasmic Membrane	COG2951	Cell envelope biogenesis, outer membrane	
26991487	PP_4807	mrdA-2	penicillin-binding protein 2	1.8	9.30E-02	Control	9.5	70229	3	Cytoplasmic Membrane	COG0768	Cell envelope biogenesis, outer membrane	
26991491	PP_4811	proA	gamma-glutamyl phosphate reductase	1.2	2.63E-01	Control	6.1	45417	16	Cytoplasmic	COG0014	Amino acid transport and metabolism	
26991499	PP_4819		Zinc finger-domain-containing protein	1.2	1.42E-01	Vanillin	4.5	49827	6	Cytoplasmic			
26991500	PP_4820		NifR3 family TIM-barrel protein	1.9	3.53E-01	Control	8.0	36488	2	Cytoplasmic	COG0042	Translation, ribosomal structure and biogenesis	
26991502	PP_4822	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyl	2.3	1.47E-03	Control	6.5	57695	30	Cytoplasmic	COG0138	Nucleotide transport and metabolism	
26991503	PP_4823	purD	phosphoribosylamine--glycine ligase	1.6	1.16E-05	Control	4.7	45837	17	Cytoplasmic	COG0151	Nucleotide transport and metabolism	
26991504	PP_4824		integral membrane sensor hybrid histidine kinase	1.8	7.69E-02	Vanillin	6.6	101587	11	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26991506	PP_4826	cobJ	precorrin-3B C17-methyltransferase	1.1	8.94E-01	Control	5.8	59159	7	Cytoplasmic	COG1010	Coenzyme metabolism	
26991507	PP_4827	cobI	precorrin-2 C(20)-methyltransferase	1.3	4.68E-01	Control	5.4	26691	3	Cytoplasmic	COG2243	Coenzyme metabolism	
26991514	PP_4834		SPFH domain-containing protein/band 7 family protein	2.3	1.69E-04	Control	5.0	31015	8	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991518	PP_4838	oprC	TonB-dependent copper receptor	42.6	1.83E-04	Vanillin	6.2	74540	28	Outer Membrane	COG1629	Inorganic ion transport and metabolism	
26991519	PP_4839		hypothetical protein	310.5	2.62E-02	Vanillin	9.6	50581	4	Cytoplasmic Membrane	COG3182	Function unknown	
26991528	PP_4848		DnaJ family curved-DNA-binding protein	1.9	1.58E-02	Vanillin	9.8	34808	15	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
26991540	PP_4860		N-acylglucosamine 2-epimerase	1.0	9.24E-01	Control	5.7	42193	4	Cytoplasmic	COG2942	Carbohydrate transport and metabolism	
26991542	PP_4862		short chain dehydrogenase/reductase family oxidoreductase	1.4	1.13E-01	Vanillin	6.3	27400	10	Cytoplasmic	COG4221	General function prediction only	
26991543	PP_4863		branched chain amino acid ABC transporter ATP-binding protein	8.8	1.59E-02	Vanillin	9.3	26312	4	Unknown	COG0410	Amino acid transport and metabolism	
26991544	PP_4864		branched chain amino acid ABC transporter ATP-binding protein	5.9	2.03E-02	Vanillin	6.6	32427	3	Cytoplasmic Membrane	COG0411	Amino acid transport and metabolism	
26991547	PP_4867		extracellular ligand-binding receptor	8.1	7.11E-04	Vanillin	6.2	40270	21	Periplasmic	COG0683	Amino acid transport and metabolism	
26991548	PP_4868	pncB	nicotinate phosphoribosyltransferase	1.9	1.37E-01	Control	6.4	46349	2	Cytoplasmic	COG1488	Coenzyme metabolism	
26991549	PP_4869	nadE	NAD synthetase	1.0	6.90E-01	Control	5.6	29273	13	Cytoplasmic	COG0171	Coenzyme metabolism	
26991553	PP_4873	dnaB	replicative DNA helicase	1.7	3.95E-02	Vanillin	4.7	51581	10	Cytoplasmic	COG0305	DNA replication, recombination, and repair	
26991554	PP_4874	rplI	50S ribosomal protein L9	19.7	1.42E-03	Control	5.3	15466	4	Cytoplasmic	COG0359	Translation, ribosomal structure and biogenesis	
26991558	PP_4879		RNA methyltransferase	1.2	7.22E-02	Vanillin	6.8	27014	6	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis	
26991559	PP_4880	vacB	ribonuclease R	1.5	2.47E-02	Vanillin	7.9	96688	27	Cytoplasmic	COG0557	Transcription	
26991560	PP_4881		iron ABC transporter periplasmic iron-binding protein	1.2	3.14E-01	Vanillin	5.0	36800	18	Periplasmic	COG1840	Inorganic ion transport and metabolism	
26991566	PP_4888		methyl-accepting chemotaxis sensory transducer	2.3	9.71E-03	Vanillin	6.1	71958	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991567	PP_4889	purA	adenylosuccinate synthetase	1.1	1.06E-01	Control	5.6	46833	18	Cytoplasmic	COG0104	Nucleotide transport and metabolism	
26991568	PP_4890	hisZ	ATP phosphoribosyltransferase regulatory subunit	1.8	4.01E-02	Control	4.7	42935	14	Cytoplasmic	COG3705	Amino acid transport and metabolism	
26991569	PP_4891	hflC	HflC protein	1.2	3.88E-01	Vanillin	9.8	33001	20	Cytoplasmic	COG0330	Posttranslational modification, protein turnover, chaperones	
26991570	PP_4892	hflK	HflK protein	1.3	4.46E-02	Vanillin	5.1	44762	21	Unknown	COG0330	Posttranslational modification, protein turnover, chaperones	
26991573	PP_4895	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	1.3	4.07E-01	Vanillin	7.1	35447	2	Cytoplasmic	COG0324	Translation, ribosomal structure and biogenesis	
26991574	PP_4896	mutL	DNA mismatch repair protein	1.2	1.86E-01	Vanillin	6.7	69745	9	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
26991575	PP_4897		N-acetylmuramoyl-L-alanine amidase	6.5	9.02E-04	Control	10.3	50741	2	Cytoplasmic Membrane	COG0860	Cell envelope biogenesis, outer membrane	
26991577	PP_4899		carbohydrate kinase, YjeF related protein	1.2	3.40E-01	Vanillin	8.4	28921	2	Unknown	COG0063	Carbohydrate transport and metabolism	
26991581	PP_4903		ribosome-associated GTPase	1.9	2.55E-01	Vanillin	6.5	37746	2	Cytoplasmic	COG1162	General function prediction only	
26991582	PP_4904	motB	flagellar motor protein MotB	1.2	3.84E-01	Vanillin	4.8	37802	4	Cytoplasmic Membrane	COG1360	Cell motility and secretion	
26991584	PP_4906		metal-dependent hydrolase HDOD	1.3	2.66E-02	Vanillin	7.7	57677	9	Unknown			
26991585	PP_4907	rhdA-2	rhodanese domain protein	1.7	2.67E-03	Vanillin	6.1	29517	10	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991586	PP_4908	psd	phosphatidylserine decarboxylase	1.0	9.60E-01	Control	8.6	31547	6	Cytoplasmic Membrane	COG0688	Lipid metabolism	
26991587	PP_4909	serB	phosphoserine phosphatase SerB	1.6	3.77E-02	Control	5.1	45033	14	Cytoplasmic	COG0560	Amino acid transport and metabolism	
26991588	PP_4910		hypothetical protein	1.0	8.20E-01	Vanillin	4.7	53632	10	Cytoplasmic	COG3726	General function prediction only	
26991589	PP_4911		hypothetical protein	1.2	3.23E-01	Control	8.5	27337	9	Periplasmic	COG3009	Function unknown	
26991590	PP_4912	parC	DNA topoisomerase IV subunit A	1.6	4.91E-02	Vanillin	6.2	83181	14	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
26991593	PP_4915	parE	DNA topoisomerase IV subunit B	1.3	7.77E-02	Vanillin	6.2	69556	18	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
26991597	PP_4919		NUDIX hydrolase	4.6	1.11E-01	Control	4.7	23607	3	Cytoplasmic			
26991601	PP_4923		TolC family type I secretion outer membrane protein	3.2	2.87E-04	Vanillin	5.2	52637	16	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
26991609	PP_4931		FAD dependent oxidoreductase	1.4	1.46E-01	Vanillin	7.2	42015	12	Cytoplasmic	COG0578	Energy production and conversion	
26991610	PP_4932		aldo/keto reductase	1.7	1.90E-02	Vanillin	6.4	29123	5	Cytoplasmic	COG0667	Energy production and conversion	
26991611	PP_4933		hypothetical protein	7.1	8.31E-02	Vanillin	10.0	37000	4	Unknown			
26991612	PP_4934		bifunctional heptose 7-phosphate kinase/heptose 1-phosphate a	1.2	1.07E-01	Control	5.8	49970	13	Cytoplasmic	COG2870	Cell envelope biogenesis, outer membrane	
26991613	PP_4935		lipid ABC transporter ATPase/inner membrane protein	2.0	1.60E-02	Vanillin	7.6	66279	15	Cytoplasmic Membrane	COG1132	Defense mechanisms	
26991616	PP_4938		glycosyl transferase	1.7	1.39E-01	Vanillin	9.4	41783	6	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26991617	PP_4939		hypothetical protein	1.2	1.52E-01	Vanillin	7.1	28978	4	Cytoplasmic			
26991618	PP_4940		hypothetical protein	1.1	7.75E-01	Control	9.1	36935	4	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26991621	PP_4943		glycosyl transferase	1.1	5.36E-01	Vanillin	9.5	40843	5	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
26991622	PP_4944		carbamoyltransferase	1.3	4.90E-03	Control	7.2	65646	15	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
26991623	PP_4945		hypothetical protein	1.6	8.99E-02	Control	7.4	31850	9	Cytoplasmic	COG2961	General function prediction only	
26991625	PP_4947	putA	trifunctional transcriptional regulator/proline dehydrogenase/p	3.6	1.33E-03	Vanillin	6.3	142580	35	Cytoplasmic	COG4230	Energy production and conversion	
26991627	PP_4949		TldD/PmbA family protein	2.6	2.12E-02	Vanillin	6.6	55611	6	Unknown	COG0312	General function prediction only	
26991628	PP_4950		hypothetical protein	2.0	1.15E-02	Vanillin	4.9	47741	5	Unknown	COG0312	General function prediction only	
26991630	PP_4952	dbpA	ATP-dependent RNA helicase DbpA	3.2	1.06E-03	Control	8.7	49685	10	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991637	PP_4959		response regulator receiver modulated diguanylate cyclase/pho	12.7	2.27E-05	Vanillin	4.8	78896	17	Cytoplasmic Membrane	COG5001	Signal transduction mechanisms	
26991638	PP_4960	fda	fructose-1,6-bisphosphate aldolase	1.1	7.66E-01	Control	5.6	38453	27	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
26991641	PP_4963	pgk	phosphoglycerate kinase	1.1	5.32E-01	Control	4.9	40005	22	Cytoplasmic	COG0126	Carbohydrate transport and metabolism	
26991642	PP_4964	epd	D-erythrose-4-phosphate dehydrogenase	1.3	1.11E-01	Vanillin	6.4	38482	3	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
26991643	PP_4965	tktA	transketolase	1.0	7.80E-01	Vanillin	5.0	72463	39	Cytoplasmic	COG0021	Carbohydrate transport and metabolism	
26991644	PP_4966		ArsR family transcriptional regulator	1.2	5.45E-01	Control	6.4	36148	6	Cytoplasmic	COG2226	Coenzyme metabolism	
26991645	PP_4967	metK	S-adenosylmethionine synthetase	1.9	5.38E-02	Control	5.1	42779	23	Cytoplasmic	COG0192	Coenzyme metabolism	

26991654	PP_4977	metF	5,10-methylenetetrahydrofolate reductase	1.2	4.02E-01	Control	6.2	32979	16	Cytoplasmic	COG0685	Amino acid transport and metabolism	
26991657	PP_4980		DEAD-box ATP dependent DNA helicase	1.2	1.47E-01	Control	10.7	68073	26	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
26991660	PP_4983		amine oxidase	1.8	7.62E-02	Vanillin	10.2	65923	21	Unknown	COG1231	Amino acid transport and metabolism	
26991661	PP_4984	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	1.8	1.46E-01	Vanillin	6.1	52453	5	Cytoplasmic	COG0161	Coenzyme metabolism	
26991665	PP_4988		chemotaxis protein CheA	2.0	8.97E-02	Vanillin	4.7	180005	11	Unknown	COG0643	Cell motility and secretion	Signal transduction mechanisms
26991670	PP_4993	gshB	glutathione synthetase	1.7	5.95E-02	Vanillin	5.1	35254	14	Cytoplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
26991675	PP_4998	pyrB	aspartate carbamoyltransferase catalytic subunit	1.0	7.91E-01	Vanillin	7.1	36344	19	Cytoplasmic	COG0540	Nucleotide transport and metabolism	
26991676	PP_4999	pyrC	dihydroorotase	1.4	3.11E-02	Control	5.4	44116	9	Cytoplasmic	COG0044	Nucleotide transport and metabolism	
26991678	PP_5001	hslU	ATP-dependent protease ATP-binding subunit HslU	1.8	1.09E-02	Control	5.7	49982	22	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
26991680	PP_5003	phaA	poly(3-hydroxyalkanoate) polymerase 1	4.1	3.78E-03	Vanillin	7.4	62241	21	Cytoplasmic	COG3243	Lipid metabolism	
26991681	PP_5004		poly(3-hydroxyalkanoate) depolymerase	3.2	3.61E-02	Vanillin	10.1	31446	2	Unknown	COG0596	General function prediction only	
26991682	PP_5005	phaC	poly(3-hydroxyalkanoate) polymerase 2	7.0	6.82E-04	Vanillin	9.6	62722	9	Cytoplasmic	COG3243	Lipid metabolism	
26991684	PP_5007		poly(hydroxyalkanoate) granule-associated protein	4.0	1.98E-04	Vanillin	10.9	26214	12	Cytoplasmic	COG3937	Function unknown	
26991688	PP_5011	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	1.0	9.68E-01	Vanillin	9.5	28397	17	Cytoplasmic	COG2226	Coenzyme metabolism	
26991695	PP_5019		16S ribosomal RNA methyltransferase RsmE	1.2	5.34E-01	Control	9.1	26126	4	Cytoplasmic Membrane	COG1385	Function unknown	
26991696	PP_5020		methyl-accepting chemotaxis sensory transducer	1.6	9.66E-03	Vanillin	4.9	69017	19	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
26991698	PP_5022		amino acid ABC transporter ATP-binding protein	5.0	1.17E-02	Control	7.6	27004	2	Cytoplasmic Membrane	COG1126	Amino acid transport and metabolism	
26991700	PP_5024		amino acid ABC transporter periplasmic amino acid-binding prot	1.1	2.19E-01	Vanillin	8.6	29848	6	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
26991701	PP_5025	mdoH	glucosyltransferase MdoH	1.2	1.18E-01	Vanillin	8.3	95875	10	Cytoplasmic Membrane	COG2943	Cell envelope biogenesis, outer membrane	
26991702	PP_5026	mdoG	glucan biosynthesis protein G	1.1	5.29E-01	Vanillin	6.5	62340	24	Periplasmic	COG3131	Inorganic ion transport and metabolism	
26991704	PP_5028	pip	proline iminopeptidase	1.6	2.14E-02	Vanillin	6.2	36589	15	Cytoplasmic	COG0596	General function prediction only	
26991711	PP_5035	hutC	histidine utilization repressor	1.2	1.02E-01	Vanillin	6.6	27624	4	Cytoplasmic	COG2188	Transcription	
26991716	PP_5040	fbp	fructose-1,6-bisphosphatase	1.3	1.83E-01	Control	5.9	37246	18	Cytoplasmic	COG0158	Carbohydrate transport and metabolism	
26991717	PP_5041	glgP	glycogen/starch/alpha-glucan phosphorylase	8.9	6.95E-04	Vanillin	6.4	92004	18	Cytoplasmic	COG0058	Carbohydrate transport and metabolism	
26991720	PP_5044		GTP-binding protein TypA	1.5	9.35E-02	Control	5.3	67157	29	Cytoplasmic Membrane	COG1217	Signal transduction mechanisms	
26991721	PP_5045	thiI	thiamine biosynthesis protein ThiI	1.5	3.44E-01	Vanillin	6.9	54945	2	Cytoplasmic	COG0301	Coenzyme metabolism	
26991722	PP_5046	glnA	glutamine synthetase, type I	1.3	6.30E-02	Control	5.1	51740	30	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991724	PP_5048	ntrC	nitrogen metabolism transcriptional regulator NtrC	1.2	3.17E-01	Control	6.0	53114	11	Cytoplasmic	COG2204	Signal transduction mechanisms	
26991732	PP_5056	pgm	phosphoglyceromutase	1.1	2.82E-01	Vanillin	4.9	55180	23	Cytoplasmic	COG0696	Carbohydrate transport and metabolism	
26991733	PP_5057		M24/M37 family peptidase	1.4	4.24E-01	Vanillin	9.8	48800	7	Outer Membrane	COG4942	Cell division and chromosome partitioning	
26991734	PP_5058		carboxyl-terminal protease	1.3	1.18E-01	Control	5.6	46333	16	Cytoplasmic Membrane	COG0793	Cell envelope biogenesis, outer membrane	
26991739	PP_5063	betB	betaine aldehyde dehydrogenase	1.7	1.07E-02	Vanillin	4.8	52986	8	Cytoplasmic	COG1012	Energy production and conversion	
26991740	PP_5064	betA	choline dehydrogenase	1.7	1.60E-02	Vanillin	6.8	62544	6	Cytoplasmic Membrane	COG2303	Amino acid transport and metabolism	
26991743	PP_5067		potassium efflux protein KefA	1.4	1.94E-01	Vanillin	8.9	122371	2	Cytoplasmic Membrane	COG3264	Cell envelope biogenesis, outer membrane	
26991746	PP_5070		ParA family protein	2.0	1.26E-02	Vanillin	4.7	28660	5	Cytoplasmic	COG1192	Cell division and chromosome partitioning	
26991750	PP_5074	hemE	uroporphyrinogen decarboxylase	1.2	7.24E-02	Vanillin	6.7	38883	6	Cytoplasmic	COG0407	Coenzyme metabolism	
26991751	PP_5075	gltD	glutamate synthase subunit beta	1.7	3.07E-02	Control	6.3	51819	23	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
26991752	PP_5076	gltB	glutamate synthase subunit alpha	1.2	2.01E-01	Vanillin	6.2	161772	59	Cytoplasmic	COG0069	Amino acid transport and metabolism	
26991753	PP_5077		sporulation domain protein	1.0	8.44E-01	Vanillin	7.1	55434	10	Unknown	COG3267	Intracellular trafficking and secretion	
26991754	PP_5078	aroB	3-dehydroquinate synthase	1.2	5.72E-01	Vanillin	6.0	39485	13	Cytoplasmic	COG0337	Amino acid transport and metabolism	
26991760	PP_5084		penicillin-binding protein, 1A family	1.2	3.38E-01	Vanillin	7.2	89193	14	Extracellular	COG5009	Cell envelope biogenesis, outer membrane	
26991761	PP_5085	maeB	malic enzyme	1.4	9.34E-03	Control	4.9	45127	29	Cytoplasmic	COG0281	Energy production and conversion	
26991764	PP_5088	priA	primosome assembly protein PriA	1.5	2.91E-01	Control	8.4	82345	3	Cytoplasmic	COG1198	DNA replication, recombination, and repair	
26991765	PP_5089	argS	arginyl-tRNA synthetase	1.2	5.10E-02	Control	5.7	63668	29	Cytoplasmic	COG0018	Translation, ribosomal structure and biogenesis	
26991766	PP_5090		sporulation domain protein	1.4	1.26E-01	Control	10.6	24964	6	Cytoplasmic Membrane	COG3087	Cell division and chromosome partitioning	
26991771	PP_5095	proC-2	pyrroline-5-carboxylate reductase	1.4	8.01E-02	Control	4.7	28258	11	Cytoplasmic	COG0345	Amino acid transport and metabolism	
26991773	PP_5097	metX	homoserine O-acetyltransferase	1.4	4.28E-02	Control	6.0	41659	8	Cytoplasmic	COG2021	Amino acid transport and metabolism	
26991777	PP_5101		coproporphyrinogen III oxidase	1.0	8.62E-01	Control	4.9	43376	3	Cytoplasmic	COG0635	Coenzyme metabolism	
26991779	PP_5103	trmB	tRNA (guanine-N(7)-)-methyltransferase	2.0	1.32E-01	Control	7.3	27203	4	Cytoplasmic	COG0220	General function prediction only	
26991780	PP_5104	thiG	thiazole synthase	1.1	5.91E-01	Vanillin	5.8	28917	12	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
26991785	PP_5109	ftsX	hypothetical protein	1.5	4.35E-02	Vanillin	6.5	36984	9	Cytoplasmic Membrane	COG2177	Cell division and chromosome partitioning	
26991786	PP_5110	ftsE	cell division ATP-binding protein FtsE	1.8	1.92E-01	Control	11.0	24830	2	Cytoplasmic Membrane	COG2884	Cell division and chromosome partitioning	
26991787	PP_5111	ftsY	signal recognition particle-docking protein FtsY	1.3	1.02E-01	Vanillin	4.9	51680	15	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
26991788	PP_5112		peptidase M16 domain protein	2.5	1.02E-01	Vanillin	5.9	50095	10	Periplasmic	COG0612	General function prediction only	
26991789	PP_5113		peptidase M16 domain protein	1.2	5.15E-02	Vanillin	8.0	52389	7	Unknown	COG0612	General function prediction only	
26991794	PP_5118		rhodanese domain protein	1.0	6.79E-01	Vanillin	5.6	30750	12	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
26991796	PP_5120		conifer aldehyde dehydrogenase	6.9	9.95E-03	Vanillin	9.2	52453	3	Cytoplasmic	COG1012	Energy production and conversion	
26991801	PP_5125	mutM	formamidopyrimidine-DNA glycosylase	1.3	2.78E-01	Vanillin	9.2	30178	2	Cytoplasmic	COG0266	DNA replication, recombination, and repair	
26991802	PP_5126		signal transduction protein	1.9	6.04E-03	Control	5.6	28452	3	Unknown	COG1639	Signal transduction mechanisms	
26991803	PP_5127		hypothetical protein	1.2	2.21E-01	Control	6.9	44126	7	Cytoplasmic	COG1092	General function prediction only	
26991804	PP_5128	ilvD	dihydroxy-acid dehydratase	1.4	8.73E-03	Control	5.8	65671	31	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
26991817	PP_5141	thyA	thymidylate synthase	1.2	3.75E-01	Vanillin	5.4	36772	5	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
26991820	PP_5144		hypothetical protein	2.0	4.23E-02	Vanillin	5.3	26452	1	Unknown	COG3332	Function unknown	
26991821	PP_5145	ptsP	PTSINtr with GAF domain, PtsP	2.7	1.20E-02	Vanillin	5.3	83337	28	Cytoplasmic	COG3605	Signal transduction mechanisms	
26991825	PP_5149	ilvA-2	threonine dehydratase	5.1	4.59E-05	Control	6.6	55023	13	Cytoplasmic	COG1171	Amino acid transport and metabolism	
26991826	PP_5150	rpiA	ribose-5-phosphate isomerase A	2.3	1.19E-01	Control	4.9	23496	4	Unknown	COG0120	Carbohydrate transport and metabolism	
26991828	PP_5152		SdiA-regulated domain protein	2.7	8.03E-03	Vanillin	4.5	33795	2	Cytoplasmic Membrane	COG3204	Function unknown	
26991829	PP_5153		fumarylacetoacetate (FAA) hydrolase	1.3	5.28E-01	Control	4.7	23906	2	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
26991830	PP_5154		FAD linked oxidase domain protein	2.7	2.57E-02	Vanillin	5.2	49990	7	Cytoplasmic	COG0277	Energy production and conversion	
26991831	PP_5155	serA	D-3-phosphoglycerate dehydrogenase	1.7	8.30E-02	Control	6.3	44339	18	Cytoplasmic	COG0111	Amino acid transport and metabolism	
26991841	PP_5165		NLPA lipoprotein	1.3	3.37E-01	Control	8.7	28159	4	Unknown	COG1464	Inorganic ion transport and metabolism	
26991844	PP_5168	cysA	sulfate ABC transporter ATPase subunit	2.7	5.24E-02	Vanillin	6.4	36972	6	Cytoplasmic Membrane	COG1118	Inorganic ion transport and metabolism	
26991846	PP_5170	cysT	sulfate ABC transporter inner membrane subunit CysT	4.5	1.25E-01	Control	9.6	29454	2	Cytoplasmic Membrane	COG0555	Posttranslational modification, protein turnover, chaperones	
26991847	PP_5171	cysP	sulfate ABC transporter periplasmic sulfate-binding protein	5.7	4.24E-04	Vanillin	9.0	37491	13	Periplasmic	COG1613	Inorganic ion transport and metabolism	
26991849	PP_5173		acriflavin resistance protein	7.0	1.93E-04	Vanillin	5.4	112277	10	Cytoplasmic Membrane	COG0841	Defense mechanisms	
26991850	PP_5174		RND efflux transporter	9.6	7.56E-04	Vanillin	5.5	38032	9	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991851	PP_5175		efflux transporter RND family, MFP subunit	7.2	2.61E-03	Vanillin	6.5	38304	12	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
26991855	PP_5179	potG	spermidine/putrescine ABC transporter ATPase	2.2	2.65E-03	Vanillin	6.5	42472	14	Cytoplasmic Membrane	COG3842	Amino acid transport and metabolism	

26991856	PP_5180	potF-1	putrescine ABC transporter periplasmic putrescine-binding prote	3.1	2.93E-05	Vanillin	8.0	39788	11	Periplasmic	COG0687	Amino acid transport and metabolism	
26991857	PP_5181	potF-2	putrescine ABC transporter periplasmic putrescine-binding prote	2.2	5.30E-05	Vanillin	6.4	40068	22	Periplasmic	COG0687	Amino acid transport and metabolism	
26991858	PP_5182		aminotransferase	5.1	1.64E-03	Vanillin	6.2	49871	12	Cytoplasmic	COG0161	Coenzyme metabolism	
26991859	PP_5183		glutamine synthetase	2.4	3.17E-03	Vanillin	4.8	50877	19	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991860	PP_5184		glutamine synthetase	2.4	4.94E-02	Vanillin	4.5	50974	9	Cytoplasmic	COG0174	Amino acid transport and metabolism	
26991861	PP_5185	argA	N-acetylglutamate synthase	1.2	1.77E-01	Control	5.9	47440	11	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991862	PP_5186	argE	acetylornithine deacetylase	2.6	1.84E-02	Control	4.9	41425	2	Cytoplasmic	COG0624	Amino acid transport and metabolism	
26991863	PP_5187		adenylate cyclase	1.1	6.62E-01	Control	5.6	52133	14	Cytoplasmic	COG3025	Function unknown	
26991868	PP_5192	gcvP-2	glycine dehydrogenase	17.9	6.59E-06	Vanillin	6.3	104037	6	Cytoplasmic	COG1003	Amino acid transport and metabolism	
26991870	PP_5194	gcvT	glycine cleavage system aminomethyltransferase T	1.9	7.33E-04	Vanillin	5.3	39379	6	Cytoplasmic	COG0404	Amino acid transport and metabolism	
26991872	PP_5196		iron ABC transporter periplasmic iron-binding protein	7.6	3.72E-04	Control	5.7	36829	7	Periplasmic	COG1840	Inorganic ion transport and metabolism	
26991873	PP_5197	ubiF	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	1.1	5.06E-01	Vanillin	6.3	44605	8	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
26991875	PP_5199	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	1.2	5.63E-01	Vanillin	7.6	43623	4	Cytoplasmic Membrane	COG0654	Coenzyme metabolism	Energy production and conversion
26991876	PP_5200	pepP	peptidase M24	1.2	2.64E-01	Vanillin	5.8	49171	7	Cytoplasmic	COG0006	Amino acid transport and metabolism	
26991882	PP_5206		secretion protein HlyD family protein	2.1	1.83E-02	Vanillin	9.6	34522	7	Cytoplasmic Membrane	COG1566	Defense mechanisms	
26991886	PP_5210		alcohol dehydrogenase, zinc-containing	12.6	2.72E-03	Vanillin	7.6	33856	7	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
26991888	PP_5212		CDP-6-deoxy-delta-3,4-glucoseen reductase	1.2	1.04E-01	Control	5.7	35566	3	Cytoplasmic	COG0543	Coenzyme metabolism	Energy production and conversion
26991889	PP_5213		UbiD family decarboxylase	1.8	5.54E-04	Control	7.8	61071	5	Cytoplasmic	COG0043	Coenzyme metabolism	
26991890	PP_5214	rho	transcription termination factor Rho	1.3	5.70E-02	Control	8.2	47041	38	Cytoplasmic	COG1158	Transcription	
26991892	PP_5216	ppx	Ppx/GppA phosphatase	1.2	8.28E-02	Vanillin	6.9	55958	22	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
26991896	PP_5220	elbB	isoprenoid biosynthesis protein with amidotransferase-like dom	1.4	9.99E-02	Control	5.0	23391	7	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
26991903	PP_5227	lysA-2	diaminopimelate decarboxylase	1.4	2.67E-01	Control	4.9	45213	15	Cytoplasmic	COG0019	Amino acid transport and metabolism	
26991904	PP_5228	dapF	diaminopimelate epimerase	1.9	4.09E-02	Control	8.2	31487	3	Cytoplasmic	COG0253	Amino acid transport and metabolism	
26991905	PP_5229		hypothetical protein	1.6	5.54E-01	Control	6.1	26395	2	Cytoplasmic	COG3159	Function unknown	
26991907	PP_5231		HAD superfamily hydrolase	1.1	6.33E-01	Control	5.1	25611	5	Cytoplasmic	COG1011	General function prediction only	
26991928	PP_5252		amidohydrolase 3	65.6	2.75E-03	Vanillin	6.4	72743	10	Unknown	COG1574	General function prediction only	
26991934	PP_5258		aldehyde dehydrogenase family protein	5.9	1.13E-04	Vanillin	5.4	53106	12	Cytoplasmic	COG1012	Energy production and conversion	
26991940	PP_5264	rep	ATP-dependent DNA helicase Rep	1.7	1.47E-01	Vanillin	5.6	76869	3	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
26991949	PP_5273		oxidoreductase	1.8	1.60E-01	Control	7.3	46651	5	Cytoplasmic	COG0665	Amino acid transport and metabolism	
26991954	PP_5278		aldehyde dehydrogenase family protein	1.7	2.22E-02	Vanillin	5.5	53053	14	Cytoplasmic	COG1012	Energy production and conversion	
26991958	PP_5282	rpmB	50S ribosomal protein L28	21.0	1.18E-01	Control	12.3	8922	5	Cytoplasmic	COG0227	Translation, ribosomal structure and biogenesis	
26991959	PP_5283		periplasmic dipeptide-binding protein	1.2	2.08E-01	Control	8.5	57512	14	Periplasmic	COG0747	Amino acid transport and metabolism	
26991961	PP_5285	coaBC	bifunctional phosphopantothenoylcysteine decarboxylase/phosp	1.1	6.58E-01	Vanillin	7.0	43126	9	Cytoplasmic	COG0452	Coenzyme metabolism	
26991964	PP_5288		phosphomannomutase	1.0	8.44E-01	Control	5.0	50271	15	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
26991965	PP_5289	argB	acetylglutamate kinase	1.4	8.08E-02	Control	5.7	31953	15	Cytoplasmic	COG0548	Amino acid transport and metabolism	
26991968	PP_5292	crc	exodeoxyribonuclease III Xth	1.2	6.96E-02	Control	4.9	29786	5	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
26991970	PP_5294	rph	ribonuclease PH	1.3	3.36E-01	Vanillin	5.9	25723	3	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis	
26991978	PP_5302	spoT	(p)ppGpp synthetase I, SpoT/RelA	1.0	8.91E-01	Control	9.2	78603	20	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
26991980	PP_5304		lipoprotein	1.4	6.19E-02	Control	5.1	26284	6	Unknown			
26991981	PP_5305		NAD-dependent epimerase/dehydratase	1.5	1.97E-01	Control	5.4	30749	4	Unknown	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
26991982	PP_5306	exbB	ferric siderophore transport system protein ExbB	2.6	2.17E-02	Control	9.5	33260	7	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
26991984	PP_5308	tonB	TonB family protein	3.4	1.49E-03	Control	10.5	26022	7	Outer Membrane	COG0810	Cell envelope biogenesis, outer membrane	
26991985	PP_5309		LysR family transcriptional regulator	1.3	4.17E-02	Control	7.0	33763	8	Cytoplasmic	COG0583	Transcription	
26991986	PP_5310	recG	ATP-dependent DNA helicase RecG	1.1	4.83E-01	Vanillin	6.8	76452	7	Cytoplasmic	COG1200	DNA replication, recombination, and repair	Transcription
26991987	PP_5311		signal transduction protein	1.3	2.69E-01	Vanillin	5.9	51775	7	Cytoplasmic	COG1639	Signal transduction mechanisms	
26991990	PP_5314	rubB	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	1.1	6.19E-01	Vanillin	5.4	40183	5	Cytoplasmic	COG1251	Energy production and conversion	
26991996	PP_5320	phoB	transcriptional regulator	1.8	5.50E-02	Vanillin	5.2	27080	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
26991997	PP_5321	phoR	PAS/PAC sensor signal transduction histidine kinase	3.5	6.38E-03	Vanillin	7.3	49063	2	Cytoplasmic Membrane	COG0642	Signal transduction mechanisms	
26992000	PP_5324		response regulator receiver protein	1.9	2.73E-03	Control	8.9	31770	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
26992002	PP_5326	pstB	phosphate transporter ATP-binding protein	1.2	3.44E-01	Vanillin	6.5	31601	6	Cytoplasmic Membrane	COG1117	Inorganic ion transport and metabolism	
26992005	PP_5329	pstS	phosphate ABC transporter phosphate-binding protein	1.9	6.07E-03	Vanillin	9.4	34955	8	Cytoplasmic Membrane	COG0226	Inorganic ion transport and metabolism	
26992011	PP_5335	purK	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.1	1.41E-01	Vanillin	5.2	38702	9	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
26992013	PP_5337		LysR family transcriptional regulator	1.3	1.36E-01	Vanillin	6.6	33517	4	Cytoplasmic	COG0583	Transcription	
26992021	PP_5345		acetyltransferase	1.0	7.63E-01	Vanillin	6.0	25042	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
26992022	PP_5346	oadA	pyruvate carboxylase subunit B	12.0	4.27E-04	Control	5.3	65626	53	Cytoplasmic	COG5016	Energy production and conversion	
26992023	PP_5347	accC-2	pyruvate carboxylase subunit A	11.7	1.47E-03	Control	6.5	51942	28	Cytoplasmic	COG0439	Lipid metabolism	
26992026	PP_5350		RpiR family transcriptional regulator	7.0	1.33E-01	Control	7.2	31028	2	Cytoplasmic	COG1737	Transcription	
26992027	PP_5351	zwf-3	glucose-6-phosphate 1-dehydrogenase	1.1	7.13E-01	Vanillin	6.6	54944	4	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
26992028	PP_5352	uvrD	DNA-dependent helicase II	1.1	4.92E-01	Vanillin	6.2	81692	15	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
26992029	PP_5353		hypothetical protein	1.1	4.03E-01	Control	7.2	30672	5	Cytoplasmic Membrane	COG4395	Function unknown	
26992033	PP_5357	pkxY	pyridoxamine kinase	1.3	4.88E-02	Control	6.4	31671	3	Cytoplasmic	COG2240	Coenzyme metabolism	
26992035	PP_5359		CobW/P47K family protein	1.3	2.68E-01	Vanillin	8.2	35772	2	Cytoplasmic Membrane	COG0523	General function prediction only	
26992037	PP_5361		CobW/P47K family protein	1.3	2.38E-01	Vanillin	4.6	45607	28	Cytoplasmic	COG0523	General function prediction only	
26992041	PP_5365		cyclopropane-fatty-acyl-phospholipid synthase	28.2	4.74E-05	Vanillin	5.9	48114	16	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
26992042	PP_5366	lpd3	dihydrolipoamide dehydrogenase	1.4	3.31E-02	Vanillin	6.0	49353	7	Cytoplasmic	COG1249	Energy production and conversion	
26992056	PP_5380	copA	copper resistance protein A	2.3	1.23E-01	Vanillin	6.0	74225	3	Periplasmic	COG2132	Secondary metabolites biosynthesis, transport, and catabolism	
26992068	PP_5392		YVTN family beta-propeller repeat-containing protein	11.9	2.72E-03	Vanillin	7.4	39354	7	Cytoplasmic	COG3391	Function unknown	
26992070	PP_5395		hypothetical protein	2.4	1.66E-03	Vanillin	5.6	31623	12	Cytoplasmic	COG1568	General function prediction only	
26992075	PP_5400		hypothetical protein	1.6	2.56E-01	Vanillin	4.7	39161	4	Unknown			
26992084	PP_5409	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.7	1.61E-03	Vanillin	6.0	66312	17	Cytoplasmic	COG0449	Cell envelope biogenesis, outer membrane	
26992086	PP_5411	glmU	UDP-N-acetylglucosamine pyrophosphorylase	1.5	6.90E-03	Control	6.7	48471	18	Cytoplasmic	COG1207	Cell envelope biogenesis, outer membrane	
26992088	PP_5413	atpD	F0F1 ATP synthase subunit beta	1.3	6.10E-02	Control	4.6	49359	51	Cytoplasmic	COG0055	Energy production and conversion	
26992089	PP_5414	atpG	F0F1 ATP synthase subunit gamma	1.4	1.35E-02	Control	9.2	31464	17	Cytoplasmic	COG0224	Energy production and conversion	
26992090	PP_5415	atpA	F0F1 ATP synthase subunit alpha	1.5	4.29E-02	Control	5.2	55352	45	Cytoplasmic	COG0056	Energy production and conversion	
325273773				367.7	3.10E-02	Control			2				
148547246				185.7	7.09E-04	Vanillin			12				
148547037				94.7	3.90E-05	Vanillin			8				
298682197				92.5	2.84E-02	Vanillin			6				

313498081	16.9	6.32E-05	Vanillin	16
374706103	16.6	3.61E-04	Vanillin	2
24982083	13.3	1.54E-03	Control	4
325275033	7.4	2.12E-05	Vanillin	8
54301780	7.3	2.11E-01	Control	2
148546522	5.3	7.43E-05	Control	7
24981833	4.2	7.30E-03	Control	10
24985446	4.1	1.44E-03	Control	4
148546519	3.9	3.88E-03	Control	14
17980438	3.9	1.09E-03	Vanillin	8
152998462	3.7	1.57E-02	Control	2
313497930	3.2	6.78E-03	Control	19
260914511	2.9	4.53E-01	Control	1
260609519	2.9	5.00E-02	Vanillin	6
148545952	2.9	7.03E-03	Control	24
170722725	2.7	4.33E-02	Control	2
24981839	2.5	1.82E-03	Control	16
148546138	2.2	1.36E-03	Control	19
24986578	2.1	1.61E-01	Vanillin	5
313501195	2.1	1.07E-02	Vanillin	21
24983623	2.0	4.50E-02	Vanillin	16
148549466	1.9	5.97E-03	Control	13
148547402	1.8	1.35E-03	Vanillin	3
148545432	1.8	2.55E-02	Vanillin	6
148549014	1.6	6.99E-02	Control	3
148550051	1.6	8.17E-02	Control	23
148545801	1.6	2.43E-02	Control	12
24986535	1.5	2.33E-02	Control	24
148549381	1.5	2.09E-01	Control	5
24983268	1.5	1.46E-02	Control	35
313496591	1.4	6.45E-02	Vanillin	7
148545799	1.4	3.99E-01	Control	5
24982449	1.4	1.71E-01	Vanillin	7
148550089	1.4	6.84E-02	Vanillin	2
24986090	1.4	1.59E-01	Control	5
148548654	1.3	4.21E-02	Control	14
313497915	1.3	1.67E-01	Control	10
148546787	1.3	3.46E-01	Vanillin	4
24982353	1.3	1.28E-02	Control	25
24987101	1.3	3.02E-01	Vanillin	10
24986054	1.3	3.01E-01	Vanillin	2
313497311	1.2	1.70E-01	Control	11
104780459	1.2	1.86E-01	Control	10
313496770	1.2	1.98E-01	Control	15
339490066	1.2	3.23E-01	Control	20
148545524	1.2	4.40E-02	Vanillin	23
24981908	1.2	9.68E-02	Control	10
148549632	1.1	5.12E-01	Control	8
330982601	1.1	7.89E-01	Control	5
148547408	1.1	9.27E-01	Vanillin	2
148546656	1.1	7.91E-01	Vanillin	3
24986476	1.1	3.78E-01	Control	73
121189	1.1	9.35E-01	Vanillin	17
24986637	1.0	9.82E-01	Control	7
104780030	1.0	9.42E-01	Vanillin	7

5.4 Teilprojekt Terpene



Gelbilder der GeLCMSMS-Analyse von auf Glucose, Oktansäure, Citronellol und Citronellsäure kultivierten Zellen von *P. aeruginosa* PAO1. Pro Kohlenstoffquelle wurden die Proben dreier biologischer Replikate auf ein Gel aufgetragen und bei 30 mA aufgetrennt. Nachdem die Front den unteren Rand des Gels erreicht hatte, wurde die Elektrophorese gestoppt und das Gel mit Coomassie gefärbt. Jede Spur wurde in 10 Fraktionen unterteilt und die markierten Bereiche aus dem Gel ausgeschnitten. Die mit A bezeichneten Teile wurden und mit Trypsin verdaut und mittels LC-ESI-MS/MS analysiert. Die mit B gekennzeichneten Teile dienten als „Backup“ und wurden bei -80°C gelagert.

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595199	PA0001	dnaA	chromosomal replication initiator protein DnaA	1.6	4.33E-02	Glucose	8.9	57722	6	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.3	2.76E-02	Citronellol	4.9	40694	22	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	1.7	1.06E-01	Glucose	5.7	90188	37	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	1.2	5.50E-01	Glucose	4.5	19115	4	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	22.2	2.17E-04	Citronellol	7.9	61755	20	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.9	2.51E-02	Glucose	4.8	73973	33	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	1.2	3.91E-01	Glucose	4.7	36109	13	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595208	PA0010	tag	DNA-3-methyladenine glycosidase I	3.5	9.72E-01	Citronellol	4.6	20780	2	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	1.1	4.73E-01	Citronellol	7.0	33028	12	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	1.4	9.42E-01	Citronellol	4.7	19365	6	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	1.4	2.42E-01	Citronellol	9.4	37586	6	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	1.7	2.90E-01	Citronellol	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	4.2	2.38E-03	Citronellol	6.3	35095	12	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	1.3	1.50E-01	Glucose	5.8	34774	12	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	1.4	6.66E-02	Citronellol	5.5	29484	4	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	3.1	6.80E-04	Glucose	5.0	28488	11	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	2.1	1.33E-03	Glucose	6.3	43680	18	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	3.0	9.56E-01	Citronellol	7.1	7863	3	Unknown	COG3360	Function unknown	
15595239	PA0041		probable hemagglutinin	12.2	8.91E-03	Citronellol	5.1	361591	3	Extracellular			
15595252	PA0054		conserved hypothetical protein	1.0	7.09E-01	Glucose	9.6	20024	2	Unknown	COG1859	Translation, ribosomal structure and biogenesis	
15595253	PA0055		hypothetical protein	1.7	1.10E-02	Citronellol	5.7	18433	11	Cytoplasmic	COG3812	Function unknown	
15595257	PA0059	osmC	osmotically inducible protein OsmC	40.2	8.14E-02	Citronellol	6.3	15610	2	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
15595263	PA0065		hypothetical protein	26.6	2.68E-02	Glucose	6.1	24951	6	Cytoplasmic	COG0546	General function prediction only	
15595264	PA0066		conserved hypothetical protein	2.2	7.40E-03	Citronellol	6.6	19198	4	Cytoplasmic	COG0663	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.2	2.81E-01	Glucose	4.9	76011	29	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	2.7	2.63E-01	Citronellol	8.9	31716	6	Periplasmic			
15595273	PA0075	pppA	PppA	4.2	8.34E-03	Citronellol	6.2	25904	3	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	1.7	3.18E-01	Glucose	4.4	23856	2	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	1.7	3.57E-01	Citronellol	6.1	48275	6	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	1.3	3.25E-01	Citronellol	4.9	18785	16	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.5	1.36E-02	Glucose	5.0	55771	34	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	1.5	3.03E-02	Citronellol	6.8	17415	11	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	1.7	7.33E-02	Citronellol	4.4	30361	8	Cytoplasmic	COG4455	General function prediction only	
15595286	PA0088	tssF1	TssF1	4.0	8.59E-02	Glucose	7.4	69483	3	Cytoplasmic	COG3519	Intracellular trafficking, secretion, and vesicular transport	
15595288	PA0090	clpV1	ClpV1	2.8	4.92E-03	Glucose	5.3	98737	25	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	6.8	3.96E-02	Citronellol	6.4	72012	11	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	10.7	3.54E-02	Citronellol	8.9	44738	5	Cytoplasmic Membrane	COG4104	Function unknown	
15595292	PA0094		hypothetical protein	1.2	8.36E-01	Citronellol	6.8	16456	4	Unknown	COG5435	Function unknown	
15595298	PA0100		hypothetical protein	3.9	4.86E-03	Citronellol	4.1	33723	3	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.1	6.97E-01	Citronellol	6.7	26622	11	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595313	PA0115		conserved hypothetical protein	1.9	3.67E-02	Citronellol	6.3	17085	6	Cytoplasmic	COG2153	General function prediction only	
15595316	PA0118		hypothetical protein	2.2	3.75E-02	Glucose	6.8	21473	5	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595320	PA0122	rahU	rahU	140.7	9.16E-06	Citronellol	4.4	14579	6	Extracellular			
15595324	PA0126		hypothetical protein	3.5	1.07E-01	Glucose	8.0	22367	2	Outer Membrane Vesicle			
15595326	PA0128		conserved hypothetical protein	4.6	9.33E-03	Glucose	4.9	12132	3	Unknown	COG2824	Inorganic ion transport and metabolism	
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.0	9.78E-01	Citronellol	6.0	53323	8	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	1.4	1.60E-01	Citronellol	6.3	20541	16	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	3.1	2.15E-02	Glucose	5.0	55835	7	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
15595342	PA0144		hypothetical protein	1.9	3.57E-01	Citronellol	8.4	22431	6	Unknown	COG3613	Nucleotide transport and metabolism	
15595343	PA0145		hypothetical protein	1.2	3.05E-01	Citronellol	4.4	18448	2	Cytoplasmic	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.5	1.06E-02	Citronellol	4.9	36163	7	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595357	PA0159		probable transcriptional regulator	1.3	4.29E-01	Glucose	6.0	34683	2	Cytoplasmic	COG0583	Transcription	
15595362	PA0164		probable gamma-glutamyltranspeptidase	2.2	2.94E-02	Citronellol	6.5	58453	2	Periplasmic	COG0405	Amino acid transport and metabolism	
15595368	PA0170		hypothetical protein	3.4	3.81E-03	Glucose	4.3	14553	5	Cytoplasmic			
15595369	PA0171		hypothetical protein	1.0	8.87E-01	Glucose	7.1	19800	13	Cytoplasmic			
15595372	PA0174		conserved hypothetical protein	54.1	6.04E-03	Citronellol	8.5	22206	2	Cytoplasmic	COG1871	Cell motility and secretion	Signal transduction mechanisms
15595374	PA0176	aer2	aerotaxis transducer Aer2	17.7	1.30E-04	Citronellol	4.8	72591	22	Cytoplasmic	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595375	PA0177		probable purine-binding chemotaxis protein	34.5	2.30E-06	Citronellol	4.3	17487	3	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595376	PA0178		probable two-component sensor	100.7	1.75E-01	Citronellol	4.5	68931	5	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	4.5	4.62E-04	Citronellol	5.9	38650	21	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595393	PA0196	pntB	pyridine nucleotide transhydrogenase, beta subunit	7.6	9.84E-02	Citronellol	7.3	49947	2	Cytoplasmic Membrane	COG1282	Energy production and conversion	
15595400	PA0203		probable binding protein component of ABC transporter	1.9	5.91E-01	Citronellol	6.3	37860	3	Periplasmic	COG0687	Amino acid transport and metabolism	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	25.8	7.94E-05	Citronellol	4.5	30343	10	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	48.2	8.96E-06	Citronellol	7.1	28496	8	Cytoplasmic			
15595424	PA0227		probable CoA transferase, subunit B	12.6	3.43E-05	Citronellol	5.4	27314	3	Cytoplasmic	COG2057	Lipid metabolism	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	1.4	1.55E-01	Citronellol	6.2	49121	4	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	2.1	5.08E-02	Citronellol	5.1	27985	3	Unknown	COG0596	General function prediction only	
15595429	PA0232	pcaC	gamma-carboxymuconolactone decarboxylase	3.3	2.06E-03	Citronellol	7.1	15084	3	Unknown	COG0599	Function unknown	
15595444	PA0247	pobA	p-hydroxybenzoate hydroxylase	194.8	1.58E-04	Citronellol	6.8	44323	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15595460	PA0263	hcpC	secreted protein Hcp	2.8	3.30E-01	Citronellol	5.8	19091	5	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.3	1.57E-01	Citronellol	5.4	51622	25	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	1.2	3.09E-02	Citronellol	6.4	45220	21	Periplasmic	COG0160	Amino acid transport and metabolism	
15595471	PA0274		hypothetical protein	119.8	1.02E-02	Citronellol	8.8	28498	2	Outer Membrane			
15595474	PA0277		conserved hypothetical protein	1.2	5.63E-01	Citronellol	6.5	26626	7	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	2.3	8.42E-03	Glucose	9.0	36433	14	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	1.3	5.42E-01	Glucose	9.1	49667	6	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.5	5.28E-02	Citronellol	4.6	41191	7	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	1.6	9.74E-02	Citronellol	4.6	50907	12	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595494	PA0297	spuA	probable glutamine amidotransferase	7.3	1.26E-03	Citronellol	6.4	26477	2	Unknown	COG2071	General function prediction only	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	1.9	1.96E-01	Glucose	5.0	50965	2	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595496	PA0299	spuC	Polyamine:pyruvate transaminase	1.6	4.59E-02	Citronellol	6.0	50453	16	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	3.5	5.40E-03	Citronellol	7.6	40629	15	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	2.1	2.76E-02	Citronellol	5.5	40069	14	Periplasmic	COG0687	Amino acid transport and metabolism	
15595505	PA0308		hypothetical protein	1.2	6.02E-01	Glucose	6.8	38245	2	Cytoplasmic	COG2267	Lipid metabolism	
15595506	PA0309		hypothetical protein	1.6	1.23E-01	Citronellol	7.6	27021	8	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	2.3	1.95E-02	Citronellol	9.7	28005	11	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15595512	PA0315		hypothetical protein	3.1	1.85E-02	Citronellol	7.2	15463	9	Unknown			
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.3	2.57E-01	Citronellol	6.5	44216	21	Periplasmic	COG0111	Amino acid transport and metabolism	
15595514	PA0317		hypothetical protein	1.0	9.08E-01	Glucose	4.9	51286	18	Periplasmic	COG0277	Energy production and conversion	
15595515	PA0318		conserved hypothetical protein	1.1	5.57E-01	Citronellol	5.3	23843	7	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15595520	PA0323		probable binding protein component of ABC transporter	17.8	2.01E-04	Citronellol	6.8	38901	5	Periplasmic	COG0687	Amino acid transport and metabolism	
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	1.1	4.05E-01	Citronellol	5.3	23721	10	Cytoplasmic	COG0120	Carbohydrate transport and metabolism	
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	1.4	2.12E-01	Glucose	6.5	55351	14	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15595532	PA0335		hypothetical protein	1.0	7.96E-01	Citronellol	4.5	24353	12	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.2	1.29E-01	Glucose	9.5	18726	5	Cytoplasmic	COG0494	DNA replication, recombination, and repair	General function prediction only
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.1	6.69E-01	Glucose	5.6	83606	21	Cytoplasmic	COG3605	Signal transduction mechanisms	
15595536	PA0339		hypothetical protein	3.4	2.87E-01	Glucose	6.7	26527	2	Unknown	COG3332	Function unknown	
15595539	PA0342	thyA	thymidylate synthase	1.1	7.83E-01	Citronellol	6.5	30016	8	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
15595547	PA0350	folA	dihydrofolate reductase	2.7	1.11E-01	Glucose	5.3	18203	5	Unknown	COG0262	Coenzyme metabolism	
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.6	5.16E-03	Glucose	6.0	65160	34	Periplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15595552	PA0355	pfpI	protease PfpI	42.6	5.83E-03	Citronellol	5.0	19246	7	Cytoplasmic	COG0693	General function prediction only	

15595553	PA0356		hypothetical protein	1.1	5.15E-01	Glucose	5.3	30360	4	Unknown	COG1639	Signal transduction mechanisms	
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	1.2	1.86E-01	Citronellol	9.0	17771	11	Cytoplasmic	COG0669	Coenzyme metabolism	
15595561	PA0364		probable oxidoreductase	23.0	1.67E-04	Citronellol	7.0	57805	9	Unknown	COG2303	Amino acid transport and metabolism	
15595562	PA0365		hypothetical protein	445.9	4.81E-02	Citronellol	7.5	19558	2	Cytoplasmic Membrane			
15595563	PA0366		probable aldehyde dehydrogenase	16.7	4.71E-04	Citronellol	9.2	52876	16	Cytoplasmic	COG1012	Energy production and conversion	
15595564	PA0367		probable transcriptional regulator	4.2	8.04E-04	Citronellol	5.9	24540	3	Cytoplasmic	COG1309	Transcription	
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	2.1	8.38E-02	Glucose	4.5	48391	9	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.5	1.41E-02	Glucose	4.8	28234	12	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
15595579	PA0382	micA	DNA mismatch repair protein MicA	2.1	9.41E-04	Glucose	8.3	25331	3	Cytoplasmic	COG0220	General function prediction only	
15595580	PA0383		conserved hypothetical protein	16.8	1.41E-05	Citronellol	8.3	50243	6	Unknown			
15595584	PA0387		conserved hypothetical protein	1.6	7.35E-01	Citronellol	6.1	21242	7	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
15595585	PA0388		hypothetical protein	1.0	8.50E-01	Citronellol	7.4	15303	3	Periplasmic			
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	1.5	1.04E-01	Glucose	4.5	28094	10	Cytoplasmic	COG0345	Amino acid transport and metabolism	
15595591	PA0394		conserved hypothetical protein	2.2	1.75E-02	Citronellol	6.7	24505	5	Cytoplasmic	COG0325	General function prediction only	
15595592	PA0395	pilT	twitching motility protein PilT	1.7	6.17E-02	Citronellol	6.9	38021	8	Cytoplasmic	COG2805	Cell motility and secretion	Intracellular trafficking and secretion
15595596	PA0399		cystathionine beta-synthase	1.1	2.91E-01	Glucose	5.5	49170	24	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15595597	PA0400		probable cystathionine gamma-lyase	1.4	3.12E-01	Citronellol	6.6	42786	10	Cytoplasmic	COG0626	Amino acid transport and metabolism	
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.1	5.01E-01	Citronellol	5.8	44150	9	Periplasmic	COG0044	Nucleotide transport and metabolism	
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.0	9.65E-01	Glucose	6.8	36629	18	Periplasmic	COG0540	Nucleotide transport and metabolism	
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.3	1.27E-02	Citronellol	5.7	18676	8	Cytoplasmic	COG2065	Nucleotide transport and metabolism	
15595604	PA0407	gshB	glutathione synthetase	2.0	1.44E-02	Citronellol	5.8	35705	16	Periplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
15595605	PA0408	pilG	twitching motility protein PilG	29.8	7.58E-04	Glucose	7.4	14718	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595607	PA0410	pilI	twitching motility protein PilI	1.4	3.10E-01	Glucose	6.6	19934	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595608	PA0411	pilJ	twitching motility protein PilJ	2.1	2.93E-01	Glucose	4.4	72528	3	Outer Membrane Vesicle	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595610	PA0413	chpA	component of chemotactic signal transduction system	1.2	4.08E-01	Glucose	4.2	268573	18	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595612	PA0415	chpC	probable chemotaxis protein	2.6	3.51E-04	Glucose	4.7	17625	6	Unknown			
15595615	PA0418		hypothetical protein	1.1	6.09E-01	Glucose	5.6	52140	3	Cytoplasmic			
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1.2	4.02E-01	Citronellol	6.3	52478	12	Cytoplasmic	COG0161	Coenzyme metabolism	
15595620	PA0423	pasP	PasP	2.4	2.54E-01	Citronellol	6.5	20776	20	Periplasmic	COG2353	Function unknown	
15595622	PA0425	mexA	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexA precursor	1.6	8.71E-02	Citronellol	9.2	40969	3	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15595623	PA0426	mexB	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB	4.8	9.02E-03	Citronellol	5.4	112790	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15595624	PA0427	oprM	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	2.8	8.40E-02	Citronellol	5.3	52598	4	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15595625	PA0428		probable ATP-dependent RNA helicase	2.6	1.64E-01	Glucose	10.7	70112	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
15595626	PA0429		hypothetical protein	4.8	3.40E-02	Glucose	7.0	40872	3	Cytoplasmic			
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	1.1	4.89E-01	Citronellol	6.5	32196	17	Periplasmic	COG0685	Amino acid transport and metabolism	
15595628	PA0431		hypothetical protein	2.3	5.19E-01	Citronellol	6.8	20639	2	Unknown	COG0317	Signal transduction mechanisms	Transcription
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	1.1	7.40E-01	Citronellol	6.0	51400	35	Periplasmic	COG0499	Coenzyme metabolism	
15595631	PA0434		hypothetical protein	16.3	2.03E-02	Citronellol	5.8	81304	5	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15595634	PA0437	codA	cytosine deaminase	1.3	3.53E-01	Citronellol	6.0	47074	6	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15595643	PA0446		conserved hypothetical protein	3.2	7.50E-05	Citronellol	5.3	43847	5	Cytoplasmic	COG1804	Energy production and conversion	
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	3.6	1.99E-03	Citronellol	6.1	43311	7	Cytoplasmic	COG1960	Lipid metabolism	
15595646	PA0449		hypothetical protein	1.2	1.94E-01	Citronellol	10.5	19808	12	Cytoplasmic	COG1607	Lipid metabolism	
15595652	PA0455	dbpA	RNA helicase DbpA	2.0	6.50E-03	Glucose	8.4	49752	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
15595656	PA0459		probable ClpA/B protease ATP binding subunit	68.6	1.31E-03	Citronellol	6.7	94143	9	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595657	PA0460		hypothetical protein	15.6	7.22E-03	Glucose	5.8	18727	2	Unknown			
15595659	PA0462		hypothetical protein	2.7	1.32E-02	Citronellol	10.6	26230	12	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15595660	PA0463	creB	two-component response regulator CreB	3.1	1.71E-01	Glucose	5.4	25573	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595664	PA0467		conserved hypothetical protein	1.5	5.79E-02	Citronellol	7.5	23301	9	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15595665	PA0468		hypothetical protein	1.0	8.47E-01	Citronellol	4.8	33594	2	Periplasmic	COG4257	Defense mechanisms	
15595666	PA0469		hypothetical protein	3.0	3.71E-03	Citronellol	4.7	32137	9	Cytoplasmic			
15595670	PA0473		probable glutathione S-transferase	5.2	4.80E-05	Citronellol	5.8	28294	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15595675	PA0478		probable N-acetyltransferase	1.7	3.17E-02	Citronellol	4.6	18109	3	Cytoplasmic	COG0456	General function prediction only	
15595679	PA0482	glcB	malate synthase G	2.9	1.83E-02	Citronellol	5.5	78659	61	Periplasmic	COG2225	Energy production and conversion	
15595681	PA0484		conserved hypothetical protein	14.4	1.71E-05	Citronellol	4.5	18553	4	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15595697	PA0500	bioB	biotin synthase	16.6	9.33E-03	Glucose	6.0	39113	11	Cytoplasmic	COG0502	Coenzyme metabolism	
15595699	PA0502		probable biotin biosynthesis protein bioH	3.1	5.07E-03	Citronellol	4.3	26494	3	Cytoplasmic	COG0596	General function prediction only	
15595700	PA0503		probable biotin synthesis protein BioC	4.0	9.57E-03	Glucose	9.0	29712	5	Unknown	COG2226	Coenzyme metabolism	
15595701	PA0504	bioD	dethiobiotin synthase	1.2	9.49E-01	Citronellol	5.3	23337	10	Cytoplasmic	COG0132	Coenzyme metabolism	
15595703	PA0506		probable acyl-CoA dehydrogenase	8.2	2.01E-05	Citronellol	5.8	65358	37	Periplasmic	COG1960	Lipid metabolism	
15595704	PA0507		probable acyl-CoA dehydrogenase	13.1	6.20E-02	Citronellol	6.4	64349	3	Cytoplasmic	COG1960	Lipid metabolism	
15595705	PA0508		probable acyl-CoA dehydrogenase	10.8	2.30E-04	Citronellol	5.1	63628	46	Cytoplasmic	COG1960	Lipid metabolism	
15595732	PA0535		probable transcriptional regulator	3.2	1.55E-01	Glucose	4.9	20231	2	Cytoplasmic	COG1396	Transcription	
15595734	PA0537		conserved hypothetical protein	1.9	5.89E-01	Citronellol	8.9	22180	7	Outer Membrane Vesicle	COG1704	Function unknown	
15595743	PA0546	metK	methionine adenosyltransferase	1.1	5.86E-01	Citronellol	5.2	42709	27	Cytoplasmic	COG0192	Coenzyme metabolism	
15595745	PA0548	tktA	transketolase	1.3	1.83E-02	Glucose	5.0	72220	39	Periplasmic	COG0021	Carbohydrate transport and metabolism	
15595747	PA0550		conserved hypothetical protein	2.2	2.07E-02	Citronellol	5.4	29834	6	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	2.3	1.28E-02	Citronellol	5.8	38743	3	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15595749	PA0552	pgk	phosphoglycerate kinase	1.6	1.68E-02	Citronellol	5.1	40404	22	Periplasmic	COG0126	Carbohydrate transport and metabolism	
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	1.6	1.65E-01	Citronellol	5.3	38574	28	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
15595755	PA0558		conserved hypothetical protein	2.8	3.18E-03	Citronellol	6.2	27987	12	Cytoplasmic	COG2226	Coenzyme metabolism	
15595756	PA0559		conserved hypothetical protein	1.8	1.07E-01	Glucose	6.5	42586	2	Cytoplasmic	COG2081	General function prediction only	
15595759	PA0562		probable hydrolase	4.3	4.00E-02	Glucose	5.4	24232	6	Cytoplasmic	COG0637	General function prediction only	
15595765	PA0568		hypothetical protein	1.7	1.88E-02	Citronellol	4.2	17683	2	Cytoplasmic			
15595768	PA0571		hypothetical protein	1.7	5.10E-01	Citronellol	5.0	22501	5	Unknown			
15595773	PA0576	rpoD	sigma factor RpoD	1.9	4.09E-02	Glucose	4.6	69643	29	Outer Membrane Vesicle	COG0568	Transcription	
15595775	PA0578		conserved hypothetical protein	2.5	3.56E-02	Citronellol	6.0	16842	3	Cytoplasmic	COG1610	Function unknown	
15595776	PA0579	rpsU	30S ribosomal protein S21	4.0	1.00E-01	Glucose	11.4	8485	3	Cytoplasmic			
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	3.0	1.09E-02	Glucose	6.2	36561	4	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
15595780	PA0583		hypothetical protein	1.1	7.75E-01	Glucose	5.6	20091	4	Cytoplasmic	COG0801	Coenzyme metabolism	
15595783	PA0586		conserved hypothetical protein	10.6	4.93E-04	Citronellol	5.1	60814	9	Cytoplasmic	COG2719	Function unknown	
15595784	PA0587		conserved hypothetical protein	19.4	1.66E-04	Citronellol	7.8	48742	9	Cytoplasmic	COG2718	Function unknown	
15595785	PA0588		conserved hypothetical protein	8.2	8.21E-06	Citronellol	5.5	73722	42	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms	
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	1.1	8.77E-01	Glucose	7.2	32019	5	Cytoplasmic			
15595789	PA0592	ksgA	rRNA (adenine-N6,N6)-dimethyltransferase	3.0	1.14E-01	Glucose	7.4	30058	6	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.1	6.92E-01	Citronellol	6.6	34891	8	Cytoplasmic	COG1995	Coenzyme metabolism	
15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.0	8.53E-01	Citronellol	5.6	48441	25	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15595792	PA0595	ostA	organic solvent tolerance protein OstA precursor	1.4	3.86E-01	Glucose	5.3	104271	4	Periplasmic	COG1452	Cell envelope biogenesis, outer membrane	
15595793	PA0596		hypothetical protein	1.3	1.33E-01	Citronellol	5.1	38185	7	Cytoplasmic	COG3178	General function prediction only	
15595794	PA0597		probable nucleotidyl transferase	1.2	1.74E-01	Glucose	6.1	24149	3	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
15595798	PA0601		probable two-component response regulator	2.0	2.94E-01	Glucose	6.5	22868	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15595801	PA0604		probable binding protein component of ABC transporter	3.4	1.09E-02	Citronellol	5.6	38167	8	Periplasmic	COG0687	Amino acid transport and metabolism	
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.9	3.31E-02	Glucose	5.1	24096	13	Cytoplasmic	COG0036	Carbohydrate transport and metabolism	
15595806	PA0609	trpE	anthranilate synthetase component I	1.0	8.06E-01	Glucose	4.7	54555	14	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
15595846	PA0649	trpG	anthranilate synthase component II	3.9	1.17E-01	Glucose	6.0	22046	4	Cytoplasmic	COG0512	Amino acid transport and metabolism	Coenzyme metabolism
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	3.8	5.80E-02	Glucose	5.6	37384	6	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	1.7	1.54E-02	Citronellol	4.6	30315	11	Cytoplasmic	COG0134	Amino acid transport and metabolism	
15595850	PA0653		conserved hypothetical protein	1.5	7.97E-02	Citronellol	6.4	15237	6	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones	
15595851	PA0654	speD	S-adenosylmethionine decarboxylase proenzyme	2.7	1.17E-01	Glucose	4.5	30446	5	Cytoplasmic	COG1586	Amino acid transport and metabolism	
15595852	PA0655		hypothetical protein	1.0	8.99E-01	Citronellol	5.3	23644	5	Unknown	COG2941	Coenzyme metabolism	
15595857	PA0660		hypothetical protein	3.2	1.44E-03	Citronellol	6.2	34814	20	Cytoplasmic	COG2070	General function prediction only	
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.4	1.31E-01	Citronellol	6.7	36684	20	Cytoplasmic	COG0002	Amino acid transport and metabolism	
15595861	PA0664		hypothetical protein	2.9	3.90E-03	Glucose	5.6	14790	3	Cytoplasmic	COG1664	Cell envelope biogenesis, outer membrane	

15595862	PA0665		conserved hypothetical protein	2.4	1.54E-01	Glucose	4.0	12484	2	Cytoplasmic	COG0316	Posttranslational modification, protein turnover, chaperones	
15595863	PA0666		conserved hypothetical protein	2.1	2.40E-03	Citronellol	5.2	39087	3	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.1	9.00E-01	Citronellol	5.6	44129	27	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis	
15595869	PA0672	hemO	heme oxygenase	3.3	1.79E-02	Glucose	4.8	21953	10	Unknown	COG3230	Inorganic ion transport and metabolism	
15595901	PA0704		probable amidase	6.9	2.13E-03	Citronellol	6.9	50605	3	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15595903	PA0706	cat	chloramphenicol acetyltransferase	1.1	8.28E-01	Citronellol	6.1	23524	3	Unknown	COG0110	General function prediction only	
15595912	PA0715		hypothetical protein	2.2	4.32E-03	Citronellol	9.9	36589	6	Cytoplasmic	COG3344	DNA replication, recombination, and repair	
15595938	PA0741		conserved hypothetical protein	2.1	1.47E-01	Citronellol	6.6	22687	6	Unknown	COG2910	General function prediction only	
15595940	PA0743		probable 3-hydroxyisobutyrate dehydrogenase	101.7	1.08E-04	Citronellol	5.3	30754	2	Cytoplasmic	COG2084	Lipid metabolism	
15595941	PA0744		probable enoyl-CoA hydratase/isomerase	6.9	1.27E-03	Citronellol	5.1	40589	6	Cytoplasmic	COG1024	Lipid metabolism	
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	2.9	2.98E-04	Citronellol	6.4	29904	13	Cytoplasmic	COG1024	Lipid metabolism	
15595943	PA0746		probable acyl-CoA dehydrogenase	5.1	3.42E-03	Citronellol	5.3	42553	2	Cytoplasmic	COG1960	Lipid metabolism	
15595944	PA0747		probable aldehyde dehydrogenase	32.6	5.14E-04	Citronellol	6.1	54564	3	Cytoplasmic	COG1012	Energy production and conversion	
15595947	PA0750	ung	uracil-DNA glycosylase	1.0	8.67E-01	Glucose	8.2	26010	7	Cytoplasmic	COG0692	DNA replication, recombination, and repair	
15595951	PA0754		hypothetical protein	5.2	1.07E-03	Citronellol	5.5	34918	14	Unknown	COG3181	Function unknown	
15595953	PA0756		probable two-component response regulator	6.8	8.81E-02	Glucose	5.2	24431	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595955	PA0758		hypothetical protein	1.5	1.81E-02	Glucose	4.7	30875	9	Cytoplasmic	COG1639	Signal transduction mechanisms	
15595956	PA0759		conserved hypothetical protein	1.1	1.96E-01	Glucose	5.2	33667	14	Unknown	COG0354	General function prediction only	
15595958	PA0761	nadB	L-aspartate oxidase	1.7	4.01E-02	Glucose	6.3	60004	10	Cytoplasmic	COG0029	Coenzyme metabolism	
15595959	PA0762	algU	sigma factor AlgU	1.5	1.50E-01	Glucose	5.4	22196	7	Cytoplasmic	COG1595	Transcription	
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	1.3	1.98E-01	Citronellol	6.1	34572	6	Periplasmic	COG3026	Signal transduction mechanisms	
15595963	PA0766	mucD	serine protease MucD precursor	1.4	2.03E-01	Glucose	7.8	50321	7	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
15595964	PA0767	lepA	GTP-binding protein LepA	5.6	1.96E-02	Glucose	5.3	66263	6	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
15595967	PA0770	rnc	ribonuclease III	1.2	2.67E-01	Glucose	6.6	25474	4	Cytoplasmic	COG0571	Transcription	
15595968	PA0771	era	GTP-binding protein Era	1.0	7.26E-01	Citronellol	6.6	34550	4	Cytoplasmic Membrane	COG1159	General function prediction only	
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.0	8.93E-01	Glucose	5.6	27228	8	Cytoplasmic	COG0854	Coenzyme metabolism	
15595971	PA0774		conserved hypothetical protein	7.6	4.06E-02	Glucose	6.4	36522	2	Cytoplasmic	COG2227	Coenzyme metabolism	
15595972	PA0775		conserved hypothetical protein	3.0	4.91E-02	Glucose	5.3	27608	3	Cytoplasmic	COG4106	General function prediction only	
15595976	PA0779		probable ATP-dependent protease	1.5	3.87E-01	Citronellol	6.8	88574	12	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15595979	PA0782	putA	proline dehydrogenase PutA	2.6	1.75E-01	Citronellol	6.0	115630	13	Periplasmic	COG4230	Energy production and conversion	
15595989	PA0792	prpD	propionate catabolic protein PrpD	2.1	1.19E-02	Citronellol	6.6	54881	7	Cytoplasmic	COG2079	General function prediction only	
15595991	PA0794		probable aconitate hydratase	1.5	3.48E-01	Citronellol	5.3	94890	12	Cytoplasmic	COG1048	Energy production and conversion	
15595992	PA0795	prpC	citrate synthase 2	2.6	2.53E-04	Citronellol	6.4	41689	14	Cytoplasmic	COG0372	Energy production and conversion	
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.6	9.46E-02	Citronellol	5.2	32137	14	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15596001	PA0804		probable oxidoreductase	2.9	6.50E-03	Citronellol	4.8	30017	4	Cytoplasmic	COG0656	General function prediction only	
15596017	PA0820		hypothetical protein	1.4	2.81E-01	Citronellol	6.9	30068	2	Cytoplasmic	COG3183	Defense mechanisms	
15596030	PA0833		hypothetical protein	1.2	6.25E-01	Citronellol	9.0	24713	6	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596032	PA0835	pta	phosphate acetyltransferase	1.4	1.15E-01	Citronellol	5.0	75696	16	Periplasmic	COG0280	Energy production and conversion	
15596033	PA0836	ackA	acetate kinase	2.6	1.31E-03	Citronellol	7.1	42421	8	Cytoplasmic	COG0282	Energy production and conversion	
15596034	PA0837	slyD	peptidyl-prolyl cis-trans isomerase SlyD	3.3	1.64E-01	Citronellol	4.2	17010	2	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15596035	PA0838		probable glutathione peroxidase	3.5	2.58E-03	Citronellol	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596037	PA0840		probable oxidoreductase	1.3	5.87E-01	Citronellol	5.5	40334	10	Cytoplasmic	COG1902	Energy production and conversion	
15596045	PA0848		probable alkyl hydroperoxide reductase	1.4	7.57E-01	Citronellol	5.1	21814	4	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15596046	PA0849	trxB2	thioredoxin reductase 2	4.8	1.12E-02	Glucose	5.4	33481	2	Cytoplasmic	COG0492	Posttranslational modification, protein turnover, chaperones	
15596048	PA0851		hypothetical protein	5.7	1.94E-02	Glucose	6.8	34024	7	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15596049	PA0852	cbpD	chitin-binding protein CbpD precursor	1.2	8.66E-01	Citronellol	6.9	41917	6	Extracellular	COG3397	Function unknown	
15596050	PA0853		probable oxidoreductase	2.9	1.14E-02	Citronellol	8.3	23485	6	Cytoplasmic	COG2249	General function prediction only	
15596051	PA0854	fumC2	fumarate hydratase	3.8	1.38E-04	Citronellol	6.1	49122	19	Cytoplasmic	COG0114	Energy production and conversion	
15596053	PA0856		hypothetical protein	2.4	1.42E-01	Glucose	10.1	19998	10	Unknown	COG3184	Function unknown	
15596055	PA0858		conserved hypothetical protein	10.6	6.58E-02	Glucose	5.7	35420	5	Cytoplasmic	COG1054	General function prediction only	
15596056	PA0859		hypothetical protein	1.6	5.76E-02	Citronellol	4.6	21466	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
15596059	PA0862		hypothetical protein	2.2	7.04E-02	Citronellol	6.5	29845	4	Cytoplasmic	COG5424	Coenzyme metabolism	
15596060	PA0863		probable oxidoreductase	3.0	6.03E-02	Citronellol	4.9	33368	3	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15596064	PA0867	mliC	membrane-bound lysozyme inhibitor of c-type lysozyme MliC	1.8	1.68E-01	Glucose	4.8	13695	7	Outer Membrane Vesicle	COG3895	General function prediction only	
15596067	PA0870	phhC	aromatic amino acid aminotransferase	2.0	2.79E-03	Citronellol	6.2	43273	7	Cytoplasmic	COG1448	Amino acid transport and metabolism	
15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	2.3	5.80E-03	Citronellol	6.4	13333	5	Cytoplasmic	COG2154	Coenzyme metabolism	
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	3.4	6.12E-05	Citronellol	6.3	71762	34	Cytoplasmic	COG0365	Lipid metabolism	
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.6	2.38E-02	Citronellol	6.8	28010	17	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596088	PA0891		hypothetical protein	2.6	7.84E-03	Citronellol	4.9	40214	4	Cytoplasmic	COG3608	General function prediction only	
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.4	1.71E-01	Citronellol	5.8	43747	26	Periplasmic	COG4992	Amino acid transport and metabolism	
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	2.7	5.00E-03	Citronellol	4.7	36930	5	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	2.9	1.29E-02	Citronellol	6.5	37245	10	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596096	PA0899	aruB	succinylarginine dihydrolase	2.0	1.75E-03	Citronellol	6.2	48875	11	Periplasmic	COG3724	Amino acid transport and metabolism	
15596098	PA0901	aruE	succinylglutamate desuccinylase	2.0	5.65E-03	Citronellol	6.0	36909	8	Cytoplasmic	COG2988	Amino acid transport and metabolism	
15596099	PA0902		hypothetical protein	1.3	3.32E-02	Glucose	6.4	35430	12	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15596100	PA0903	alaS	alanyl-tRNA synthetase	1.2	4.80E-01	Glucose	5.2	94701	43	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.0	9.52E-01	Citronellol	5.0	44388	30	Cytoplasmic	COG0527	Amino acid transport and metabolism	
15596112	PA0915		conserved hypothetical protein	5.4	1.61E-02	Glucose	6.3	17514	6	Cytoplasmic	COG4807	Function unknown	
15596113	PA0916		conserved hypothetical protein	1.1	7.31E-01	Glucose	4.6	48961	3	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis	
15596123	PA0926		hypothetical protein	1.9	2.80E-01	Glucose	8.5	15829	3	Cytoplasmic			
15596129	PA0932	cysM	cysteine synthase B	1.3	1.84E-01	Citronellol	5.5	32448	15	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596131	PA0934	relA	GTP pyrophosphokinase	3.2	2.46E-02	Glucose	7.6	83815	15	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15596132	PA0935		conserved hypothetical protein	1.1	6.05E-01	Glucose	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only	
15596134	PA0937		conserved hypothetical protein	1.1	6.31E-01	Glucose	9.7	20789	2	Cytoplasmic	COG3122	Function unknown	
15596140	PA0943		hypothetical protein	1.5	9.24E-02	Citronellol	8.7	27183	15	Periplasmic			
15596141	PA0944	purN	phosphoribosylaminoimidazole synthetase	1.2	3.22E-01	Glucose	7.2	24734	2	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	1.1	6.94E-01	Glucose	4.5	37122	17	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
15596144	PA0947		conserved hypothetical protein	7.1	1.09E-02	Glucose	6.0	26843	4	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	2.5	2.97E-01	Citronellol	6.8	20744	6	Unknown	COG0655	General function prediction only	
15596153	PA0956	proS	prolyl-tRNA synthetase	1.8	5.49E-04	Glucose	5.1	63103	30	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis	
15596154	PA0957		hypothetical protein	12.1	1.77E-03	Citronellol	6.3	14622	5	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	2.1	1.60E-01	Citronellol	4.8	48360	11	Periplasmic			
15596156	PA0959		hypothetical protein	1.8	9.23E-01	Citronellol	6.5	23069	4	Cytoplasmic	COG0537	Nucleotide transport and metabolism	Carbohydrate transport and metabolism
15596159	PA0962		probable dna-binding stress protein	1.4	6.04E-01	Citronellol	4.7	17493	11	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.9	1.48E-02	Glucose	5.2	66207	39	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis	
15596161	PA0964	pmpR	pqsR-mediated PQS regulator, PmpR	1.1	8.71E-01	Citronellol	4.4	26557	2	Cytoplasmic	COG0217	Function unknown	
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.1	7.84E-01	Citronellol	6.1	21927	12	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
15596165	PA0968		conserved hypothetical protein	7.1	2.41E-01	Glucose	8.7	16672	2	Cytoplasmic	COG0824	General function prediction only	
15596166	PA0969	tolQ	TolQ protein	2.0	6.52E-01	Citronellol	6.3	25250	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
15596169	PA0972	tolB	TolB protein	1.5	1.29E-01	Citronellol	9.2	47720	16	Periplasmic	COG0823	Intracellular trafficking and secretion	
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	2.1	1.90E-01	Glucose	6.3	17925	5	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596171	PA0974		conserved hypothetical protein	1.7	1.33E-01	Citronellol	8.7	29097	6	Outer Membrane Vesicle	COG1729	Function unknown	
15596173	PA0976		conserved hypothetical protein	1.4	5.88E-02	Glucose	4.7	23900	4	Unknown	COG0603	General function prediction only	
15596178	PA0981		hypothetical protein	3.5	6.12E-02	Citronellol	6.4	21871	3	Unknown			
15596192	PA0995	ogt	methylated-DNA--protein-cysteine methyltransferase	16.1	4.16E-03	Glucose	7.6	19253	2	Cytoplasmic	COG0350	DNA replication, recombination, and repair	
15596194	PA0997	pqsB	PqsB	2.9	4.53E-03	Glucose	4.6	30501	5	Cytoplasmic	COG0332	acyl-carrier-protein	
15596195	PA0998	pqsC	PqsC	3.8	2.34E-03	Glucose	4.9	38238	3	Cytoplasmic	COG0332	acyl-carrier-protein	
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	10.2	6.67E-04	Glucose	5.3	36378	5	Cytoplasmic	COG0332	acyl-carrier-protein	
15596201	PA1004	nadA	quinolinate synthetase A	1.5	9.61E-04	Glucose	5.4	38418	5	Cytoplasmic	COG0379	Coenzyme metabolism	
15596202	PA1005		conserved hypothetical protein	3.3	3.99E-02	Citronellol	8.4	52994	5	Periplasmic	COG4783	General function prediction only	
15596205	PA1008	bcp	bacterioferritin comigratory protein	1.8	5.44E-03	Citronellol	7.3	17352	11	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones	
15596206	PA1009		hypothetical protein	1.1	9.98E-01	Citronellol	5.6	20585	3	Cytoplasmic	COG2716	Amino acid transport and metabolism	

15596207	PA1010	dapA	dihydrodipicolinate synthase	1.0	9.75E-01	Glucose	6.4	31449	24	Periplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
15596208	PA1011		hypothetical protein	1.0	8.50E-01	Glucose	4.7	43055	10	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane	
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.3	3.30E-01	Citronellol	5.1	26831	18	Periplasmic	COG0152	Nucleotide transport and metabolism	
15596212	PA1015		probable transcriptional regulator	3.5	3.40E-03	Citronellol	7.0	28853	3	Cytoplasmic	COG1414	Transcription	
15596220	PA1023		probable short-chain dehydrogenase	3.2	6.52E-03	Citronellol	6.7	32821	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596223	PA1026		hypothetical protein	1.4	2.90E-01	Citronellol	4.8	17184	2	Cytoplasmic			
15596224	PA1027		probable aldehyde dehydrogenase	1.5	1.31E-01	Citronellol	6.8	57291	4	Cytoplasmic	COG1012	Energy production and conversion	
15596230	PA1033		probable glutathione S-transferase	1.4	2.97E-01	Citronellol	6.8	24527	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596233	PA1036		hypothetical protein	1.1	7.84E-01	Citronellol	4.6	19537	3	Unknown			
15596236	PA1039		conserved hypothetical protein	1.2	9.55E-01	Citronellol	6.7	17189	3	Unknown	COG3012	Function unknown	
15596237	PA1040		hypothetical protein	1.7	2.77E-02	Citronellol	6.0	18721	6	Unknown			
15596238	PA1041		probable outer membrane protein precursor	33.4	3.46E-03	Citronellol	5.1	21747	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
15596240	PA1043		hypothetical protein	3.8	2.62E-02	Glucose	8.2	27276	3	Periplasmic			
15596244	PA1047		probable esterase	1.8	1.91E-02	Citronellol	6.1	42335	6	Periplasmic	COG1680	Defense mechanisms	
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	2.4	4.50E-03	Citronellol	6.8	24860	8	Cytoplasmic	COG0259	Coenzyme metabolism	
15596250	PA1053		conserved hypothetical protein	1.3	4.39E-01	Glucose	10.1	15649	2	Outer Membrane Vesicle	COG3133	Cell envelope biogenesis, outer membrane	
15596258	PA1061		conserved hypothetical protein	1.5	5.35E-02	Citronellol	6.6	39952	16	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596259	PA1062		hypothetical protein	3.5	3.07E-02	Glucose	6.5	19155	5	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane	
15596261	PA1064		hypothetical protein	2.0	8.00E-01	Citronellol	5.1	24172	3	Periplasmic	COG3650	Function unknown	
15596262	PA1065		conserved hypothetical protein	8.0	8.36E-04	Citronellol	6.8	17989	2	Unknown	COG3189	Function unknown	
15596263	PA1066		probable short-chain dehydrogenase	2.2	3.04E-03	Citronellol	7.6	23376	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596265	PA1068		probable heat shock protein (hsp90 family)	3.3	4.42E-03	Glucose	5.7	70659	14	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596266	PA1069		hypothetical protein	1.7	2.18E-02	Glucose	4.3	86114	25	Cytoplasmic			
15596267	PA1070	braG	branched-chain amino acid transport protein BraG	19.5	2.35E-02	Citronellol	6.6	25592	3	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	4.3	2.67E-03	Citronellol	5.5	39769	27	Periplasmic	COG0683	Amino acid transport and metabolism	
15596286	PA1089		conserved hypothetical protein	1.8	2.51E-01	Glucose	5.0	22471	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596287	PA1090		hypothetical protein	2.4	4.41E-04	Citronellol	5.3	24703	4	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane	
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	5.7	6.73E-02	Citronellol	5.2	187155	25	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane	
15596289	PA1092	fliC	flagellin type B	5.1	1.52E-03	Citronellol	5.2	49242	19	Periplasmic	COG1344	Cell motility and secretion	
15596291	PA1094	fliD	flagellar capping protein FliD	2.1	3.69E-02	Citronellol	7.1	49449	13	Periplasmic	COG1345	Cell motility and secretion	
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.3	2.86E-01	Glucose	5.0	55277	11	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596324	PA1127		probable oxidoreductase	5.3	3.68E-03	Glucose	5.2	36474	5	Cytoplasmic	COG0667	Energy production and conversion	
15596332	PA1135		conserved hypothetical protein	7.5	2.45E-05	Citronellol	6.4	31898	10	Cytoplasmic	COG0693	General function prediction only	
15596337	PA1140		conserved hypothetical protein	1.9	4.76E-02	Citronellol	6.3	31614	4	Cytoplasmic	COG3257	General function prediction only	
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucleotide reductase	4.6	2.11E-03	Glucose	4.5	47386	17	Periplasmic	COG0208	Nucleotide transport and metabolism	
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	3.4	2.50E-03	Glucose	5.7	107105	55	Periplasmic	COG0209	Nucleotide transport and metabolism	
15596354	PA1157		probable two-component response regulator	1.0	9.78E-01	Glucose	4.7	26373	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596358	PA1161	rrmA	rRNA methyltransferase	2.7	5.76E-03	Glucose	7.9	29644	4	Cytoplasmic	COG2226	Coenzyme metabolism	
15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	1.2	3.02E-01	Glucose	5.0	41077	10	Cytoplasmic	COG0624	Amino acid transport and metabolism	
15596362	PA1165	pcpS	PcpS	1.5	1.19E-01	Glucose	7.0	26715	3	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism	
15596363	PA1166		hypothetical protein	14.2	1.95E-04	Citronellol	7.3	28156	8	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596368	PA1171		probable transglycolase	1.7	5.61E-02	Citronellol	9.3	42682	5	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane	
15596370	PA1173	napB	cytochrome c-type protein NapB precursor	24.3	7.84E-05	Citronellol	8.3	17918	3	Periplasmic	COG3043	Energy production and conversion	
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	12.3	3.15E-03	Citronellol	8.6	92942	27	Periplasmic	COG0243	Energy production and conversion	
15596376	PA1179	phoP	two-component response regulator PhoP	1.0	6.43E-01	Glucose	5.2	25650	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596384	PA1187		probable acyl-CoA dehydrogenase	26.2	1.99E-05	Citronellol	6.5	42350	9	Cytoplasmic	COG1960	Lipid metabolism	
15596385	PA1188		hypothetical protein	23.1	2.31E-04	Citronellol	6.0	42128	3	Cytoplasmic	COG1804	Energy production and conversion	
15596389	PA1192		conserved hypothetical protein	1.7	7.88E-03	Glucose	6.5	31260	4	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
15596390	PA1193		hypothetical protein	2.0	8.54E-02	Glucose	9.1	25292	5	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15596397	PA1200		conserved hypothetical protein	1.7	1.29E-01	Citronellol	5.1	24597	6	Cytoplasmic	COG4122	General function prediction only	
15596399	PA1202		probable hydrolase	4.3	3.12E-03	Citronellol	4.8	22471	11	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596401	PA1204		conserved hypothetical protein	1.4	4.28E-01	Citronellol	6.5	20224	5	Cytoplasmic	COG0431	General function prediction only	
15596403	PA1206		hypothetical protein	1.5	2.21E-01	Glucose	4.4	17690	6	Cytoplasmic			
15596413	PA1216		hypothetical protein	11.3	1.03E-03	Citronellol	6.1	28573	6	Cytoplasmic	COG4976	General function prediction only	
15596422	PA1225		probable NAD(P)H dehydrogenase	3.6	5.01E-02	Glucose	7.0	22551	6	Cytoplasmic	COG2249	General function prediction only	
15596431	PA1234		hypothetical protein	3.0	4.20E-02	Glucose	4.6	18460	2	Cytoplasmic			
15596457	PA1260		amino acid ABC transporter periplasmic binding protein	19.8	1.46E-04	Citronellol	5.2	29142	6	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596469	PA1272	cobO	cob(I)alamin adenosyltransferase	1.0	8.91E-01	Citronellol	8.0	22292	4	Cytoplasmic	COG2109	Coenzyme metabolism	
15596473	PA1276	cobC	cobalamin biosynthetic protein CobC	1.3	2.03E-01	Glucose	8.0	36657	2	Cytoplasmic	COG0079	Amino acid transport and metabolism	
15596475	PA1278	cobP	cobinamide kinase	2.8	1.37E-01	Glucose	5.4	18862	3	Cytoplasmic	COG2087	Coenzyme metabolism	
15596476	PA1279	cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.0	8.75E-01	Glucose	6.6	36531	4	Cytoplasmic	COG2038	Coenzyme metabolism	
15596477	PA1280		hypothetical protein	1.6	9.15E-01	Citronellol	6.7	21591	3	Cytoplasmic	COG0406	General function prediction only	
15596480	PA1283		probable transcriptional regulator	1.2	4.52E-01	Glucose	4.9	20307	2	Unknown	COG1309	Transcription	
15596484	PA1287		probable glutathione peroxidase	3.7	1.87E-02	Citronellol	8.3	20217	10	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596485	PA1288		probable outer membrane protein precursor	2.0	2.97E-01	Citronellol	6.0	45561	9	Periplasmic	COG2067	Lipid metabolism	
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	1.4	3.89E-02	Citronellol	5.3	30597	11	Periplasmic	COG2897	Inorganic ion transport and metabolism	
15596491	PA1294	rnd	ribonuclease D	1.4	3.27E-01	Citronellol	4.8	43066	7	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
15596501	PA1304		probable oligopeptidase	1.7	1.32E-01	Glucose	4.7	75881	19	Periplasmic	COG1770	Amino acid transport and metabolism	
15596504	PA1307		conserved hypothetical protein	2.5	2.97E-03	Citronellol	5.7	28544	4	Cytoplasmic	COG0121	General function prediction only	
15596521	PA1324		hypothetical protein	6.9	8.53E-04	Citronellol	5.8	18303	5	Unknown			
15596532	PA1335		probable two-component response regulator	1.8	2.97E-02	Citronellol	6.9	46687	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596534	PA1337	ansB	glutaminase-asparaginase	4.5	5.84E-04	Citronellol	7.3	38644	20	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	2.7	1.52E-02	Citronellol	6.2	59874	15	Periplasmic	COG0405	Amino acid transport and metabolism	
15596538	PA1341		amino acid ABC transporter membrane protein	5.4	6.25E-01	Citronellol	9.3	27593	2	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
15596539	PA1342		probable binding protein component of ABC transporter	3.3	4.96E-03	Citronellol	8.6	33054	43	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596541	PA1344		probable short-chain dehydrogenase	5.8	9.85E-04	Citronellol	4.9	27397	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596554	PA1357		conserved hypothetical protein	4.3	3.22E-02	Glucose	5.3	16789	2	Cytoplasmic	COG2606	Function unknown	
15596568	PA1371		hypothetical protein	2.1	2.41E-02	Citronellol	5.2	27419	2	Unknown	COG5619	Function unknown	
15596569	PA1372		hypothetical protein	1.2	2.79E-01	Citronellol	5.5	79820	20	Cytoplasmic	COG3972	General function prediction only	
15596572	PA1375	pdxB	erythronate-4-phosphate dehydrogenase	1.2	1.09E-01	Citronellol	5.5	41001	5	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	2.8	1.34E-03	Citronellol	5.0	66760	13	Cytoplasmic	COG4579	Signal transduction mechanisms	
15596574	PA1377		conserved hypothetical protein	1.5	1.21E-02	Glucose	7.9	20068	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596599	PA1402		hypothetical protein	2.9	7.04E-02	Citronellol	4.7	23753	6	Cytoplasmic	COG4122	General function prediction only	
15596627	PA1430	lasR	transcriptional regulator LasR	1.9	3.28E-01	Glucose	6.5	26618	3	Cytoplasmic	COG2771	Transcription	
15596637	PA1440		hypothetical protein	1.3	6.91E-02	Citronellol	3.9	22382	3	Cytoplasmic	COG3318	General function prediction only	
15596639	PA1442		conserved hypothetical protein	2.3	1.69E-02	Citronellol	10.3	18760	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
15596640	PA1443	fliM	flagellar motor switch protein FliM	1.3	1.01E-01	Citronellol	5.0	36282	5	Cytoplasmic	COG1868	Cell motility and secretion	
15596641	PA1444	fliN	flagellar motor switch protein FliN	2.9	3.99E-01	Citronellol	4.0	16620	4	Cytoplasmic Membrane	COG1886	Cell motility and secretion	Intracellular trafficking and secretion
15596651	PA1454	fleN	flagellar synthesis regulator FleN	6.9	2.85E-02	Citronellol	8.7	30037	3	Cytoplasmic Membrane	COG0455	Cell motility	
15596652	PA1455	fliA	sigma factor FliA	2.3	3.11E-03	Citronellol	5.9	27522	4	Cytoplasmic	COG1191	Transcription	
15596654	PA1457	cheZ	chemotaxis protein CheZ	1.1	6.27E-01	Glucose	4.6	29622	11	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
15596655	PA1458		probable two-component sensor	2.1	1.29E-01	Glucose	4.3	79737	19	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15596656	PA1459		probable methyltransferase	2.0	4.50E-02	Glucose	8.6	39004	10	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
15596659	PA1462		probable plasmid partitioning protein	1.2	7.72E-01	Citronellol	10.1	28407	4	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
15596661	PA1464		probable purine-binding chemotaxis protein	2.1	6.76E-03	Citronellol	4.1	17536	11	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15596667	PA1470		probable short-chain dehydrogenase	5.6	1.30E-04	Citronellol	4.9	25365	8	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596669	PA1472		conserved hypothetical protein	1.8	2.63E-02	Citronellol	5.8	21138	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	1.6	1.84E-01	Citronellol	8.6	36485	18	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15596692	PA1495		hypothetical protein	2.6	8.87E-03	Citronellol	5.9	23443	2	Unknown	COG4339	Function unknown	
15596713	PA1516		hypothetical protein	4.4	1.10E-01	Citronellol	4.8	18896	6	Cytoplasmic	COG3195	Function unknown	
15596723	PA1526		probable transcriptional regulator	2.7	1.12E-01	Citronellol	7.8	25070	2	Cytoplasmic	COG1802	Transcription	
15596724	PA1527		conserved hypothetical protein	7.0	1.97E-01	Citronellol	4.8	131580	11	Cytoplasmic	COG1196	Cell division and chromosome partitioning	

15596725	PA1528	zipA	cell division protein ZipA	1.8	5.00E-01	Citronellol	5.7	32236	4	Outer Membrane Vesicle	COG3115	Cell division and chromosome partitioning	
15596726	PA1529	lig	DNA ligase	1.0	9.37E-01	Glucose	5.1	86767	24	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	9.5	1.04E-02	Glucose	4.4	73309	12	Cytoplasmic	COG2812	DNA replication, recombination, and repair	
15596731	PA1534	recR	recombination protein RecR	1.2	4.12E-01	Glucose	6.0	21173	7	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
15596732	PA1535		citronellyl-CoA dehydrogenase	65.5	1.63E-05	Citronellol	5.6	42041	22	Cytoplasmic	COG1960	Lipid metabolism	
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.5	2.73E-01	Citronellol	4.6	19804	7	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15596741	PA1544	anr	transcriptional regulator Anr	1.3	3.61E-01	Glucose	5.2	27129	9	Cytoplasmic	COG0664	Signal transduction mechanisms	
15596747	PA1550		hypothetical protein	4.4	1.45E-01	Citronellol	5.1	20338	2	Outer Membrane Vesicle	COG3198	Function unknown	
15596749	PA1552	ccoP1	Cytochrome c oxidase, cbb3-type, CcoP subunit	2.0	1.49E-01	Glucose	6.0	34644	3	Outer Membrane Vesicle	COG2010	Energy production and conversion	
15596750	PA1553	ccoO1	Cytochrome c oxidase, cbb3-type, CcoO subunit	2.2	5.56E-01	Citronellol	8.2	22758	7	Outer Membrane Vesicle	COG2993	Energy production and conversion	
15596759	PA1562	acnA	aconitate hydratase 1	3.7	1.06E-02	Citronellol	5.4	99147	42	Cytoplasmic	COG1048	Energy production and conversion	
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	1.7	2.90E-02	Citronellol	5.2	30777	9	Cytoplasmic	COG2084	Lipid metabolism	
15596776	PA1579		hypothetical protein	3.5	8.48E-02	Citronellol	8.2	22110	12	Periplasmic			
15596777	PA1580	gltA	citrate synthase	1.2	1.87E-01	Citronellol	7.0	47695	33	Periplasmic	COG0372	Energy production and conversion	
15596778	PA1581	sdhC	succinate dehydrogenase (C subunit)	1.2	6.30E-01	Citronellol	10.4	13738	3	Outer Membrane Vesicle	COG2009	Energy production and conversion	
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	2.0	1.23E-03	Glucose	6.5	63532	24	Periplasmic	COG1053	Energy production and conversion	
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	2.0	5.07E-03	Glucose	6.9	26155	11	Outer Membrane Vesicle	COG0479	Energy production and conversion	
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	1.1	8.79E-01	Glucose	6.5	105877	46	Outer Membrane Vesicle	COG0567	Energy production and conversion	
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	1.3	4.51E-01	Citronellol	5.2	42887	30	Periplasmic	COG0508	Energy production and conversion	
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.0	9.63E-01	Glucose	7.0	50165	28	Periplasmic	COG1249	Energy production and conversion	
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	1.0	7.86E-01	Glucose	6.1	41542	28	Periplasmic	COG0045	Energy production and conversion	
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	1.3	2.47E-01	Glucose	6.0	30266	26	Periplasmic	COG0074	Energy production and conversion	
15596793	PA1596	htpG	heat shock protein HtpG	2.0	9.98E-04	Glucose	4.9	71667	50	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596794	PA1597		hypothetical protein	1.1	6.88E-01	Citronellol	5.9	25791	9	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.2	2.94E-01	Glucose	5.3	42806	23	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	1.3	1.24E-01	Citronellol	6.9	18747	11	Cytoplasmic	COG0764	Lipid metabolism	
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.2	1.93E-01	Citronellol	6.2	36773	15	Cytoplasmic	COG0240	Energy production and conversion	
15596813	PA1616		conserved hypothetical protein	1.8	4.74E-01	Glucose	6.4	16715	5	Unknown	COG2062	Signal transduction mechanisms	
15596814	PA1617		probable AMP-binding enzyme	38.9	5.19E-03	Citronellol	7.2	61370	14	Cytoplasmic	COG1022	Lipid metabolism	
15596815	PA1618		conserved hypothetical protein	1.7	8.92E-01	Citronellol	7.0	15595	7	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596819	PA1622		probable hydrolase	16.5	3.07E-06	Citronellol	7.1	31290	9	Cytoplasmic	COG0596	General function prediction only	
15596820	PA1623		conserved hypothetical protein	2.2	3.79E-02	Citronellol	6.1	24924	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596821	PA1624		hypothetical protein	1.1	2.92E-01	Citronellol	6.4	29533	3	Periplasmic			
15596836	PA1639		hypothetical protein	2.9	7.41E-02	Glucose	5.4	22457	5	Periplasmic			
15596839	PA1642	selD	selenophosphate synthetase	1.1	5.01E-01	Glucose	4.7	36354	10	Cytoplasmic	COG0709	Amino acid transport and metabolism	
15596841	PA1644		conserved hypothetical protein	1.1	6.91E-01	Glucose	5.5	21838	6	Unknown	COG1853	General function prediction only	
15596845	PA1648		probable oxidoreductase	4.2	1.23E-03	Citronellol	6.1	36168	6	Cytoplasmic	COG2130	General function prediction only	
15596851	PA1654		probable aminotransferase	1.7	1.04E-01	Glucose	5.3	43311	3	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
15596852	PA1655		probable glutathione S-transferase	2.4	3.24E-01	Citronellol	5.3	22738	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596854	PA1657		conserved hypothetical protein	1.5	1.53E-01	Glucose	4.5	18165	2	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15596855	PA1658		conserved hypothetical protein	27.0	1.27E-02	Glucose	5.1	55560	2	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.4	2.35E-01	Glucose	7.6	20236	10	Outer Membrane Vesicle	COG0302	Coenzyme metabolism	
15596874	PA1677		conserved hypothetical protein	1.3	3.11E-01	Citronellol	6.5	21034	9	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596875	PA1678		probable DNA methylase	6.0	3.90E-02	Citronellol	4.4	34229	4	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
15596878	PA1681	aroC	chorismate synthase	1.4	2.04E-01	Citronellol	6.6	38987	5	Cytoplasmic	COG0082	Amino acid transport and metabolism	
15596880	PA1683		probable sugar aldolase	1.7	4.94E-02	Citronellol	6.5	22868	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	2.4	2.02E-01	Citronellol	5.0	20552	7	Cytoplasmic	COG1791	Function unknown	
15596883	PA1686	alkA	DNA-3-methyladenine glycosidase II	1.4	3.50E-01	Glucose	6.9	32211	2	Unknown	COG0122	DNA replication, recombination, and repair	
15596884	PA1687	speE	spermidine synthase	1.2	4.32E-01	Glucose	4.9	32238	8	Periplasmic	COG0421	Amino acid transport and metabolism	
15596886	PA1689		conserved hypothetical protein	35.0	1.04E-02	Citronellol	6.5	77984	6	Outer Membrane Vesicle	COG1368	Cell envelope biogenesis, outer membrane	
15596923	PA1726	bglX	periplasmic beta-glucosidase	1.1	7.02E-01	Glucose	7.1	83003	7	Periplasmic	COG1472	Carbohydrate transport and metabolism	
15596930	PA1733		conserved hypothetical protein	9.2	6.35E-04	Citronellol	5.3	26467	7	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones	
15596933	PA1736		probable acyl-CoA thiolase	30.2	7.10E-05	Citronellol	5.3	42102	19	Cytoplasmic	COG0183	Lipid metabolism	
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	25.9	3.17E-05	Citronellol	6.7	76666	36	Cytoplasmic	COG1250	Lipid metabolism	
15596939	PA1742	pauD2	Glutamine amidotransferase class I	5.2	5.18E-03	Glucose	5.0	27361	4	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	3.4	8.40E-03	Citronellol	7.8	24412	11	Cytoplasmic	COG1024	Lipid metabolism	
15596946	PA1749		hypothetical protein	1.1	7.11E-01	Citronellol	10.0	17672	3	Unknown	COG2388	General function prediction only	
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.1	1.72E-01	Glucose	6.5	39132	11	Cytoplasmic	COG0722	Amino acid transport and metabolism	
15596949	PA1752		hypothetical protein	1.2	4.57E-01	Glucose	6.7	34141	8	Cytoplasmic	COG1893	Coenzyme metabolism	
15596950	PA1753		conserved hypothetical protein	1.3	4.74E-01	Glucose	4.7	18372	3	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596951	PA1754	cysB	transcriptional regulator CysB	2.6	1.16E-01	Citronellol	7.0	36110	10	Periplasmic	COG0583	Transcription	
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	1.1	6.26E-01	Citronellol	6.4	30215	10	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15596954	PA1757	thrH	homoserine kinase	2.0	4.92E-03	Glucose	5.0	23501	9	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596956	PA1759		probable transcriptional regulator	3.1	3.85E-03	Citronellol	6.3	101111	10	Unknown	COG2909	Transcription	
15596965	PA1768		hypothetical protein	1.9	3.93E-03	Citronellol	9.6	19720	6	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15596966	PA1769		conserved hypothetical protein	1.2	4.43E-01	Glucose	6.1	31074	10	Cytoplasmic	COG1806	Function unknown	
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.7	8.93E-02	Glucose	4.8	85798	75	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
15596969	PA1772		probable methyltransferase	5.9	1.70E-06	Citronellol	4.6	17404	8	Cytoplasmic	COG0684	Coenzyme metabolism	
15596972	PA1775	cmpX	conserved cytoplasmic membrane protein, CmpX protein	1.7	8.08E-01	Citronellol	8.8	29019	2	Outer Membrane Vesicle			
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precursor	1.7	2.02E-01	Glucose	4.8	37639	13	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596984	PA1787	acnB	aconitate hydratase 2	1.3	2.62E-01	Citronellol	5.0	93595	80	Periplasmic	COG1049	Energy production and conversion	
15596986	PA1789		hypothetical protein	3.8	3.81E-03	Citronellol	5.3	31273	8	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596987	PA1790		hypothetical protein	1.9	1.50E-01	Glucose	6.7	23312	4	Cytoplasmic	COG4445	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	1.6	1.61E-02	Citronellol	6.2	18126	12	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.9	3.79E-03	Glucose	5.6	62912	34	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	1.2	6.18E-01	Citronellol	5.4	51245	23	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis	
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase	1.0	1.00E+00	Citronellol	5.8	30549	11	Periplasmic	COG0190	Coenzyme metabolism	
15596997	PA1800	tig	trigger factor	1.3	1.29E-01	Citronellol	4.5	48582	32	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
15596998	PA1801	clpP	ClpP	1.1	8.02E-01	Citronellol	6.4	23502	16	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15596999	PA1802	clpX	ClpX	1.5	5.39E-02	Glucose	4.8	46991	27	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
15597000	PA1803	lon	Lon protease	1.4	2.79E-01	Glucose	6.0	88647	35	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15597001	PA1804	hupB	DNA-binding protein HU	4.1	6.06E-02	Glucose	10.8	9054	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	1.5	2.72E-01	Glucose	4.7	68741	5	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	1.4	1.28E-02	Citronellol	5.7	28006	7	Cytoplasmic Membrane	COG0623	acyl-carrier-protein	
15597007	PA1810		probable binding protein component of ABC transporter	1.2	2.86E-01	Glucose	6.5	70473	12	Periplasmic	COG4166	Amino acid transport and metabolism	
15597010	PA1813		probable hydroxyacylglutathione hydrolase	2.4	1.91E-02	Citronellol	6.3	28865	5	Cytoplasmic	COG0491	General function prediction only	
15597012	PA1815	rnhA	ribonuclease H	1.2	1.99E-01	Glucose	8.7	16697	6	Unknown	COG0328	DNA replication, recombination, and repair	
15597013	PA1816	dnaQ	DNA polymerase III, epsilon chain	2.0	2.14E-02	Glucose	5.0	26814	8	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	2.1	1.79E-02	Citronellol	6.1	82757	14	Cytoplasmic	COG1982	Amino acid transport and metabolism	
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	8.3	4.60E-04	Citronellol	5.4	29957	11	Cytoplasmic	COG1024	Lipid metabolism	
15597019	PA1822	fimL	hypothetical protein	1.1	8.58E-01	Glucose	4.9	60868	3	Cytoplasmic			
15597020	PA1823		conserved hypothetical protein	1.6	3.96E-02	Citronellol	4.9	31356	5	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
15597025	PA1828		probable short-chain dehydrogenase	3.4	1.91E-03	Citronellol	7.4	26919	15	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597026	PA1829		hypothetical protein	3.5	3.17E-03	Citronellol	5.9	40833	8	Cytoplasmic	COG3173	General function prediction only	
15597028	PA1831		hypothetical protein	2.7	1.77E-02	Citronellol	6.3	26378	6	Cytoplasmic	COG0406	General function prediction only	
15597030	PA1833		probable oxidoreductase	2.2	2.10E-03	Citronellol	5.2	34552	16	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597034	PA1837		hypothetical protein	1.5	3.24E-01	Glucose	4.7	18765	6	Cytoplasmic	COG3749	Function unknown	
15597035	PA1838	cysI	sulfite reductase	1.3	2.21E-01	Glucose	5.9	62132	26	Periplasmic	COG0155	Inorganic ion transport and metabolism	
15597038	PA1841		hypothetical protein	6.4	9.76E-03	Glucose	5.1	18654	6	Cytoplasmic	COG3760	Function unknown	
15597040	PA1843	metH	methionine synthase	2.7	2.67E-01	Citronellol	4.6	135062	46	Periplasmic	COG1410	Amino acid transport and metabolism	
15597042	PA1845		hypothetical protein	1.1	5.61E-01	Glucose	4.6	18757	2	Unknown			
15597043	PA1846	cti	cis/trans isomerase	17.8	2.41E-04	Glucose	6.0	86517	8	Periplasmic			

15597044	PA1847	nfuA	NfuA	1.4	4.20E-01	Glucose	4.2	21136	10	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	1.6	3.01E-01	Citronellol	6.8	26377	4	Periplasmic	COG0725	Inorganic ion transport and metabolism	
15597077	PA1880		probable oxidoreductase	7.4	7.36E-06	Citronellol	7.4	77656	19	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597078	PA1881		probable oxidoreductase	16.3	1.35E-03	Citronellol	7.7	15959	4	Cytoplasmic	COG2080	Energy production and conversion	
15597084	PA1887		hypothetical protein	223.8	2.70E-02	Citronellol	8.0	24376	2	Unknown			
15597087	PA1890		probable glutathione S-transferase	1.3	6.07E-02	Glucose	7.0	23440	14	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597091	PA1894		hypothetical protein	3.1	7.71E-02	Glucose	5.3	26179	11	Unknown			
15597110	PA1914		conserved hypothetical protein	17.2	6.00E-04	Citronellol	6.9	46125	6	Extracellular			
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	1.1	7.58E-01	Glucose	5.7	86211	6	Cytoplasmic	COG0620	Amino acid transport and metabolism	
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	26.1	2.13E-04	Citronellol	8.4	33860	14	Periplasmic	COG1879	Carbohydrate transport and metabolism	
15597145	PA1949	rbsR	ribose operon repressor RbsR	3.1	2.27E-03	Citronellol	7.2	36446	6	Cytoplasmic	COG1609	Transcription	
15597146	PA1950	rbsK	ribokinase	2.5	1.11E-03	Citronellol	4.9	31846	7	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597160	PA1964		probable ATP-binding component of ABC transporter	3.9	1.48E-03	Glucose	4.8	57917	12	Cytoplasmic	COG0488	General function prediction only	
15597178	PA1982	exaA	quinoprotein ethanol dehydrogenase	2.6	1.48E-02	Citronellol	7.1	68123	6	Periplasmic	COG4993	Carbohydrate transport and metabolism	
15597180	PA1984	exaC	NAD+ dependent aldehyde dehydrogenase ExaC	52.4	4.33E-02	Citronellol	5.4	54892	2	Periplasmic	COG1012	Energy production and conversion	
15597183	PA1987	pqqC	pyrroloquinoline quinone biosynthesis protein C	3.3	1.82E-02	Citronellol	7.4	29449	3	Cytoplasmic	COG5424	Coenzyme metabolism	
15597190	PA1994		hypothetical protein	6.4	3.18E-02	Citronellol	4.7	21561	6	Cytoplasmic	COG3554	Function unknown	
15597193	PA1997		probable AMP-binding enzyme	5.6	5.99E-04	Citronellol	6.5	71929	8	Cytoplasmic	COG0365	Lipid metabolism	
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	65.3	2.39E-06	Citronellol	5.0	25244	4	Cytoplasmic	COG1788	Lipid metabolism	
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	36.9	2.22E-05	Citronellol	4.6	23187	12	Cytoplasmic	COG2057	Lipid metabolism	
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	21.6	4.27E-05	Citronellol	6.4	40405	24	Cytoplasmic	COG0183	Lipid metabolism	
15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase	29.7	1.55E-05	Citronellol	5.6	26727	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597203	PA2007	maiA	maleylacetoacetate isomerase	4.6	3.53E-04	Citronellol	6.9	23685	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597204	PA2008	fahA	fumarylacetoacetase	2.6	6.09E-03	Citronellol	6.0	46341	4	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase	24.2	2.97E-07	Citronellol	6.0	31837	12	Cytoplasmic	COG0119	Amino acid transport and metabolism	
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containing)	46.4	2.10E-04	Citronellol	5.6	71282	29	Cytoplasmic	COG4770	Lipid metabolism	
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase	48.3	9.99E-06	Citronellol	5.2	28947	13	Cytoplasmic	COG1024	Lipid metabolism	
15597210	PA2014	liuB	methylcrotonyl-CoA carboxylase, beta-subunit	71.5	1.07E-05	Citronellol	6.7	57433	31	Cytoplasmic	COG4799	Lipid metabolism	
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase	52.9	4.52E-05	Citronellol	5.5	42209	35	Cytoplasmic	COG1960	Lipid metabolism	
15597212	PA2016	liuR	regulator of liu genes	52.8	2.65E-02	Citronellol	5.4	15631	5	Extracellular	COG0789	Transcription	
15597216	PA2020		probable transcriptional regulator	3.5	1.85E-01	Glucose	7.1	23695	2	Cytoplasmic	COG1309	Transcription	
15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase	1.2	4.32E-01	Citronellol	5.1	31236	21	Periplasmic	COG1210	Cell envelope biogenesis, outer membrane	
15597220	PA2024		probable ring-cleaving dioxygenase	23.1	5.01E-04	Citronellol	5.6	15373	4	Unknown	COG0346	Amino acid transport and metabolism	
15597221	PA2025	gor	glutathione reductase	2.3	1.18E-03	Citronellol	6.3	49237	15	Cytoplasmic	COG1249	Energy production and conversion	
15597230	PA2034		hypothetical protein	5.8	1.38E-01	Glucose	6.3	24525	4	Cytoplasmic	COG2242	Coenzyme metabolism	
15597240	PA2044		hypothetical protein	2.3	7.31E-04	Glucose	6.1	70083	15	Periplasmic	COG1305	Amino acid transport and metabolism	
15597267	PA2071	fusA2	elongation factor G	6.0	7.93E-04	Citronellol	4.9	77574	19	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15597272	PA2076		probable transcriptional regulator	7.0	1.10E-03	Glucose	6.0	32458	4	Cytoplasmic	COG0583	Transcription	
15597276	PA2080	kynU	kynureninase KynU	1.9	1.47E-02	Citronellol	5.3	46294	10	Cytoplasmic	COG3844	Amino acid transport and metabolism	
15597277	PA2081	kynB	kynurenine formamidase, KynB	6.7	2.43E-02	Citronellol	5.2	23152	4	Cytoplasmic	COG1878	Amino acid transport and metabolism	
15597278	PA2082	kynR	KynR	1.5	1.14E-01	Citronellol	6.5	17846	3	Cytoplasmic	COG1522	Transcription	
15597365	PA2169		hypothetical protein	123.2	1.40E-04	Citronellol	4.9	16843	2	Cytoplasmic			
15597380	PA2184		conserved hypothetical protein	15.2	1.03E-03	Citronellol	4.7	18990	2	Cytoplasmic	COG3685	Function unknown	
15597393	PA2197		conserved hypothetical protein	3.1	1.09E-03	Citronellol	6.3	37135	12	Cytoplasmic	COG2130	General function prediction only	
15597394	PA2198		hypothetical protein	1.9	4.73E-04	Citronellol	5.2	12944	4	Cytoplasmic	COG1359	Function unknown	
15597395	PA2199		probable dehydrogenase	2.3	5.90E-04	Citronellol	5.4	30886	8	Cytoplasmic	COG2084	Lipid metabolism	
15597400	PA2204		probable binding protein component of ABC transporter	1.9	3.98E-02	Glucose	9.7	29309	15	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15597418	PA2222		hypothetical protein	5.2	2.71E-03	Citronellol	5.0	23441	6	Unknown			
15597425	PA2229		conserved hypothetical protein	1.1	2.72E-01	Citronellol	6.5	26560	5	Cytoplasmic	COG2258	Function unknown	
15597428	PA2232	pslB	PslB	1.6	9.67E-02	Glucose	6.0	53515	16	Periplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15597449	PA2253	ansA	L-asparaginase I	1.0	6.34E-01	Glucose	5.3	34755	4	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15597455	PA2259	ptxS	transcriptional regulator PtxS	35.4	2.31E-04	Glucose	6.9	37359	3	Cytoplasmic	COG1609	Transcription	
15597456	PA2260		hypothetical protein	26.5	8.13E-05	Glucose	6.0	28980	16	Cytoplasmic			
15597457	PA2261		probable 2-ketogluconate kinase	20.9	1.68E-03	Glucose	5.7	34041	11	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597459	PA2263		probable 2-hydroxyacid dehydrogenase	75.1	1.76E-06	Glucose	8.7	35615	19	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15597460	PA2264		conserved hypothetical protein	1.2	4.41E-01	Glucose	5.4	26359	3	Outer Membrane Vesicle			
15597461	PA2265		gluconate dehydrogenase	5.7	5.27E-05	Glucose	7.3	64716	15	Periplasmic	COG2303	Amino acid transport and metabolism	
15597467	PA2271		probable acetyltransferase	1.3	5.06E-01	Citronellol	6.2	19165	3	Cytoplasmic			
15597486	PA2290	gcd	glucose dehydrogenase	2.1	4.65E-01	Citronellol	6.2	86218	2	Outer Membrane Vesicle	COG4993	Carbohydrate transport and metabolism	
15597487	PA2291		probable glucose-sensitive porin	3.1	1.85E-04	Glucose	5.5	50499	2	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
15597497	PA2301		hypothetical protein	1.7	1.35E-01	Glucose	6.5	19330	7	Cytoplasmic	COG2606	Function unknown	
15597498	PA2302	ambE	AmbE	5.5	2.29E-02	Citronellol	4.8	229041	99	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597499	PA2303	ambD	AmbD	2.0	2.55E-02	Citronellol	6.6	38657	6	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597500	PA2304	ambC	AmbC	3.9	6.57E-03	Citronellol	6.8	40696	5	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597501	PA2305	ambB	AmbB	4.7	1.99E-01	Citronellol	6.3	134446	27	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597516	PA2320	gntR	transcriptional regulator GntR	2.6	5.58E-02	Glucose	8.2	37147	3	Cytoplasmic	COG1609	Transcription	
15597517	PA2321		gluconokinase	71.6	5.12E-05	Glucose	7.1	18456	14	Unknown	COG3265	Carbohydrate transport and metabolism	
15597519	PA2323		probable glyceraldehyde-3-phosphate dehydrogenase	23.0	2.11E-05	Glucose	6.4	59960	41	Cytoplasmic	COG1012	Energy production and conversion	
15597527	PA2331		hypothetical protein	2.5	4.46E-01	Citronellol	5.0	19904	4	Unknown	COG2128	Function unknown	
15597562	PA2366		uricase PuuD	2.4	4.33E-02	Citronellol	5.7	55042	5	Cytoplasmic Membrane	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15597563	PA2367		hypothetical protein	34.1	7.18E-03	Citronellol	4.6	17636	5	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15597567	PA2371		probable ClpA/B-type protease	3.7	5.67E-02	Citronellol	5.1	92424	2	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597568	PA2372		hypothetical protein	483.2	2.56E-04	Citronellol	8.4	21241	2	Unknown			
15597574	PA2378		probable aldehyde dehydrogenase	1.1	3.14E-01	Citronellol	8.4	83665	19	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ	1.0	8.40E-01	Glucose	7.1	84039	26	Periplasmic	COG2366	General function prediction only	
15597582	PA2386	pvdA	L-ornithine N5-oxygenase	18.4	6.48E-05	Glucose	6.5	49478	20	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
15597590	PA2394	pvdN	PvdN	1.1	6.99E-01	Glucose	7.3	47981	13	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
15597591	PA2395	pvdO	PvdO	1.4	1.79E-01	Citronellol	5.4	31070	8	Periplasmic	COG1262	Function unknown	
15597592	PA2396	pvdF	pyoverdine synthetase F	1.4	1.81E-01	Glucose	5.0	31039	21	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15597594	PA2398	fpvA	ferripyoverdine receptor	1.7	1.95E-01	Glucose	5.3	91167	28	Periplasmic	COG4773	Inorganic ion transport and metabolism	
15597595	PA2399	pvdD	pyoverdine synthetase D	2.0	3.63E-01	Glucose	5.0	273645	61	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
110645305	PA2400	pvdJ	PvdJ	2.4	2.66E-01	Glucose	5.1	240213	10	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597598	PA2402		probable non-ribosomal peptide synthetase	3.1	1.24E-01	Glucose	5.1	569179	219	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597603	PA2407		probable adhesion protein	1.4	1.23E-01	Citronellol	9.6	34309	7	Periplasmic	COG0803	Inorganic ion transport and metabolism	
15597606	PA2410		hypothetical protein	2.0	2.79E-02	Citronellol	5.0	31732	10	Unknown	COG0803	Inorganic ion transport and metabolism	
15597607	PA2411		probable thioesterase	14.1	1.69E-03	Glucose	5.4	27846	17	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	
15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, PvdH	13.5	1.17E-03	Glucose	6.5	50215	20	Cytoplasmic	COG0160	Amino acid transport and metabolism	
15597615	PA2419		probable hydrolase	2.9	6.67E-04	Citronellol	6.5	24272	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15597620	PA2424	pvdL	PvdL	5.7	3.14E-02	Glucose	5.1	480292	210	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597638	PA2442	gcvT2	glycine cleavage system protein T2	1.6	1.51E-01	Citronellol	6.4	39882	16	Periplasmic	COG0404	Amino acid transport and metabolism	
15597640	PA2444	glyA2	serine hydroxymethyltransferase	10.3	4.13E-02	Glucose	6.5	44974	4	Periplasmic	COG0112	Amino acid transport and metabolism	
15597641	PA2445	gcvP2	glycine cleavage system protein P2	5.0	4.96E-03	Glucose	6.0	103918	46	Periplasmic	COG1003	Amino acid transport and metabolism	
15597644	PA2448		hypothetical protein	41.9	2.75E-02	Citronellol	6.6	62839	2	Periplasmic	COG1574	General function prediction only	
15597651	PA2455		hypothetical protein	1.8	4.14E-01	Citronellol	5.6	20332	2	Cytoplasmic	COG3153	General function prediction only	
15597655	PA2459		hypothetical protein	3.3	7.34E-02	Glucose	5.6	23801	3	Cytoplasmic			
15597658	PA2462		hypothetical protein	7.0	1.27E-02	Citronellol	5.1	573168	46	Outer Membrane Vesicle	COG3210	Intracellular trafficking and secretion	
15597660	PA2464		hypothetical protein	1.3	1.93E-01	Glucose	4.6	17626	5	Periplasmic			
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG	1.2	3.10E-01	Citronellol	7.1	28053	3	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15597677	PA2481		hypothetical protein	6.8	1.35E-03	Citronellol	8.5	31249	2	Periplasmic	COG3258	Energy production and conversion	
15597679	PA2483		conserved hypothetical protein	1.4	1.39E-01	Citronellol	6.2	36102	6	Cytoplasmic	COG2141	Energy production and conversion	
15597687	PA2491		probable oxidoreductase	2.2	3.62E-02	Citronellol	5.3	36832	17	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexE precursor	1.7	6.50E-02	Citronellol	8.8	45031	10	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	

15597690	PA2494	mexF	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF	2.5	1.26E-01	Citronellol	5.4	115509	10	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15597691	PA2495	oprN	Multidrug efflux outer membrane protein OprN precursor	1.9	2.09E-01	Citronellol	5.1	51165	6	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15597692	PA2496		hypothetical protein	2.9	8.00E-02	Glucose	6.6	19483	2	Cytoplasmic	COG2318	Function unknown	
15597699	PA2503		hypothetical protein	9.0	6.68E-02	Citronellol	4.6	45895	3	Cytoplasmic			
15597700	PA2504		hypothetical protein	27.1	1.24E-04	Citronellol	4.3	22822	5	Cytoplasmic	COG4859	Function unknown	
15597703	PA2507	catA	catechol 1,2-dioxygenase	36.5	1.15E-05	Citronellol	5.1	34160	11	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
15597711	PA2515	xylL	cis-1,2-dihydroxycyclohexa-3,4-diene carboxylate dehydrogenase	158.2	2.47E-03	Citronellol	5.2	27240	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597713	PA2517	xylY	toluate 1,2-dioxygenase beta subunit	76.9	6.83E-04	Citronellol	4.9	19191	2	Cytoplasmic	COG5517	Secondary metabolites biosynthesis, transport, and catabolism	
15597725	PA2529		hypothetical protein	1.2	2.97E-01	Glucose	5.6	52681	6	Cytoplasmic	COG0312	General function prediction only	
15597726	PA2530		hypothetical protein	12.2	1.60E-01	Citronellol	5.7	48959	4	Unknown	COG0312	General function prediction only	
15597727	PA2531		probable aminotransferase	4.5	7.88E-03	Citronellol	9.4	40715	2	Unknown	COG0079	Amino acid transport and metabolism	
15597728	PA2532	tpx	thiol peroxidase	2.4	7.77E-04	Citronellol	4.9	17234	14	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
15597741	PA2545	xthA	exodeoxyribonuclease III	1.3	1.55E-01	Citronellol	6.4	31003	9	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15597746	PA2550		probable acyl-CoA dehydrogenase	5.4	1.29E-01	Citronellol	6.6	45482	4	Cytoplasmic	COG1960	Lipid metabolism	
15597747	PA2551		probable transcriptional regulator	2.5	1.05E-02	Citronellol	9.9	35144	2	Cytoplasmic	COG0583	Transcription	
15597748	PA2552		probable acyl-CoA dehydrogenase	15.4	1.40E-03	Citronellol	5.6	40908	9	Cytoplasmic	COG1960	Lipid metabolism	
15597749	PA2553		probable acyl-CoA thiolase	17.1	1.19E-04	Citronellol	5.9	41400	16	Cytoplasmic	COG0183	Lipid metabolism	
15597750	PA2554		probable short-chain dehydrogenase	13.9	1.66E-04	Citronellol	6.6	26394	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597751	PA2555		probable AMP-binding enzyme	7.2	1.94E-03	Citronellol	6.1	60159	5	Cytoplasmic	COG0365	Lipid metabolism	
15597753	PA2557		probable AMP-binding enzyme	49.7	7.56E-06	Citronellol	6.1	62629	22	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15597758	PA2562		hypothetical protein	2.6	2.22E-01	Citronellol	10.0	17384	2	Unknown			
15597768	PA2572		probable two-component response regulator	93.3	2.40E-02	Citronellol	5.4	50757	2	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15597771	PA2575		hypothetical protein	2.6	7.15E-02	Citronellol	6.4	22222	13	Unknown	COG3560	General function prediction only	
15597773	PA2577		probable transcriptional regulator	2.4	1.74E-02	Citronellol	8.0	16459	3	Cytoplasmic	COG1522	Transcription	
15597778	PA2582		hypothetical protein	1.6	9.26E-01	Citronellol	10.5	19446	7	Unknown	COG3109	Signal transduction mechanisms	
15597782	PA2586	gacA	response regulator GacA	6.8	2.11E-04	Glucose	6.1	23576	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15597797	PA2601		probable transcriptional regulator	1.4	3.21E-01	Glucose	5.5	32375	2	Cytoplasmic	COG0583	Transcription	
15597799	PA2603		probable thiosulfate sulfurtransferase	3.8	1.23E-01	Glucose	5.0	57285	2	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15597807	PA2611	cysG	siroheme synthase	8.1	2.94E-02	Glucose	6.3	50370	8	Cytoplasmic	COG0007	Coenzyme metabolism	
15597808	PA2612	serS	seryl-tRNA synthetase	1.2	4.88E-01	Glucose	5.3	47231	19	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis	
15597809	PA2613		conserved hypothetical protein	3.4	1.16E-02	Glucose	6.3	49047	3	Cytoplasmic	COG2256	DNA replication, recombination, and repair	
15597810	PA2614	lolA	periplasmic chaperone LolA	1.3	8.31E-01	Citronellol	5.8	23072	13	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane	
15597812	PA2616	trxB1	thioredoxin reductase 1	1.4	3.14E-01	Glucose	5.2	33818	9	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones	
15597814	PA2618		hypothetical protein	10.0	2.12E-03	Citronellol	8.5	27826	2	Cytoplasmic	COG2935	Posttranslational modification, protein turnover, chaperones	
15597815	PA2619	infA	initiation factor	2.4	2.27E-01	Glucose	9.6	8303	4	Cytoplasmic	COG0361	Translation, ribosomal structure and biogenesis	
15597816	PA2620	clpA	ATP-binding protease component ClpA	1.3	3.33E-01	Glucose	5.9	84010	22	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597818	PA2622	cspD	cold-shock protein CspD	2.6	9.59E-02	Citronellol	5.6	9600	4	Cytoplasmic	COG1278	Transcription	
15597819	PA2623	icd	isocitrate dehydrogenase	2.7	5.56E-03	Citronellol	4.9	45577	49	Periplasmic	COG0538	Energy production and conversion	
15597820	PA2624	idh	isocitrate dehydrogenase	4.5	2.03E-03	Glucose	6.1	81633	51	Periplasmic	COG2838	Energy production and conversion	
15597821	PA2625		conserved hypothetical protein	1.0	9.82E-01	Citronellol	5.2	17525	6	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15597822	PA2626	trmU	tRNA methyltransferase	1.2	5.39E-02	Glucose	5.9	41886	2	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
15597823	PA2627		conserved hypothetical protein	1.7	2.40E-01	Glucose	10.9	23030	3	Unknown	COG2915	General function prediction only	
15597825	PA2629	purB	adenylosuccinate lyase	1.4	8.27E-03	Glucose	5.7	50500	22	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15597826	PA2630		conserved hypothetical protein	1.3	2.11E-01	Glucose	4.1	44057	4	Cytoplasmic	COG2850	Function unknown	
15597827	PA2631		probable acetyl transferase	1.3	3.88E-01	Glucose	4.8	16040	7	Cytoplasmic	COG2153	General function prediction only	
15597830	PA2634	aceA	isocitrate lyase AceA	5.8	7.03E-05	Citronellol	5.9	58886	50	Periplasmic	COG2224	Energy production and conversion	
15597834	PA2638	nuoB	NADH dehydrogenase I chain B	1.1	9.16E-01	Citronellol	5.1	25425	2	Cytoplasmic Membrane	COG0377	Energy production and conversion	
15597835	PA2639	nuoD	NADH dehydrogenase I chain C,D	2.5	1.13E-02	Glucose	6.7	68323	6	Cytoplasmic	COG0649	Energy production and conversion	
15597836	PA2640	nuoE	NADH dehydrogenase I chain E	1.5	4.45E-02	Glucose	4.8	18088	2	Cytoplasmic	COG1905	Energy production and conversion	
15597837	PA2641	nuoF	NADH dehydrogenase I chain F	3.7	4.92E-02	Glucose	7.0	48678	3	Cytoplasmic	COG1894	Energy production and conversion	
15597838	PA2642	nuoG	NADH dehydrogenase I chain G	2.8	3.62E-03	Glucose	6.0	98999	15	Outer Membrane Vesicle	COG1034	Energy production and conversion	
15597840	PA2644	nuoI	NADH Dehydrogenase I chain I	6.4	2.43E-01	Citronellol	6.7	20578	3	Cytoplasmic	COG1143	Energy production and conversion	
15597846	PA2650		conserved hypothetical protein	2.0	7.36E-02	Glucose	5.7	29513	5	Cytoplasmic	COG2226	Coenzyme metabolism	
15597853	PA2657		probable two-component response regulator	1.3	1.92E-01	Glucose	5.9	24729	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15597875	PA2679		hypothetical protein	5.2	1.57E-03	Citronellol	5.2	27641	3	Cytoplasmic	COG2226	Coenzyme metabolism	
15597878	PA2682		conserved hypothetical protein	2.3	1.67E-02	Citronellol	5.4	45495	3	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15597879	PA2683		probable serine/threonine dehydratase, degradative	1.0	9.28E-01	Citronellol	6.4	33957	3	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15597880	PA2684		conserved hypothetical protein	2.7	1.04E-01	Citronellol	6.6	145819	5	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane	
15597888	PA2692		probable transcriptional regulator	1.3	7.97E-02	Citronellol	6.5	19143	4	Cytoplasmic	COG1959	Transcription	
15597894	PA2698		probable hydrolase	1.9	2.55E-01	Citronellol	5.3	25051	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15597895	PA2699		hypothetical protein	8.1	7.62E-04	Citronellol	6.2	67906	3	Unknown	COG1574	General function prediction only	
15597898	PA2702	tse2	Tse2	2.0	7.48E-03	Glucose	6.8	17657	2	Extracellular			
15597903	PA2707		hypothetical protein	2.7	6.72E-03	Citronellol	6.1	32205	20	Cytoplasmic	COG0714	General function prediction only	
15597905	PA2709	cysK	cysteine synthase A	1.8	1.14E-02	Citronellol	6.6	34309	17	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15597913	PA2717	cpo	chloroperoxidase precursor	11.1	2.31E-03	Citronellol	5.9	30435	8	Cytoplasmic	COG0596	General function prediction only	
15597916	PA2720		hypothetical protein	1.2	4.29E-01	Citronellol	4.7	23816	5	Cytoplasmic			
15597917	PA2721		hypothetical protein	38.7	5.22E-05	Citronellol	4.6	17356	3	Cytoplasmic	COG3865	Function unknown	
15597921	PA2725		probable chaperone	5.2	6.61E-03	Glucose	6.2	68829	9	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597928	PA2732		hypothetical protein	5.6	1.35E-01	Citronellol	6.2	128671	26	Cytoplasmic	COG0610	Defense mechanisms	
15597930	PA2734		hypothetical protein	1.3	2.65E-01	Glucose	6.1	48703	10	Cytoplasmic	COG0732	Defense mechanisms	
15597931	PA2735		probable restriction-modification system protein	1.4	4.76E-02	Glucose	5.4	89570	27	Cytoplasmic	COG0286	Defense mechanisms	
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit	1.2	3.30E-01	Glucose	5.1	86799	37	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis	
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit	1.5	1.75E-01	Citronellol	5.8	38063	16	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis	
15597937	PA2741	rplT	50S ribosomal protein L20	1.0	5.57E-01	Glucose	12.3	13365	6	Outer Membrane Vesicle	COG0292	Translation, ribosomal structure and biogenesis	
15597939	PA2743	infC	translation initiation factor IF-3	1.8	2.31E-01	Glucose	10.3	20864	8	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
15597940	PA2744	thrS	threonyl-tRNA synthetase	1.9	2.69E-03	Glucose	6.3	73080	41	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis	
15597951	PA2755	eco	ecotin precursor	1.6	6.90E-02	Citronellol	6.5	17228	8	Periplasmic	COG4574	General function prediction only	
15597956	PA2760	oprQ	OprQ	1.3	5.52E-01	Citronellol	5.5	46850	13	Periplasmic			
15597960	PA2764		hypothetical protein	4.4	3.57E-04	Citronellol	6.0	24519	10	Cytoplasmic			
15597961	PA2765		hypothetical protein	1.2	4.41E-01	Citronellol	4.5	32396	13	Unknown	COG2837	Inorganic ion transport and metabolism	
15597966	PA2770		hypothetical protein	1.4	1.47E-01	Glucose	4.7	28258	7	Cytoplasmic	COG0384	General function prediction only	
15597988	PA2792		hypothetical protein	1.2	5.47E-01	Glucose	6.4	22070	4	Unknown			
15597990	PA2794		pseudaminidase	10.3	4.43E-03	Citronellol	6.2	47151	6	Unknown			
15597991	PA2795		conserved hypothetical protein	4.0	1.46E-02	Glucose	7.1	36929	2	Cytoplasmic	COG0042	Translation, ribosomal structure and biogenesis	
15597992	PA2796	tal	transaldolase	1.4	3.76E-02	Citronellol	4.9	33946	23	Cytoplasmic	COG0176	Carbohydrate transport and metabolism	
15597993	PA2797		hypothetical protein	3.3	2.54E-03	Glucose	4.6	17710	7	Cytoplasmic	COG1366	Signal transduction mechanisms	
15597994	PA2798		probable two-component response regulator	1.1	7.70E-01	Citronellol	4.6	43485	6	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription
15597996	PA2800		conserved hypothetical protein	2.9	2.37E-01	Glucose	5.3	26148	4	Periplasmic	COG2853	Cell envelope biogenesis, outer membrane	
15598002	PA2806		conserved hypothetical protein	1.8	1.33E-01	Glucose	5.4	30848	9	Cytoplasmic	COG2904	Function unknown	
15598008	PA2812		probable ATP-binding component of ABC transporter	2.8	1.99E-02	Citronellol	6.3	34540	6	Cytoplasmic Membrane	COG1131	Defense mechanisms	
15598009	PA2813		probable glutathione S-transferase	2.9	1.34E-01	Citronellol	4.8	23405	14	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598011	PA2815		probable acyl-CoA dehydrogenase	3.9	1.19E-02	Citronellol	5.9	88762	2	Outer Membrane Vesicle	COG1960	Lipid metabolism	
15598017	PA2821		probable glutathione S-transferase	1.1	6.70E-01	Citronellol	6.1	24716	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598018	PA2822		conserved hypothetical protein	1.1	3.30E-01	Glucose	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms	
15598019	PA2823		conserved hypothetical protein	1.4	1.28E-01	Glucose	5.7	33760	9	Cytoplasmic	COG2607	General function prediction only	
15598022	PA2826		probable glutathione peroxidase	6.0	1.81E-04	Citronellol	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15598024	PA2828		probable aminotransferase	1.2	4.16E-01	Citronellol	6.1	44799	9	Periplasmic	COG0436	Amino acid transport and metabolism	
15598025	PA2829		hypothetical protein	1.3	3.65E-01	Glucose	5.2	16432	4	Unknown			
15598027	PA2831		conserved hypothetical protein	1.6	1.03E-01	Citronellol	5.3	42933	8	Cytoplasmic	COG2866	Amino acid transport and metabolism	
15598028	PA2832	tpm	thiopurine methyltransferase	1.4	9.37E-02	Citronellol	4.7	24875	4	Cytoplasmic			
15598036	PA2840		probable ATP-dependent RNA helicase	8.8	3.40E-02	Glucose	9.0	62107	3	Outer Membrane Vesicle	COG0513	DNA replication, recombination, and repair	Transcription
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	6.6	1.25E-04	Citronellol	5.4	28612	8	Cytoplasmic	COG1024	Lipid metabolism	

15598046	PA2850	ohr	organic hydroperoxide resistance protein	5.1	5.09E-01	Citronellol	7.4	14522	2	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
15598047	PA2851	efp	translation elongation factor P	1.1	1.71E-01	Citronellol	4.5	20985	8	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis	
15598049	PA2853	oprI	Outer membrane lipoprotein OprI precursor	1.2	5.94E-01	Glucose	8.5	8835	2	Outer Membrane			
15598050	PA2854		conserved hypothetical protein	1.3	2.00E-01	Glucose	5.6	34799	11	Periplasmic	COG1376	Function unknown	
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	1.7	1.34E-01	Citronellol	5.9	21037	7	Periplasmic	COG2755	Amino acid transport and metabolism	
15598058	PA2862	lipA	lactonizing lipase precursor	1400.2	2.05E-04	Citronellol	6.9	32723	6	Extracellular	COG1075	General function prediction only	
15598062	PA2866	mttC	secretion protein MttC	1.1	5.36E-01	Citronellol	6.1	29544	2	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598065	PA2869		hypothetical protein	3.4	4.23E-03	Citronellol	8.7	18206	4	Cytoplasmic Membrane	COG3915	Function unknown	
15598067	PA2871		hypothetical protein	1.5	4.49E-02	Citronellol	5.4	28695	15	Unknown	COG1946	Lipid metabolism	
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	1.1	5.98E-01	Glucose	5.3	24394	12	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
15598081	PA2885	atuR	putative repressor of atu genes	4.3	1.85E-03	Citronellol	4.9	22057	4	Unknown	COG1309	Transcription	
15598082	PA2886	atuA	expressed protein with apparent function in citronellol catabolism	101.1	1.99E-06	Citronellol	5.1	64435	27	Cytoplasmic			
15598083	PA2887	atuB	putative dehydrogenase involved in catabolism of citronellol	108.4	9.09E-09	Citronellol	7.3	30751	23	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598084	PA2888	atuC	geranyl-CoA carboxylase, beta-subunit	57.5	2.61E-05	Citronellol	6.5	57328	25	Cytoplasmic	COG4799	Lipid metabolism	
15598085	PA2889	atuD	citronellyl-CoA dehydrogenase, AtuD	106.3	7.83E-06	Citronellol	6.3	42714	44	Cytoplasmic	COG1960	Lipid metabolism	
15598086	PA2890	atuE	putative isohexenylglutaconyl-CoA hydratase	52.7	6.18E-07	Citronellol	5.2	27717	15	Cytoplasmic	COG1024	Lipid metabolism	
15598087	PA2891	atuF	geranyl-CoA carboxylase, alpha-subunit (biotin-containing)	37.7	9.75E-05	Citronellol	6.1	71747	31	Cytoplasmic	COG4770	Lipid metabolism	
15598088	PA2892	atuG	GCase, alpha-subunit (biotin-containing)	86.3	3.50E-07	Citronellol	7.2	29631	23	Cytoplasmic	COG4221	General function prediction only	
15598098	PA2902		hypothetical protein	1.3	2.29E-01	Glucose	4.8	30448	2	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	1.1	3.48E-01	Glucose	6.3	27275	4	Cytoplasmic	COG2243	Coenzyme metabolism	
15598101	PA2905	cobH	precorrin isomerase CobH	2.0	1.54E-01	Glucose	5.7	21650	7	Cytoplasmic	COG2082	Coenzyme metabolism	
15598114	PA2918		probable short-chain dehydrogenase	4.8	4.38E-04	Citronellol	7.2	26738	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598135	PA2939		probable aminopeptidase	21.3	1.49E-04	Citronellol	4.8	57511	18	Extracellular	COG2234	General function prediction only	
15598136	PA2940		probable acyl-CoA thiolase	398.8	2.95E-02	Citronellol	5.5	39211	2	Cytoplasmic	COG0183	Lipid metabolism	
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	2.5	2.06E-01	Glucose	5.2	138499	5	Cytoplasmic	COG1429	Coenzyme metabolism	
15598141	PA2945		conserved hypothetical protein	1.0	8.63E-01	Citronellol	4.9	41175	5	Cytoplasmic	COG0523	General function prediction only	
15598146	PA2950	pfmß	proton motive force protein, PMF	1.0	8.14E-01	Glucose	4.8	43528	23	Cytoplasmic	COG3007	Function unknown	
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	2.2	4.02E-03	Citronellol	4.8	31423	19	Periplasmic	COG2025	Energy production and conversion	
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	2.3	6.13E-03	Citronellol	9.6	26377	23	Outer Membrane Vesicle	COG2086	Energy production and conversion	
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	1.4	1.45E-01	Citronellol	5.6	59896	15	Outer Membrane Vesicle	COG0644	Energy production and conversion	
15598150	PA2954		hypothetical protein	1.4	6.34E-01	Citronellol	4.9	21240	7	Cytoplasmic	COG3816	Function unknown	
15598154	PA2958		hypothetical protein	3.0	9.81E-04	Citronellol	6.3	42109	2	Cytoplasmic	COG0520	Posttranslational modification, protein turnover, chaperones	
15598155	PA2959		conserved hypothetical protein	1.3	1.61E-01	Glucose	5.3	28114	6	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598157	PA2961	holB	DNA polymerase III, delta prime subunit	4.5	2.43E-02	Glucose	6.6	35746	6	Cytoplasmic	COG0470	DNA replication, recombination, and repair	
15598158	PA2962	tmk	thymidylate kinase	1.5	1.44E-01	Glucose	4.9	23077	8	Cytoplasmic	COG0125	Nucleotide transport and metabolism	
15598160	PA2964	pabC	4-amino-4-deoxychorismate lyase	1.8	1.41E-02	Citronellol	5.7	29886	4	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.5	2.29E-01	Glucose	5.8	43465	9	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598162	PA2966	acpP	acyl carrier protein	1.9	2.48E-01	Citronellol	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	3.0	1.27E-03	Glucose	6.6	25585	15	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	2.8	9.97E-04	Glucose	4.8	32444	13	Periplasmic	COG0331	Lipid metabolism	
15598168	PA2972		conserved hypothetical protein	1.9	3.77E-01	Citronellol	6.0	21054	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15598170	PA2974		probable hydrolase	2.4	2.35E-02	Glucose	5.4	25322	3	Cytoplasmic	COG0546	General function prediction only	
15598172	PA2976	rne	ribonuclease E	1.1	6.43E-01	Glucose	4.6	117463	39	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis	
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	1.3	1.52E-01	Glucose	6.7	37595	3	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
15598174	PA2978	ptpA	phosphotyrosine protein phosphatase	1.1	6.54E-01	Glucose	6.1	17152	7	Cytoplasmic	COG0394	Signal transduction mechanisms	
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.2	4.10E-01	Citronellol	5.4	27646	12	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	1.7	3.95E-02	Glucose	6.7	51161	19	Cytoplasmic	COG1249	Energy production and conversion	
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	3.5	2.42E-01	Citronellol	5.7	128763	36	Periplasmic	COG1197	DNA replication, recombination, and repair	Transcription
15598199	PA3003		hypothetical protein	1.1	4.67E-01	Glucose	4.5	22474	8	Periplasmic			
15598200	PA3004		5'-methylthioinosine phosphorylase	1.2	4.17E-01	Citronellol	6.6	26266	7	Cytoplasmic	COG0005	Nucleotide transport and metabolism	
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.6	1.01E-01	Glucose	6.2	36101	10	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
15598203	PA3007	lexA	repressor protein LexA	3.2	3.43E-02	Citronellol	6.5	22506	2	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
15598206	PA3010		hypothetical protein	2.3	9.74E-01	Citronellol	4.6	19071	2	Unknown			
15598207	PA3011	topA	DNA topoisomerase I	1.0	9.55E-01	Citronellol	8.7	97282	56	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	8.0	3.24E-03	Citronellol	6.8	41643	32	Cytoplasmic	COG0183	Lipid metabolism	
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	4.1	1.65E-03	Citronellol	5.6	76954	45	Periplasmic	COG1250	Lipid metabolism	
15598211	PA3015		hypothetical protein	8.8	1.49E-02	Citronellol	5.9	30469	4	Unknown			
15598215	PA3019		probable ATP-binding component of ABC transporter	4.6	4.84E-03	Glucose	5.0	71155	15	Cytoplasmic	COG0488	General function prediction only	
15598217	PA3021		hypothetical protein	1.1	7.85E-01	Glucose	7.8	14206	4	Unknown	COG3755	Function unknown	
15598218	PA3022		hypothetical protein	1.0	8.49E-01	Glucose	5.9	29579	14	Cytoplasmic	COG3217	General function prediction only	
15598219	PA3023		conserved hypothetical protein	10.1	2.56E-05	Citronellol	4.7	31504	6	Cytoplasmic	COG1597	Lipid metabolism	General function prediction only
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.5	4.19E-02	Citronellol	5.0	43359	6	Cytoplasmic	COG0303	Coenzyme metabolism	
15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	1.7	4.07E-04	Citronellol	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism	
15598226	PA3030	mobA	molybdopterin-guanine dinucleotide biosynthesis protein MobA	1.9	2.11E-01	Glucose	7.6	21870	4	Cytoplasmic	COG0746	Coenzyme metabolism	
15598227	PA3031		hypothetical protein	21.1	6.12E-01	Glucose	4.7	8012	2	Outer Membrane Vesicle			
15598228	PA3032	snr1	cytochrome c Snr1	19.8	5.38E-04	Citronellol	6.8	52500	6	Cytoplasmic	COG1858	Inorganic ion transport and metabolism	
15598234	PA3038		probable porin	34.5	1.69E-03	Citronellol	7.1	46712	9	Periplasmic			
15598239	PA3043		conserved hypothetical protein	1.9	5.35E-02	Citronellol	6.5	50083	7	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15598244	PA3048		conserved hypothetical protein	1.2	5.00E-01	Glucose	8.0	81155	9	Cytoplasmic	COG0116	DNA replication, recombination, and repair	
15598249	PA3053		probable hydrolytic enzyme	1.2	8.99E-02	Citronellol	8.0	37485	4	Periplasmic	COG0596	General function prediction only	
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	21.2	1.24E-02	Citronellol	6.1	182637	11	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism	
15598266	PA3070		conserved hypothetical protein	2.2	1.42E-02	Citronellol	4.9	36148	2	Cytoplasmic	COG0714	General function prediction only	
15598276	PA3080		hypothetical protein	33.3	8.40E-05	Citronellol	4.8	38479	10	Unknown	COG4447	General function prediction only	
15598277	PA3081		conserved hypothetical protein	10.4	6.31E-03	Citronellol	9.2	50680	7	Periplasmic			
15598278	PA3082	gbt	glycine betaine transmethylase	2.2	1.03E-01	Citronellol	4.5	71403	2	Periplasmic			
15598279	PA3083	pepN	aminopeptidase N	1.5	2.61E-01	Citronellol	4.9	100046	52	Periplasmic	COG0308	Amino acid transport and metabolism	
15598280	PA3084		hypothetical protein	1.6	7.46E-02	Citronellol	7.6	29990	2	Cytoplasmic			
15598284	PA3088		conserved hypothetical protein	1.5	8.49E-02	Citronellol	7.3	32140	4	Cytoplasmic	COG0061	Coenzyme metabolism	
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	8.1	7.79E-04	Citronellol	7.2	72969	18	Cytoplasmic	COG1902	Energy production and conversion	
15598302	PA3106		probable short-chain dehydrogenase	1.2	5.79E-01	Citronellol	4.6	26997	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598303	PA3107	metZ	O-succinylhomoserine sulfhydrylase	1.1	6.75E-01	Glucose	6.3	43185	14	Periplasmic	COG0626	Amino acid transport and metabolism	
15598304	PA3108	purF	amidophosphoribosyltransferase	2.3	3.32E-03	Glucose	6.8	55370	20	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism	
15598307	PA3111	folC	folylpolyglutamate synthetase	3.0	9.98E-02	Glucose	5.0	46505	4	Cytoplasmic	COG0285	Coenzyme metabolism	
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	1.2	5.36E-01	Citronellol	7.1	31843	13	Periplasmic	COG0777	Lipid metabolism	
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	1.4	5.73E-01	Glucose	6.8	22280	5	Cytoplasmic	COG0135	Amino acid transport and metabolism	
15598312	PA3116		probable aspartate-semialdehyde dehydrogenase	13.6	2.37E-02	Glucose	4.5	35349	3	Cytoplasmic	COG0136	Amino acid transport and metabolism	
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	1.1	6.22E-01	Citronellol	5.5	40494	24	Periplasmic	COG0136	Amino acid transport and metabolism	
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.6	8.56E-02	Citronellol	4.8	39120	12	Cytoplasmic	COG0473	Amino acid transport and metabolism	
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	1.2	4.20E-01	Citronellol	4.7	24011	16	Cytoplasmic	COG0066	Amino acid transport and metabolism	
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	1.6	6.98E-02	Glucose	6.3	51042	18	Cytoplasmic	COG0065	Amino acid transport and metabolism	
15598318	PA3122		probable transcriptional regulator	1.5	3.74E-01	Glucose	6.4	32835	4	Cytoplasmic	COG0583	Transcription	
15598319	PA3123		conserved hypothetical protein	5.0	8.82E-03	Citronellol	4.6	13516	6	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
15598322	PA3126	ibpA	heat-shock protein IbpA	9.1	7.04E-05	Glucose	6.1	16583	3	Cytoplasmic	COG0071	Posttranslational modification, protein turnover, chaperones	
15598323	PA3127		hypothetical protein	4.3	1.52E-03	Citronellol	5.0	29403	11	Unknown			
15598324	PA3128		probable short-chain dehydrogenase	3.9	2.86E-04	Citronellol	6.8	26219	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598326	PA3130		hypothetical protein	2.4	2.30E-02	Glucose	5.2	16555	6	Unknown	COG0824	General function prediction only	
15598327	PA3131		probable aldolase	1.9	3.77E-02	Glucose	5.3	22852	9	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598330	PA3134	gltX	glutamyl-tRNA synthetase	1.1	9.95E-01	Citronellol	6.7	56749	25	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15598334	PA3138	uvrB	excinuclease ABC subunit B	1.3	2.60E-01	Glucose	5.1	76067	15	Cytoplasmic	COG0556	DNA replication, recombination, and repair	
15598335	PA3139		probable amino acid aminotransferase	1.0	7.66E-01	Glucose	6.6	43319	25	Periplasmic	COG1448	Amino acid transport and metabolism	
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	1.2	2.64E-01	Glucose	5.8	38907	19	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane	
15598346	PA3150	wbpG	LPS biosynthesis protein WbpG	1.1	9.54E-01	Glucose	8.3	43471	2	Outer Membrane Vesicle	COG0037	Cell cycle control, cell division, chromosome partitioning	

15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	1.3	1.80E-01	Citronellol	5.7	27448	8	Cytoplasmic	COG0107	Amino acid transport and metabolism	
15598348	PA3152	hisH2	glutamine amidotransferase	2.1	7.64E-02	Glucose	7.1	22663	9	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase, wbpE	1.4	7.11E-02	Citronellol	6.0	38924	18	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-acetyltransferase, WbpD	1.8	2.82E-02	Glucose	7.8	20562	5	Cytoplasmic	COG1045	Amino acid transport and metabolism	
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	1.8	1.37E-02	Glucose	6.6	35717	20	Cytoplasmic	COG0673	General function prediction only	
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.1	5.52E-01	Glucose	5.2	48155	35	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane	
15598358	PA3162	rpsA	30S ribosomal protein S1	1.0	9.76E-01	Glucose	4.6	61869	30	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis	
15598359	PA3163	cmk	cytidylate kinase	1.1	5.03E-01	Citronellol	4.8	24637	12	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	11.1	3.19E-04	Glucose	4.8	39483	12	Cytoplasmic	COG0079	Amino acid transport and metabolism	
15598362	PA3166	pheA	chorismate mutase	1.2	4.27E-01	Citronellol	6.3	40632	13	Cytoplasmic	COG0077	Amino acid transport and metabolism	
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.1	6.50E-01	Citronellol	4.7	39917	18	Periplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
15598364	PA3168	gyrA	DNA gyrase subunit A	1.2	3.73E-01	Glucose	4.6	101134	53	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.3	3.09E-02	Glucose	5.1	39425	10	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis	
15598366	PA3170		conserved hypothetical protein	1.5	8.01E-02	Citronellol	5.5	48493	5	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	2.2	4.44E-03	Glucose	6.3	25860	7	Cytoplasmic	COG2227	Coenzyme metabolism	
15598368	PA3172		probable hydrolase	1.1	5.03E-01	Citronellol	5.0	24944	11	Cytoplasmic	COG0546	General function prediction only	
15598369	PA3173		probable short-chain dehydrogenase	1.1	7.17E-01	Glucose	4.9	26332	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598376	PA3180		hypothetical protein	37.8	1.66E-02	Glucose	4.7	16863	2	Unknown	COG1051	Nucleotide transport and metabolism	
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	22.3	1.41E-04	Glucose	7.6	23953	15	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598378	PA3182	pgl	6-phosphogluconolactonase	32.2	3.84E-06	Glucose	6.5	25571	13	Unknown	COG0363	Carbohydrate transport and metabolism	
15598379	PA3183	zwf	glucose-6-phosphate 1-dehydrogenase	5.8	7.15E-03	Glucose	5.7	55620	24	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
15598382	PA3186	oprB	Glucose/carbohydrate outer membrane porin OprB precursor	5.3	2.92E-01	Glucose	5.5	50753	6	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
15598383	PA3187		probable ATP-binding component of ABC transporter	4.6	1.51E-02	Glucose	7.5	42240	4	Outer Membrane Vesicle	COG3839	Carbohydrate transport and metabolism	
15598386	PA3190		probable binding protein component of ABC sugar transporter	16.2	3.17E-06	Glucose	5.8	45131	29	Periplasmic	COG1653	Carbohydrate transport and metabolism	
15598388	PA3192	gltR	two-component response regulator GltR	7.4	4.81E-03	Glucose	5.7	27381	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15598389	PA3193	glk	glucokinase	6.2	5.98E-05	Glucose	5.0	34606	10	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
15598390	PA3194	edd	phosphogluconate dehydratase	4.6	1.18E-02	Glucose	6.7	65182	27	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	23.2	4.15E-05	Glucose	6.6	36170	25	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15598392	PA3196		hypothetical protein	2.8	6.47E-03	Citronellol	3.9	19293	2	Unknown			
15598395	PA3199		conserved hypothetical protein	1.8	1.84E-01	Citronellol	6.7	23144	4	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15598401	PA3205		hypothetical protein	14.7	1.80E-03	Citronellol	10.5	16696	2	Unknown	COG3678	Intracellular trafficking and secretion	Cell motility and secretio
15598404	PA3208		conserved hypothetical protein	2.5	4.47E-01	Citronellol	6.5	19948	13	Cytoplasmic Membrane	COG0778	Energy production and conversion	
15598410	PA3214		hypothetical protein	1.5	7.99E-01	Citronellol	10.4	23214	4	Unknown	COG3218	General function prediction only	
15598421	PA3225		probable transcriptional regulator	3.3	6.60E-04	Citronellol	7.4	34098	5	Cytoplasmic	COG0583	Transcription	
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.3	2.50E-01	Citronellol	8.5	20104	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15598429	PA3233		hypothetical protein	12.0	5.87E-05	Citronellol	6.3	66563	2	Cytoplasmic	COG2905	Signal transduction mechanisms	
15598439	PA3243	minC	cell division inhibitor MinC	1.1	5.41E-01	Citronellol	6.5	28124	9	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
15598440	PA3244	minD	cell division inhibitor MinD	1.2	1.66E-01	Glucose	5.5	29617	21	Periplasmic	COG2894	Cell division and chromosome partitioning	
15598442	PA3246	rluA	pseudouridine synthase RluA	1.0	7.66E-01	Glucose	7.0	24339	5	Cytoplasmic	COG0564	Translation, ribosomal structure and biogenesis	
15598443	PA3247		hypothetical protein	3.0	4.60E-02	Citronellol	6.0	46658	11	Cytoplasmic	COG1362	Amino acid transport and metabolism	
15598446	PA3250		hypothetical protein	28.8	1.42E-03	Citronellol	6.2	38285	12	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15598451	PA3255		hypothetical protein	1.4	4.86E-02	Citronellol	4.4	21635	9	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15598452	PA3256		probable oxidoreductase	1.1	4.30E-01	Citronellol	5.2	33387	14	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15598453	PA3257	prc	periplasmic tail-specific protease	1.0	8.49E-01	Citronellol	6.6	78182	34	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.4	2.42E-01	Glucose	4.8	26845	12	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones	
15598459	PA3263		conserved hypothetical protein	1.4	5.31E-02	Glucose	4.7	34015	20	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
15598466	PA3270		hypothetical protein	1.4	1.50E-01	Citronellol	9.9	21901	4	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15598473	PA3277		probable short-chain dehydrogenase	1.4	3.49E-01	Citronellol	6.5	29251	3	Cytoplasmic	COG0300	General function prediction only	
15598482	PA3286		hypothetical protein	1.8	1.56E-02	Citronellol	6.4	38139	15	Periplasmic	COG0332	acyl-carrier-protein	
15598483	PA3287		conserved hypothetical protein	3.0	6.52E-04	Citronellol	5.5	18194	2	Periplasmic	COG0666	General function prediction only	
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	5.6	5.88E-04	Citronellol	7.5	61654	24	Outer Membrane Vesicle	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	6.1	7.09E-04	Citronellol	7.2	61736	10	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598498	PA3302		conserved hypothetical protein	2.0	2.69E-01	Citronellol	5.0	16901	7	Unknown	COG2030	Lipid metabolism	
15598504	PA3308	hepA	RNA helicase HepA	1.1	6.96E-01	Glucose	4.8	106839	25	Periplasmic	COG0553	Transcription	DNA replication, recombination, and repair
15598505	PA3309		conserved hypothetical protein	12.6	1.46E-04	Citronellol	5.4	16496	11	Periplasmic	COG0589	Signal transduction mechanisms	
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.4	1.19E-01	Glucose	5.5	30908	8	Cytoplasmic	COG2084	Lipid metabolism	
15598509	PA3313		hypothetical protein	1.3	2.95E-01	Citronellol	10.2	36539	18	Periplasmic	COG3221	Inorganic ion transport and metabolism	
15598522	PA3326	clpP2	ClpP2	4.6	3.49E-02	Citronellol	5.4	22142	13	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15598523	PA3327		probable non-ribosomal peptide synthetase	14.9	9.52E-03	Citronellol	5.5	259403	53	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15598525	PA3329		hypothetical protein	12.7	1.54E-03	Citronellol	6.2	49134	7	Cytoplasmic			
15598527	PA3331		cytochrome P450	7.7	1.31E-03	Citronellol	5.7	46345	2	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
15598528	PA3332		conserved hypothetical protein	8.3	2.37E-04	Citronellol	5.5	15920	10	Cytoplasmic	COG3631	General function prediction only	
15598529	PA3333	fabH2	3-oxoacyl-[acyl-carrier-protein] synthase III	7.8	3.36E-04	Citronellol	5.0	34003	7	Cytoplasmic	COG0332	acyl-carrier-protein	
15598537	PA3341		probable transcriptional regulator	2.6	4.62E-01	Citronellol	8.6	16071	2	Cytoplasmic	COG1846	Transcription	
15598540	PA3344	recQ	ATP-dependent DNA helicase RecQ	2.4	2.20E-03	Glucose	5.8	79449	6	Cytoplasmic	COG0514	DNA replication, recombination, and repair	
15598544	PA3348		probable chemotaxis protein methyltransferase	1.1	6.39E-01	Citronellol	9.6	30615	7	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
15598545	PA3349		probable chemotaxis protein	1.1	5.49E-01	Glucose	6.1	34402	13	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15598549	PA3353		hypothetical protein	1.1	3.04E-01	Glucose	6.8	29852	12	Cytoplasmic	COG5581	Signal transduction mechanisms	
15598553	PA3357	dsdA	D-serine dehydratase	1.3	6.85E-02	Glucose	6.0	48200	7	Cytoplasmic	COG3048	Amino acid transport and metabolism	
15598562	PA3366	amiE	aliphatic amidase	120.3	7.45E-02	Citronellol	5.1	38495	2	Cytoplasmic	COG0388	General function prediction only	
15598593	PA3397	fpr	NADP+-dependent ferredoxin reductase	1.3	2.22E-01	Citronellol	5.9	29518	22	Periplasmic	COG1018	Energy production and conversion	
15598610	PA3414		hypothetical protein	1.3	4.51E-01	Glucose	8.1	20918	2	Unknown			
15598614	PA3418	ldh	leucine dehydrogenase	31.8	5.26E-05	Citronellol	5.9	35633	7	Cytoplasmic	COG0334	Amino acid transport and metabolism	
15598617	PA3421		conserved hypothetical protein	18.2	4.13E-05	Citronellol	9.2	50690	5	Unknown			
15598622	PA3426		probable enoyl CoA-hydratase/isomerase	2.5	1.82E-02	Citronellol	4.5	26998	3	Cytoplasmic	COG1024	Lipid metabolism	
15598623	PA3427		probable short-chain dehydrogenases	4.9	1.61E-02	Citronellol	5.8	32323	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598626	PA3430		probable aldolase	19.2	3.79E-06	Citronellol	6.6	27993	6	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15598633	PA3437	folM	dihydromonapterin reductase, FolM	1.5	7.17E-01	Citronellol	7.0	25403	2	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	1.2	5.24E-01	Glucose	7.6	20833	4	Cytoplasmic	COG0302	Coenzyme metabolism	
15598636	PA3440		conserved hypothetical protein	1.2	5.63E-01	Citronellol	5.7	11637	2	Unknown	COG3492	Function unknown	
15598646	PA3450		probable antioxidant protein	1.5	5.40E-02	Glucose	5.2	24164	9	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598649	PA3453		conserved hypothetical protein	1.2	1.65E-01	Glucose	5.4	24160	10	Unknown	COG3132	Function unknown	
15598654	PA3458		probable transcriptional regulator	1.0	9.87E-01	Citronellol	5.6	17599	3	Unknown	COG1846	Transcription	
15598657	PA3461		conserved hypothetical protein	6.2	8.88E-04	Citronellol	5.1	43294	8	Cytoplasmic	COG1363	Carbohydrate transport and metabolism	
15598666	PA3470		hypothetical protein	3.0	1.39E-02	Glucose	5.2	16673	3	Unknown	COG0494	DNA replication, recombination, and repair	General function prediction only
15598667	PA3471		probable malic enzyme	3.4	1.97E-04	Glucose	5.2	62420	22	Periplasmic	COG0281	Energy production and conversion	
15598673	PA3477	rhlR	transcriptional regulator RhlR	1.8	6.13E-01	Citronellol	7.2	27577	3	Cytoplasmic	COG2771	Transcription	
15598676	PA3480		probable deoxycytidine triphosphate deaminase	1.6	6.92E-01	Citronellol	6.3	21154	8	Cytoplasmic	COG0717	Nucleotide transport and metabolism	
15598677	PA3481		conserved hypothetical protein	1.5	9.96E-03	Citronellol	5.1	38889	9	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
15598678	PA3482	metG	methionyl-tRNA synthetase	1.7	2.07E-03	Glucose	5.4	74903	31	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis	
15598704	PA3508		probable transcriptional regulator	15.4	5.49E-02	Citronellol	5.8	30877	2	Cytoplasmic	COG1414	Transcription	
15598720	PA3524	gloA1	lactoylglutathione lyase	1.0	4.68E-01	Citronellol	4.7	14251	2	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15598721	PA3525	argG	argininosuccinate synthase	1.3	8.17E-02	Glucose	5.3	45297	20	Periplasmic	COG0137	Amino acid transport and metabolism	
15598723	PA3527	pyrC	dihydroorotase	1.5	5.59E-02	Citronellol	6.6	38406	13	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
15598724	PA3528	rnt	ribonuclease T	1.1	5.63E-01	Glucose	4.8	24723	9	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15598725	PA3529		alkylhydroperoxide reductase C	1.5	1.72E-02	Glucose	5.3	21822	15	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.2	2.37E-01	Glucose	5.7	33924	16	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15598735	PA3539		conserved hypothetical protein	1.3	7.59E-02	Glucose	6.7	29560	13	Cytoplasmic	COG3022	Function unknown	
15598748	PA3552	arnB	ArnB	6.3	1.71E-04	Citronellol	8.0	41867	1	Cytoplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598750	PA3554	arnA	ArnA	1.2	4.31E-01	Glucose	6.7	74360	2	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis	
15598758	PA3562	frlI	phosphotransferase system transporter enzyme I, FrlI	1.2	6.41E-01	Citronellol	4.8	101572	4	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598759	PA3563	fruR	fructose transport system repressor FruR	2.3	2.02E-02	Citronellol	6.4	36369	4	Cytoplasmic	COG1609	Transcription	

15598763	PA3567		probable oxidoreductase	1.2	2.57E-01	Glucose	6.6	36678	5	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15598764	PA3568		probable acetyl-coa synthetase	20.7	1.78E-01	Citronellol	6.7	68990	4	Cytoplasmic	COG0365	Lipid metabolism	
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	28.7	6.58E-05	Citronellol	6.4	53663	7	Cytoplasmic	COG1012	Energy production and conversion	
15598774	PA3578		conserved hypothetical protein	2.1	4.89E-03	Citronellol	4.9	28906	6	Cytoplasmic Membrane	COG0384	General function prediction only	
15598775	PA3579		probable carbohydrate kinase	1.0	8.20E-01	Citronellol	5.6	54207	4	Cytoplasmic	COG0554	Energy production and conversion	
15598778	PA3582	glpK	glycerol kinase	6.5	3.32E-03	Citronellol	5.9	55966	23	Cytoplasmic	COG0554	Energy production and conversion	
15598783	PA3587	metR	transcriptional regulator MetR	1.2	3.86E-01	Citronellol	5.6	34216	3	Cytoplasmic	COG0583	Transcription	
15598800	PA3604	erdR	response regulator ErdR	1.3	1.77E-01	Citronellol	4.8	23531	11	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598806	PA3610	potD	polyamine transport protein PotD	6.0	7.19E-03	Glucose	5.5	39260	7	Periplasmic	COG0687	Amino acid transport and metabolism	
15598809	PA3613		hypothetical protein	8.3	5.68E-04	Citronellol	6.4	88379	11	Periplasmic	COG3957	Carbohydrate transport and metabolism	
15598810	PA3614		hypothetical protein	3.6	1.75E-04	Citronellol	7.0	51921	7	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
15598811	PA3615		hypothetical protein	4.8	3.87E-03	Citronellol	6.0	40465	8	Cytoplasmic	COG1611	General function prediction only	
15598813	PA3617	recA	RecA protein	1.2	5.17E-01	Citronellol	5.2	36879	13	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
15598814	PA3618		conserved hypothetical protein	2.3	1.65E-01	Glucose	5.0	17715	4	Unknown	COG1546	General function prediction only	
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.7	5.96E-02	Glucose	6.1	94977	21	Cytoplasmic	COG0249	DNA replication, recombination, and repair	
15598817	PA3621	fdxA	ferredoxin I	1.1	7.73E-01	Citronellol	3.7	12159	3	Cytoplasmic	COG1146	Energy production and conversion	
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	1.9	3.32E-02	Glucose	6.1	23407	5	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones	
15598821	PA3625	surE	survival protein SurE	1.5	4.72E-02	Glucose	5.2	26368	5	Unknown	COG0496	General function prediction only	
15598823	PA3627	ygbB	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.5	5.18E-01	Glucose	7.1	16662	3	Cytoplasmic	COG0245	Lipid metabolism	
15598824	PA3628		probable esterase	3.2	1.78E-03	Citronellol	6.3	31243	7	Unknown	COG0627	General function prediction only	
15598825	PA3629	adhC	alcohol dehydrogenase class III	3.4	2.87E-04	Citronellol	5.4	39208	7	Cytoplasmic	COG1062	Energy production and conversion	
15598829	PA3633	ygbP	4-diphosphocytidyl-2-C-methylerythritol synthase	1.1	6.90E-01	Glucose	5.2	25613	4	Cytoplasmic	COG1211	Lipid metabolism	
15598831	PA3635	eno	enolase	1.3	1.13E-01	Glucose	4.8	45195	22	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	1.1	4.86E-01	Glucose	6.5	31143	21	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
15598833	PA3637	pyrG	CTP synthase	1.8	6.49E-03	Glucose	5.4	59617	34	Periplasmic	COG0504	Nucleotide transport and metabolism	
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)	1.6	9.59E-02	Glucose	5.2	34947	25	Outer Membrane Vesicle	COG0825	Lipid metabolism	
15598836	PA3640	dnaE	DNA polymerase III, alpha chain	1.6	8.94E-01	Citronellol	5.1	130904	42	Cytoplasmic	COG0587	DNA replication, recombination, and repair	
15598838	PA3642	rnhB	ribonuclease HII	4.4	9.89E-02	Glucose	6.5	21771	5	Cytoplasmic	COG0164	DNA replication, recombination, and repair	
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase	1.6	3.76E-02	Citronellol	7.1	28010	8	Cytoplasmic	COG1043	acyl carrier protein	
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	3.5	6.76E-03	Citronellol	7.6	16774	6	Cytoplasmic	COG0764	Lipid metabolism	
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase	1.5	3.88E-01	Citronellol	6.2	36191	3	Cytoplasmic	COG1044	3-hydroxymyristoyl	
15598843	PA3647		probable outer membrane protein precursor	2.0	1.25E-01	Citronellol	10.0	19058	8	Unknown	COG2825	Cell envelope biogenesis, outer membrane	
15598844	PA3648	oprB6	outer membrane protein OprB6	2.8	1.14E-01	Glucose	4.8	88286	5	Periplasmic	COG4775	Cell envelope biogenesis, outer membrane	
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase	1.0	9.09E-01	Glucose	5.7	42508	7	Unknown	COG0743	Lipid metabolism	
15598849	PA3653	frr	ribosome recycling factor	1.8	4.20E-01	Citronellol	5.9	20485	18	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis	
15598850	PA3654	pyrH	uridylate kinase	1.2	3.96E-01	Glucose	5.4	26272	13	Periplasmic	COG0528	Nucleotide transport and metabolism	
15598851	PA3655	tsf	elongation factor Ts	1.3	1.80E-01	Glucose	5.0	30653	33	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis	
15598852	PA3656	rpsB	30S ribosomal protein S2	1.5	4.82E-01	Glucose	9.0	27336	15	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis	
15598853	PA3657	map	methionine aminopeptidase	1.7	2.45E-03	Citronellol	6.3	29086	8	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis	
15598854	PA3658	glnD	protein-PII uridylyltransferase	1.4	5.34E-01	Citronellol	5.5	103403	4	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones	
15598855	PA3659		probable aminotransferase	2.0	1.32E-02	Glucose	5.5	44544	7	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase	1.2	1.18E-01	Citronellol	6.0	35973	12	Periplasmic	COG2171	Amino acid transport and metabolism	
15598870	PA3674		hypothetical protein	1.7	1.82E-02	Citronellol	7.6	14393	2	Periplasmic	COG3126	Function unknown	
15598871	PA3675		hypothetical protein	2.5	1.89E-02	Glucose	9.4	23645	7	Unknown			
15598874	PA3678		probable transcriptional regulator	3.8	1.16E-01	Citronellol	6.3	23150	9	Cytoplasmic	COG1309	Transcription	
15598878	PA3682		hypothetical protein	1.9	4.29E-03	Citronellol	5.0	29150	8	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15598881	PA3685		conserved hypothetical protein	1.1	4.97E-01	Glucose	4.8	24180	5	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones	
15598882	PA3686	adk	adenylate kinase	2.0	1.36E-02	Citronellol	6.4	23107	16	Cytoplasmic	COG0563	Nucleotide transport and metabolism	
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase	2.9	4.47E-03	Citronellol	6.2	97839	21	Cytoplasmic	COG2352	Energy production and conversion	
15598887	PA3691		hypothetical protein	5.6	8.59E-02	Citronellol	8.5	14468	3	Outer Membrane Vesicle			
15598888	PA3692	lptF	Lipotoxon F, LptF	4.4	6.17E-02	Citronellol	9.9	28514	5	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
15598889	PA3693		conserved hypothetical protein	1.3	9.81E-01	Citronellol	7.0	18219	3	Unknown	COG2110	General function prediction only	
15598892	PA3696		conserved hypothetical protein	1.5	1.90E-01	Glucose	5.4	26551	4	Unknown	COG2013	Function unknown	
15598894	PA3698		hypothetical protein	2.1	1.95E-01	Citronellol	4.5	20351	4	Unknown			
15598896	PA3700	lysS	lysyl-tRNA synthetase	1.6	1.40E-02	Glucose	5.0	57329	35	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis	
15598897	PA3702	wspR	WspR	4.6	7.13E-03	Citronellol	5.6	37887	2	Cytoplasmic	COG3706	Signal transduction mechanisms	
15598911	PA3716		hypothetical protein	1.4	4.45E-01	Glucose	4.1	60503	3	Outer Membrane Vesicle			
15598916	PA3721	nalC	NalC	1.3	8.50E-01	Citronellol	5.7	23533	2	Cytoplasmic	COG1309	Transcription	
15598918	PA3723		probable FMN oxidoreductase	13.2	9.95E-05	Citronellol	6.3	40319	14	Cytoplasmic	COG1902	Energy production and conversion	
15598921	PA3726		conserved hypothetical protein	1.4	2.33E-01	Glucose	4.8	20596	6	Cytoplasmic	COG4681	Function unknown	
15598922	PA3727		hypothetical protein	2.6	9.64E-03	Glucose	4.9	26461	2	Cytoplasmic	COG1502	Lipid metabolism	
15598923	PA3728		hypothetical protein	2.2	4.06E-01	Citronellol	4.9	197133	58	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning	
15598926	PA3731		conserved hypothetical protein	1.1	5.34E-01	Glucose	7.5	24893	7	Cytoplasmic	COG1842	Transcription	Signal transduction mechanisms
15598927	PA3732		conserved hypothetical protein	1.3	7.19E-02	Citronellol	4.0	15959	3	Unknown	COG3789	Function unknown	
15598930	PA3735	thrC	threonine synthase	1.0	1.00E+00	Citronellol	6.6	51795	22	Periplasmic	COG0498	Amino acid transport and metabolism	
15598931	PA3736	hom	homoserine dehydrogenase	1.5	8.95E-03	Glucose	5.1	46192	16	Cytoplasmic	COG0460	Amino acid transport and metabolism	
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC	1.7	2.97E-02	Glucose	8.8	26095	8	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15598935	PA3740		hypothetical protein	1.7	1.98E-01	Glucose	10.0	24754	2	Unknown			
15598937	PA3742	rplS	50S ribosomal protein L19	3.5	1.75E-01	Glucose	11.1	13032	3	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
15598938	PA3743	trmD	tRNA (guanine-N1)-methyltransferase	1.6	6.92E-02	Glucose	4.9	28359	2	Cytoplasmic	COG0336	Translation, ribosomal structure and biogenesis	
15598941	PA3746	ffh	signal recognition particle protein Ffh	1.3	8.08E-01	Citronellol	10.3	69359	3	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2	1.5	2.28E-02	Citronellol	6.1	42342	18	Periplasmic	COG0027	Nucleotide transport and metabolism	
15598948	PA3753		conserved hypothetical protein	1.9	2.84E-02	Citronellol	7.0	18509	5	Cytoplasmic	COG0663	General function prediction only	
15598949	PA3754		hypothetical protein	2.8	2.13E-02	Citronellol	4.5	22855	3	Cytoplasmic			
15598950	PA3755		conserved hypothetical protein	2.1	5.49E-01	Citronellol	4.6	20829	2	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15598954	PA3759		probable aminotransferase	7.2	1.71E-02	Citronellol	5.7	36123	3	Cytoplasmic	COG2222	Cell envelope biogenesis, outer membrane	
15598955	PA3760		N-Acetyl-D-Glucosamine phosphotransferase system transporter	1.9	1.00E-01	Citronellol	5.4	89195	2	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase	2.1	3.44E-01	Citronellol	4.8	140646	62	Periplasmic	COG0046	Nucleotide transport and metabolism	
15598960	PA3765		hypothetical protein	1.1	9.68E-01	Citronellol	6.3	20903	2	Unknown	COG3644	Function unknown	
15598962	PA3767		conserved hypothetical protein	1.2	5.42E-01	Citronellol	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15598964	PA3769	guaA	GMP synthase	1.5	1.24E-01	Glucose	5.6	57959	34	Periplasmic	COG0519	Nucleotide transport and metabolism	
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase	1.4	8.90E-02	Glucose	6.7	51707	32	Periplasmic	COG0516	Nucleotide transport and metabolism	
15598972	PA3777	xseA	exodeoxyribonuclease VII large subunit	1.3	4.09E-01	Glucose	11.4	51231	2	Cytoplasmic	COG1570	DNA replication, recombination, and repair	
15598974	PA3779		hypothetical protein	3.3	1.70E-02	Citronellol	5.3	37696	5	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15598978	PA3783		hypothetical protein	1.3	8.09E-02	Glucose	6.4	23091	7	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15598980	PA3785		conserved hypothetical protein	14.0	1.08E-03	Citronellol	6.8	17000	8	Periplasmic	COG2847	Inorganic ion transport and metabolism	
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precursor	1.9	4.20E-02	Citronellol	6.4	79303	7	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15598990	PA3795		probable oxidoreductase	3.9	1.82E-02	Citronellol	5.3	34803	6	Cytoplasmic	COG0667	Energy production and conversion	
15598992	PA3797		conserved hypothetical protein	1.3	1.48E-01	Citronellol	5.8	29996	4	Cytoplasmic	COG0388	General function prediction only	
15598993	PA3798		probable aminotransferase	1.2	1.98E-01	Citronellol	6.2	42594	8	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598996	PA3801		conserved hypothetical protein	3.0	6.46E-01	Citronellol	4.8	23108	5	Outer Membrane Vesicle	COG2976	Function unknown	
15598997	PA3802	hisS	histidyl-tRNA synthetase	1.2	1.48E-01	Glucose	5.0	47480	16	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE	1.0	8.84E-01	Citronellol	6.4	40056	14	Cytoplasmic	COG0821	Lipid metabolism	
15599000	PA3805	pilF	type 4 fimbrial biogenesis protein PilF	1.7	8.28E-02	Glucose	7.3	28537	3	Periplasmic	COG3063	Cell motility and secretion	Intracellular trafficking and secretion
15599001	PA3806		conserved hypothetical protein	4.4	9.90E-01	Glucose	8.4	41700	2	Cytoplasmic	COG0820	General function prediction only	
15599002	PA3807	ndk	nucleoside diphosphate kinase	1.2	5.58E-01	Glucose	5.3	15592	13	Cytoplasmic	COG0105	Nucleotide transport and metabolism	
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]	1.1	9.34E-01	Citronellol	4.0	12241	5	Cytoplasmic	COG0633	Energy production and conversion	
15599005	PA3810	hscA	heat shock protein HscA	2.1	6.19E-04	Glucose	4.6	66446	19	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599006	PA3811	hscB	heat shock protein HscB	1.6	7.02E-01	Citronellol	4.6	20203	3	Cytoplasmic	COG1076	Posttranslational modification, protein turnover, chaperones	
15599008	PA3813	iscU	probable iron-binding protein IscU	1.7	3.31E-01	Glucose	5.8	13753	4	Cytoplasmic	COG0822	Energy production and conversion	
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)	1.0	9.70E-01	Glucose	5.9	44666	25	Cytoplasmic	COG1104	Amino acid transport and metabolism	
15599010	PA3815	iscR	IscR	1.6	9.63E-03	Glucose	6.9	17853	7	Unknown	COG1959	Transcription	

15599012	PA3817		probable methyltransferase	1.1	5.87E-01	Citronellol	6.2	28493	8	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis		
15599013	PA3818		extragenic suppressor protein SuhB	2.5	7.94E-02	Glucose	6.6	29521	10	Periplasmic	COG0483	Carbohydrate transport and metabolism		
15599014	PA3819		conserved hypothetical protein	1.8	4.01E-01	Citronellol	9.4	18941	2	Outer Membrane	COG3134	Function unknown		
15599017	PA3822		conserved hypothetical protein	1.1	7.21E-01	Citronellol	9.6	11862	2	Outer Membrane Vesicle	COG1862	Intracellular trafficking and secretion		
15599018	PA3823	tgt	queuine tRNA-ribosyltransferase	2.7	5.85E-02	Glucose	6.9	41205	3	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis		
15599027	PA3832	holC	DNA polymerase III, chi subunit	1.6	9.43E-02	Glucose	5.7	16109	2	Cytoplasmic	COG2927	DNA replication, recombination, and repair		
15599029	PA3834	valS	valyl-tRNA synthetase	1.1	6.29E-01	Glucose	5.2	107707	44	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis		
15599031	PA3836		hypothetical protein	2.3	7.30E-03	Citronellol	8.7	34220	21	Periplasmic	COG2984	General function prediction only		
15599039	PA3844		hypothetical protein	2.0	3.10E-01	Citronellol	4.8	22795	4	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones		
15599041	PA3846		hypothetical protein	3.6	7.47E-02	Citronellol	5.1	19892	7	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15599044	PA3849		conserved hypothetical protein	2.8	6.73E-02	Citronellol	5.1	37930	4	Cytoplasmic	COG3081	General function prediction only		
15599045	PA3850		hypothetical protein	3.3	2.74E-01	Glucose	4.4	33613	2	Unknown				
15599047	PA3852		hypothetical protein	3.2	2.13E-03	Citronellol	5.4	33979	7	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
15599051	PA3856		hypothetical protein	2.0	2.90E-02	Citronellol	9.9	18327	2	Unknown				
15599053	PA3858		probable amino acid-binding protein	7.7	5.00E-05	Citronellol	7.9	37043	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15599054	PA3859		carboxylesterase	1.0	6.17E-01	Citronellol	4.9	23420	4	Unknown	COG0400	General function prediction only		
15599055	PA3860		probable AMP-binding enzyme	21.0	9.98E-06	Citronellol	6.2	68986	22	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15599060	PA3865		probable amino acid binding protein	1.7	1.52E-01	Citronellol	6.1	28433	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15599061	PA3866		pyocin protein	2.4	2.28E-01	Citronellol	8.8	80731	5	Extracellular				
15599074	PA3879	narL	two-component response regulator NarL	3.9	8.65E-03	Citronellol	4.8	24255	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
15599081	PA3886		hypothetical protein	1.2	3.46E-01	Glucose	4.9	32290	4	Cytoplasmic	COG0647	Carbohydrate transport and metabolism		
15599091	PA3896		probable 2-hydroxyacid dehydrogenase	1.2	4.82E-01	Glucose	8.2	35632	8	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism	
15599098	PA3903	prfC	peptide chain release factor 3	1.5	1.64E-02	Citronellol	5.7	59865	10	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis		
15599100	PA3905		hypothetical protein	5.5	2.18E-03	Glucose	7.7	20024	5	Unknown				
15599103	PA3908		hypothetical protein	1.0	9.56E-01	Citronellol	5.0	27294	7	Cytoplasmic				
15599113	PA3918	moaC	molybdopterin biosynthetic protein C	1.2	3.75E-01	Citronellol	7.0	17306	12	Cytoplasmic	COG0315	Coenzyme metabolism		
15599114	PA3919		conserved hypothetical protein	3.6	6.68E-04	Citronellol	6.3	51700	12	Cytoplasmic	COG1875	General function prediction only		
15599117	PA3922		conserved hypothetical protein	13.8	2.09E-04	Citronellol	9.0	51229	36	Periplasmic				
15599118	PA3923		hypothetical protein	6.7	4.15E-03	Citronellol	4.7	69590	13	Outer Membrane				
15599119	PA3924		probable medium-chain acyl-CoA ligase	3.1	2.51E-04	Citronellol	6.0	62315	22	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15599120	PA3925		probable acyl-CoA thiolase	6.6	1.42E-04	Citronellol	6.4	40553	29	Cytoplasmic	COG0183	Lipid metabolism		
15599126	PA3931		conserved hypothetical protein	1.1	9.77E-01	Citronellol	8.6	28101	11	Periplasmic	COG1464	Inorganic ion transport and metabolism		
15599136	PA3941		hypothetical protein	2.6	3.57E-01	Citronellol	5.8	22025	4	Cytoplasmic	COG0546	General function prediction only		
15599137	PA3942	tesB	acyl-CoA thioesterase II	1.2	4.95E-01	Glucose	5.8	32934	4	Cytoplasmic	COG1946	Lipid metabolism		
15599139	PA3944		conserved hypothetical protein	1.1	7.14E-01	Citronellol	5.3	21857	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis		
15599140	PA3945		conserved hypothetical protein	2.0	5.15E-01	Citronellol	5.7	22403	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis		
15599143	PA3948	rocA1	Two-component response regulator RocA1	1.9	2.20E-01	Glucose	6.8	22996	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
15599146	PA3951		conserved hypothetical protein	1.6	1.72E-02	Glucose	7.5	18088	4	Unknown	COG1432	Function unknown		
15599160	PA3965		probable transcriptional regulator	2.2	5.67E-02	Citronellol	5.7	19289	9	Cytoplasmic	COG1522	Transcription		
15599167	PA3972		probable acyl-CoA dehydrogenase	14.4	7.71E-05	Citronellol	6.4	60338	30	Cytoplasmic	COG1960	Lipid metabolism		
15599170	PA3975	thiD	phosphomethylpyrimidine kinase	2.2	5.93E-02	Glucose	6.2	27979	3	Periplasmic	COG0351	Coenzyme metabolism		
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase	1.1	8.26E-01	Citronellol	7.1	22146	3	Unknown	COG0352	Coenzyme metabolism		
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase	1.1	3.68E-01	Citronellol	5.6	45398	21	Cytoplasmic	COG0001	Coenzyme metabolism		
15599173	PA3978		hypothetical protein	1.3	1.21E-01	Citronellol	4.3	19636	2	Unknown	COG0790	General function prediction only		
15599175	PA3980		conserved hypothetical protein	3.4	6.76E-02	Glucose	5.8	49978	3	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis		
15599178	PA3983		conserved hypothetical protein	1.2	6.54E-02	Glucose	4.6	31549	7	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism		
15599182	PA3987	leuS	leucyl-tRNA synthetase	1.3	3.94E-01	Glucose	5.5	97647	43	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis		
15599183	PA3988		hypothetical protein	1.9	1.92E-01	Glucose	5.0	22884	9	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane		
15599184	PA3989	holA	DNA polymerase III, delta subunit	7.0	3.38E-02	Glucose	6.9	37378	4	Unknown	COG1466	DNA replication, recombination, and repair		
15599191	PA3996	lis	lipoate synthase	8.0	7.00E-03	Glucose	6.9	36733	7	Cytoplasmic	COG0320	Coenzyme metabolism		
15599192	PA3997	lipB	lipoate-protein ligase B	2.2	3.55E-02	Glucose	6.0	23856	4	Cytoplasmic	COG0321	Coenzyme metabolism		
15599199	PA4004		conserved hypothetical protein	1.4	1.35E-01	Glucose	9.2	17791	4	Cytoplasmic	COG1576	Function unknown		
15599201	PA4006	nadD	nicotinic acid mononucleotide adenylyltransferase	1.4	1.03E-01	Citronellol	6.4	23801	3	Cytoplasmic	COG1057	Coenzyme metabolism		
15599202	PA4007	proA	gamma-glutamyl phosphate reductase	1.1	6.66E-01	Citronellol	5.2	45044	15	Periplasmic	COG0014	Amino acid transport and metabolism		
15599205	PA4010		hypothetical protein	1.4	1.14E-01	Citronellol	8.8	26949	6	Cytoplasmic	COG2094	DNA replication, recombination, and repair		
15599210	PA4015		conserved hypothetical protein	4.4	9.36E-04	Citronellol	5.6	16700	12	Cytoplasmic	COG2030	Lipid metabolism		
15599212	PA4017		conserved hypothetical protein	1.5	2.34E-01	Glucose	7.1	23164	5	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15599214	PA4019		probable aromatic acid decarboxylase	1.6	4.29E-02	Citronellol	4.8	22367	2	Cytoplasmic	COG0163	Coenzyme metabolism		
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	1.1	6.64E-01	Glucose	6.4	48469	5	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane		
15599217	PA4022	hdhA	hydrazone dehydrogenase, HdhA	3.6	1.15E-03	Citronellol	5.5	54979	24	Outer Membrane Vesicle	COG1012	Energy production and conversion		
15599221	PA4026		probable acetyltransferase	5.3	6.72E-04	Citronellol	7.0	18049	9	Cytoplasmic	COG0456	General function prediction only		
15599226	PA4031	ppa	inorganic pyrophosphatase	1.3	3.76E-01	Glucose	4.9	19396	12	Cytoplasmic	COG0221	Energy production and conversion		
15599230	PA4035		hypothetical protein	2.3	1.10E-04	Citronellol	6.3	35895	5	Periplasmic	COG4254	Function unknown		
15599238	PA4043	ispA	geranyltranstransferase	2.8	7.32E-02	Glucose	5.1	31464	6	Cytoplasmic	COG0142	Coenzyme metabolism		
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase	3.2	5.83E-04	Glucose	5.5	68049	8	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism	
15599243	PA4048		hypothetical protein	3.1	1.53E-01	Citronellol	9.4	23085	2	Unknown	COG3577	General function prediction only		
15599247	PA4052	nusB	NusB protein	1.1	9.39E-01	Citronellol	8.5	17675	6	Unknown	COG0781	Transcription		
15599248	PA4053	ribE	6,7-dimethyl-8-ribityllumazine synthase	1.2	8.13E-01	Glucose	5.8	16413	5	Cytoplasmic	COG0054	Coenzyme metabolism		
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	2.6	7.77E-03	Citronellol	5.1	39438	13	Cytoplasmic	COG0108	Coenzyme metabolism		
15599250	PA4055	ribC	riboflavin synthase alpha chain	1.1	7.66E-01	Glucose	6.4	23469	6	Cytoplasmic	COG0307	Coenzyme metabolism		
15599251	PA4056	ribD	riboflavin-specific deaminase/reductase	5.5	4.31E-03	Glucose	7.3	39764	2	Cytoplasmic	COG0117	Coenzyme metabolism		
15599252	PA4057	nrdR	NrdR	1.0	9.19E-01	Glucose	8.0	17925	7	Cytoplasmic	COG1327	Transcription		
15599256	PA4061		probable thioredoxin	1.4	1.39E-01	Citronellol	4.4	31878	15	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones		
15599258	PA4063		hypothetical protein	8.6	1.25E-01	Glucose	6.4	21235	2	Periplasmic				
15599262	PA4067	oprG	Outer membrane protein OprG precursor	3.9	3.41E-01	Glucose	4.7	25193	2	Periplasmic	COG3047	Cell envelope biogenesis, outer membrane		
15599263	PA4068		probable epimerase	1.0	8.41E-01	Citronellol	5.7	33310	14	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15599264	PA4069		hypothetical protein	1.2	5.62E-01	Glucose	6.3	32939	6	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane		
15599274	PA4079		probable dehydrogenase	2.0	2.85E-02	Citronellol	5.1	24319	8	Extracellular	COG0300	General function prediction only		
15599310	PA4115		conserved hypothetical protein	1.4	2.60E-01	Citronellol	7.1	51130	4	Cytoplasmic	COG1611	General function prediction only		
15599311	PA4116	bphO	heme oxygenase, BphO	1.1	3.01E-01	Glucose	4.9	21464	2	Cytoplasmic	COG3230	Inorganic ion transport and metabolism		
15599346	PA4151	acoB	acetoin catabolism protein AcoB	61.9	3.62E-03	Citronellol	4.8	36437	3	Cytoplasmic	COG0022	Energy production and conversion		
15599357	PA4162		probable short-chain dehydrogenase	1.3	6.55E-01	Citronellol	8.0	24857	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15599358	PA4163		hypothetical protein	1.0	8.89E-01	Citronellol	4.7	60494	19	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis		
15599375	PA4180		probable acetolactate synthase large subunit	1.8	6.03E-02	Glucose	6.3	59806	6	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase		
15599390	PA4195		probable binding protein component of ABC transporter	2.0	3.59E-03	Glucose	7.9	29539	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15599393	PA4198		probable AMP-binding enzyme	1.1	3.40E-01	Glucose	6.2	59548	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15599394	PA4199		probable acyl-CoA dehydrogenase	1.9	5.65E-02	Citronellol	5.0	63926	10	Cytoplasmic	COG1960	Lipid metabolism		
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	1.8	1.06E-01	Citronellol	4.9	36533	5	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane		
15599397	PA4202		hypothetical protein	1.2	2.20E-01	Citronellol	8.1	36782	8	Cytoplasmic	COG2070	General function prediction only		
15599399	PA4204	ppgL	periplasmic gluconolactonase, PpgL	1.2	5.89E-01	Citronellol	7.4	41616	8	Periplasmic	COG2706	Carbohydrate transport and metabolism		
15599423	PA4227	pchR	transcriptional regulator PchR	91.0	8.70E-03	Glucose	7.4	32339	2	Cytoplasmic	COG2207	Transcription		
15599428	PA4232	ssb	single-stranded DNA-binding protein	1.6	7.68E-01	Citronellol	5.3	18557	10	Cytoplasmic	COG0629	DNA replication, recombination, and repair		
15599430	PA4234	uvrA	excinuclease ABC subunit A	1.7	2.69E-01	Citronellol	6.6	104456	35	Cytoplasmic	COG0178	DNA replication, recombination, and repair		
15599431	PA4235	bfrA	bacterioferritin	1.2	2.84E-01	Glucose	4.8	17940	9	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism		
15599432	PA4236	katA	catalase	4.9	1.22E-04	Citronellol	6.7	55589	26	Periplasmic	COG0753	Inorganic ion transport and metabolism		
15599433	PA4237	rplQ	50S ribosomal protein L17	1.3	6.04E-01	Citronellol	11.1	14504	4	Outer Membrane Vesicle	COG0203	Translation, ribosomal structure and biogenesis		
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.0	8.28E-01	Glucose	4.6	36649	18	Outer Membrane Vesicle	COG0202	Transcription		
15599435	PA4239	rpsD	30S ribosomal protein S4	2.8	9.15E-02	Glucose	10.5	23277	15	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis		
15599436	PA4240	rpsK	30S ribosomal protein S11	5.6	4.44E-02	Glucose	11.5	13630	7	Outer Membrane Vesicle	COG0100	Translation, ribosomal structure and biogenesis		
15599437	PA4241	rpsM	30S ribosomal protein S13	2.8	1.93E-01	Glucose	11.5	13265	10	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis		
15599440	PA4244	rplO	50S ribosomal protein L15	1.3	7.88E-01	Citronellol	11.6	15174	7	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis		
15599442	PA4246	rpsE	30S ribosomal protein S5	3.0	8.10E-02	Glucose	10.6	17625	12	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis		

15599444	PA4248	rplF	50S ribosomal protein L6	1.0	8.81E-01	Citronellol	10.5	19099	9	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
15599445	PA4249	rpsH	30S ribosomal protein S8	6.1	6.60E-02	Glucose	10.2	14171	6	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
15599446	PA4250	rpsN	30S ribosomal protein S14	5.9	4.17E-02	Glucose	11.9	11565	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
15599447	PA4251	rplE	50S ribosomal protein L5	1.1	7.82E-01	Citronellol	10.3	20392	15	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis	
15599448	PA4252	rplX	50S ribosomal protein L24	6.4	1.21E-01	Glucose	11.0	11470	5	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis	
15599449	PA4253	rplN	50S ribosomal protein L14	2.2	2.32E-01	Glucose	11.4	13412	6	Outer Membrane Vesicle	COG0093	Translation, ribosomal structure and biogenesis	
15599452	PA4256	rplP	50S ribosomal protein L16	1.2	6.16E-01	Glucose	11.8	15401	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
15599453	PA4257	rpsC	30S ribosomal protein S3	1.7	1.57E-01	Glucose	10.8	25838	14	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis	
15599454	PA4258	rplV	50S ribosomal protein L22	2.5	3.14E-01	Glucose	10.9	11911	2	Cytoplasmic	COG0091	Translation, ribosomal structure and biogenesis	
15599456	PA4260	rplB	50S ribosomal protein L2	1.7	3.26E-01	Glucose	11.8	29579	6	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
15599457	PA4261	rplW	50S ribosomal protein L23	4.2	1.02E-01	Glucose	10.8	10950	3	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
15599458	PA4262	rplD	50S ribosomal protein L4	1.2	8.39E-01	Citronellol	10.6	21640	5	Outer Membrane Vesicle	COG0088	Translation, ribosomal structure and biogenesis	
15599459	PA4263	rplC	50S ribosomal protein L3	1.1	8.05E-01	Glucose	10.6	22592	4	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis	
15599461	PA4265	tufA	elongation factor Tu	1.1	3.08E-01	Citronellol	5.0	43337	54	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
15599462	PA4266	fusA1	elongation factor G	1.6	9.22E-02	Glucose	4.8	77752	79	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15599463	PA4267	rpsG	30S ribosomal protein S7	1.2	6.28E-01	Glucose	10.9	17504	15	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis	
15599464	PA4268	rpsL	30S ribosomal protein S12	1.5	3.85E-01	Glucose	11.6	13799	5	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	4.1	2.44E-01	Citronellol	7.1	154364	104	Outer Membrane Vesicle	COG0086	Transcription	
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	3.5	3.48E-01	Citronellol	5.6	150837	117	Periplasmic	COG0085	Transcription	
15599468	PA4272	rplJ	50S ribosomal protein L10	1.7	2.04E-01	Citronellol	9.5	17602	8	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
15599469	PA4273	rplA	50S ribosomal protein L1	1.7	2.93E-02	Citronellol	10.3	24234	13	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis	
15599470	PA4274	rplK	50S ribosomal protein L11	3.6	5.85E-02	Glucose	10.4	14907	5	Outer Membrane Vesicle	COG0080	Translation, ribosomal structure and biogenesis	
15599471	PA4275	nusG	transcription antitermination protein NusG	1.0	8.82E-01	Citronellol	5.8	20130	14	Cytoplasmic	COG0250	Transcription	
15599474	PA4278		hypothetical protein	2.1	1.32E-01	Glucose	5.9	26077	2	Unknown			
15599475	PA4279		hypothetical protein	1.1	5.95E-01	Citronellol	5.4	26758	5	Cytoplasmic	COG1521	Transcription	
15599478	PA4282		probable exonuclease	3.0	7.04E-01	Citronellol	5.5	138959	10	Extracellular	COG0419	DNA replication, recombination, and repair	
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	2.3	5.35E-02	Citronellol	6.7	79084	5	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	7.2	1.65E-01	Citronellol	5.5	139379	15	Unknown	COG1074	DNA replication, recombination, and repair	
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	1.7	3.80E-02	Citronellol	5.3	132646	10	Cytoplasmic	COG1330	DNA replication, recombination, and repair	
15599482	PA4286		hypothetical protein	1.7	7.34E-02	Citronellol	5.2	24815	3	Unknown	COG0095	Coenzyme metabolism	
15599492	PA4296	pprB	two-component response regulator, PprB	23.5	5.85E-02	Citronellol	6.7	30557	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599504	PA4308		conserved hypothetical protein	2.4	9.99E-03	Citronellol	6.5	53246	11	Unknown	COG0433	Replication, recombination, and repair	
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	1.3	1.09E-01	Glucose	6.5	32410	9	Periplasmic	COG0788	Nucleotide transport and metabolism	
15599511	PA4315	mvaT	transcriptional regulator MvaT, P16 subunit	1.0	8.24E-01	Glucose	10.1	14180	2	Cytoplasmic			
15599512	PA4316	sbcB	exodeoxyribonuclease I	1.4	2.90E-01	Glucose	5.4	55449	8	Cytoplasmic	COG2925	DNA replication, recombination, and repair	
15599513	PA4317		hypothetical protein	2.3	8.69E-01	Citronellol	9.2	26709	2	Cytoplasmic Membrane			
15599518	PA4322		conserved hypothetical protein	1.4	6.86E-02	Citronellol	6.2	36661	8	Cytoplasmic	COG0714	General function prediction only	
15599525	PA4329	pykA	pyruvate kinase II	2.4	8.58E-03	Glucose	6.7	52252	30	Periplasmic	COG0469	Carbohydrate transport and metabolism	
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	39.3	7.61E-06	Citronellol	6.7	28152	14	Cytoplasmic	COG1024	Lipid metabolism	
15599527	PA4331		probable ferredoxin reductase	1.6	1.34E-01	Citronellol	7.3	33842	2	Cytoplasmic	COG0543	Coenzyme metabolism	Energy production and conversion
15599529	PA4333		probable fumarase	3.1	2.42E-02	Glucose	5.2	54763	27	Periplasmic	COG1951	Energy production and conversion	
15599532	PA4336		conserved hypothetical protein	2.6	2.63E-01	Citronellol	6.0	20993	5	Cytoplasmic	COG0693	General function prediction only	
15599536	PA4340		hypothetical protein	2.1	3.14E-01	Citronellol	6.1	20988	6	Periplasmic			
15599541	PA4345		hypothetical protein	1.9	3.40E-01	Glucose	4.8	22161	2	Unknown	COG2353	Function unknown	
15599545	PA4349		hypothetical protein	1.6	1.16E-01	Citronellol	6.2	31671	10	Unknown	COG1960	Lipid metabolism	
15599548	PA4352		conserved hypothetical protein	5.8	6.85E-02	Citronellol	6.2	30972	3	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms	
15599552	PA4356	xenB	xenobiotic reductase	1.4	8.76E-02	Citronellol	4.9	37796	21	Periplasmic	COG1902	Energy production and conversion	
15599562	PA4366	sodB	superoxide dismutase	1.6	1.30E-01	Citronellol	5.2	21351	8	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein precursor	1.2	3.77E-01	Citronellol	4.5	47230	22	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
15599568	PA4372		hypothetical protein	5.6	3.29E-02	Glucose	6.0	38323	7	Outer Membrane Vesicle	COG3489	General function prediction only	
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	1.6	2.25E-02	Citronellol	6.7	45690	3	Cytoplasmic	COG1488	Coenzyme metabolism	
15599577	PA4381		probable two-component response regulator	1.5	3.74E-01	Glucose	5.9	25235	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599581	PA4385	groEL	GroEL protein	1.4	2.42E-02	Glucose	4.8	57086	63	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
15599582	PA4386	groES	GroES protein	1.1	5.82E-01	Citronellol	4.9	10267	7	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
15599584	PA4388		hypothetical protein	1.3	1.60E-01	Citronellol	6.4	26982	7	Cytoplasmic	COG0748	Inorganic ion transport and metabolism	
15599585	PA4389		probable short-chain dehydrogenase	4.7	3.00E-03	Citronellol	7.3	26720	22	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599591	PA4395		conserved hypothetical protein	2.1	2.16E-02	Citronellol	8.2	18044	14	Cytoplasmic	COG1666	Function unknown	
15599595	PA4399		conserved hypothetical protein	1.2	9.51E-01	Citronellol	6.1	21065	4	Cytoplasmic	COG2096	Coenzyme transport and metabolism	
15599596	PA4400		probable pyrophosphohydrolase	1.5	1.70E-01	Citronellol	5.1	34022	5	Cytoplasmic	COG0352	Coenzyme metabolism	
15599597	PA4401		probable glutathione S-transferase	1.4	1.77E-02	Citronellol	5.4	23789	15	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599598	PA4402	argJ	glutamate N-acetyltransferase	1.2	5.53E-01	Glucose	5.3	41762	19	Cytoplasmic	COG1364	Amino acid transport and metabolism	
15599599	PA4403	secA	secretion protein SecA	1.3	2.84E-01	Glucose	5.4	103854	39	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion	
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.1	4.26E-01	Glucose	5.0	33435	15	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane	
15599603	PA4407	ftsZ	cell division protein FtsZ	10.5	5.39E-04	Glucose	4.7	41218	11	Periplasmic	COG0206	Cell division and chromosome partitioning	
15599604	PA4408	ftsA	cell division protein FtsA	4.1	6.92E-03	Glucose	5.0	44646	12	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.1	5.37E-01	Citronellol	4.7	34363	10	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.1	7.01E-01	Citronellol	6.1	51949	7	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.4	9.09E-02	Citronellol	5.7	48080	18	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane	
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.7	4.99E-03	Citronellol	6.5	47412	14	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1.3	2.82E-01	Citronellol	5.1	51263	18	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
15599616	PA4420		conserved hypothetical protein	1.7	1.21E-01	Citronellol	7.7	34640	11	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane	
15599619	PA4423		conserved hypothetical protein	1.5	2.82E-01	Glucose	7.2	65629	6	Periplasmic	COG3107	General function prediction only	
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	1.7	1.17E-01	Glucose	4.7	21413	9	Cytoplasmic	COG0279	Carbohydrate transport and metabolism	
15599622	PA4426		conserved hypothetical protein	1.4	2.21E-01	Citronellol	9.8	20619	5	Outer Membrane Vesicle	COG2823	General function prediction only	
15599623	PA4427	sspB	stringent starvation protein B	3.1	1.24E-01	Glucose	4.3	14548	3	Unknown	COG2969	General function prediction only	
15599624	PA4428	sspA	stringent starvation protein A	1.5	4.82E-02	Citronellol	6.1	23615	6	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599625	PA4429		probable cytochrome c1 precursor	2.7	9.14E-02	Citronellol	7.5	28993	6	Outer Membrane Vesicle	COG2857	Energy production and conversion	
15599627	PA4431		probable iron-sulfur protein	1.1	8.63E-01	Citronellol	6.5	20828	4	Outer Membrane Vesicle	COG0723	Energy production and conversion	
15599628	PA4432	rpsI	30S ribosomal protein S9	1.2	4.93E-01	Glucose	11.8	14615	5	Outer Membrane Vesicle	COG0103	Translation, ribosomal structure and biogenesis	
15599629	PA4433	rplM	50S ribosomal protein L13	1.4	4.63E-01	Citronellol	10.4	16029	5	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis	
15599630	PA4434		probable oxidoreductase	2.8	1.66E-03	Citronellol	5.7	38644	5	Periplasmic	COG0667	Energy production and conversion	
15599631	PA4435		probable acyl-CoA dehydrogenase	31.6	1.17E-04	Citronellol	6.1	42128	20	Cytoplasmic	COG1960	Lipid metabolism	
15599634	PA4438		conserved hypothetical protein	1.9	9.49E-03	Glucose	6.2	41993	4	Cytoplasmic	COG1485	General function prediction only	
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.0	7.69E-01	Glucose	5.8	48961	17	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis	
15599636	PA4440		hypothetical protein	1.6	4.55E-02	Citronellol	6.2	22315	5	Unknown	COG2945	General function prediction only	
15599637	PA4441		hypothetical protein	1.3	9.06E-01	Citronellol	6.3	16386	4	Outer Membrane Vesicle	COG3105	Function unknown	
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	3.1	1.96E-03	Glucose	5.6	69268	26	Periplasmic	COG2895	Inorganic ion transport and metabolism	
15599639	PA4443	cysD	ATP sulfurylase small subunit	2.4	5.49E-03	Glucose	7.1	35478	12	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15599641	PA4445		conserved hypothetical protein	1.2	3.51E-01	Citronellol	5.3	27360	8	Cytoplasmic	COG0327	Function unknown	
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	1.2	1.16E-01	Glucose	6.0	38655	11	Periplasmic	COG0079	Amino acid transport and metabolism	
15599644	PA4448	hisD	histidinol dehydrogenase	1.0	9.11E-01	Glucose	4.9	47179	26	Periplasmic	COG0141	Amino acid transport and metabolism	
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	1.3	3.34E-01	Glucose	9.3	22844	17	Cytoplasmic	COG0040	Amino acid transport and metabolism	
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.2	2.63E-02	Glucose	5.5	44645	22	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane	
15599649	PA4453		conserved hypothetical protein	1.1	2.84E-01	Glucose	9.7	23760	13	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
15599650	PA4454		conserved hypothetical protein	2.6	2.40E-01	Glucose	4.7	16557	3	Outer Membrane Vesicle	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
15599653	PA4457		arabinose-5-phosphate isomerase KdsD	1.1	7.55E-01	Glucose	5.6	34179	14	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
15599654	PA4458		conserved hypothetical protein	1.2	6.31E-02	Citronellol	5.6	19334	11	Cytoplasmic	COG1778	General function prediction only	
15599656	PA4460		conserved hypothetical protein	1.0	8.77E-01	Glucose	9.6	19126	10	Periplasmic	COG1934	Function unknown	
15599657	PA4461		probable ATP-binding component of ABC transporter	2.1	1.18E-01	Glucose	6.7	26450	2	Outer Membrane Vesicle	COG1137	General function prediction only	
15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.2	3.61E-01	Glucose	4.4	56054	7	Cytoplasmic	COG1508	Transcription	
15599660	PA4464	ptsN	nitrogen regulatory IIA protein	1.1	9.99E-01	Citronellol	4.7	16730	3	Cytoplasmic	COG1762	Carbohydrate transport and metabolism	Signal transduction mechanisms
15599661	PA4465		conserved hypothetical protein	1.5	2.29E-02	Citronellol	5.7	32218	7	Cytoplasmic	COG1660	General function prediction only	

15599664	PA4468	sodM	superoxide dismutase	1.4	2.65E-01	Glucose	6.2	22506	7	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599666	PA4470	fumC1	fumarate hydratase	2.8	4.16E-02	Citronellol	5.9	48695	20	Cytoplasmic	COG0114	Energy production and conversion	
15599668	PA4472	pmbA	PmbA protein	2.8	8.88E-03	Citronellol	5.5	47908	11	Cytoplasmic	COG0312	General function prediction only	
15599670	PA4474		conserved hypothetical protein	2.0	1.67E-03	Citronellol	5.0	50266	8	Cytoplasmic	COG0312	General function prediction only	
15599671	PA4475		conserved hypothetical protein	3.2	3.82E-05	Citronellol	6.8	30724	10	Cytoplasmic	COG0388	General function prediction only	
15599673	PA4477	cafA	cytoplasmic axial filament protein	1.4	2.05E-01	Citronellol	5.0	54665	13	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
15599674	PA4478		conserved hypothetical protein	1.1	7.14E-01	Glucose	4.7	20974	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15599677	PA4481	mreB	rod shape-determining protein MreB	2.1	1.17E-02	Glucose	5.1	36976	17	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning	
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.2	4.88E-01	Glucose	5.5	51862	27	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.2	4.51E-01	Glucose	5.1	53081	31	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis	
15599685	PA4489		conserved hypothetical protein	2.1	5.15E-02	Citronellol	5.3	167428	19	Outer Membrane Vesicle	COG2373	General function prediction only	
15599686	PA4490		conserved hypothetical protein	2.0	1.13E-01	Glucose	10.3	23969	2	Cytoplasmic Membrane	COG3234	Function unknown	
15599689	PA4493	roxR	RoxR	1.8	3.16E-01	Citronellol	5.3	20616	9	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription
15599691	PA4495		hypothetical protein	2.8	1.10E-02	Citronellol	5.9	24879	11	Periplasmic	COG3471	Function unknown	
15599692	PA4496		probable binding protein component of ABC transporter	6.0	1.21E-03	Citronellol	7.6	60077	27	Periplasmic	COG0747	Amino acid transport and metabolism	
15599693	PA4497		probable binding protein component of ABC transporter	15.6	1.12E-03	Citronellol	7.0	59496	2	Periplasmic	COG0747	Amino acid transport and metabolism	
15599694	PA4498		probable metallopeptidase	77.5	3.24E-02	Citronellol	6.2	44126	3	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15599695	PA4499		probable transcriptional regulator	1.2	4.92E-01	Glucose	6.2	20435	3	Cytoplasmic	COG1396	Transcription	
15599698	PA4502		probable binding protein component of ABC transporter	7.1	2.10E-03	Citronellol	6.6	58611	3	Periplasmic	COG0747	Amino acid transport and metabolism	
15599704	PA4508		probable transcriptional regulator	2.6	3.94E-02	Citronellol	6.7	17334	3	Cytoplasmic	COG1522	Transcription	
15599711	PA4515		conserved hypothetical protein	1.7	1.41E-01	Glucose	6.6	25616	3	Cytoplasmic	COG3128	Function unknown	
15599715	PA4519	speC	ornithine decarboxylase	1.1	2.96E-01	Glucose	4.7	43559	19	Cytoplasmic	COG0019	Amino acid transport and metabolism	
15599718	PA4522	ampD	beta-lactamase expression regulator AmpD	1.1	6.75E-01	Citronellol	5.5	21028	3	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	1.1	5.80E-01	Glucose	5.1	30552	14	Cytoplasmic	COG0157	Coenzyme metabolism	
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	7.0	1.43E-03	Citronellol	6.6	15512	6	Outer Membrane Vesicle	COG4969	Cell motility and secretion	Intracellular trafficking and secretion
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	1.1	4.25E-01	Citronellol	5.7	62328	6	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15599725	PA4529	coaE	dephosphocoenzyme A kinase	2.7	2.28E-02	Glucose	6.8	22843	8	Cytoplasmic	COG0237	Coenzyme metabolism	
15599729	PA4533		hypothetical protein	1.7	3.21E-01	Glucose	9.5	17613	4	Periplasmic			
15599738	PA4542	clpB	ClpB protein	1.3	2.03E-01	Glucose	5.1	95005	40	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15599739	PA4543		conserved hypothetical protein	1.3	1.76E-01	Citronellol	7.5	26047	6	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
15599743	PA4547	pilR	two-component response regulator PilR	3.0	7.03E-02	Glucose	5.9	49737	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599744	PA4548		probable D-amino acid oxidase	1.4	1.45E-01	Glucose	6.5	39413	4	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism	
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	2.8	3.82E-02	Citronellol	6.4	126583	8	Periplasmic	COG3419	Cell motility and secretion	Intracellular trafficking and secretion
15599753	PA4557	lytB	LytB protein	1.2	1.25E-01	Glucose	5.2	34762	4	Cytoplasmic	COG0761	Lipid metabolism	
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.7	3.56E-02	Glucose	4.3	15984	8	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	1.3	3.09E-01	Glucose	6.1	105464	44	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	1.1	2.70E-01	Citronellol	9.1	34340	9	Cytoplasmic	COG0196	Coenzyme metabolism	
15599760	PA4564		conserved hypothetical protein	4.0	1.16E-02	Glucose	9.2	16724	5	Periplasmic	COG3045	Function unknown	
15599761	PA4565	proB	glutamate 5-kinase	1.1	4.84E-01	Glucose	7.3	39845	7	Cytoplasmic	COG0263	Amino acid transport and metabolism	
15599762	PA4566	obg	GTP-binding protein Obg	1.2	7.46E-01	Citronellol	4.5	44338	4	Cytoplasmic	COG0536	General function prediction only	
15599764	PA4568	rplU	50S ribosomal protein L21	1.5	5.77E-01	Glucose	10.6	11654	2	Outer Membrane Vesicle	COG0261	Translation, ribosomal structure and biogenesis	
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.1	8.17E-01	Citronellol	4.6	34851	15	Cytoplasmic	COG0142	Coenzyme metabolism	
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	2.3	3.69E-04	Glucose	4.5	21795	7	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15599772	PA4576		probable ATP-dependent protease	1.3	2.20E-01	Glucose	4.7	90222	37	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
15599784	PA4588	gdhA	glutamate dehydrogenase	1.7	1.05E-02	Glucose	6.0	48856	25	Unknown	COG0334	Amino acid transport and metabolism	
15599791	PA4595		probable ATP-binding component of ABC transporter	1.8	7.65E-03	Glucose	5.4	61302	29	Periplasmic	COG0488	General function prediction only	
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.0	8.16E-01	Glucose	6.0	45157	20	Periplasmic	COG0112	Amino acid transport and metabolism	
15599800	PA4604		conserved hypothetical protein	5.6	1.02E-01	Glucose	4.5	37256	3	Cytoplasmic	COG0523	General function prediction only	
15599809	PA4613	katB	catalase	10.0	6.34E-04	Citronellol	8.6	57131	4	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
15599810	PA4614	mscL	conductance mechanosensitive channel	1.1	9.88E-01	Citronellol	4.6	14432	4	Outer Membrane Vesicle	COG1970	Cell envelope biogenesis, outer membrane	
15599811	PA4615		probable oxidoreductase	1.4	4.18E-03	Citronellol	5.2	29377	9	Cytoplasmic	COG1018	Energy production and conversion	
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	4.4	4.01E-02	Glucose	4.7	219755	3	Extracellular			
15599822	PA4626	hprA	glycerate dehydrogenase	1.1	5.26E-01	Citronellol	6.7	34285	13	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599823	PA4627		conserved hypothetical protein	2.5	1.36E-01	Glucose	8.1	35937	2	Cytoplasmic	COG2813	Translation, ribosomal structure and biogenesis	
15599828	PA4632		hypothetical protein	1.4	3.42E-01	Citronellol	7.6	29159	3	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15599829	PA4633		probable chemotaxis transducer	2.4	2.48E-02	Citronellol	4.5	76623	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15599830	PA4634		hypothetical protein	3.0	1.65E-01	Glucose	8.7	22996	2	Unknown	COG2135	Function unknown	
15599835	PA4639		hypothetical protein	1.3	4.41E-01	Citronellol	9.8	20736	8	Outer Membrane Vesicle			
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.9	1.28E-02	Glucose	7.0	55498	7	Cytoplasmic	COG0579	General function prediction only	
15599839	PA4644		hypothetical protein	55.0	1.97E-02	Glucose	5.9	17109	2	Unknown			
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	2.0	3.57E-01	Citronellol	5.6	20639	14	Cytoplasmic	COG0634	Nucleotide transport and metabolism	
15599841	PA4646	upp	uracil phosphoribosyltransferase	1.2	6.08E-01	Glucose	7.0	22938	20	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
15599846	PA4651	cupE4	Pilin assembly chaperone CupE4	43.5	1.70E-03	Citronellol	9.7	28981	3	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
15599851	PA4656		conserved hypothetical protein	1.1	8.86E-01	Glucose	8.3	33852	2	Cytoplasmic	COG1090	General function prediction only	
15599852	PA4657		hypothetical protein	1.9	8.40E-03	Citronellol	6.8	35913	8	Unknown	COG3380	General function prediction only	
15599856	PA4661	pagL	Lipid A 3-O-deacylase	1.0	9.86E-01	Glucose	6.3	18393	9	Periplasmic			
15599857	PA4662	murI	glutamate racemase	1.1	4.45E-01	Citronellol	5.2	28274	4	Cytoplasmic	COG0796	Cell envelope biogenesis, outer membrane	
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	3.5	1.30E-02	Glucose	5.6	26686	5	Cytoplasmic	COG0476	Coenzyme metabolism	
15599860	PA4665	prfA	peptide chain release factor 1	1.6	7.42E-02	Citronellol	4.8	40040	5	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis	
15599864	PA4669	ipk	isopentenyl monophosphate kinase	2.2	1.32E-01	Glucose	6.6	30843	5	Unknown	COG1947	Lipid metabolism	
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.6	4.91E-02	Glucose	6.5	34008	23	Periplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
15599866	PA4671		probable ribosomal protein L25	1.5	2.73E-01	Citronellol	6.2	21962	13	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis	
15599867	PA4672		peptidyl-tRNA hydrolase	4.0	5.17E-03	Glucose	9.8	20772	5	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis	
15599868	PA4673		conserved hypothetical protein	1.1	5.62E-01	Glucose	4.8	40078	15	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
15599870	PA4675		probable TonB-dependent receptor	2.1	6.96E-02	Glucose	5.2	80952	10	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599871	PA4676		probable carbonic anhydrase	1.4	9.89E-02	Glucose	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15599873	PA4678	rimI	peptide n-acetyltransferase RimI	1.4	1.97E-01	Glucose	6.2	17095	3	Cytoplasmic	COG0456	General function prediction only	
15599874	PA4679		hypothetical protein	1.7	1.88E-01	Glucose	5.0	24841	4	Unknown			
15599881	PA4686		hypothetical protein	39.0	5.24E-04	Glucose	5.3	106827	23	Periplasmic	COG1196	Cell division and chromosome partitioning	
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	1.7	3.10E-02	Glucose	5.5	36149	20	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.1	9.30E-01	Citronellol	5.7	36424	30	Periplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	1.5	2.25E-01	Glucose	6.3	17784	10	Cytoplasmic	COG0440	Amino acid transport and metabolism	
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.3	2.56E-02	Glucose	6.8	62986	30	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
15599895	PA4701		conserved hypothetical protein	1.0	9.55E-01	Glucose	6.0	58344	30	Periplasmic	COG2187	Function unknown	
15599898	PA4704	cbpA	cAMP-binding protein A	5.6	1.65E-04	Citronellol	5.2	29671	2	Cytoplasmic	COG0664	Signal transduction mechanisms	
15599902	PA4708	phuT	Heme-transport protein, PhuT	1.3	8.91E-02	Glucose	7.8	31037	16	Periplasmic	COG4558	Inorganic ion transport and metabolism	
15599903	PA4709		probable hemin degrading factor	2.4	4.04E-02	Glucose	5.6	39057	7	Cytoplasmic	COG3720	Inorganic ion transport and metabolism	
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR precursor	1.1	8.38E-01	Citronellol	5.9	84724	4	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599909	PA4715		probable aminotransferase	2.9	2.74E-02	Glucose	8.1	46064	3	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599910	PA4716		hypothetical protein	1.4	5.32E-01	Citronellol	5.0	30850	3	Cytoplasmic	COG0384	General function prediction only	
15599911	PA4717		conserved hypothetical protein	10.6	2.60E-03	Citronellol	6.1	31861	2	Unknown	COG2321	General function prediction only	
15599914	PA4720	trmA	tRNA (uracil-5-)-methyltransferase	1.2	4.14E-01	Glucose	7.0	41206	3	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis	
15599916	PA4722		probable aminotransferase	1.1	3.78E-01	Citronellol	5.7	42567	7	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599917	PA4723	dksA	suppressor protein DksA	1.9	3.75E-04	Citronellol	4.8	17344	11	Periplasmic	COG1734	Signal transduction mechanisms	
15599920	PA4726	cbrB	two-component response regulator CbrB	2.1	1.98E-03	Glucose	5.5	52286	16	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	12.9	3.08E-03	Glucose	4.6	18014	3	Cytoplasmic	COG0801	Coenzyme metabolism	
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.4	2.32E-02	Glucose	5.8	27874	11	Periplasmic	COG0413	Coenzyme metabolism	
15599924	PA4730	panC	pantoate--beta-alanine ligase	1.2	2.88E-01	Glucose	6.5	30836	11	Cytoplasmic	COG0414	Coenzyme metabolism	
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.1	6.02E-01	Glucose	6.6	61944	18	Periplasmic	COG0166	Carbohydrate transport and metabolism	
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	6.8	4.65E-04	Citronellol	6.2	71624	22	Cytoplasmic	COG0365	Lipid metabolism	
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.5	5.54E-02	Glucose	4.8	75421	58	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis	
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	3.3	2.77E-02	Glucose	6.9	33378	8	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis	

15599938	PA4744	infB	translation initiation factor IF-2	1.5	5.00E-02	Glucose	6.0	90912	43	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis	
15599939	PA4745	nusA	N utilization substance protein A	1.7	1.67E-01	Glucose	4.3	54658	21	Periplasmic	COG0195	Transcription	
15599940	PA4746		conserved hypothetical protein	1.8	3.81E-01	Glucose	4.3	17139	2	Cytoplasmic	COG0779	Function unknown	
15599941	PA4747	secG	secretion protein SecG	1.0	6.31E-01	Glucose	5.1	13207	2	Outer Membrane Vesicle	COG1314	Intracellular trafficking and secretion	
15599942	PA4748	tpiA	triosephosphate isomerase	2.2	2.34E-02	Glucose	5.3	25621	8	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
15599943	PA4749	glmM	phosphoglucosamine mutase	1.1	7.89E-01	Citronellol	6.0	47796	10	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15599944	PA4750	folP	dihydropteroate synthase	1.0	7.85E-01	Citronellol	5.4	30490	7	Cytoplasmic	COG0294	Coenzyme metabolism	
15599945	PA4751	ftsH	cell division protein FtsH	1.3	7.02E-02	Glucose	5.6	69955	2	Outer Membrane Vesicle	COG0465	Posttranslational modification, protein turnover, chaperones	
15599949	PA4755	greA	transcription elongation factor GreA	1.3	6.85E-01	Citronellol	4.7	17158	11	Periplasmic	COG0782	Function unknown	
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	2.9	2.22E-01	Citronellol	4.8	117330	76	Periplasmic	COG0458	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.2	2.31E-01	Citronellol	5.2	40810	11	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.0	9.47E-01	Citronellol	6.0	28324	18	Periplasmic	COG0289	Amino acid transport and metabolism	
15599954	PA4760	dnaJ	DnaJ protein	2.2	8.19E-02	Glucose	7.4	40260	4	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
15599955	PA4761	dnaK	DnaK protein	2.0	3.12E-02	Glucose	4.5	68403	55	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599956	PA4762	grpE	heat shock protein GrpE	1.1	9.33E-01	Citronellol	4.2	20702	10	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
15599958	PA4764	fur	ferric uptake regulation protein	1.1	5.49E-01	Citronellol	5.9	15234	9	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15599962	PA4768	smpB	SmpB protein	11.4	4.85E-02	Glucose	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones	
15599975	PA4781		cyclic di-GMP phosphodiesterase	51.2	1.13E-02	Citronellol	5.0	43628	5	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15599978	PA4784		probable transcriptional regulator	1.1	9.29E-01	Citronellol	6.5	16733	2	Cytoplasmic	COG1522	Transcription	
15599987	PA4793		hypothetical protein	3.2	2.80E-04	Citronellol	8.4	21281	2	Periplasmic			
15599990	PA4796		hypothetical protein	2.3	8.47E-04	Citronellol	4.8	17129	4	Unknown	COG0509	Amino acid transport and metabolism	
15600003	PA4809	fdhE	FdhE protein	1.1	5.09E-01	Glucose	5.8	33830	2	Cytoplasmic	COG3058	Posttranslational modification, protein turnover, chaperones	
15600006	PA4813	lipC	lipase LipC	4970.4	4.76E-03	Citronellol	5.8	32341	2	Extracellular	COG1075	General function prediction only	
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.7	3.00E-02	Glucose	5.2	70667	14	Periplasmic	COG1166	Amino acid transport and metabolism	
15600034	PA4841		conserved hypothetical protein	2.6	2.43E-01	Citronellol	4.4	19733	4	Unknown	COG1443	Lipid metabolism	
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	1.2	5.67E-01	Glucose	4.7	16455	10	Unknown	COG0511	Lipid metabolism	
15600041	PA4848	accC	biotin carboxylase	1.5	9.80E-02	Glucose	6.3	48888	20	Periplasmic	COG0439	Lipid metabolism	
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	1.4	7.25E-02	Glucose	4.2	32000	4	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis	
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	1.7	6.89E-02	Glucose	6.5	57665	29	Periplasmic	COG0138	Nucleotide transport and metabolism	
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	1.2	4.28E-01	Citronellol	4.7	45212	22	Periplasmic	COG0151	Nucleotide transport and metabolism	
15600059	PA4866		conserved hypothetical protein	2.2	1.67E-02	Citronellol	6.3	18743	3	Unknown	COG1247	Cell envelope biogenesis, outer membrane	
15600061	PA4868	ureC	urease alpha subunit	1.2	1.67E-01	Glucose	6.2	60611	4	Cytoplasmic	COG0804	Amino acid transport and metabolism	
15600065	PA4872		hypothetical protein	1.5	2.54E-02	Glucose	5.4	31320	9	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15600067	PA4874		conserved hypothetical protein	13.6	1.37E-03	Citronellol	10.3	14433	8	Periplasmic			
15600069	PA4876	osmE	osmotically inducible lipoprotein OsmE	13.1	8.39E-03	Citronellol	8.8	12523	2	Outer Membrane Vesicle			
15600073	PA4880		probable bacterioferritin	11.3	2.31E-03	Citronellol	4.4	20217	8	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
15600083	PA4890	desT	DesT	2.5	6.17E-01	Citronellol	9.1	22899	3	Cytoplasmic	COG1309	Transcription	
15600086	PA4893	ureG	urease accessory protein UreG	1.2	5.36E-01	Citronellol	4.6	21991	3	Cytoplasmic	COG0378	Posttranslational modification, protein turnover, chaperones	Transcription
15600092	PA4899		probable aldehyde dehydrogenase	7.7	2.57E-04	Citronellol	5.8	52697	7	Cytoplasmic	COG1012	Energy production and conversion	
15600100	PA4907		probable short-chain dehydrogenase	1.0	9.97E-01	Citronellol	5.1	27384	13	Cytoplasmic	COG4221	General function prediction only	
15600102	PA4909		probable ATP-binding component of ABC transporter	46.7	9.42E-01	Citronellol	7.8	26262	2	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
15600106	PA4913		probable binding protein component of ABC transporter	22.6	7.78E-04	Citronellol	6.6	39798	18	Periplasmic	COG0683	Amino acid transport and metabolism	
15600109	PA4916		hypothetical protein	3.6	7.85E-02	Glucose	6.5	25457	2	Unknown	COG1051	Nucleotide transport and metabolism	
15600111	PA4918		hypothetical protein	1.4	1.24E-01	Citronellol	4.7	23821	11	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	1.3	1.80E-01	Glucose	6.3	46095	15	Cytoplasmic	COG1488	Coenzyme metabolism	
15600113	PA4920	nadE	NH3-dependent NAD synthetase	1.9	1.96E-02	Glucose	5.4	29696	18	Periplasmic	COG0171	Coenzyme metabolism	
15600115	PA4922	azu	azurin precursor	1.3	3.32E-01	Glucose	6.9	16008	10	Periplasmic	COG3241	Energy production and conversion	
15600116	PA4923		conserved hypothetical protein	1.3	9.19E-01	Citronellol	5.2	20725	3	Unknown	COG1611	General function prediction only	
15600124	PA4931	dnaB	replicative DNA helicase	1.2	3.00E-01	Glucose	4.7	51589	7	Cytoplasmic	COG0305	DNA replication, recombination, and repair	
15600125	PA4932	rplI	50S ribosomal protein L9	1.6	5.97E-02	Glucose	5.3	15532	7	Periplasmic	COG0359	Translation, ribosomal structure and biogenesis	
15600128	PA4935	rpsF	30S ribosomal protein S6	1.3	4.14E-01	Glucose	4.6	16165	14	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis	
15600131	PA4938	purA	adenylosuccinate synthetase	1.8	1.12E-02	Glucose	6.0	46814	23	Periplasmic	COG0104	Nucleotide transport and metabolism	
15600132	PA4939		conserved hypothetical protein	1.2	1.81E-01	Glucose	4.8	42546	13	Cytoplasmic	COG3705	Amino acid transport and metabolism	
15600141	PA4948		conserved hypothetical protein	2.7	3.82E-02	Glucose	4.7	16463	3	Cytoplasmic	COG0802	General function prediction only	
15600142	PA4949		conserved hypothetical protein	1.3	4.73E-01	Citronellol	7.6	51550	8	Unknown	COG0063	Carbohydrate transport and metabolism	
15600144	PA4951	orn	oligoribonuclease	3.9	3.42E-03	Citronellol	5.6	20826	4	Cytoplasmic	COG1949	RNA processing and modification	
15600148	PA4955		hypothetical protein	1.9	6.33E-03	Citronellol	10.0	56255	3	Cytoplasmic Membrane			
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	1.6	3.47E-02	Glucose	5.3	29391	8	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15600150	PA4957	psd	phosphatidylserine decarboxylase	4.5	1.04E-01	Glucose	7.9	32001	2	Outer Membrane Vesicle	COG0688	Lipid metabolism	
15600152	PA4959	fimX	FimX	2.1	4.71E-02	Glucose	4.9	75992	12	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15600153	PA4960		probable phosphoserine phosphatase	1.1	5.90E-01	Citronellol	4.9	46438	9	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15600157	PA4964	parC	topoisomerase IV subunit A	1.2	1.95E-01	Glucose	5.9	83364	15	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15600160	PA4967	parE	topoisomerase IV subunit B	1.5	1.56E-01	Glucose	5.9	69178	5	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
15600161	PA4968		conserved hypothetical protein	1.0	1.00E+00	Glucose	6.8	22645	6	Unknown	COG3150	General function prediction only	
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	1.4	3.97E-01	Glucose	4.8	30498	2	Cytoplasmic	COG1409	General function prediction only	
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.5	8.89E-02	Citronellol	4.7	23133	7	Cytoplasmic			
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	3.0	7.28E-04	Glucose	5.8	69784	21	Cytoplasmic	COG0422	Coenzyme metabolism	
15600167	PA4974		probable outer membrane protein precursor	1.0	8.09E-01	Citronellol	5.9	53405	8	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15600168	PA4975		NAD(P)H quinone oxidoreductase	1.7	1.93E-01	Citronellol	6.0	26315	2	Cytoplasmic	COG2249	General function prediction only	
15600180	PA4987		probable transcriptional regulator	2.0	5.51E-01	Citronellol	5.6	22368	3	Cytoplasmic	COG1917	Function unknown	
15600184	PA4991		hypothetical protein	1.1	5.11E-01	Glucose	8.0	42109	3	Cytoplasmic	COG0578	Energy production and conversion	
15600185	PA4992		hypothetical protein	1.3	1.84E-01	Glucose	6.4	29030	7	Cytoplasmic	COG0667	Energy production and conversion	
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.3	9.38E-02	Citronellol	6.2	50348	21	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane	
15600191	PA4998		conserved hypothetical protein	1.3	2.07E-01	Glucose	10.0	24986	3	Cytoplasmic			
15600194	PA5001		hypothetical protein	1.0	8.80E-01	Glucose	8.7	36625	7	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
15600198	PA5005		probable carbamoyl transferase	2.6	5.13E-03	Glucose	6.9	66047	6	Outer Membrane Vesicle	COG2192	Posttranslational modification, protein turnover, chaperones	
15600205	PA5012	waaF	heptosyltransferase II	7.8	3.77E-02	Glucose	8.0	38409	5	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane	
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.1	7.30E-01	Glucose	6.2	34084	24	Periplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	1.7	8.51E-02	Citronellol	5.2	110102	23	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
15600208	PA5015	aceE	pyruvate dehydrogenase	1.6	4.64E-01	Glucose	5.6	99563	61	Periplasmic	COG2609	Energy production and conversion	
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	2.4	1.21E-01	Glucose	5.0	56676	26	Periplasmic	COG0508	Energy production and conversion	
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	2.3	2.04E-02	Citronellol	5.0	23517	6	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
15600212	PA5019		conserved hypothetical protein	1.8	1.33E-02	Citronellol	6.0	31882	7	Cytoplasmic	COG2961	General function prediction only	
15600213	PA5020		probable acyl-CoA dehydrogenase	2.9	2.16E-01	Citronellol	6.2	66235	2	Cytoplasmic	COG1960	Lipid metabolism	
15600216	PA5023		conserved hypothetical protein	1.4	6.43E-02	Citronellol	5.6	55025	2	Cytoplasmic	COG0397	Function unknown	
15600218	PA5025	metY	homocysteine synthase	1.0	6.54E-01	Glucose	6.5	45177	10	Cytoplasmic	COG2873	Amino acid transport and metabolism	
15600219	PA5026		hypothetical protein	148.7	3.20E-05	Citronellol	6.3	16786	3	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	1.7	1.35E-01	Citronellol	6.3	38792	10	Cytoplasmic	COG0407	Coenzyme metabolism	
15600228	PA5035	gltD	glutamate synthase small chain	2.3	8.89E-04	Glucose	6.4	52625	26	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
15600229	PA5036	gltB	glutamate synthase large chain precursor	1.6	7.18E-01	Citronellol	6.0	161607	76	Cytoplasmic	COG0069	Amino acid transport and metabolism	
15600231	PA5038	aroB	3-dehydroquinate synthase	1.5	6.54E-03	Citronellol	5.6	40109	10	Cytoplasmic	COG0337	Amino acid transport and metabolism	
15600232	PA5039	aroK	shikimate kinase	1.7	3.23E-01	Glucose	8.8	19205	2	Cytoplasmic	COG0703	Amino acid transport and metabolism	
15600239	PA5046		malic enzyme	1.1	6.75E-01	Glucose	4.8	45428	37	Periplasmic	COG0281	Energy production and conversion	
15600244	PA5051	argS	arginyl-tRNA synthetase	1.1	6.31E-01	Glucose	5.2	65199	19	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis	
15600246	PA5053	hslV	heat shock protein HslV	1.3	3.09E-01	Citronellol	6.7	18767	8	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones	
15600247	PA5054	hslU	heat shock protein HslU	1.2	2.38E-01	Glucose	5.4	50082	17	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
15600253	PA5060	phaF	polyhydroxyalkanoate synthesis protein PhaF	14.0	2.43E-02	Citronellol	11.1	30577	2	Cytoplasmic	COG3937	Function unknown	
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	1.9	3.97E-03	Glucose	9.5	28254	12	Cytoplasmic	COG2226	Coenzyme metabolism	
15600257	PA5064		hypothetical protein	2.2	1.25E-02	Glucose	6.0	22767	5	Cytoplasmic	COG3165	Function unknown	
15600259	PA5066	hisI	phosphoribosyl-AMP cyclohydrolase	1.0	8.92E-01	Citronellol	6.0	15375	8	Cytoplasmic	COG0139	Amino acid transport and metabolism	
15600261	PA5068	tatA	translocation protein TatA	6.2	3.17E-01	Citronellol	7.7	9190	1	Cytoplasmic Membrane	COG1826	Intracellular trafficking and secretion	
15600264	PA5071		conserved hypothetical protein	1.6	1.92E-01	Glucose	9.1	26065	4	Cytoplasmic	COG1385	Function unknown	

15600269	PA5076		probable binding protein component of ABC transporter	1.3	1.11E-01	Citronellol	7.6	29736	23	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600270	PA5077	mdoH	periplasmic glucans biosynthesis protein MdoH	2.1	3.07E-01	Glucose	8.9	96994	2	Outer Membrane Vesicle	COG2943	Cell envelope biogenesis, outer membrane	
15600271	PA5078		conserved hypothetical protein	1.4	2.27E-02	Citronellol	7.0	59444	19	Periplasmic	COG3131	Inorganic ion transport and metabolism	
15600272	PA5079		conserved hypothetical protein	1.0	9.29E-01	Glucose	6.3	15530	4	Unknown	COG1490	Translation, ribosomal structure and biogenesis	
15600273	PA5080		prolyl aminopeptidase	1.3	2.40E-01	Citronellol	6.2	36515	15	Cytoplasmic	COG0596	General function prediction only	
15600274	PA5081		hypothetical protein	4.5	5.02E-03	Citronellol	4.7	17918	4	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600275	PA5082		probable binding protein component of ABC transporter	7.1	2.25E-02	Citronellol	8.2	32866	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	2.2	3.07E-03	Citronellol	5.9	29791	5	Cytoplasmic	COG3741	Amino acid transport and metabolism	
15600285	PA5092	hutI	imidazolone-5-propionate hydrolase HutI	4.9	7.32E-03	Citronellol	6.0	43425	2	Cytoplasmic	COG1228	Secondary metabolites biosynthesis, transport, and catabolism	
15600293	PA5100	hutU	urocanase	57.3	2.59E-02	Citronellol	6.3	61161	3	Cytoplasmic	COG2987	Amino acid transport and metabolism	
15600297	PA5104		conserved hypothetical protein	7.9	1.37E-01	Citronellol	5.6	21415	3	Unknown	COG3758	Function unknown	
15600298	PA5105	hutC	histidine utilization repressor HutC	6.4	2.11E-02	Citronellol	7.4	27779	2	Cytoplasmic	COG2188	Transcription	
15600302	PA5109		hypothetical protein	1.5	5.39E-01	Citronellol	5.1	22697	7	Cytoplasmic	COG3803	Function unknown	
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	1.4	4.00E-02	Glucose	5.9	37216	15	Periplasmic	COG0158	Carbohydrate transport and metabolism	
15600304	PA5111	gloA3	lactoylglutathione lyase	1.7	5.39E-01	Citronellol	4.8	20215	6	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15600305	PA5112	estA	esterase EstA	15.2	1.12E-01	Citronellol	4.5	69608	3	Periplasmic	COG3240	Lipid metabolism	General function prediction only
15600308	PA5115		conserved hypothetical protein	4.9	8.19E-02	Citronellol	5.2	20998	2	Cytoplasmic			
15600310	PA5117	typA	regulatory protein TypA	2.3	7.56E-03	Glucose	5.0	66903	19	Periplasmic	COG1217	Signal transduction mechanisms	
15600311	PA5118	thiI	thiazole biosynthesis protein ThiI	4.6	2.47E-02	Glucose	6.7	54849	2	Cytoplasmic	COG0301	Coenzyme metabolism	
15600312	PA5119	glnA	glutamine synthetase	1.3	1.42E-01	Glucose	5.0	51944	21	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism	
15600318	PA5125	ntrC	two-component response regulator NtrC	1.9	1.86E-01	Glucose	5.8	52753	6	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600321	PA5128	secB	secretion protein SecB	1.8	1.98E-02	Citronellol	4.2	18146	11	Periplasmic	COG1952	Intracellular trafficking and secretion	
15600324	PA5131	pgm	phosphoglycerate mutase	1.6	2.63E-02	Glucose	4.9	55601	25	Periplasmic	COG0696	Carbohydrate transport and metabolism	
15600327	PA5134		probable carboxyl-terminal protease	1.4	1.05E-01	Glucose	5.4	46018	4	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15600330	PA5137		hypothetical protein	2.4	4.90E-03	Citronellol	7.5	27991	7	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600331	PA5138		hypothetical protein	1.2	4.32E-02	Citronellol	4.9	27915	8	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600332	PA5139		hypothetical protein	1.2	6.85E-01	Glucose	5.8	27565	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	1.3	4.19E-01	Citronellol	4.7	25938	4	Cytoplasmic	COG0106	Amino acid transport and metabolism	
15600335	PA5142	hisH1	glutamine amidotransferase	1.3	1.51E-01	Glucose	6.3	23666	13	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	1.2	4.34E-01	Citronellol	6.5	21937	6	Cytoplasmic	COG0131	Amino acid transport and metabolism	
15600339	PA5146		hypothetical protein	1.0	9.93E-01	Citronellol	8.3	80849	6	Outer Membrane Vesicle	COG2982	Cell envelope biogenesis, outer membrane	
15600342	PA5149		conserved hypothetical protein	1.1	3.44E-01	Citronellol	6.8	39433	2	Unknown	COG0673	General function prediction only	
15600343	PA5150		probable short-chain dehydrogenase	2.4	2.02E-03	Citronellol	6.2	26191	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic binding protein	5.5	1.02E-03	Citronellol	4.9	27561	18	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	1.3	1.48E-01	Citronellol	5.9	39542	16	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	1.2	3.81E-01	Citronellol	6.1	33106	10	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	1.6	2.87E-02	Citronellol	5.0	32457	16	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.3	2.44E-01	Glucose	6.0	20766	10	Unknown	COG1898	Cell envelope biogenesis, outer membrane	
15600359	PA5166	dctD	DctD	2.3	7.26E-03	Glucose	5.5	50864	5	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600360	PA5167	dctP	DctP	7.3	7.10E-04	Citronellol	8.8	37051	19	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15600364	PA5171	arcA	arginine deiminase	27.9	1.74E-04	Citronellol	5.5	46436	33	Cytoplasmic	COG2235	Amino acid transport and metabolism	
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	37.9	1.71E-04	Citronellol	6.6	38108	22	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15600366	PA5173	arcC	carbamate kinase	19.6	4.23E-05	Citronellol	5.0	33080	13	Cytoplasmic	COG0549	Amino acid transport and metabolism	
15600367	PA5174		probable beta-ketoacyl synthase	9.8	5.00E-04	Glucose	6.0	68763	32	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	1.1	8.10E-01	Citronellol	4.8	29779	7	Cytoplasmic	COG1218	Inorganic ion transport and metabolism	
15600369	PA5176		conserved hypothetical protein	1.9	2.61E-03	Citronellol	4.5	20983	9	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600370	PA5177		probable hydrolase	3.4	1.66E-02	Glucose	5.9	25629	4	Cytoplasmic	COG1011	General function prediction only	
15600377	PA5184		hypothetical protein	1.5	3.92E-02	Citronellol	8.8	20417	11	Periplasmic	COG1605	Amino acid transport and metabolism	
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	7.6	4.95E-04	Citronellol	5.2	44810	9	Cytoplasmic	COG1250	Lipid metabolism	
15600383	PA5190		probable nitroreductase	1.4	3.62E-02	Glucose	6.0	22450	11	Cytoplasmic	COG0778	Energy production and conversion	
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.0	9.05E-01	Glucose	5.1	55732	35	Periplasmic	COG1866	Energy production and conversion	
15600386	PA5193	yrfI	heat shock protein HSP33	1.9	1.46E-02	Glucose	4.5	32834	9	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
15600393	PA5200	amgR	AmgR	1.1	4.74E-01	Citronellol	6.6	27924	12	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600394	PA5201		conserved hypothetical protein	1.6	1.87E-02	Glucose	6.3	84963	36	Periplasmic	COG2183	Transcription	
15600396	PA5203	gshA	glutamate--cysteine ligase	1.5	5.98E-02	Citronellol	4.9	59205	15	Cytoplasmic	COG2918	Coenzyme metabolism	
15600397	PA5204	argA	N-acetylglutamate synthase	1.1	5.95E-01	Citronellol	6.5	47858	12	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600403	PA5210		probable secretion pathway ATPase	1.4	1.17E-01	Glucose	6.5	65981	4	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15600406	PA5213	gcvP1	glycine cleavage system protein P1	16.9	5.69E-04	Citronellol	6.5	104710	15	Cytoplasmic	COG1003	Amino acid transport and metabolism	
15600407	PA5214	gcvH1	glycine cleavage system protein H1	1.5	7.80E-01	Citronellol	3.9	13642	4	Unknown	COG0509	Amino acid transport and metabolism	
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	1.6	4.55E-02	Citronellol	5.4	38907	8	Periplasmic	COG0404	Amino acid transport and metabolism	
15600410	PA5217		probable binding protein component of ABC iron transporter	3.9	1.05E-02	Citronellol	6.4	36292	6	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15600417	PA5224	pepP	aminopeptidase P	1.3	1.52E-01	Citronellol	5.1	49710	19	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15600418	PA5225		hypothetical protein	1.6	2.89E-02	Glucose	4.0	19358	5	Unknown	COG3079	Function unknown	
15600421	PA5228		conserved hypothetical protein	1.2	9.32E-01	Citronellol	12.0	23077	2	Unknown	COG0212	Coenzyme metabolism	
15600422	PA5229		conserved hypothetical protein	2.2	2.59E-03	Citronellol	7.5	16871	7	Unknown	COG2947	Function unknown	
15600427	PA5234		probable oxidoreductase	1.7	8.24E-02	Citronellol	7.0	34011	11	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15600430	PA5237		conserved hypothetical protein	9.8	1.88E-01	Glucose	6.5	54621	2	Cytoplasmic	COG0043	Coenzyme metabolism	
15600432	PA5239	rho	transcription termination factor Rho	1.4	2.85E-01	Citronellol	6.8	47069	23	Periplasmic	COG1158	Transcription	
15600433	PA5240	trxA	thioredoxin	1.2	3.17E-01	Citronellol	4.5	11870	8	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15600434	PA5241	ppx	exopolyphosphatase	1.1	7.19E-01	Citronellol	6.7	56419	14	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
15600435	PA5242	ppk	polyphosphate kinase	1.6	1.63E-01	Citronellol	7.7	83151	24	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	2.6	1.66E-02	Citronellol	4.8	37005	7	Cytoplasmic	COG0113	Coenzyme metabolism	
15600438	PA5245		conserved hypothetical protein	2.1	3.64E-02	Citronellol	4.7	23426	14	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
15600445	PA5252		probable ATP-binding component of ABC transporter	11.7	5.84E-04	Glucose	5.9	70871	13	Cytoplasmic	COG0488	General function prediction only	
15600447	PA5254		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.3	7.91E-01	Citronellol	5.4	23047	2	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15600448	PA5255	algQ	Alginate regulatory protein AlgQ	1.9	1.03E-01	Glucose	4.6	18011	2	Cytoplasmic	COG3160	Transcription	
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	1.3	2.70E-02	Citronellol	4.8	27247	5	Unknown	COG1587	Coenzyme metabolism	
15600453	PA5260	hemC	porphobilinogen deaminase	1.6	5.19E-02	Citronellol	5.3	33641	5	Cytoplasmic	COG0181	Coenzyme metabolism	
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	11.5	2.39E-04	Citronellol	7.3	27608	10	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
15600456	PA5263	argH	argininosuccinate lyase	1.3	3.47E-01	Citronellol	5.5	51640	21	Periplasmic	COG0165	Amino acid transport and metabolism	
15600467	PA5274	rnk	nucleoside diphosphate kinase regulator	37.6	7.52E-02	Glucose	4.2	14405	2	Cytoplasmic	COG0782	Function unknown	
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.6	1.85E-02	Citronellol	5.4	45490	23	Periplasmic	COG0019	Amino acid transport and metabolism	
15600471	PA5278	dapF	diaminopimelate epimerase	1.1	6.94E-01	Glucose	7.7	30320	6	Cytoplasmic	COG0253	Amino acid transport and metabolism	
15600472	PA5279		conserved hypothetical protein	1.5	2.06E-01	Glucose	5.3	25767	3	Cytoplasmic	COG3159	Function unknown	
15600474	PA5281		probable hydrolase	6.0	1.84E-02	Glucose	5.9	25852	3	Cytoplasmic	COG1011	General function prediction only	
15600481	PA5288	glnK	nitrogen regulatory protein P-II 2	2.4	3.06E-01	Citronellol	5.2	12286	2	Cytoplasmic Membrane	COG0347	Amino acid transport and metabolism	
15600489	PA5296	rep	ATP-dependent DNA helicase Rep	13.0	1.50E-03	Glucose	6.0	77041	2	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
15600491	PA5298		xanthine phosphoribosyltransferase	1.2	4.58E-01	Glucose	6.6	20575	8	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15600494	PA5301	pauR	probable transcriptional regulator	1.8	6.16E-01	Citronellol	5.3	19944	5	Cytoplasmic	COG1396	Transcription	
15600501	PA5308	lrp	leucine-responsive regulatory protein	1.6	2.16E-01	Citronellol	8.3	18868	2	Cytoplasmic	COG1522	Transcription	
15600505	PA5312	pauC	Aldehyde dehydrogenase	2.0	2.13E-02	Citronellol	5.3	53143	25	Periplasmic	COG1012	Energy production and conversion	
15600506	PA5313	gabT2	Transaminase	4.6	6.16E-04	Citronellol	6.7	48347	2	Cytoplasmic	COG0161	Coenzyme metabolism	
15600510	PA5317		probable binding protein component of ABC dipeptide transporter	1.8	4.64E-02	Glucose	7.0	57880	8	Periplasmic	COG0747	Amino acid transport and metabolism	
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine decarboxylase	1.2	1.01E-01	Citronellol	6.3	43133	11	Cytoplasmic	COG0452	Coenzyme metabolism	
15600515	PA5322	algC	phosphomannomutase AlgC	1.2	3.41E-01	Glucose	5.0	50295	24	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15600516	PA5323	argB	acetylglutamate kinase	1.1	5.66E-01	Glucose	6.8	31849	21	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600522	PA5329		conserved hypothetical protein	2.8	3.69E-03	Citronellol	5.0	17712	6	Cytoplasmic	COG0824	General function prediction only	
15600523	PA5330		hypothetical protein	2.0	2.68E-01	Citronellol	9.4	22434	8	Unknown			
15600524	PA5331	pyrE	orotate phosphoribosyltransferase	1.0	7.58E-01	Glucose	5.1	23320	12	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
15600525	PA5332	crc	catabolite repression control protein	1.4	6.22E-02	Glucose	5.2	29844	10	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15600527	PA5334	rph	ribonuclease PH	1.2	4.95E-01	Citronellol	5.9	25654	6	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis	
15600528	PA5335		conserved hypothetical protein	1.1	5.40E-01	Citronellol	5.8	31708	13	Cytoplasmic	COG1561	Function unknown	

15600529	PA5336	gmk	guanylate kinase	1.7	3.98E-02	Glucose	5.3	23102	11	Cytoplasmic	COG0194	Nucleotide transport and metabolism		
15600530	PA5337	rpoZ	RNA polymerase omega subunit	11.6	2.71E-02	Glucose	4.0	9775	3	Unknown	COG1758	Transcription		
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.6	2.37E-02	Glucose	9.4	78861	13	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
15600532	PA5339		conserved hypothetical protein	1.1	7.34E-01	Glucose	4.8	13610	6	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis		
15600536	PA5343		hypothetical protein	1.1	6.52E-01	Glucose	6.2	30778	10	Unknown	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15600537	PA5344	oxyR	OxyR	1.1	5.97E-01	Glucose	6.7	34295	10	Cytoplasmic	COG0583	Transcription		
15600539	PA5346	sadB	SadB	4.4	5.31E-02	Glucose	6.0	51427	3	Cytoplasmic	COG1639	Signal transduction mechanisms		
15600540	PA5347		hypothetical protein	2.5	1.61E-01	Glucose	11.1	14726	3	Unknown				
15600541	PA5348		probable DNA-binding protein	50.1	1.93E-03	Citronellol	11.3	9695	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair		
15600542	PA5349		probable rubredoxin reductase	1.0	8.95E-01	Citronellol	5.5	40617	11	Cytoplasmic	COG1251	Energy production and conversion		
15600550	PA5357		hypothetical protein	1.5	2.03E-02	Citronellol	4.7	19512	9	Cytoplasmic	COG3161	Coenzyme metabolism		
15600552	PA5359		hypothetical protein	42.4	4.83E-04	Citronellol	8.0	16472	4	Periplasmic	COG4315	Function unknown		
15600557	PA5364		probable two-component response regulator	1.7	1.89E-02	Citronellol	9.4	32401	2	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU	1.5	1.51E-02	Glucose	5.0	27487	4	Cytoplasmic	COG0704	Inorganic ion transport and metabolism		
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding protein, PstS	1.4	4.88E-02	Glucose	9.5	34473	8	Periplasmic	COG0226	Inorganic ion transport and metabolism		
15600564	PA5371		conserved hypothetical protein	2.1	1.70E-02	Citronellol	4.5	14555	2	Unknown	COG1607	Lipid metabolism		
15600566	PA5373	betB	betaine aldehyde dehydrogenase	1.0	9.32E-01	Glucose	5.0	53332	5	Cytoplasmic	COG1012	Energy production and conversion		
15600567	PA5374	betI	transcriptional regulator BetI	2.3	4.11E-01	Citronellol	9.0	21861	4	Unknown	COG1309	Transcription		
15600571	PA5378		hypothetical protein	2.2	1.92E-03	Citronellol	7.3	34427	12	Periplasmic	COG2113	Amino acid transport and metabolism		
15600588	PA5395		conserved hypothetical protein	5.1	7.74E-03	Citronellol	7.8	18513	3	Unknown	COG3558	Function unknown		
15600606	PA5413	ltaA	low specificity l-threonine aldolase	1.2	1.91E-01	Glucose	5.0	38213	8	Cytoplasmic	COG2008	Amino acid transport and metabolism		
15600607	PA5414		hypothetical protein	1.4	9.35E-01	Citronellol	5.8	22547	2	Outer Membrane Vesicle				
15600614	PA5421	fdhA	glutathione-independent formaldehyde dehydrogenase	14.3	3.63E-05	Citronellol	6.8	42008	2	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only	
15600616	PA5423		hypothetical protein	1.4	9.89E-01	Citronellol	5.7	20002	2	Periplasmic	COG3495	Function unknown		
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase	1.0	9.93E-01	Citronellol	5.4	38496	9	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism		
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	1.4	1.69E-02	Glucose	6.2	16889	10	Unknown	COG0041	Nucleotide transport and metabolism		
15600622	PA5429	aspA	aspartate ammonia-lyase	4.5	2.98E-03	Citronellol	5.6	51069	10	Periplasmic	COG1027	Amino acid transport and metabolism		
15600626	PA5433		conserved hypothetical protein	2.3	5.22E-01	Citronellol	9.0	25584	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis		
15600628	PA5435		probable transcarboxylase subunit	4.6	7.87E-05	Glucose	5.7	66095	49	Cytoplasmic	COG5016	Energy production and conversion		
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase	3.1	3.90E-03	Glucose	6.6	51816	21	Cytoplasmic	COG0439	Lipid metabolism		
15600632	PA5439		probable glucose-6-phosphate dehydrogenase	1.8	3.93E-02	Citronellol	7.2	54573	4	Cytoplasmic	COG0364	Carbohydrate transport and metabolism		
15600634	PA5441		hypothetical protein	1.1	7.50E-01	Glucose	4.6	80036	35	Periplasmic				
15600636	PA5443	uvrD	DNA helicase II	2.8	1.86E-03	Glucose	5.7	81494	13	Cytoplasmic	COG0210	DNA replication, recombination, and repair		
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase	4.8	8.73E-04	Citronellol	6.5	36399	14	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane		
15600647	PA5454	rmd	oxidoreductase Rmd	6.2	3.47E-04	Citronellol	6.7	33910	7	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15600652	PA5459		hypothetical protein	2.0	1.29E-02	Citronellol	4.7	30701	6	Cytoplasmic	COG2226	Coenzyme metabolism		
15600674	PA5481		hypothetical protein	7.0	1.27E-03	Citronellol	5.2	17366	3	Periplasmic				
15600676	PA5483	algB	two-component response regulator AlgB	1.1	5.10E-01	Citronellol	5.2	49323	8	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA	1.4	5.96E-01	Citronellol	6.4	23375	11	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones		
15600683	PA5490	cc4	cytochrome c4 precursor	2.1	5.01E-01	Citronellol	7.6	20735	5	Outer Membrane Vesicle	COG2863	Energy production and conversion		
15600685	PA5492		conserved hypothetical protein	2.2	1.73E-01	Glucose	7.1	23786	6	Unknown	COG0218	General function prediction only		
15600686	PA5493	polA	DNA polymerase I	1.2	4.57E-01	Citronellol	4.8	99792	45	Periplasmic	COG0749	DNA replication, recombination, and repair		
15600692	PA5499	np20	transcriptional regulator np20	1.0	6.79E-01	Glucose	6.9	18216	2	Cytoplasmic	COG0735	Inorganic ion transport and metabolism		
15600698	PA5505		probable TonB-dependent receptor	1.3	1.61E-03	Glucose	8.7	28065	16	Periplasmic	COG1464	Inorganic ion transport and metabolism		
15600700	PA5507		hypothetical protein	1.1	8.14E-01	Citronellol	6.4	24262	6	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15600709	PA5516	pdxY	pyridoxamine kinase	1.1	4.90E-01	Citronellol	6.0	31285	6	Cytoplasmic	COG2240	Coenzyme metabolism		
15600712	PA5519		conserved hypothetical protein	1.0	8.54E-01	Glucose	7.5	21215	2	Unknown	COG1607	Lipid metabolism		
15600713	PA5520		hypothetical protein	1.4	1.63E-01	Citronellol	5.1	26250	4	Unknown				
15600714	PA5521		probable short-chain dehydrogenase	1.3	6.13E-02	Citronellol	5.8	26894	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15600716	PA5523		probable aminotransferase	14.0	2.91E-03	Citronellol	6.7	48908	3	Cytoplasmic	COG0001	Coenzyme metabolism		
15600717	PA5524		probable short-chain dehydrogenase	1.7	1.73E-03	Citronellol	5.0	27158	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15600735	PA5542		hypothetical protein	4.6	5.44E-04	Citronellol	6.3	45872	9	Unknown	COG1680	Defense mechanisms		
15600738	PA5545		conserved hypothetical protein	10.2	1.19E-04	Citronellol	7.8	33627	13	Periplasmic	COG2358	General function prediction only		
15600739	PA5546		conserved hypothetical protein	13.9	3.38E-04	Citronellol	5.7	44096	9	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane		
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.7	4.07E-03	Glucose	5.9	66294	26	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane		
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	1.6	4.53E-02	Citronellol	6.2	48851	14	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane		
15600747	PA5554	atpD	ATP synthase beta chain	2.0	5.04E-03	Citronellol	4.7	49499	43	Periplasmic	COG0055	Energy production and conversion		
15600748	PA5555	atpG	ATP synthase gamma chain	1.6	2.15E-01	Citronellol	8.1	31553	16	Outer Membrane Vesicle	COG0224	Energy production and conversion		
15600749	PA5556	atpA	ATP synthase alpha chain	2.1	1.07E-02	Citronellol	5.1	55393	31	Periplasmic	COG0056	Energy production and conversion		
15600750	PA5557	atpH	ATP synthase delta chain	3.8	7.30E-02	Citronellol	5.9	19260	13	Outer Membrane Vesicle	COG0712	Energy production and conversion		
15600751	PA5558	atpF	ATP synthase B chain	1.3	1.32E-01	Citronellol	5.8	16924	10	Outer Membrane Vesicle	COG0711	Energy production and conversion		
15600753	PA5560	atpB	ATP synthase A chain	1.6	3.54E-01	Glucose	6.5	31921	2	Outer Membrane Vesicle	COG0356	Energy production and conversion		
15600755	PA5562	spoOJ	chromosome partitioning protein SpoOJ	1.2	5.70E-01	Glucose	10.0	31969	3	Cytoplasmic	COG1475	Transcription		
15600756	PA5563	soj	chromosome partitioning protein Soj	2.7	8.82E-02	Glucose	6.1	28609	2	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning		
15600757	PA5564	gidB	glucose inhibited division protein B	1.1	1.83E-01	Glucose	6.3	23735	5	Unknown	COG0357	Cell envelope biogenesis, outer membrane		
15600758	PA5565	gidA	glucose-inhibited division protein A	4.7	1.10E-04	Glucose	6.5	69605	8	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning		
15600761	PA5568		conserved hypothetical protein	3.0	2.42E-02	Glucose	8.0	64074	2	Outer Membrane Vesicle	COG0706	Intracellular trafficking and secretion		
15600762	PA5569	rnpA	ribonuclease P protein component	1.6	8.35E-03	Citronellol	11.5	15282	3	Unknown	COG0594	Translation, ribosomal structure and biogenesis		
375041995				1.7	4.74E-01	Glucose			87					
346058816				1.2	2.62E-01	Citronellol			33					
22001796				1.7	1.41E-03	Glucose			27					
375041914				14.2	1.11E-02	Citronellol			21					
313110180				1.0	7.93E-01	Citronellol			25					
118572621				1.4	1.28E-01	Citronellol			13					
239949862				2.1	1.25E-02	Citronellol			14					
107103488				1.7	2.13E-02	Citronellol			12					
107104524				1.5	7.73E-03	Citronellol			13					
375044686				11.0	1.02E-02	Glucose			12					
308198348				1.5	4.90E-02	Citronellol			12					
334834247				1.1	4.64E-01	Glucose			14					
239949861				1.6	9.10E-03	Citronellol			12					
107099134				1.2	1.01E-01	Citronellol			13					
313111914				24.1	1.03E-02	Citronellol			10					
254236126				1.1	9.76E-01	Glucose			9					
375041918				1.6	4.44E-01	Citronellol			9					
282403589				1.2	5.04E-01	Citronellol			8					
344189438				1.0	7.85E-01	Citronellol			8					
107104057				1.1	4.50E-01	Glucose			7					
107100575				3.2	4.05E-02	Citronellol			7					
296389665				1.4	2.01E-01	Glucose			6					
107101116				1.3	1.36E-01	Glucose			7					
254236426				1.6	4.38E-04	Citronellol			6					
107103573				1.3	6.89E-02	Citronellol			5					
313112332				2.1	5.24E-02	Glucose			5					
116053335				6.5	1.06E-02	Citronellol			4					
70732985				2.4	9.85E-02	Citronellol			3					
359783701				3.4	4.04E-02	Glucose			3					
107102888				2.9	9.24E-04	Citronellol			3					
107101938				2.2	1.53E-02	Citronellol			3					
107102668				1.3	9.01E-02	Citronellol			3					
355639818				1.8	3.80E-01	Citronellol			3					
107099288				1.3	4.31E-01	Glucose			2					

359782167	1.4	4.26E-01	Glucose	3
295698607	3.1	1.97E-01	Glucose	2
258591310	5.7	8.16E-01	Citronellol	2
254240896	4.2	3.19E-01	Citronellol	2
331007094	6.8	2.97E-01	Citronellol	2
312386137	1.2	5.83E-01	Glucose	2
302186668	4.7	2.77E-01	Citronellol	2
157830859	3.0	1.93E-01	Glucose	1
330807576	4.1	9.99E-06	Citronellol	2
374702386	9.0	1.20E-02	Citronellol	2
226944916	4.4	1.60E-02	Citronellol	3
334141306	6.2	8.37E-03	Citronellol	3
104782430	25.6	1.51E-03	Citronellol	3
116052531	3.9	3.90E-03	Citronellol	2
244539066	1.4	1.74E-01	Citronellol	2
146307419	1.8	2.16E-01	Glucose	2
330808408	2.4	1.88E-01	Citronellol	2
104780339	1.7	2.23E-02	Citronellol	1
357405980	1.4	2.43E-01	Glucose	2
374702598	9.8	8.85E-02	Glucose	1
104781332	1.2	4.95E-01	Citronellol	3
254236849	4.5	3.30E-02	Citronellol	2
116049588	9.7	3.38E-07	Citronellol	2
107103974	1.6	7.70E-02	Citronellol	2
107104298	1.1	6.47E-01	Glucose	2

5.4.1.2 GeLCMSMS_P_aeruginosa_PAO1_Glucose_Oktansäure_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595199	PA0001	dnaA	chromosomal replication initiator protein DnaA	1.63	5.86E-03	Oktansaeure	8.9	57722	11	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.17	9.31E-02	Oktansaeure	4.9	40694	17	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	1.52	3.09E-03	Glucose	5.7	90188	40	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	1.15	9.74E-01	Glucose	4.5	19115	3	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	13.76	9.57E-06	Oktansaeure	7.9	61755	4	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.06	4.43E-01	Glucose	4.8	73973	39	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	1.62	2.30E-02	Glucose	4.7	36109	13	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595208	PA0010	tag	DNA-3-methyladenine glycosidase I	2	4.03E-01	Oktansaeure	4.6	20780	2	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	1.38	1.71E-01	Glucose	7.0	33028	12	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	1.66	1.70E-02	Oktansaeure	4.7	19365	6	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	1.35	3.40E-01	Oktansaeure	9.4	37586	6	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	2.3	2.66E-02	Oktansaeure	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	2.03	7.76E-03	Oktansaeure	6.3	35095	10	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	1.51	2.76E-02	Glucose	5.8	34774	9	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	1.29	2.47E-01	Oktansaeure	5.5	29484	3	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	2.66	6.04E-04	Glucose	5.0	28488	11	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	1.91	5.59E-03	Glucose	6.3	43680	16	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	2.87	1.28E-02	Oktansaeure	7.1	7863	2	Unknown	COG3360	Function unknown	
15595243	PA0045		hypothetical protein	1.32	3.86E-01	Oktansaeure	9.6	24395	2	Periplasmic	COG1462	Cell envelope biogenesis, outer membrane	
15595252	PA0054		conserved hypothetical protein	2.84	4.45E-02	Oktansaeure	9.6	20024	3	Unknown	COG1859	Translation, ribosomal structure and biogenesis	
15595253	PA0055		hypothetical protein	1.03	8.65E-01	Glucose	5.7	18433	11	Cytoplasmic	COG3812	Function unknown	
15595263	PA0065		hypothetical protein	6.77	2.89E-02	Glucose	6.1	24951	6	Cytoplasmic	COG0546	General function prediction only	
15595264	PA0066		conserved hypothetical protein	1.08	7.06E-01	Oktansaeure	6.6	19198	2	Cytoplasmic	COG0663	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.25	1.71E-01	Oktansaeure	4.9	76011	31	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	1.74	2.25E-01	Oktansaeure	8.9	31716	7	Periplasmic			
15595273	PA0075	pppA	PppA	2.91	1.07E-02	Oktansaeure	6.2	25904	7	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	1.07	6.44E-01	Glucose	4.4	23856	3	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	2.11	2.08E-02	Oktansaeure	6.1	48275	7	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595280	PA0082	tssA1	TssA1	1.91	8.79E-03	Oktansaeure	4.1	36647	2	Cytoplasmic	COG3515	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	1.14	4.63E-01	Oktansaeure	4.9	18785	18	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.4	2.32E-02	Oktansaeure	5.0	55771	40	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	1.28	2.13E-01	Oktansaeure	6.8	17415	12	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	1.67	3.38E-01	Glucose	4.4	30361	7	Cytoplasmic	COG4455	General function prediction only	
15595286	PA0088	tssF1	TssF1	2.45	1.94E-02	Oktansaeure	7.4	69483	5	Cytoplasmic	COG3519	Intracellular trafficking, secretion, and vesicular transport	
15595288	PA0090	clpV1	ClpV1	1.22	6.02E-01	Oktansaeure	5.3	98737	39	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	2.28	6.28E-02	Oktansaeure	6.4	72012	14	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	4.11	8.27E-02	Oktansaeure	8.9	44738	3	Cytoplasmic Membrane	COG4104	Function unknown	
15595292	PA0094		hypothetical protein	1.24	6.53E-01	Oktansaeure	6.8	16456	4	Unknown	COG5435	Function unknown	
15595298	PA0100		hypothetical protein	2.19	6.15E-03	Oktansaeure	4.1	33723	5	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.07	5.65E-01	Glucose	6.7	26622	9	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595313	PA0115		conserved hypothetical protein	1.38	3.86E-01	Glucose	6.3	17085	6	Cytoplasmic	COG2153	General function prediction only	
15595316	PA0118		hypothetical protein	1.22	4.33E-01	Oktansaeure	6.8	21473	4	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595320	PA0122	rahU	rahU	75.56	5.72E-04	Oktansaeure	4.4	14579	7	Extracellular			
15595324	PA0126		hypothetical protein	1.31	6.83E-01	Oktansaeure	8.0	22367	2	Outer Membrane Vesicle			
15595326	PA0128		conserved hypothetical protein	1.35	1.40E-01	Glucose	4.9	12132	3	Unknown	COG2824	Inorganic ion transport and metabolism	
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.36	1.15E-01	Glucose	6.0	53323	7	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	2.27	4.90E-03	Oktansaeure	6.3	20541	14	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	2.36	7.22E-03	Glucose	5.0	55835	8	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
119167454	PA0143	nuh	purine nucleosidase Nuh	1.17	4.22E-01	Glucose	7.7	37542	14	Periplasmic	COG1957	Nucleotide transport and metabolism	
15595342	PA0144		hypothetical protein	3.25	1.06E-02	Oktansaeure	8.4	22431	7	Unknown	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.07	8.50E-01	Oktansaeure	4.9	36163	5	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595357	PA0159		probable transcriptional regulator	1.45	1.64E-01	Oktansaeure	6.0	34683	2	Cytoplasmic	COG0583	Transcription	
15595362	PA0164		probable gamma-glutamyltranspeptidase	1.46	1.72E-01	Oktansaeure	6.5	58453	3	Periplasmic	COG0405	Amino acid transport and metabolism	
15595367	PA0169	siaD	SiaD	1.02	8.50E-01	Oktansaeure	9.5	26792	2	Cytoplasmic	COG2199	Signal transduction mechanisms	
15595368	PA0170		hypothetical protein	1.12	5.85E-01	Glucose	4.3	14553	5	Cytoplasmic			
15595369	PA0171		hypothetical protein	1.35	4.26E-01	Glucose	7.1	19800	12	Cytoplasmic			
15595374	PA0176	aer2	aerotaxis transducer Aer2	14.67	4.41E-03	Oktansaeure	4.8	72591	24	Cytoplasmic	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595375	PA0177		probable purine-binding chemotaxis protein	10.2	6.74E-03	Oktansaeure	4.3	17487	3	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595376	PA0178		probable two-component sensor	229.68	1.56E-03	Oktansaeure	4.5	68931	2	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595380	PA0182		probable short-chain dehydrogenase	1.13	3.03E-01	Glucose	4.7	25230	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	3.97	2.11E-04	Oktansaeure	5.9	38650	17	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	10.2	2.57E-02	Oktansaeure	4.5	30343	4	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	9.62	6.70E-02	Oktansaeure	7.1	28496	2	Cytoplasmic			
15595422	PA0225		probable transcriptional regulator	5.72	9.27E-02	Oktansaeure	6.9	19993	2	Cytoplasmic	COG1476	Transcription	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	3.75	1.19E-01	Oktansaeure	6.2	49121	4	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	1.19	9.95E-01	Oktansaeure	5.1	27985	3	Unknown	COG0596	General function prediction only	
15595429	PA0232	pcaC	gamma-carboxymuconolactone decarboxylase	1.05	9.28E-01	Glucose	7.1	15084	2	Unknown	COG0599	Function unknown	
15595456	PA0259		hypothetical protein	3.81	1.46E-04	Oktansaeure	5.0	52444	7	Unknown			
15595457	PA0260		hypothetical protein	8.87	3.00E-03	Oktansaeure	7.0	78202	2	Unknown			
15595460	PA0263	hcpC	secreted protein Hcp	56.2	2.68E-04	Oktansaeure	5.8	19091	8	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.24	9.97E-02	Oktansaeure	5.4	51622	23	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	1.85	1.62E-04	Oktansaeure	6.4	45220	19	Periplasmic	COG0160	Amino acid transport and metabolism	
15595474	PA0277		conserved hypothetical protein	1.72	1.44E-01	Oktansaeure	6.5	26626	7	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	2	7.18E-04	Oktansaeure	9.0	36433	14	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	1.58	3.03E-01	Oktansaeure	9.1	49667	7	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.32	2.52E-01	Oktansaeure	4.6	41191	5	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	1.36	1.54E-01	Oktansaeure	4.6	50907	8	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	2.33	1.23E-03	Oktansaeure	5.0	50965	7	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595496	PA0299	spuC	Polyamine:pyruvate transaminase	1.25	2.15E-01	Oktansaeure	6.0	50453	14	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	1.55	6.52E-02	Oktansaeure	7.6	40629	12	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	1.55	3.09E-02	Oktansaeure	5.5	40069	13	Periplasmic	COG0687	Amino acid transport and metabolism	
15595506	PA0309		hypothetical protein	1.51	6.43E-02	Oktansaeure	7.6	27021	7	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	1.2	2.68E-01	Glucose	9.7	28005	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15595512	PA0315		hypothetical protein	1.56	2.04E-01	Glucose	7.2	15463	7	Unknown			
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.2	2.41E-01	Oktansaeure	6.5	44216	17	Periplasmic	COG0111	Amino acid transport and metabolism	
15595514	PA0317		hypothetical protein	1.66	9.22E-03	Glucose	4.9	51286	14	Periplasmic	COG0277	Energy production and conversion	
15595515	PA0318		conserved hypothetical protein	1.24	1.01E-02	Oktansaeure	5.3	23843	6	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	1.53	3.54E-02	Glucose	5.3	23721	11	Cytoplasmic	COG0120	Carbohydrate transport and metabolism	
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	2.25	8.50E-03	Glucose	6.5	55351	14	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15595532	PA0335		hypothetical protein	1.5	2.29E-01	Oktansaeure	4.5	24353	14	Cytoplasmic	COG0560	Amino acid transport and metabolism	

15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.1	7.91E-01	Glucose	9.5	18726	5	Cytoplasmic	COG0494	DNA replication, recombination, and repair	General function prediction only
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.11	5.16E-01	Oktansaeure	5.6	83606	24	Cytoplasmic	COG3605	Signal transduction mechanisms	
15595536	PA0339		hypothetical protein	1.06	7.92E-01	Glucose	6.7	26527	2	Unknown	COG3332	Function unknown	
15595539	PA0342	thyA	thymidylate synthase	1.54	1.37E-01	Glucose	6.5	30016	7	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
15595547	PA0350	folA	dihydrofolate reductase	1.14	5.01E-01	Glucose	5.3	18203	7	Unknown	COG0262	Coenzyme metabolism	
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.44	1.58E-01	Glucose	6.0	65160	35	Periplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15595552	PA0355	pfpI	protease PfpI	17.03	1.10E-03	Oktansaeure	5.0	19246	7	Cytoplasmic	COG0693	General function prediction only	
15595553	PA0356		hypothetical protein	1.07	5.44E-01	Glucose	5.3	30360	4	Unknown	COG1639	Signal transduction mechanisms	
15595554	PA0357	mutM	formamidopyrimidine-DNA glycosylase	3	1.08E-01	Oktansaeure	9.6	30046	2	Cytoplasmic	COG0266	DNA replication, recombination, and repair	
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	1.42	1.75E-01	Glucose	9.0	17771	12	Cytoplasmic	COG0669	Coenzyme metabolism	
15595566	PA0369		hypothetical protein	1.09	8.31E-01	Oktansaeure	3.8	10556	2	Unknown			
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	1.31	2.04E-01	Glucose	4.5	48391	10	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.64	1.68E-02	Glucose	4.8	28234	15	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
15595579	PA0382	micA	DNA mismatch repair protein MicA	1.42	7.89E-03	Glucose	8.3	25331	3	Cytoplasmic	COG0220	General function prediction only	
15595584	PA0387		conserved hypothetical protein	1.58	3.24E-01	Oktansaeure	6.1	21242	9	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
15595585	PA0388		hypothetical protein	3.24	2.88E-01	Glucose	7.4	15303	2	Periplasmic			
15595589	PA0392		conserved hypothetical protein	1.27	4.56E-01	Glucose	10.1	21745	2	Cytoplasmic Membrane			
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	1.03	9.43E-01	Oktansaeure	4.5	28094	9	Cytoplasmic	COG0345	Amino acid transport and metabolism	
15595591	PA0394		conserved hypothetical protein	1.02	8.20E-01	Glucose	6.7	24505	3	Cytoplasmic	COG0325	General function prediction only	
15595592	PA0395	pilT	twitching motility protein PilT	1.18	1.99E-01	Oktansaeure	6.9	38021	9	Cytoplasmic	COG2805	Cell motility and secretion	Intracellular trafficking and secretion
15595596	PA0399		cystathionine beta-synthase	1.1	2.40E-01	Oktansaeure	5.5	49170	20	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15595597	PA0400		probable cystathionine gamma-lyase	1.76	1.13E-02	Oktansaeure	6.6	42786	7	Cytoplasmic	COG0626	Amino acid transport and metabolism	
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.26	5.79E-01	Oktansaeure	5.8	44150	7	Periplasmic	COG0044	Nucleotide transport and metabolism	
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.11	2.65E-01	Glucose	6.8	36629	11	Periplasmic	COG0540	Nucleotide transport and metabolism	
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.01	9.05E-01	Oktansaeure	5.7	18676	7	Cytoplasmic	COG2065	Nucleotide transport and metabolism	
15595604	PA0407	gshB	glutathione synthetase	1.46	2.13E-01	Oktansaeure	5.8	35705	17	Periplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
15595605	PA0408	pilG	twitching motility protein PilG	1.41	3.89E-01	Glucose	7.4	14718	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595607	PA0410	pilI	twitching motility protein PilI	1.79	1.97E-01	Oktansaeure	6.6	19934	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595608	PA0411	pilJ	twitching motility protein PilJ	1.41	2.27E-01	Oktansaeure	4.4	72528	2	Outer Membrane Vesicle	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595610	PA0413	chpA	component of chemotactic signal transduction system	1.46	1.74E-01	Oktansaeure	4.2	268573	24	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595612	PA0415	chpC	probable chemotaxis protein	1.15	4.97E-01	Glucose	4.7	17625	6	Unknown			
15595615	PA0418		hypothetical protein	1.33	1.45E-01	Oktansaeure	5.6	52140	6	Cytoplasmic			
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1.26	1.73E-01	Glucose	6.3	52478	7	Cytoplasmic	COG0161	Coenzyme metabolism	
15595620	PA0423	pasP	PasP	5.03	2.61E-03	Oktansaeure	6.5	20776	19	Periplasmic	COG2353	Function unknown	
15595622	PA0425	mexA	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexA precursor	3.4	3.07E-03	Oktansaeure	9.2	40969	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15595623	PA0426	mexB	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB	1.83	6.54E-02	Oktansaeure	5.4	112790	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15595624	PA0427	oprM	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	2.94	1.35E-01	Oktansaeure	5.3	52598	4	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15595625	PA0428		probable ATP-dependent RNA helicase	1.36	7.33E-01	Glucose	10.7	70112	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
15595626	PA0429		hypothetical protein	1.04	7.38E-01	Glucose	7.0	40872	2	Cytoplasmic			
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	1.19	3.40E-01	Glucose	6.5	32196	16	Periplasmic	COG0685	Amino acid transport and metabolism	
15595628	PA0431		hypothetical protein	1.97	8.50E-03	Oktansaeure	6.8	20639	2	Unknown	COG0317	Signal transduction mechanisms	Transcription
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	1.42	1.88E-02	Glucose	6.0	51400	27	Periplasmic	COG0499	Coenzyme metabolism	
15595631	PA0434		hypothetical protein	5.2	5.67E-03	Oktansaeure	5.8	81304	12	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15595634	PA0437	codA	cytosine deaminase	1.38	1.26E-01	Glucose	6.0	47074	6	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15595643	PA0446		conserved hypothetical protein	2.12	1.76E-02	Oktansaeure	5.3	43847	3	Cytoplasmic	COG1804	Energy production and conversion	
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	2.88	2.57E-04	Oktansaeure	6.1	43311	3	Cytoplasmic	COG1960	Lipid metabolism	
15595646	PA0449		hypothetical protein	1.5	1.18E-01	Glucose	10.5	19808	13	Cytoplasmic	COG1607	Lipid metabolism	
15595652	PA0455	dbpA	RNA helicase DbpA	1.32	2.14E-02	Glucose	8.4	49752	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
15595657	PA0460		hypothetical protein	1.72	2.76E-01	Glucose	5.8	18727	2	Unknown			
15595659	PA0462		hypothetical protein	1.36	1.70E-01	Oktansaeure	10.6	26230	9	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15595660	PA0463	creB	two-component response regulator CreB	1.05	8.01E-01	Glucose	5.4	25573	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595664	PA0467		conserved hypothetical protein	1.5	1.59E-01	Oktansaeure	7.5	23301	9	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15595665	PA0468		hypothetical protein	2.05	4.42E-02	Oktansaeure	4.8	33594	2	Periplasmic	COG4257	Defense mechanisms	
15595666	PA0469		hypothetical protein	2.38	2.92E-02	Oktansaeure	4.7	32137	10	Cytoplasmic			
15595670	PA0473		probable glutathione S-transferase	1.24	1.70E-01	Glucose	5.8	28294	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15595675	PA0478		probable N-acetyltransferase	1.18	7.14E-01	Glucose	4.6	18109	3	Cytoplasmic	COG0456	General function prediction only	
15595679	PA0482	glcB	malate synthase G	4.82	1.96E-03	Oktansaeure	5.5	78659	69	Periplasmic	COG2225	Energy production and conversion	
15595681	PA0484		conserved hypothetical protein	3.51	5.43E-02	Oktansaeure	4.5	18553	3	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15595684	PA0487		probable molybdenum transport regulator	1.3	4.52E-01	Oktansaeure	9.2	26948	2	Cytoplasmic	COG2005	General function prediction only	
15595697	PA0500	bioB	biotin synthase	6.46	2.65E-02	Glucose	6.0	39113	12	Cytoplasmic	COG0502	Coenzyme metabolism	
15595698	PA0501	bioF	8-amino-7-oxononanoate synthase	1.54	1.80E-01	Glucose	5.9	42237	2	Cytoplasmic	COG0156	Coenzyme metabolism	
15595699	PA0502		probable biotin biosynthesis protein bioH	1.38	2.44E-01	Oktansaeure	4.3	26494	2	Cytoplasmic	COG0596	General function prediction only	
15595700	PA0503		probable biotin synthesis protein BioC	1.98	2.06E-02	Glucose	9.0	29712	6	Unknown	COG2226	Coenzyme metabolism	
15595701	PA0504	bioD	dethiobiotin synthase	1.17	7.94E-01	Oktansaeure	5.3	23337	10	Cytoplasmic	COG0132	Coenzyme metabolism	
15595703	PA0506		probable acyl-CoA dehydrogenase	6.87	1.79E-03	Oktansaeure	5.8	65358	40	Periplasmic	COG1960	Lipid metabolism	
15595704	PA0507		probable acyl-CoA dehydrogenase	1.44	7.44E-02	Oktansaeure	6.4	64349	2	Cytoplasmic	COG1960	Lipid metabolism	
15595705	PA0508		probable acyl-CoA dehydrogenase	10.98	8.69E-05	Oktansaeure	5.1	63628	43	Cytoplasmic	COG1960	Lipid metabolism	
15595716	PA0519	nirS	nitrite reductase precursor	23.03	6.66E-03	Oktansaeure	8.2	62653	4	Periplasmic	COG2010	Energy production and conversion	
15595724	PA0527	dnr	transcriptional regulator Dnr	5.34	4.88E-02	Oktansaeure	6.7	25933	2	Cytoplasmic	COG0664	Signal transduction mechanisms	
15595732	PA0535		probable transcriptional regulator	1.6	1.30E-01	Oktansaeure	4.9	20231	4	Cytoplasmic	COG1396	Transcription	
15595734	PA0537		conserved hypothetical protein	1.81	1.78E-01	Oktansaeure	8.9	22180	8	Outer Membrane Vesicle	COG1704	Function unknown	
15595743	PA0546	metK	methionine adenosyltransferase	1.15	2.04E-01	Oktansaeure	5.2	42709	24	Cytoplasmic	COG0192	Coenzyme metabolism	
15595745	PA0548	tktA	transketolase	1.01	9.01E-01	Glucose	5.0	72220	39	Periplasmic	COG0021	Carbohydrate transport and metabolism	
15595747	PA0550		conserved hypothetical protein	1.73	1.23E-02	Oktansaeure	5.4	29834	5	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	1.24	2.33E-01	Oktansaeure	5.8	38743	4	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15595749	PA0552	pgk	phosphoglycerate kinase	1.36	7.22E-02	Oktansaeure	5.1	40404	18	Periplasmic	COG0126	Carbohydrate transport and metabolism	
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	1.13	3.65E-01	Glucose	5.3	38574	23	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
15595755	PA0558		conserved hypothetical protein	1.4	3.05E-02	Oktansaeure	6.2	27987	13	Cytoplasmic	COG2226	Coenzyme metabolism	
15595759	PA0562		probable hydrolase	1.02	7.87E-01	Glucose	5.4	24232	7	Cytoplasmic	COG0637	General function prediction only	
15595765	PA0568		hypothetical protein	1.02	7.90E-01	Oktansaeure	4.2	17683	3	Cytoplasmic			
15595768	PA0571		hypothetical protein	2.62	7.82E-03	Oktansaeure	5.0	22501	5	Unknown			
15595773	PA0576	rpoD	sigma factor RpoD	1.53	1.04E-01	Glucose	4.6	69643	31	Outer Membrane Vesicle	COG0568	Transcription	
15595776	PA0579	rpsU	30S ribosomal protein S21	3.48	6.78E-02	Glucose	11.4	8485	3	Cytoplasmic			
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	1.23	2.70E-01	Glucose	6.2	36561	5	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
15595780	PA0583		hypothetical protein	1.31	4.10E-01	Oktansaeure	5.6	20091	4	Cytoplasmic	COG0801	Coenzyme metabolism	
15595783	PA0586		conserved hypothetical protein	6.4	5.31E-03	Oktansaeure	5.1	60814	11	Cytoplasmic	COG2719	Function unknown	
15595784	PA0587		conserved hypothetical protein	11.68	2.80E-03	Oktansaeure	7.8	48742	9	Cytoplasmic	COG2718	Function unknown	
15595785	PA0588		conserved hypothetical protein	9.51	5.03E-03	Oktansaeure	5.5	73722	47	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms	
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	1.24	3.10E-01	Glucose	7.2	32019	5	Cytoplasmic			
15595789	PA0592	ksgA	rRNA (adenine-N6,N6)-dimethyltransferase	1.03	8.26E-01	Oktansaeure	7.4	30058	6	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.41	1.15E-01	Glucose	6.6	34891	10	Cytoplasmic	COG1995	Coenzyme metabolism	

15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.22	9.46E-03	Oktansaeure	5.6	48441	17	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones		
15595792	PA0595	ostA	organic solvent tolerance protein OstA precursor	1.53	3.53E-01	Glucose	5.3	104271	3	Periplasmic	COG1452	Cell envelope biogenesis, outer membrane		
15595793	PA0596		hypothetical protein	1.24	1.72E-01	Oktansaeure	5.1	38185	9	Cytoplasmic	COG3178	General function prediction only		
15595794	PA0597		probable nucleotidyl transferase	1.11	4.17E-01	Glucose	6.1	24149	3	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis	
15595798	PA0601		probable two-component response regulator	21.58	8.92E-02	Glucose	6.5	22868	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
15595801	PA0604		probable binding protein component of ABC transporter	1.24	4.37E-01	Oktansaeure	5.6	38167	6	Periplasmic	COG0687	Amino acid transport and metabolism		
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.4	1.69E-01	Oktansaeure	5.1	24096	13	Cytoplasmic	COG0036	Carbohydrate transport and metabolism		
15595806	PA0609	trpE	anthranilate synthetase component I	1.23	1.20E-01	Glucose	4.7	54555	15	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism	
15595830	PA0633		hypothetical protein	1.5	8.18E-01	Oktansaeure	4.7	17539	2	Outer Membrane Vesicle				
15595846	PA0649	trpG	anthranilate synthase component II	1.3	6.29E-01	Glucose	6.0	22046	4	Cytoplasmic	COG0512	Amino acid transport and metabolism	Coenzyme metabolism	
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	1.36	2.38E-01	Glucose	5.6	37384	7	Cytoplasmic	COG0547	Amino acid transport and metabolism		
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	1.13	4.56E-01	Glucose	4.6	30315	11	Cytoplasmic	COG0134	Amino acid transport and metabolism		
15595850	PA0653		conserved hypothetical protein	1.66	2.25E-01	Glucose	6.4	15237	6	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones		
15595851	PA0654	speD	S-adenosylmethionine decarboxylase proenzyme	3.85	1.00E-02	Glucose	4.5	30446	4	Cytoplasmic	COG1586	Amino acid transport and metabolism		
15595852	PA0655		hypothetical protein	1.23	3.10E-01	Oktansaeure	5.3	23644	6	Unknown	COG2941	Coenzyme metabolism		
15595854	PA0657		probable ATPase	1.26	2.95E-01	Oktansaeure	6.0	54551	2	Cytoplasmic Membrane	COG0464	Posttranslational modification, protein turnover, chaperones		
15595855	PA0658		probable short-chain dehydrogenase	1.12	2.67E-02	Oktansaeure	10.4	29174	2	Cytoplasmic	COG0300	General function prediction only		
15595857	PA0660		hypothetical protein	1.62	1.27E-01	Oktansaeure	6.2	34814	18	Cytoplasmic	COG2070	General function prediction only		
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.01	9.87E-01	Oktansaeure	6.7	36684	13	Cytoplasmic	COG0002	Amino acid transport and metabolism		
15595861	PA0664		hypothetical protein	1.11	5.18E-01	Oktansaeure	5.6	14790	3	Cytoplasmic	COG1664	Cell envelope biogenesis, outer membrane		
15595862	PA0665		conserved hypothetical protein	2.93	5.65E-02	Glucose	4.0	12484	2	Cytoplasmic	COG0316	Posttranslational modification, protein turnover, chaperones		
15595863	PA0666		conserved hypothetical protein	1.31	1.40E-01	Oktansaeure	5.2	39087	2	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones		
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.07	5.46E-01	Glucose	5.6	44129	26	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis		
15595869	PA0672	hemO	heme oxygenase	1.04	7.09E-01	Glucose	4.8	21953	12	Unknown	COG3230	Inorganic ion transport and metabolism		
15595903	PA0706	cat	chloramphenicol acetyltransferase	1.01	8.23E-01	Glucose	6.1	23524	3	Unknown	COG0110	General function prediction only		
15595912	PA0715		hypothetical protein	1.63	1.49E-01	Oktansaeure	9.9	36589	3	Cytoplasmic	COG3344	DNA replication, recombination, and repair		
15595938	PA0741		conserved hypothetical protein	2.62	2.80E-02	Oktansaeure	6.6	22687	6	Unknown	COG2910	General function prediction only		
15595940	PA0743		probable 3-hydroxyisobutyrate dehydrogenase	32.62	2.64E-02	Oktansaeure	5.3	30754	2	Cytoplasmic	COG2084	Lipid metabolism		
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	1.65	3.48E-01	Oktansaeure	6.4	29904	14	Cytoplasmic	COG1024	Lipid metabolism		
15595944	PA0747		probable aldehyde dehydrogenase	17.65	3.39E-02	Oktansaeure	6.1	54564	2	Cytoplasmic	COG1012	Energy production and conversion		
15595947	PA0750	ung	uracil-DNA glycosylase	1.24	1.60E-01	Glucose	8.2	26010	7	Cytoplasmic	COG0692	DNA replication, recombination, and repair		
15595951	PA0754		hypothetical protein	3.52	5.28E-02	Oktansaeure	5.5	34918	16	Unknown	COG3181	Function unknown		
15595953	PA0756		probable two-component response regulator	1.42	1.61E-01	Oktansaeure	5.2	24431	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15595955	PA0758		hypothetical protein	1.11	6.01E-01	Oktansaeure	4.7	30875	8	Cytoplasmic	COG1639	Signal transduction mechanisms		
15595956	PA0759		conserved hypothetical protein	1.09	3.47E-01	Oktansaeure	5.2	33667	15	Unknown	COG0354	General function prediction only		
15595958	PA0761	nadB	L-aspartate oxidase	1.21	6.97E-02	Glucose	6.3	60004	10	Cytoplasmic	COG0029	Coenzyme metabolism		
15595959	PA0762	algU	sigma factor AlgU	1.13	8.51E-01	Oktansaeure	5.4	22196	8	Cytoplasmic	COG1595	Transcription		
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	1.24	4.83E-01	Oktansaeure	6.1	34572	4	Periplasmic	COG3026	Signal transduction mechanisms		
15595963	PA0766	mucD	serine protease MucD precursor	1.38	5.84E-02	Oktansaeure	7.8	50321	8	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones		
15595964	PA0767	lepA	GTP-binding protein LepA	1.46	1.44E-01	Oktansaeure	5.3	66263	9	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane		
15595967	PA0770	rnc	ribonuclease III	1.2	3.40E-01	Glucose	6.6	25474	4	Cytoplasmic	COG0571	Transcription		
15595968	PA0771	era	GTP-binding protein Era	1.16	3.50E-02	Oktansaeure	6.6	34550	6	Cytoplasmic Membrane	COG1159	General function prediction only		
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.05	7.00E-01	Glucose	5.6	27228	7	Cytoplasmic	COG0854	Coenzyme metabolism		
15595971	PA0774		conserved hypothetical protein	4.07	3.51E-02	Glucose	6.4	36522	2	Cytoplasmic	COG2227	Coenzyme metabolism		
15595972	PA0775		conserved hypothetical protein	2.21	7.01E-04	Glucose	5.3	27608	3	Cytoplasmic	COG4106	General function prediction only		
15595976	PA0779		probable ATP-dependent protease	1.31	8.39E-01	Glucose	6.8	88574	12	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones		
15595979	PA0782	putA	proline dehydrogenase PutA	2.52	2.05E-02	Oktansaeure	6.0	115630	19	Periplasmic	COG4230	Energy production and conversion		
15595989	PA0792	prpD	propionate catabolic protein PrpD	2.74	9.39E-03	Oktansaeure	6.6	54881	6	Cytoplasmic	COG2079	General function prediction only		
15595991	PA0794		probable aconitate hydratase	1.65	6.91E-02	Glucose	5.3	94890	10	Cytoplasmic	COG1048	Energy production and conversion		
15595992	PA0795	prpC	citrate synthase 2	1.47	2.55E-02	Oktansaeure	6.4	41689	12	Cytoplasmic	COG0372	Energy production and conversion		
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.05	7.14E-01	Oktansaeure	5.2	32137	10	Cytoplasmic	COG2513	Carbohydrate transport and metabolism		
15596001	PA0804		probable oxidoreductase	1.51	3.52E-01	Glucose	4.8	30017	2	Cytoplasmic	COG0656	General function prediction only		
15596004	PA0807	ampDh3	AmpDh3	2.83	3.59E-03	Oktansaeure	6.3	28720	2	Outer Membrane Vesicle	COG3023	Cell envelope biogenesis, outer membrane		
15596029	PA0832		conserved hypothetical protein	1.13	3.02E-01	Glucose	6.2	23483	2	Cytoplasmic	COG0491	General function prediction only		
15596030	PA0833		hypothetical protein	1.15	3.98E-01	Oktansaeure	9.0	24713	7	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane		
15596032	PA0835	pta	phosphate acetyltransferase	2.09	4.48E-04	Oktansaeure	5.0	75696	18	Periplasmic	COG0280	Energy production and conversion		
15596033	PA0836	ackA	acetate kinase	2.7	6.99E-03	Oktansaeure	7.1	42421	4	Cytoplasmic	COG0282	Energy production and conversion		
15596034	PA0837	slyD	peptidyl-prolyl cis-trans isomerase SlyD	2.5	1.16E-01	Oktansaeure	4.2	17010	3	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones		
15596035	PA0838		probable glutathione peroxidase	1.44	2.22E-01	Oktansaeure	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones		
15596037	PA0840		probable oxidoreductase	1.01	8.52E-01	Glucose	5.5	40334	10	Cytoplasmic	COG1902	Energy production and conversion		
15596045	PA0848		probable alkyl hydroperoxide reductase	1.2	4.09E-01	Glucose	5.1	21814	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones		
15596046	PA0849	trxB2	thioredoxin reductase 2	1.74	1.53E-02	Glucose	5.4	33481	2	Cytoplasmic	COG0492	Posttranslational modification, protein turnover, chaperones		
15596048	PA0851		hypothetical protein	3.27	4.17E-02	Glucose	6.8	34024	8	Cytoplasmic	COG1171	Amino acid transport and metabolism		
15596049	PA0852	cbpD	chitin-binding protein CbpD precursor	3.19	8.19E-04	Oktansaeure	6.9	41917	9	Extracellular	COG3397	Function unknown		
15596050	PA0853		probable oxidoreductase	1.85	1.57E-02	Oktansaeure	8.3	23485	6	Cytoplasmic	COG2249	General function prediction only		
15596051	PA0854	fumC2	fumarate hydratase	2.27	5.71E-04	Oktansaeure	6.1	49122	16	Cytoplasmic	COG0114	Energy production and conversion		
15596053	PA0856		hypothetical protein	1.31	4.97E-01	Glucose	10.1	19998	9	Unknown	COG3184	Function unknown		
15596055	PA0858		conserved hypothetical protein	1.28	2.29E-01	Glucose	5.7	35420	5	Cytoplasmic	COG1054	General function prediction only		
15596056	PA0859		hypothetical protein	2.65	3.00E-02	Oktansaeure	4.6	21466	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones		
15596059	PA0862		hypothetical protein	1.39	3.84E-01	Oktansaeure	6.5	29845	4	Cytoplasmic	COG5424	Coenzyme metabolism		
15596060	PA0863		probable oxidoreductase	1.34	4.63E-01	Oktansaeure	4.9	33368	4	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only	
15596062	PA0865	hpd	4-hydroxyphenylpyruvate dioxygenase	44.03	3.96E-02	Oktansaeure	4.9	39913	6	Periplasmic	COG3185	Amino acid transport and metabolism	General function prediction only	
15596064	PA0867	mliC	membrane-bound lysozyme inhibitor of c-type lysozyme MliC	1.03	8.29E-01	Oktansaeure	4.8	13695	7	Outer Membrane Vesicle	COG3895	General function prediction only		
15596067	PA0870	phhC	aromatic amino acid aminotransferase	1.66	1.54E-02	Oktansaeure	6.2	43273	6	Cytoplasmic	COG1448	Amino acid transport and metabolism		
15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	1.07	8.78E-01	Oktansaeure	6.4	13333	4	Cytoplasmic	COG2154	Coenzyme metabolism		
15596069	PA0872	phhA	phenylalanine-4-hydroxylase	9.09	8.03E-02	Oktansaeure	5.6	30322	2	Cytoplasmic	COG3186	Amino acid transport and metabolism		
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	3.13	3.75E-03	Oktansaeure	6.3	71762	31	Cytoplasmic	COG0365	Lipid metabolism		
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.37	1.63E-01	Oktansaeure	6.8	28010	19	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15596088	PA0891		hypothetical protein	1.69	5.78E-02	Oktansaeure	4.9	40214	3	Cytoplasmic	COG3608	General function prediction only		
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.18	7.83E-02	Oktansaeure	5.8	43747	23	Periplasmic	COG4992	Amino acid transport and metabolism		
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	1.55	8.80E-02	Oktansaeure	4.7	36930	5	Cytoplasmic	COG3138	Amino acid transport and metabolism		
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	1.29	3.08E-01	Oktansaeure	6.5	37245	7	Cytoplasmic	COG3138	Amino acid transport and metabolism		
15596095	PA0898	aruD	succinylglutamate 5-semialdehyde dehydrogenase	1.2	4.02E-01	Glucose	6.2	51510	7	Periplasmic	COG1012	Energy production and conversion		
15596096	PA0899	aruB	succinylarginine dihydrolase	1.04	3.51E-01	Glucose	6.2	48875	7	Periplasmic	COG3724	Amino acid transport and metabolism		
15596098	PA0901	aruE	succinylglutamate desuccinylase	1.26	1.86E-01	Oktansaeure	6.0	36909	7	Cytoplasmic	COG2988	Amino acid transport and metabolism		
15596099	PA0902		hypothetical protein	1.7	5.07E-02	Glucose	6.4	35430	10	Cytoplasmic	COG2008	Amino acid transport and metabolism		
15596100	PA0903	alaS	alanyl-tRNA synthetase	1.69	5.22E-02	Glucose	5.2	94701	43	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis		
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.7	6.49E-03	Glucose	5.0	44388	29	Cytoplasmic	COG0527	Amino acid transport and metabolism		
15596112	PA0915		conserved hypothetical protein	2.58	2.13E-02	Glucose	6.3	17514	7	Cytoplasmic	COG4807	Function unknown		
15596113	PA0916		conserved hypothetical protein	3.45	3.30E-02	Glucose	4.6	48961	2	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis		
15596123	PA0926		hypothetical protein	1.65	2.20E-01	Glucose	8.5	15829	2	Cytoplasmic				

15596129	PA0932	cysM	cysteine synthase B	1.35	2.48E-01	Glucose	5.5	32448	13	Cytoplasmic	COG0031	Amino acid transport and metabolism		
15596131	PA0934	relA	GTP pyrophosphokinase	1.47	3.16E-02	Oktansaeure	7.6	83815	24	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
15596132	PA0935		conserved hypothetical protein	1.45	3.78E-02	Oktansaeure	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only		
15596134	PA0937		conserved hypothetical protein	2.62	6.35E-02	Oktansaeure	9.7	20789	3	Cytoplasmic	COG3122	Function unknown		
15596140	PA0943		hypothetical protein	1.07	9.11E-01	Oktansaeure	8.7	27183	16	Periplasmic				
15596141	PA0944	purN	phosphoribosylaminoimidazole synthetase	1.36	9.00E-02	Glucose	7.2	24734	2	Cytoplasmic	COG0299	Nucleotide transport and metabolism		
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	1.62	2.97E-02	Glucose	4.5	37122	11	Cytoplasmic	COG0150	Nucleotide transport and metabolism		
15596144	PA0947		conserved hypothetical protein	1.28	1.17E-01	Glucose	6.0	26843	6	Cytoplasmic	COG0593	DNA replication, recombination, and repair		
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	1.89	2.61E-01	Oktansaeure	6.8	20744	7	Unknown	COG0655	General function prediction only		
15596153	PA0956	proS	prolyl-tRNA synthetase	1.11	9.58E-02	Glucose	5.1	63103	31	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis		
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	1.54	4.02E-01	Glucose	4.8	48360	9	Periplasmic				
15596156	PA0959		hypothetical protein	4.34	3.81E-01	Glucose	6.5	23069	2	Cytoplasmic	COG0537	Nucleotide transport and metabolism	Carbohydrate transport and metabolism	
15596159	PA0962		probable dna-binding stress protein	1.49	2.61E-01	Oktansaeure	4.7	17493	12	Cytoplasmic	COG0783	Inorganic ion transport and metabolism		
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.1	2.86E-01	Glucose	5.2	66207	40	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis		
15596161	PA0964	pmpR	pqsR-mediated PQS regulator, PmpR	1.04	9.75E-01	Oktansaeure	4.4	26557	4	Cytoplasmic	COG0217	Function unknown		
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.07	9.48E-01	Oktansaeure	6.1	21927	12	Cytoplasmic	COG0632	DNA replication, recombination, and repair		
15596164	PA0967	ruvB	Holliday junction DNA helicase RuvB	1.23	6.09E-01	Oktansaeure	5.2	38932	3	Cytoplasmic	COG2255	DNA replication, recombination, and repair		
15596165	PA0968		conserved hypothetical protein	2.23	7.64E-01	Glucose	8.7	16672	2	Cytoplasmic	COG0824	General function prediction only		
15596166	PA0969	tolQ	TolQ protein	1.6	3.28E-01	Oktansaeure	6.3	25250	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion		
15596169	PA0972	tolB	TolB protein	1.32	2.17E-01	Oktansaeure	9.2	47720	14	Periplasmic	COG0823	Intracellular trafficking and secretion		
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	2.17	1.12E-01	Glucose	6.3	17925	6	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane		
15596171	PA0974		conserved hypothetical protein	1.06	7.80E-01	Oktansaeure	8.7	29097	7	Outer Membrane Vesicle	COG1729	Function unknown		
15596173	PA0976		conserved hypothetical protein	1.89	8.74E-03	Glucose	4.7	23900	4	Unknown	COG0603	General function prediction only		
15596178	PA0981		hypothetical protein	1.54	4.12E-01	Oktansaeure	6.4	21871	2	Unknown				
15596192	PA0995	ogt	methylated-DNA--protein-cysteine methyltransferase	1.51	8.49E-03	Oktansaeure	7.6	19253	3	Cytoplasmic	COG0350	DNA replication, recombination, and repair		
15596194	PA0997	pqsB	PqsB	5.18	3.49E-03	Oktansaeure	4.6	30501	10	Cytoplasmic	COG0332	acyl-carrier-protein		
15596195	PA0998	pqsC	PqsC	5.63	1.09E-02	Oktansaeure	4.9	38238	11	Cytoplasmic	COG0332	acyl-carrier-protein		
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	4.53	8.07E-04	Oktansaeure	5.3	36378	19	Cytoplasmic	COG0332	acyl-carrier-protein		
15596197	PA1000	pqsE	Quinolone signal response protein	9.54	5.54E-04	Oktansaeure	5.3	34306	7	Cytoplasmic	COG0491	General function prediction only		
15596201	PA1004	nadA	quinolinate synthetase A	1.65	6.10E-03	Glucose	5.4	38418	3	Cytoplasmic	COG0379	Coenzyme metabolism		
15596202	PA1005		conserved hypothetical protein	2.43	1.80E-02	Oktansaeure	8.4	52994	5	Periplasmic	COG4783	General function prediction only		
15596205	PA1008	bcp	bacterioferritin comigratory protein	1.28	3.49E-01	Glucose	7.3	17352	12	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones		
15596206	PA1009		hypothetical protein	2.41	7.29E-02	Oktansaeure	5.6	20585	4	Cytoplasmic	COG2716	Amino acid transport and metabolism		
15596207	PA1010	dapA	dihydrodipicolinate synthase	1.17	4.20E-01	Glucose	6.4	31449	27	Periplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane	
15596208	PA1011		hypothetical protein	1.2	4.23E-02	Glucose	4.7	43055	10	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane		
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.36	9.38E-02	Glucose	5.1	26831	18	Periplasmic	COG0152	Nucleotide transport and metabolism		
15596220	PA1023		probable short-chain dehydrogenase	1.61	1.29E-01	Oktansaeure	6.7	32821	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15596223	PA1026		hypothetical protein	1.98	1.29E-01	Glucose	4.8	17184	3	Cytoplasmic				
15596224	PA1027		probable aldehyde dehydrogenase	1.06	9.76E-01	Glucose	6.8	57291	3	Cytoplasmic	COG1012	Energy production and conversion		
15596230	PA1033		probable glutathione S-transferase	1.67	1.26E-01	Oktansaeure	6.8	24527	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
15596233	PA1036		hypothetical protein	1.4	3.16E-01	Oktansaeure	4.6	19537	2	Unknown				
15596236	PA1039		conserved hypothetical protein	1.38	3.21E-01	Oktansaeure	6.7	17189	2	Unknown	COG3012	Function unknown		
15596237	PA1040		hypothetical protein	1.02	7.72E-01	Oktansaeure	6.0	18721	5	Unknown				
15596240	PA1043		hypothetical protein	1.33	2.83E-01	Glucose	8.2	27276	3	Periplasmic				
15596244	PA1047		probable esterase	1.35	1.93E-02	Oktansaeure	6.1	42335	6	Periplasmic	COG1680	Defense mechanisms		
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	1.94	1.05E-02	Oktansaeure	6.8	24860	7	Cytoplasmic	COG0259	Coenzyme metabolism		
15596250	PA1053		conserved hypothetical protein	1.31	3.16E-02	Glucose	10.1	15649	3	Outer Membrane Vesicle	COG3133	Cell envelope biogenesis, outer membrane		
15596258	PA1061		conserved hypothetical protein	1.15	3.34E-01	Glucose	6.6	39952	15	Cytoplasmic	COG0031	Amino acid transport and metabolism		
15596259	PA1062		hypothetical protein	1.45	3.99E-01	Glucose	6.5	19155	4	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane		
15596261	PA1064		hypothetical protein	1.11	6.83E-01	Oktansaeure	5.1	24172	2	Periplasmic	COG3650	Function unknown		
15596263	PA1066		probable short-chain dehydrogenase	2.04	1.79E-02	Oktansaeure	7.6	23376	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15596266	PA1069		hypothetical protein	1.19	3.75E-01	Glucose	4.3	86114	28	Cytoplasmic				
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	1.56	1.38E-01	Oktansaeure	5.5	39769	18	Periplasmic	COG0683	Amino acid transport and metabolism		
15596285	PA1088		hypothetical protein	1.1	4.84E-01	Glucose	4.8	28800	2	Cytoplasmic	COG2226	Coenzyme metabolism		
15596286	PA1089		conserved hypothetical protein	1.04	6.31E-01	Glucose	5.0	22471	4	Cytoplasmic	COG0560	Amino acid transport and metabolism		
15596287	PA1090		hypothetical protein	1.4	2.34E-01	Oktansaeure	5.3	24703	4	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane		
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	1	9.85E-01	Glucose	5.2	187155	19	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane		
15596289	PA1092	fliC	flagellin type B	1.34	1.43E-01	Oktansaeure	5.2	49242	10	Periplasmic	COG1344	Cell motility and secretion		
15596291	PA1094	fliD	flagellar capping protein FliD	1.09	5.91E-01	Oktansaeure	7.1	49449	10	Periplasmic	COG1345	Cell motility and secretion		
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.11	1.41E-02	Oktansaeure	5.0	55277	10	Cytoplasmic	COG2204	Signal transduction mechanisms		
15596321	PA1124	dgt	deoxyguanosinetriphosphate triphosphohydrolase	2.58	4.09E-02	Oktansaeure	6.5	56741	1	Cytoplasmic	COG0232	Nucleotide transport and metabolism		
15596324	PA1127		probable oxidoreductase	4.5	4.96E-04	Glucose	5.2	36474	8	Cytoplasmic	COG0667	Energy production and conversion		
15596332	PA1135		conserved hypothetical protein	2.99	3.10E-02	Oktansaeure	6.4	31898	9	Cytoplasmic	COG0693	General function prediction only		
15596336	PA1139		hypothetical protein	1.3	3.17E-01	Oktansaeure	5.1	29336	2	Periplasmic	COG2340	Function unknown		
15596337	PA1140		conserved hypothetical protein	1.4	2.18E-01	Oktansaeure	6.3	31614	4	Cytoplasmic	COG3257	General function prediction only		
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucleotide reductase	1.96	7.73E-02	Glucose	4.5	47386	19	Periplasmic	COG0208	Nucleotide transport and metabolism		
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	2.11	1.46E-02	Glucose	5.7	107105	59	Periplasmic	COG0209	Nucleotide transport and metabolism		
15596354	PA1157		probable two-component response regulator	1.02	9.43E-01	Oktansaeure	4.7	26373	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15596358	PA1161	rrmA	rRNA methyltransferase	1.05	6.90E-01	Glucose	7.9	29644	5	Cytoplasmic	COG2226	Coenzyme metabolism		
15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	1.08	5.01E-01	Oktansaeure	5.0	41077	10	Cytoplasmic	COG0624	Amino acid transport and metabolism		
15596362	PA1165	pcpS	PcpS	1.22	4.31E-01	Glucose	7.0	26715	4	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism		
15596363	PA1166		hypothetical protein	4.83	3.95E-03	Oktansaeure	7.3	28156	6	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism		
15596366	PA1169		probable lipoxygenase	2.23	7.08E-01	Oktansaeure	6.8	74803	4	Periplasmic				
15596368	PA1171		probable transglycolase	2.2	7.50E-04	Oktansaeure	9.3	42682	7	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane		
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	19.37	2.88E-03	Oktansaeure	8.6	92942	9	Periplasmic	COG0243	Energy production and conversion		
15596376	PA1179	phoP	two-component response regulator PhoP	1.25	1.98E-01	Oktansaeure	5.2	25650	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15596385	PA1188		hypothetical protein	4.81	5.72E-02	Oktansaeure	6.0	42128	2	Cytoplasmic	COG1804	Energy production and conversion		
15596389	PA1192		conserved hypothetical protein	1.64	2.16E-02	Glucose	6.5	31260	6	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning		
15596390	PA1193		hypothetical protein	1.47	2.78E-01	Glucose	9.1	25292	6	Cytoplasmic	COG2818	DNA replication, recombination, and repair		
15596397	PA1200		conserved hypothetical protein	1.45	2.40E-01	Oktansaeure	5.1	24597	4	Cytoplasmic	COG4122	General function prediction only		
15596399	PA1202		probable hydrolase	2.83	6.47E-02	Oktansaeure	4.8	22471	12	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15596401	PA1204		conserved hypothetical protein	1.56	1.59E-01	Oktansaeure	6.5	20224	5	Cytoplasmic	COG0431	General function prediction only		
15596403	PA1206		hypothetical protein	1.02	8.03E-01	Oktansaeure	4.4	17690	7	Cytoplasmic				
15596413	PA1216		hypothetical protein	12.73	3.75E-03	Oktansaeure	6.1	28573	9	Cytoplasmic	COG4976	General function prediction only		
15596422	PA1225		probable NAD(P)H dehydrogenase	1.96	7.10E-02	Glucose	7.0	22551	6	Cytoplasmic	COG2249	General function prediction only		
15596431	PA1234		hypothetical protein	1.09	2.73E-01	Oktansaeure	4.6	18460	2	Cytoplasmic				
15596469	PA1272	cobO	cob(I)alamin adenosyltransferase	1.99	1.46E-01	Oktansaeure	8.0	22292	7	Cytoplasmic	COG2109	Coenzyme metabolism		
15596473	PA1276	cobC	cobalamin biosynthetic protein CobC	1.67	9.20E-02	Glucose	8.0	36657	2	Cytoplasmic	COG0079	Amino acid transport and metabolism		
15596475	PA1278	cobP	cobinamide kinase	2	5.20E-02	Glucose	5.4	18862	3	Cytoplasmic	COG2087	Coenzyme metabolism		
15596476	PA1279	cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.45	1.04E-01	Glucose	6.6	36531	4	Cytoplasmic	COG2038	Coenzyme metabolism		
15596477	PA1280		hypothetical protein	1.52	2.37E-01	Oktansaeure	6.7	21591	4	Cytoplasmic	COG0406	General function prediction only		

15596480	PA1283		probable transcriptional regulator	1.67	1.46E-02	Oktansaeure	4.9	20307	3	Unknown	COG1309	Transcription	
15596484	PA1287		probable glutathione peroxidase	1.16	5.01E-01	Oktansaeure	8.3	20217	10	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596485	PA1288		probable outer membrane protein precursor	2.62	1.06E-02	Oktansaeure	6.0	45561	10	Periplasmic	COG2067	Lipid metabolism	
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	1.34	2.09E-01	Oktansaeure	5.3	30597	13	Periplasmic	COG2897	Inorganic ion transport and metabolism	
15596491	PA1294	rnd	ribonuclease D	1.1	4.77E-01	Oktansaeure	4.8	43066	7	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
15596493	PA1296		probable 2-hydroxyacid dehydrogenase	1	6.04E-01	Oktansaeure	5.6	33730	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596501	PA1304		probable oligopeptidase	1.01	9.76E-01	Glucose	4.7	75881	21	Periplasmic	COG1770	Amino acid transport and metabolism	
15596504	PA1307		conserved hypothetical protein	1.86	1.17E-01	Oktansaeure	5.7	28544	3	Cytoplasmic	COG0121	General function prediction only	
15596521	PA1324		hypothetical protein	3.35	4.12E-03	Oktansaeure	5.8	18303	3	Unknown			
15596523	PA1326	ilvA2	threonine dehydratase, biosynthetic	5.79	3.60E-03	Glucose	6.5	55903	2	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15596534	PA1337	ansB	glutaminase-asparaginase	1.78	4.69E-03	Oktansaeure	7.3	38644	12	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	1.69	5.50E-02	Glucose	6.2	59874	9	Periplasmic	COG0405	Amino acid transport and metabolism	
15596539	PA1342		probable binding protein component of ABC transporter	1.4	4.54E-01	Oktansaeure	8.6	33054	38	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596541	PA1344		probable short-chain dehydrogenase	2.59	2.11E-02	Oktansaeure	4.9	27397	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596554	PA1357		conserved hypothetical protein	1.66	1.90E-02	Glucose	5.3	16789	2	Cytoplasmic	COG2606	Function unknown	
15596564	PA1367		hypothetical protein	1.07	6.42E-01	Glucose	4.5	29789	2	Cytoplasmic	COG0384	General function prediction only	
15596567	PA1370		hypothetical protein	1.17	6.69E-01	Oktansaeure	6.3	69499	2	Cytoplasmic			
15596568	PA1371		hypothetical protein	1.22	6.61E-01	Oktansaeure	5.2	27419	2	Unknown	COG5619	Function unknown	
15596569	PA1372		hypothetical protein	1.1	5.58E-01	Oktansaeure	5.5	79820	20	Cytoplasmic	COG3972	General function prediction only	
15596572	PA1375	pdxB	erythronate-4-phosphate dehydrogenase	1.25	1.30E-01	Oktansaeure	5.5	41001	3	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	1.45	2.57E-01	Oktansaeure	5.0	66760	14	Cytoplasmic	COG4579	Signal transduction mechanisms	
15596574	PA1377		conserved hypothetical protein	1.09	8.02E-01	Glucose	7.9	20068	6	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596599	PA1402		hypothetical protein	4.76	2.42E-02	Oktansaeure	4.7	23753	5	Cytoplasmic	COG4122	General function prediction only	
15596627	PA1430	lasR	transcriptional regulator LasR	1.94	4.17E-02	Oktansaeure	6.5	26618	11	Cytoplasmic	COG2771	Transcription	
15596637	PA1440		hypothetical protein	1.44	2.01E-01	Oktansaeure	3.9	22382	3	Cytoplasmic	COG3318	General function prediction only	
15596639	PA1442		conserved hypothetical protein	1.55	1.55E-01	Glucose	10.3	18760	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
15596640	PA1443	fliM	flagellar motor switch protein FliM	1.11	4.25E-01	Glucose	5.0	36282	3	Cytoplasmic	COG1868	Cell motility and secretion	
15596641	PA1444	fliN	flagellar motor switch protein FliN	2.33	1.46E-01	Oktansaeure	4.0	16620	4	Cytoplasmic Membrane	COG1886	Cell motility and secretion	Intracellular trafficking and secretion
15596651	PA1454	fleN	flagellar synthesis regulator FleN	2.04	3.20E-01	Oktansaeure	8.7	30037	2	Cytoplasmic Membrane	COG0455	Cell motility	
15596652	PA1455	fliA	sigma factor FliA	1.4	1.74E-01	Oktansaeure	5.9	27522	4	Cytoplasmic	COG1191	Transcription	
15596654	PA1457	cheZ	chemotaxis protein CheZ	1.15	5.61E-01	Oktansaeure	4.6	29622	11	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
15596655	PA1458		probable two-component sensor	1.05	8.36E-01	Glucose	4.3	79737	20	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15596656	PA1459		probable methyltransferase	1.1	3.86E-01	Oktansaeure	8.6	39004	11	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
15596659	PA1462		probable plasmid partitioning protein	1.35	1.83E-01	Oktansaeure	10.1	28407	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
15596661	PA1464		probable purine-binding chemotaxis protein	1.11	5.97E-01	Glucose	4.1	17536	12	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15596667	PA1470		probable short-chain dehydrogenase	7.33	1.14E-02	Oktansaeure	4.9	25365	7	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596669	PA1472		conserved hypothetical protein	1	8.10E-01	Oktansaeure	5.8	21138	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	1.59	3.40E-02	Oktansaeure	8.6	36485	17	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15596692	PA1495		hypothetical protein	1.62	8.09E-02	Oktansaeure	5.9	23443	2	Unknown	COG4339	Function unknown	
15596706	PA1509		hypothetical protein	7.1	1.75E-04	Oktansaeure	6.8	42364	6	Cytoplasmic			
15596707	PA1510		hypothetical protein	8.68	3.68E-04	Oktansaeure	5.1	63320	11	Unknown			
15596708	PA1511		conserved hypothetical protein	29.75	2.12E-04	Oktansaeure	6.4	93635	8	Cytoplasmic	COG3501	Function unknown	
15596713	PA1516		hypothetical protein	4.29	4.93E-03	Oktansaeure	4.8	18896	6	Cytoplasmic	COG3195	Function unknown	
15596723	PA1526		probable transcriptional regulator	3.09	7.06E-02	Oktansaeure	7.8	25070	3	Cytoplasmic	COG1802	Transcription	
15596724	PA1527		conserved hypothetical protein	1.07	9.28E-01	Glucose	4.8	131580	10	Cytoplasmic	COG1196	Cell division and chromosome partitioning	
15596725	PA1528	zipA	cell division protein ZipA	1.64	8.29E-03	Oktansaeure	5.7	32236	3	Outer Membrane Vesicle	COG3115	Cell division and chromosome partitioning	
15596726	PA1529	lig	DNA ligase	1.44	2.31E-01	Glucose	5.1	86767	21	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	1.41	3.92E-02	Glucose	4.4	73309	12	Cytoplasmic	COG2812	DNA replication, recombination, and repair	
15596731	PA1534	recR	recombination protein RecR	1.24	8.80E-01	Oktansaeure	6.0	21173	7	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.23	3.68E-01	Glucose	4.6	19804	8	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15596741	PA1544	anr	transcriptional regulator Anr	1.17	4.52E-01	Glucose	5.2	27129	8	Cytoplasmic	COG0664	Signal transduction mechanisms	
15596747	PA1550		hypothetical protein	5.72	3.70E-02	Oktansaeure	5.1	20338	2	Outer Membrane Vesicle	COG3198	Function unknown	
15596749	PA1552	ccoP1	Cytochrome c oxidase, cbb3-type, CcoP subunit	2.12	8.92E-02	Glucose	6.0	34644	2	Outer Membrane Vesicle	COG2010	Energy production and conversion	
15596750	PA1553	ccoO1	Cytochrome c oxidase, cbb3-type, CcoO subunit	1.4	4.80E-01	Oktansaeure	8.2	22758	7	Outer Membrane Vesicle	COG2993	Energy production and conversion	
15596759	PA1562	acnA	aconitate hydratase 1	1.11	5.15E-01	Oktansaeure	5.4	99147	38	Cytoplasmic	COG1048	Energy production and conversion	
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	1.4	2.61E-01	Oktansaeure	5.2	30777	11	Cytoplasmic	COG2084	Lipid metabolism	
15596776	PA1579		hypothetical protein	4.52	4.47E-03	Oktansaeure	8.2	22110	13	Periplasmic			
15596777	PA1580	gltA	citrate synthase	1.49	5.56E-04	Oktansaeure	7.0	47695	27	Periplasmic	COG0372	Energy production and conversion	
15596778	PA1581	sdhC	succinate dehydrogenase (C subunit)	2.05	4.99E-03	Glucose	10.4	13738	3	Outer Membrane Vesicle	COG2009	Energy production and conversion	
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	1.24	2.27E-01	Oktansaeure	6.5	63532	29	Periplasmic	COG1053	Energy production and conversion	
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	2.04	4.77E-02	Glucose	6.9	26155	12	Outer Membrane Vesicle	COG0479	Energy production and conversion	
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	1.62	2.83E-01	Glucose	6.5	105877	47	Outer Membrane Vesicle	COG0567	Energy production and conversion	
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	1.11	8.89E-01	Glucose	5.2	42887	22	Periplasmic	COG0508	Energy production and conversion	
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.27	2.30E-01	Oktansaeure	7.0	50165	23	Periplasmic	COG1249	Energy production and conversion	
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	1.23	3.39E-02	Glucose	6.1	41542	28	Periplasmic	COG0045	Energy production and conversion	
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	1.45	8.36E-02	Glucose	6.0	30266	27	Periplasmic	COG0074	Energy production and conversion	
15596790	PA1593		hypothetical protein	1.48	1.96E-01	Glucose	6.3	16817	2	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596793	PA1596	htpG	heat shock protein HtpG	1.17	1.44E-01	Glucose	4.9	71667	52	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596794	PA1597		hypothetical protein	1.19	3.36E-01	Glucose	5.9	25791	12	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.48	1.23E-01	Glucose	5.3	42806	18	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	1.83	4.39E-02	Glucose	6.9	18747	11	Cytoplasmic	COG0764	Lipid metabolism	
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.13	5.83E-01	Oktansaeure	6.2	36773	16	Cytoplasmic	COG0240	Energy production and conversion	
15596813	PA1616		conserved hypothetical protein	1.01	9.38E-01	Glucose	6.4	16715	5	Unknown	COG2062	Signal transduction mechanisms	
15596815	PA1618		conserved hypothetical protein	1.74	4.03E-01	Glucose	7.0	15595	7	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596820	PA1623		conserved hypothetical protein	1.95	5.35E-02	Oktansaeure	6.1	24924	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596821	PA1624		hypothetical protein	1.6	1.42E-02	Oktansaeure	6.4	29533	5	Periplasmic			
15596836	PA1639		hypothetical protein	3.66	4.79E-03	Oktansaeure	5.4	22457	5	Periplasmic			
15596839	PA1642	selD	selenophosphate synthetase	1.25	3.67E-01	Glucose	4.7	36354	12	Cytoplasmic	COG0709	Amino acid transport and metabolism	
15596841	PA1644		conserved hypothetical protein	1.23	4.73E-01	Glucose	5.5	21838	6	Unknown	COG1853	General function prediction only	
15596845	PA1648		probable oxidoreductase	2.16	7.37E-03	Oktansaeure	6.1	36168	4	Cytoplasmic	COG2130	General function prediction only	
15596851	PA1654		probable aminotransferase	1	9.06E-01	Glucose	5.3	43311	4	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
15596852	PA1655		probable glutathione S-transferase	2.84	4.29E-02	Oktansaeure	5.3	22738	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596854	PA1657		conserved hypothetical protein	7.78	1.96E-04	Oktansaeure	4.5	18165	8	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15596855	PA1658		conserved hypothetical protein	7.95	1.21E-05	Oktansaeure	5.1	55560	11	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15596859	PA1662		probable ClpA/B-type protease	22.14	5.84E-04	Oktansaeure	5.5	95774	29	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15596863	PA1666		hypothetical protein	20.7	6.49E-04	Oktansaeure	7.4	18440	3	Unknown	COG3521	Intracellular trafficking, secretion, and vesicular transport	
15596864	PA1667		hypothetical protein	25.01	7.70E-04	Oktansaeure	6.5	49689	5	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15596870	PA1673		hypothetical protein	40.64	1.46E-03	Oktansaeure	6.2	17853	5	Cytoplasmic	COG2703	Inorganic ion transport and metabolism	
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.35	2.97E-01	Glucose	7.6	20236	11	Outer Membrane Vesicle	COG0302	Coenzyme metabolism	
15596874	PA1677		conserved hypothetical protein	1.93	3.62E-02	Oktansaeure	6.5	21034	12	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596875	PA1678		probable DNA methylase	1.04	8.89E-01	Oktansaeure	4.4	34229	5	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	

15596878	PA1681	aroC	chorismate synthase	1.24	5.51E-01	Oktansaeure	6.6	38987	7	Cytoplasmic	COG0082	Amino acid transport and metabolism	
15596880	PA1683		probable sugar aldolase	1.45	2.10E-01	Oktansaeure	6.5	22868	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	2.84	1.50E-02	Oktansaeure	5.0	20552	8	Cytoplasmic	COG1791	Function unknown	
15596883	PA1686	alkA	DNA-3-methyladenine glycosidase II	1.14	3.98E-01	Oktansaeure	6.9	32211	2	Unknown	COG0122	DNA replication, recombination, and repair	
15596884	PA1687	speE	spermidine synthase	1.44	1.62E-01	Glucose	4.9	32238	8	Periplasmic	COG0421	Amino acid transport and metabolism	
15596923	PA1726	bglX	periplasmic beta-glucosidase	1.3	1.21E-01	Glucose	7.1	83003	7	Periplasmic	COG1472	Carbohydrate transport and metabolism	
15596930	PA1733		conserved hypothetical protein	2.78	2.55E-02	Oktansaeure	5.3	26467	2	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones	
15596931	PA1734		hypothetical protein	3.63	2.67E-01	Oktansaeure	8.2	30246	2	Unknown	COG2857	Energy production and conversion	
15596933	PA1736		probable acyl-CoA thiolase	11.21	9.26E-04	Oktansaeure	5.3	42102	6	Cytoplasmic	COG0183	Lipid metabolism	
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	8.22	5.53E-05	Oktansaeure	6.7	76666	30	Cytoplasmic	COG1250	Lipid metabolism	
15596939	PA1742	pauD2	Glutamine amidotransferase class I	1.03	9.25E-01	Oktansaeure	5.0	27361	5	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
15596943	PA1746		hypothetical protein	299.26	1.19E-03	Oktansaeure	6.6	18189	5	Outer Membrane Vesicle	COG2110	General function prediction only	
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	6.66	1.84E-03	Oktansaeure	7.8	24412	13	Cytoplasmic	COG1024	Lipid metabolism	
15596946	PA1749		hypothetical protein	1.25	4.38E-01	Oktansaeure	10.0	17672	2	Unknown	COG2388	General function prediction only	
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.02	8.45E-01	Oktansaeure	6.5	39132	13	Cytoplasmic	COG0722	Amino acid transport and metabolism	
15596949	PA1752		hypothetical protein	1.37	2.30E-01	Oktansaeure	6.7	34141	11	Cytoplasmic	COG1893	Coenzyme metabolism	
15596950	PA1753		conserved hypothetical protein	2.91	2.00E-01	Oktansaeure	4.7	18372	4	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596951	PA1754	cysB	transcriptional regulator CysB	2.7	2.31E-02	Oktansaeure	7.0	36110	7	Periplasmic	COG0583	Transcription	
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	2.21	4.83E-04	Glucose	6.4	30215	8	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15596954	PA1757	thrH	homoserine kinase	1.03	8.62E-01	Oktansaeure	5.0	23501	10	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596956	PA1759		probable transcriptional regulator	2.93	8.69E-02	Oktansaeure	6.3	101111	10	Unknown	COG2909	Transcription	
15596957	PA1760		probable transcriptional regulator	3.65	3.76E-01	Oktansaeure	6.8	101628	4	Cytoplasmic	COG2909	Transcription	
15596965	PA1768		hypothetical protein	1.26	2.66E-01	Oktansaeure	9.6	19720	6	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15596966	PA1769		conserved hypothetical protein	1.17	3.74E-01	Glucose	6.1	31074	12	Cytoplasmic	COG1806	Function unknown	
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.58	9.67E-02	Glucose	4.8	85798	73	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
15596969	PA1772		probable methyltransferase	4.17	6.50E-05	Oktansaeure	4.6	17404	8	Cytoplasmic	COG0684	Coenzyme metabolism	
15596972	PA1775	cmpX	conserved cytoplasmic membrane protein, CmpX protein	1.12	6.05E-01	Oktansaeure	8.8	29019	3	Outer Membrane Vesicle			
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precursor	1.11	7.59E-01	Glucose	4.8	37639	15	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596984	PA1787	acnB	aconitate hydratase 2	1.39	1.64E-01	Glucose	5.0	93595	68	Periplasmic	COG1049	Energy production and conversion	
15596986	PA1789		hypothetical protein	5.8	6.80E-04	Oktansaeure	5.3	31273	12	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596987	PA1790		hypothetical protein	1.9	6.73E-02	Oktansaeure	6.7	23312	5	Cytoplasmic	COG4445	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	1.11	7.92E-01	Glucose	6.2	18126	12	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.39	1.76E-01	Glucose	5.6	62912	35	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	1.53	1.24E-01	Glucose	5.4	51245	16	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis	
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase	1.2	3.16E-01	Glucose	5.8	30549	12	Periplasmic	COG0190	Coenzyme metabolism	
15596997	PA1800	tig	trigger factor	1.18	2.35E-01	Glucose	4.5	48582	29	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
15596998	PA1801	clpP	ClpP	1.5	7.10E-02	Oktansaeure	6.4	23502	15	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15596999	PA1802	clpX	ClpX	1.64	5.91E-03	Glucose	4.8	46991	24	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
15597000	PA1803	lon	Lon protease	1.19	5.69E-01	Glucose	6.0	88647	33	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15597001	PA1804	hupB	DNA-binding protein HU	1.12	5.59E-01	Oktansaeure	10.8	9054	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	1.5	1.54E-01	Oktansaeure	4.7	68741	6	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	1.23	2.45E-01	Oktansaeure	5.7	28006	7	Cytoplasmic Membrane	COG0623	acyl-carrier-protein	
15597007	PA1810		probable binding protein component of ABC transporter	1.31	1.38E-01	Oktansaeure	6.5	70473	17	Periplasmic	COG4166	Amino acid transport and metabolism	
15597010	PA1813		probable hydroxyacylglutathione hydrolase	1.04	8.47E-01	Oktansaeure	6.3	28865	3	Cytoplasmic	COG0491	General function prediction only	
15597012	PA1815	rnhA	ribonuclease H	1.32	1.81E-01	Glucose	8.7	16697	6	Unknown	COG0328	DNA replication, recombination, and repair	
15597013	PA1816	dnaQ	DNA polymerase III, epsilon chain	1.51	4.02E-02	Glucose	5.0	26814	8	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	1.5	6.79E-03	Oktansaeure	6.1	82757	13	Cytoplasmic	COG1982	Amino acid transport and metabolism	
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	1.43	9.28E-01	Oktansaeure	5.4	29957	4	Cytoplasmic	COG1024	Lipid metabolism	
15597019	PA1822	fimL	hypothetical protein	1.3	3.13E-01	Glucose	4.9	60868	4	Cytoplasmic			
15597020	PA1823		conserved hypothetical protein	1.02	8.32E-01	Glucose	4.9	31356	4	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
15597025	PA1828		probable short-chain dehydrogenase	1.61	1.06E-02	Oktansaeure	7.4	26919	14	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597026	PA1829		hypothetical protein	2.38	1.84E-03	Oktansaeure	5.9	40833	7	Cytoplasmic	COG3173	General function prediction only	
15597028	PA1831		hypothetical protein	2.21	3.32E-03	Oktansaeure	6.3	26378	7	Cytoplasmic	COG0406	General function prediction only	
15597030	PA1833		probable oxidoreductase	1.59	1.24E-02	Oktansaeure	5.2	34552	11	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597033	PA1836		probable transcriptional regulator	5.12	3.23E-03	Oktansaeure	7.0	21316	2	Cytoplasmic	COG1309	Transcription	
15597034	PA1837		hypothetical protein	1.67	5.00E-03	Glucose	4.7	18765	6	Cytoplasmic	COG3749	Function unknown	
15597035	PA1838	cysI	sulfite reductase	1.53	6.83E-02	Glucose	5.9	62132	23	Periplasmic	COG0155	Inorganic ion transport and metabolism	
15597038	PA1841		hypothetical protein	1.4	3.69E-02	Glucose	5.1	18654	7	Cytoplasmic	COG3760	Function unknown	
15597040	PA1843	metH	methionine synthase	1.69	3.40E-02	Glucose	4.6	135062	44	Periplasmic	COG1410	Amino acid transport and metabolism	
15597041	PA1844	tse1	Tse1	1.14	6.31E-01	Oktansaeure	8.8	16443	2	Extracellular			
15597042	PA1845		hypothetical protein	4.14	3.29E-02	Oktansaeure	4.6	18757	3	Unknown			
15597043	PA1846	cti	cis/trans isomerase	1.13	4.00E-01	Glucose	6.0	86517	11	Periplasmic			
15597044	PA1847	nfuA	NfuA	1.21	5.94E-01	Oktansaeure	4.2	21136	10	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	1.73	7.84E-02	Glucose	6.8	26377	2	Periplasmic	COG0725	Inorganic ion transport and metabolism	
15597077	PA1880		probable oxidoreductase	1.71	2.11E-03	Oktansaeure	7.4	77656	6	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597084	PA1887		hypothetical protein	765.03	2.71E-02	Oktansaeure	8.0	24376	3	Unknown			
15597087	PA1890		probable glutathione S-transferase	2.26	2.70E-02	Oktansaeure	7.0	23440	12	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597089	PA1892		hypothetical protein	5.47	4.26E-02	Glucose	7.1	27699	2	Unknown			
15597091	PA1894		hypothetical protein	1.01	8.53E-01	Oktansaeure	5.3	26179	12	Unknown			
15597099	PA1902	phzD2	phenazine biosynthesis protein PhzD	4.72	3.26E-01	Oktansaeure	5.6	23195	3	Unknown	COG1535	Secondary metabolites biosynthesis, transport, and catabolism	
15599411	PA1905	phzG2	probable pyridoxamine 5'-phosphate oxidase	25.23	1.70E-03	Oktansaeure	6.4	24367	3	Cytoplasmic	COG0259	Coenzyme metabolism	
15597109	PA1913		hypothetical protein	2.04	1.29E-01	Oktansaeure	8.4	25410	2	Unknown			
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	4.44	6.91E-04	Oktansaeure	5.7	86211	22	Cytoplasmic	COG0620	Amino acid transport and metabolism	
15597126	PA1930		probable chemotaxis transducer	220.86	2.61E-02	Oktansaeure	6.5	47801	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	6.47	5.81E-02	Oktansaeure	8.4	33860	6	Periplasmic	COG1879	Carbohydrate transport and metabolism	
15597145	PA1949	rbsR	ribose operon repressor RbsR	1.61	3.49E-02	Oktansaeure	7.2	36446	5	Cytoplasmic	COG1609	Transcription	
15597146	PA1950	rbsK	ribokinase	1.14	4.98E-01	Oktansaeure	4.9	31846	4	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597160	PA1964		probable ATP-binding component of ABC transporter	1.84	3.60E-02	Glucose	4.8	57917	14	Cytoplasmic	COG0488	General function prediction only	
15597190	PA1994		hypothetical protein	2.8	1.18E-02	Oktansaeure	4.7	21561	6	Cytoplasmic	COG3554	Function unknown	
15597193	PA1997		probable AMP-binding enzyme	4.62	9.35E-03	Oktansaeure	6.5	71929	5	Cytoplasmic	COG0365	Lipid metabolism	
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	29.32	7.61E-05	Oktansaeure	5.0	25244	5	Cytoplasmic	COG1788	Lipid metabolism	
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	23.88	2.87E-04	Oktansaeure	4.6	23187	15	Cytoplasmic	COG2057	Lipid metabolism	
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	12.35	9.78E-06	Oktansaeure	6.4	40405	22	Cytoplasmic	COG0183	Lipid metabolism	
15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase	23.84	1.14E-04	Oktansaeure	5.6	26727	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597203	PA2007	maiA	maleylacetoacetate isomerase	1.46	3.68E-01	Oktansaeure	6.9	23685	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597204	PA2008	fahA	fumarylacetoacetase	4.29	9.27E-02	Oktansaeure	6.0	46341	3	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase	1.08	6.25E-01	Glucose	6.0	31837	4	Cytoplasmic	COG0119	Amino acid transport and metabolism	
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containing)	2.44	8.29E-02	Oktansaeure	5.6	71282	2	Cytoplasmic	COG4770	Lipid metabolism	
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase	1.24	5.18E-01	Oktansaeure	5.2	28947	5	Cytoplasmic	COG1024	Lipid metabolism	
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase	2.13	2.89E-02	Oktansaeure	5.5	42209	3	Cytoplasmic	COG1960	Lipid metabolism	
15597216	PA2020		probable transcriptional regulator	2.84	6.03E-02	Oktansaeure	7.1	23695	3	Cytoplasmic	COG1309	Transcription	

15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase	1.13	6.91E-01	Oktansaeure	5.1	31236	23	Periplasmic	COG1210	Cell envelope biogenesis, outer membrane	
15597221	PA2025	gor	glutathione reductase	2.11	7.42E-04	Oktansaeure	6.3	49237	13	Cytoplasmic	COG1249	Energy production and conversion	
15597230	PA2034		hypothetical protein	3.92	1.98E-02	Oktansaeure	6.3	24525	7	Cytoplasmic	COG2242	Coenzyme metabolism	
15597240	PA2044		hypothetical protein	1.59	4.93E-02	Glucose	6.1	70083	18	Periplasmic	COG1305	Amino acid transport and metabolism	
15597267	PA2071	fusA2	elongation factor G	2.67	2.62E-02	Oktansaeure	4.9	77574	17	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15597272	PA2076		probable transcriptional regulator	2.38	2.81E-02	Glucose	6.0	32458	4	Cytoplasmic	COG0583	Transcription	
15597276	PA2080	kynU	kynureninase KynU	1.65	4.08E-03	Oktansaeure	5.3	46294	7	Cytoplasmic	COG3844	Amino acid transport and metabolism	
15597277	PA2081	kynB	kynurenine formamidase, KynB	2.61	1.16E-01	Oktansaeure	5.2	23152	3	Cytoplasmic	COG1878	Amino acid transport and metabolism	
15597278	PA2082	kynR	KynR	1.04	7.66E-01	Oktansaeure	6.5	17846	4	Cytoplasmic	COG1522	Transcription	
15597315	PA2119		alcohol dehydrogenase (Zn-dependent)	46.63	7.19E-04	Oktansaeure	5.4	38561	4	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
15597380	PA2184		conserved hypothetical protein	4.65	5.59E-03	Oktansaeure	4.7	18990	2	Cytoplasmic	COG3685	Function unknown	
15597393	PA2197		conserved hypothetical protein	1.93	3.27E-05	Oktansaeure	6.3	37135	14	Cytoplasmic	COG2130	General function prediction only	
15597394	PA2198		hypothetical protein	1.42	2.03E-01	Oktansaeure	5.2	12944	6	Cytoplasmic	COG1359	Function unknown	
15597395	PA2199		probable dehydrogenase	1.78	4.61E-02	Oktansaeure	5.4	30886	10	Cytoplasmic	COG2084	Lipid metabolism	
15597400	PA2204		probable binding protein component of ABC transporter	1.68	4.02E-02	Oktansaeure	9.7	29309	18	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15597418	PA2222		hypothetical protein	2.36	4.40E-02	Oktansaeure	5.0	23441	5	Unknown			
15597425	PA2229		conserved hypothetical protein	1.03	9.53E-01	Oktansaeure	6.5	26560	7	Cytoplasmic	COG2258	Function unknown	
15597428	PA2232	pslB	PslB	1.13	4.35E-01	Oktansaeure	6.0	53515	13	Periplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15597449	PA2253	ansA	L-asparaginase I	1.15	4.36E-01	Glucose	5.3	34755	4	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15597455	PA2259	ptxS	transcriptional regulator PtxS	12.29	3.59E-03	Glucose	6.9	37359	3	Cytoplasmic	COG1609	Transcription	
15597456	PA2260		hypothetical protein	36.54	2.86E-06	Glucose	6.0	28980	16	Cytoplasmic			
15597457	PA2261		probable 2-ketogluconate kinase	37.55	1.25E-04	Glucose	5.7	34041	10	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597459	PA2263		probable 2-hydroxyacid dehydrogenase	58.92	1.91E-05	Glucose	8.7	35615	19	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15597460	PA2264		conserved hypothetical protein	17.02	5.50E-04	Glucose	5.4	26359	3	Outer Membrane Vesicle			
15597461	PA2265		gluconate dehydrogenase	9.75	1.03E-03	Glucose	7.3	64716	13	Periplasmic	COG2303	Amino acid transport and metabolism	
15597467	PA2271		probable acetyltransferase	1.41	7.46E-02	Oktansaeure	6.2	19165	2	Cytoplasmic			
15597487	PA2291		probable glucose-sensitive porin	4.33	6.33E-02	Glucose	5.5	50499	3	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane	
15597496	PA2300	chiC	chitinase	11.02	3.53E-03	Oktansaeure	5.1	53042	6	Extracellular	COG3469	Carbohydrate transport and metabolism	
15597497	PA2301		hypothetical protein	1.67	1.84E-02	Oktansaeure	6.5	19330	10	Cytoplasmic	COG2606	Function unknown	
15597498	PA2302	ambE	AmbE	2.14	1.01E-01	Oktansaeure	4.8	229041	104	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597499	PA2303	ambD	AmbD	2.31	2.87E-03	Oktansaeure	6.6	38657	7	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597500	PA2304	ambC	AmbC	2.82	9.24E-03	Oktansaeure	6.8	40696	5	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597501	PA2305	ambB	AmbB	1.14	5.22E-01	Oktansaeure	6.3	134446	25	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597516	PA2320	gntR	transcriptional regulator GntR	4.8	1.64E-03	Glucose	8.2	37147	3	Cytoplasmic	COG1609	Transcription	
15597517	PA2321		gluconokinase	309.88	4.45E-05	Glucose	7.1	18456	13	Unknown	COG3265	Carbohydrate transport and metabolism	
15597518	PA2322		gluconate permease	33.6	2.43E-04	Glucose	8.0	47296	2	Cytoplasmic Membrane	COG2610	Carbohydrate transport and metabolism	Amino acid transport and metabolism
15597519	PA2323		probable glyceraldehyde-3-phosphate dehydrogenase	25.93	3.48E-05	Glucose	6.4	59960	41	Cytoplasmic	COG1012	Energy production and conversion	
15597526	PA2330		hypothetical protein	3.07	7.17E-02	Oktansaeure	6.6	37680	4	Unknown	COG1960	Lipid metabolism	
15597527	PA2331		hypothetical protein	14.59	4.48E-03	Oktansaeure	5.0	19904	6	Unknown	COG2128	Function unknown	
15597561	PA2365		conserved hypothetical protein	27.54	9.20E-04	Oktansaeure	4.4	20177	4	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15597562	PA2366		uricase PuuD	1.47	4.46E-02	Oktansaeure	5.7	55042	5	Cytoplasmic Membrane	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15597563	PA2367		hypothetical protein	5.57	1.96E-03	Oktansaeure	4.6	17636	3	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15597574	PA2378		probable aldehyde dehydrogenase	4.74	3.85E-04	Glucose	8.4	83665	17	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ	1.25	4.57E-01	Oktansaeure	7.1	84039	23	Periplasmic	COG2366	General function prediction only	
15597582	PA2386	pvdA	L-ornithine N5-oxygenase	1.1	6.90E-01	Oktansaeure	6.5	49478	23	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
15597590	PA2394	pvdN	PvdN	2.09	3.25E-02	Oktansaeure	7.3	47981	11	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
15597591	PA2395	pvdO	PvdO	1.93	9.62E-02	Oktansaeure	5.4	31070	11	Periplasmic	COG1262	Function unknown	
15597592	PA2396	pvdF	pyoverdine synthetase F	1.53	1.52E-01	Oktansaeure	5.0	31039	23	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15597594	PA2398	fpvA	ferripyoverdine receptor	1.11	5.50E-01	Oktansaeure	5.3	91167	28	Periplasmic	COG4773	Inorganic ion transport and metabolism	
15597595	PA2399	pvdD	pyoverdine synthetase D	1.38	3.92E-01	Oktansaeure	5.0	273645	66	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
110645305	PA2400	pvdJ	PvdJ	1.18	5.67E-01	Oktansaeure	5.1	240213	12	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597598	PA2402		probable non-ribosomal peptide synthetase	1.27	4.99E-01	Oktansaeure	5.1	569179	233	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597603	PA2407		probable adhesion protein	1.92	2.97E-02	Oktansaeure	9.6	34309	8	Periplasmic	COG0803	Inorganic ion transport and metabolism	
15597606	PA2410		hypothetical protein	1.93	4.84E-02	Oktansaeure	5.0	31732	10	Unknown	COG0803	Inorganic ion transport and metabolism	
15597607	PA2411		probable thioesterase	1.47	4.18E-02	Glucose	5.4	27846	17	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	
15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, PvdH	1.17	2.56E-01	Glucose	6.5	50215	21	Cytoplasmic	COG0160	Amino acid transport and metabolism	
15597620	PA2424	pvdL	PvdL	1.05	6.70E-01	Oktansaeure	5.1	480292	217	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597638	PA2442	gcvT2	glycine cleavage system protein T2	1.59	2.19E-01	Oktansaeure	6.4	39882	15	Periplasmic	COG0404	Amino acid transport and metabolism	
15597640	PA2444	glyA2	serine hydroxymethyltransferase	1.35	4.59E-01	Oktansaeure	6.5	44974	6	Periplasmic	COG0112	Amino acid transport and metabolism	
15597641	PA2445	gcvP2	glycine cleavage system protein P2	2.24	1.73E-02	Glucose	6.0	103918	46	Periplasmic	COG1003	Amino acid transport and metabolism	
15597646	PA2450		hypothetical protein	1.3	8.76E-02	Oktansaeure	6.4	34331	5	Periplasmic			
15597651	PA2455		hypothetical protein	2.8	3.71E-03	Oktansaeure	5.6	20332	3	Cytoplasmic	COG3153	General function prediction only	
15597655	PA2459		hypothetical protein	3.35	5.81E-02	Glucose	5.6	23801	3	Cytoplasmic			
15597658	PA2462		hypothetical protein	1.52	2.64E-01	Oktansaeure	5.1	573168	39	Outer Membrane Vesicle	COG3210	Intracellular trafficking and secretion	
15597660	PA2464		hypothetical protein	1.32	5.99E-03	Glucose	4.6	17626	5	Periplasmic			
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG	1.01	8.70E-01	Glucose	7.1	28053	5	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15597679	PA2483		conserved hypothetical protein	1.48	2.71E-01	Oktansaeure	6.2	36102	6	Cytoplasmic	COG2141	Energy production and conversion	
15597687	PA2491		probable oxidoreductase	1.28	3.59E-01	Oktansaeure	5.3	36832	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexE precursor	1.54	5.69E-02	Glucose	8.8	45031	7	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15597690	PA2494	mexF	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF	3.37	3.03E-02	Glucose	5.4	115509	6	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15597691	PA2495	oprN	Multidrug efflux outer membrane protein OprN precursor	2.39	4.48E-02	Glucose	5.1	51165	4	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15597692	PA2496		hypothetical protein	1.41	4.39E-01	Oktansaeure	6.6	19483	2	Cytoplasmic	COG2318	Function unknown	
15597699	PA2503		hypothetical protein	1.54	3.41E-01	Oktansaeure	4.6	45895	3	Cytoplasmic			
15597700	PA2504		hypothetical protein	3.32	1.81E-02	Oktansaeure	4.3	22822	2	Cytoplasmic	COG4859	Function unknown	
15597703	PA2507	catA	catechol 1,2-dioxygenase	5.33	1.39E-01	Oktansaeure	5.1	34160	2	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
15597725	PA2529		hypothetical protein	1.17	4.33E-01	Glucose	5.6	52681	5	Cytoplasmic	COG0312	General function prediction only	
15597726	PA2530		hypothetical protein	1.55	3.08E-01	Oktansaeure	5.7	48959	4	Unknown	COG0312	General function prediction only	
15597727	PA2531		probable aminotransferase	7.98	1.19E-02	Oktansaeure	9.4	40715	6	Unknown	COG0079	Amino acid transport and metabolism	
15597728	PA2532	tpx	thiol peroxidase	1.08	7.26E-01	Oktansaeure	4.9	17234	14	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
15597741	PA2545	xthA	exodeoxyribonuclease III	1.04	8.84E-01	Oktansaeure	6.4	31003	8	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15597747	PA2551		probable transcriptional regulator	1.41	1.55E-01	Oktansaeure	9.9	35144	4	Cytoplasmic	COG0583	Transcription	
15597749	PA2553		probable acyl-CoA thiolase	3.34	1.46E-03	Oktansaeure	5.9	41400	5	Cytoplasmic	COG0183	Lipid metabolism	
15597750	PA2554		probable short-chain dehydrogenase	2.06	5.63E-02	Oktansaeure	6.6	26394	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597758	PA2562		hypothetical protein	1.93	4.14E-02	Oktansaeure	10.0	17384	2	Unknown			
15597763	PA2567		hypothetical protein	2.24	5.97E-01	Oktansaeure	4.8	65617	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15597771	PA2575		hypothetical protein	4.03	4.78E-03	Oktansaeure	6.4	22222	12	Unknown	COG3560	General function prediction only	
15597773	PA2577		probable transcriptional regulator	1.47	1.40E-01	Oktansaeure	8.0	16459	2	Cytoplasmic	COG1522	Transcription	
15597775	PA2579	kynA	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing) KynA	1.2	1.64E-01	Glucose	6.5	32931	2	Cytoplasmic	COG3483	Amino acid transport and metabolism	
15597778	PA2582		hypothetical protein	2.57	3.58E-02	Oktansaeure	10.5	19446	8	Unknown	COG3109	Signal transduction mechanisms	
15597782	PA2586	gacA	response regulator GacA	1.27	4.18E-01	Oktansaeure	6.1	23576	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15597788	PA2592		probable periplasmic spermidine/putrescine-binding protein	3.82	6.19E-04	Oktansaeure	6.7	40725	7	Periplasmic	COG0687	Amino acid transport and metabolism	

15597790	PA2594		conserved hypothetical protein	2.2	7.54E-02	Oktansaeure	9.2	34686	5	Periplasmic	COG0715	Inorganic ion transport and metabolism		
15597797	PA2601		probable transcriptional regulator	1.25	4.39E-01	Glucose	5.5	32375	2	Cytoplasmic	COG0583	Transcription		
15597799	PA2603		probable thiosulfate sulfurtransferase	1	8.69E-01	Oktansaeure	5.0	57285	2	Cytoplasmic	COG2897	Inorganic ion transport and metabolism		
15597805	PA2609		hypothetical protein	1.08	6.01E-01	Glucose	6.7	36625	4	Cytoplasmic	COG0547	Amino acid transport and metabolism		
15597807	PA2611	cysG	siroheme synthase	1.46	1.02E-01	Glucose	6.3	50370	8	Cytoplasmic	COG0007	Coenzyme metabolism		
15597808	PA2612	serS	seryl-tRNA synthetase	1.31	1.47E-02	Glucose	5.3	47231	17	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis		
15597809	PA2613		conserved hypothetical protein	1.06	8.21E-01	Glucose	6.3	49047	2	Cytoplasmic	COG2256	DNA replication, recombination, and repair		
15597810	PA2614	lolA	periplasmic chaperone LolA	1.97	2.51E-02	Oktansaeure	5.8	23072	15	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane		
15597812	PA2616	trxB1	thioredoxin reductase 1	1.21	1.81E-01	Oktansaeure	5.2	33818	11	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones		
15597814	PA2618		hypothetical protein	4.5	1.90E-02	Oktansaeure	8.5	27826	2	Cytoplasmic	COG2935	Posttranslational modification, protein turnover, chaperones		
15597815	PA2619	infA	initiation factor	3.22	3.41E-02	Glucose	9.6	8303	4	Cytoplasmic	COG0361	Translation, ribosomal structure and biogenesis		
15597816	PA2620	clpA	ATP-binding protease component ClpA	2.23	1.91E-02	Oktansaeure	5.9	84010	31	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones		
15597818	PA2622	cspD	cold-shock protein CspD	1.38	8.83E-02	Oktansaeure	5.6	9600	5	Cytoplasmic	COG1278	Transcription		
15597819	PA2623	icd	isocitrate dehydrogenase	1.23	1.63E-01	Oktansaeure	4.9	45577	37	Periplasmic	COG0538	Energy production and conversion		
15597820	PA2624	idh	isocitrate dehydrogenase	2.07	1.23E-02	Glucose	6.1	81633	57	Periplasmic	COG2838	Energy production and conversion		
15597821	PA2625		conserved hypothetical protein	1.97	2.31E-02	Glucose	5.2	17525	6	Cytoplasmic	COG1051	Nucleotide transport and metabolism		
15597823	PA2627		conserved hypothetical protein	1.75	7.90E-03	Oktansaeure	10.9	23030	3	Unknown	COG2915	General function prediction only		
15597825	PA2629	purB	adenylosuccinate lyase	1.24	2.45E-01	Glucose	5.7	50500	10	Cytoplasmic	COG0015	Nucleotide transport and metabolism		
15597826	PA2630		conserved hypothetical protein	4.08	3.70E-02	Glucose	4.1	44057	2	Cytoplasmic	COG2850	Function unknown		
15597827	PA2631		probable acetyl transferase	1.01	9.06E-01	Oktansaeure	4.8	16040	5	Cytoplasmic	COG2153	General function prediction only		
15597828	PA2632		hypothetical protein	3.24	5.22E-02	Oktansaeure	8.0	23249	2	Unknown				
15597830	PA2634	aceA	isocitrate lyase AceA	13.15	1.57E-05	Oktansaeure	5.9	58886	56	Periplasmic	COG2224	Energy production and conversion		
15597834	PA2638	nuoB	NADH dehydrogenase I chain B	1.77	1.23E-01	Glucose	5.1	25425	2	Cytoplasmic Membrane	COG0377	Energy production and conversion		
15597835	PA2639	nuoD	NADH dehydrogenase I chain C,D	1.04	9.14E-01	Oktansaeure	6.7	68323	8	Cytoplasmic	COG0649	Energy production and conversion		
15597836	PA2640	nuoE	NADH dehydrogenase I chain E	2.96	2.16E-02	Glucose	4.8	18088	2	Cytoplasmic	COG1905	Energy production and conversion		
15597837	PA2641	nuoF	NADH dehydrogenase I chain F	2.04	1.44E-01	Glucose	7.0	48678	3	Cytoplasmic	COG1894	Energy production and conversion		
15597838	PA2642	nuoG	NADH dehydrogenase I chain G	2.67	4.12E-02	Glucose	6.0	98999	16	Outer Membrane Vesicle	COG1034	Energy production and conversion		
15597846	PA2650		conserved hypothetical protein	1.43	8.16E-02	Glucose	5.7	29513	5	Cytoplasmic	COG2226	Coenzyme metabolism		
15597853	PA2657		probable two-component response regulator	1.03	9.23E-01	Oktansaeure	5.9	24729	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15597875	PA2679		hypothetical protein	3.22	2.33E-02	Oktansaeure	5.2	27641	5	Cytoplasmic	COG2226	Coenzyme metabolism		
15597878	PA2682		conserved hypothetical protein	1.5	1.93E-01	Glucose	5.4	45495	2	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism		
15597879	PA2683		probable serine/threonine dehydratase, degradative	2.17	2.21E-01	Oktansaeure	6.4	33957	3	Cytoplasmic	COG1171	Amino acid transport and metabolism		
15597880	PA2684		conserved hypothetical protein	1.2	5.20E-01	Oktansaeure	6.6	145819	5	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane		
15597881	PA2685	vgrG4	VgrG4	1.68	3.66E-02	Oktansaeure	6.3	81620	4	Cytoplasmic	COG3501	Function unknown		
15597888	PA2692		probable transcriptional regulator	1.8	3.98E-03	Oktansaeure	6.5	19143	3	Cytoplasmic	COG1959	Transcription		
15597898	PA2702	tse2	Tse2	1.46	7.49E-02	Oktansaeure	6.8	17657	2	Extracellular				
15597903	PA2707		hypothetical protein	3.3	3.60E-03	Oktansaeure	6.1	32205	20	Cytoplasmic	COG0714	General function prediction only		
15597905	PA2709	cysK	cysteine synthase A	1.33	7.46E-02	Oktansaeure	6.6	34309	18	Cytoplasmic	COG0031	Amino acid transport and metabolism		
15597913	PA2717	cpo	chloroperoxidase precursor	3.84	3.39E-03	Oktansaeure	5.9	30435	4	Cytoplasmic	COG0596	General function prediction only		
15597916	PA2720		hypothetical protein	1.13	7.33E-01	Oktansaeure	4.7	23816	5	Cytoplasmic				
15597917	PA2721		hypothetical protein	3.69	2.49E-02	Oktansaeure	4.6	17356	2	Cytoplasmic	COG3865	Function unknown		
15597921	PA2725		probable chaperone	1.72	3.03E-03	Oktansaeure	6.2	68829	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones		
15597928	PA2732		hypothetical protein	1.01	8.92E-01	Oktansaeure	6.2	128671	24	Cytoplasmic	COG0610	Defense mechanisms		
15597930	PA2734		hypothetical protein	1.26	3.06E-02	Glucose	6.1	48703	9	Cytoplasmic	COG0732	Defense mechanisms		
15597931	PA2735		probable restriction-modification system protein	1.1	7.31E-01	Glucose	5.4	89570	31	Cytoplasmic	COG0286	Defense mechanisms		
15597933	PA2737		conserved hypothetical protein	2.23	8.79E-02	Oktansaeure	10.2	10254	2	Unknown	COG0789	Transcription		
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit	1.36	1.52E-01	Glucose	5.1	86799	37	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis		
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit	1.05	6.01E-01	Oktansaeure	5.8	38063	9	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis		
15597937	PA2741	rplT	50S ribosomal protein L20	1.08	6.71E-01	Glucose	12.3	13365	7	Outer Membrane Vesicle	COG0292	Translation, ribosomal structure and biogenesis		
15597939	PA2743	infC	translation initiation factor IF-3	1.91	1.46E-01	Oktansaeure	10.3	20864	10	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis		
15597940	PA2744	thrS	threonyl-tRNA synthetase	1.37	4.35E-02	Glucose	6.3	73080	39	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis		
15597951	PA2755	eco	ecotin precursor	1.14	2.91E-01	Glucose	6.5	17228	8	Periplasmic	COG4574	General function prediction only		
15597956	PA2760	oprQ	OprQ	1.08	9.46E-01	Oktansaeure	5.5	46850	14	Periplasmic				
15597960	PA2764		hypothetical protein	1.41	1.26E-01	Oktansaeure	6.0	24519	8	Cytoplasmic				
15597961	PA2765		hypothetical protein	1.8	3.31E-02	Glucose	4.5	32396	13	Unknown	COG2837	Inorganic ion transport and metabolism		
15597966	PA2770		hypothetical protein	1.58	4.49E-02	Glucose	4.7	28258	7	Cytoplasmic	COG0384	General function prediction only		
15597988	PA2792		hypothetical protein	1.97	2.10E-02	Oktansaeure	6.4	22070	3	Unknown				
15597991	PA2795		conserved hypothetical protein	2.04	1.91E-02	Glucose	7.1	36929	2	Cytoplasmic	COG0042	Translation, ribosomal structure and biogenesis		
15597992	PA2796	tal	transaldolase	1.19	3.73E-01	Oktansaeure	4.9	33946	19	Cytoplasmic	COG0176	Carbohydrate transport and metabolism		
15597993	PA2797		hypothetical protein	1.23	1.00E-01	Glucose	4.6	17710	5	Cytoplasmic	COG1366	Signal transduction mechanisms		
15597994	PA2798		probable two-component response regulator	1.27	1.63E-01	Oktansaeure	4.6	43485	7	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription	
15597996	PA2800		conserved hypothetical protein	1.63	2.53E-01	Oktansaeure	5.3	26148	4	Periplasmic	COG2853	Cell envelope biogenesis, outer membrane		
15598002	PA2806		conserved hypothetical protein	1.58	4.35E-02	Glucose	5.4	30848	11	Cytoplasmic	COG2904	Function unknown		
15598005	PA2809	copR	two-component response regulator, CopR	1.66	2.70E-01	Oktansaeure	4.6	25716	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15598008	PA2812		probable ATP-binding component of ABC transporter	1.23	4.95E-01	Oktansaeure	6.3	34540	2	Cytoplasmic Membrane	COG1131	Defense mechanisms		
15598009	PA2813		probable glutathione S-transferase	2.33	3.24E-02	Oktansaeure	4.8	23405	13	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
15598011	PA2815		probable acyl-CoA dehydrogenase	4.62	1.50E-02	Oktansaeure	5.9	88762	3	Outer Membrane Vesicle	COG1960	Lipid metabolism		
15598017	PA2821		probable glutathione S-transferase	1.49	4.35E-02	Oktansaeure	6.1	24716	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
15598018	PA2822		conserved hypothetical protein	1.85	1.78E-02	Glucose	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms		
15598019	PA2823		conserved hypothetical protein	1.57	1.59E-02	Glucose	5.7	33760	9	Cytoplasmic	COG2607	General function prediction only		
15598022	PA2826		probable glutathione peroxidase	1.1	2.58E-01	Glucose	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones		
15598024	PA2828		probable aminotransferase	1.37	2.38E-01	Oktansaeure	6.1	44799	8	Periplasmic	COG0436	Amino acid transport and metabolism		
15598025	PA2829		hypothetical protein	1.61	1.78E-02	Glucose	5.2	16432	6	Unknown				
15598027	PA2831		conserved hypothetical protein	1	8.83E-01	Oktansaeure	5.3	42933	7	Cytoplasmic	COG2866	Amino acid transport and metabolism		
15598028	PA2832	tpm	thiopurine methyltransferase	1.18	2.19E-01	Glucose	4.7	24875	4	Cytoplasmic				
15598036	PA2840		probable ATP-dependent RNA helicase	1.1	7.57E-01	Oktansaeure	9.0	62107	3	Outer Membrane Vesicle	COG0513	DNA replication, recombination, and repair	Transcription	
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	1.6	1.69E-02	Oktansaeure	5.4	28612	5	Cytoplasmic	COG1024	Lipid metabolism		
15598039	PA2843		probable aldolase	2.06	9.20E-04	Oktansaeure	6.1	49851	4	Cytoplasmic	COG3200	Amino acid transport and metabolism		
15598047	PA2851	efp	translation elongation factor P	1.1	5.69E-01	Glucose	4.5	20985	9	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis		
15598049	PA2853	oprI	Outer membrane lipoprotein OprI precursor	2.49	8.67E-02	Oktansaeure	8.5	8835	2	Outer Membrane				
15598050	PA2854		conserved hypothetical protein	1.55	4.35E-03	Glucose	5.6	34799	10	Periplasmic	COG1376	Function unknown		
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	1.29	2.57E-01	Glucose	5.9	21037	8	Periplasmic	COG2755	Amino acid transport and metabolism		
15598062	PA2866	mttC	secretion protein MttC	1.01	9.55E-01	Oktansaeure	6.1	29544	3	Cytoplasmic	COG0084	DNA replication, recombination, and repair		
15598065	PA2869		hypothetical protein	1.12	5.78E-01	Oktansaeure	8.7	18206	4	Cytoplasmic Membrane	COG3915	Function unknown		
15598067	PA2871		hypothetical protein	1.21	3.02E-01	Glucose	5.4	28695	14	Unknown	COG1946	Lipid metabolism		
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	1.32	2.46E-01	Glucose	5.3	24394	12	Cytoplasmic	COG0284	Nucleotide transport and metabolism		
15598081	PA2885	atuR	putative repressor of atu genes	1.85	1.42E-01	Oktansaeure	4.9	22057	4	Unknown	COG1309	Transcription		
15598095	PA2899		probable transcriptional regulator	14.28	9.39E-04	Oktansaeure	7.6	23250	8	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription	
15598098	PA2902		hypothetical protein	1.28	1.30E-01	Glucose	4.8	30448	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15598099	PA2903	cobJ	precorrin-3 methylase CobJ	1.39	3.02E-01	Glucose	5.9	58950	2	Cytoplasmic	COG1010	Coenzyme metabolism		
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	2.04	4.70E-03	Glucose	6.3	27275	4	Cytoplasmic	COG2243	Coenzyme metabolism		

15598101	PA2905	cobH	precorrin isomerase CobH	1.43	1.57E-01	Glucose	5.7	21650	7	Cytoplasmic	COG2082	Coenzyme metabolism		
15598114	PA2918		probable short-chain dehydrogenase	1.63	1.84E-02	Oktansaeure	7.2	26738	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598135	PA2939		probable aminopeptidase	1.96	4.34E-02	Oktansaeure	4.8	57511	8	Extracellular	COG2234	General function prediction only		
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	1.36	5.71E-01	Glucose	5.2	138499	4	Cytoplasmic	COG1429	Coenzyme metabolism		
15598141	PA2945		conserved hypothetical protein	1.55	2.81E-01	Glucose	4.9	41175	3	Cytoplasmic	COG0523	General function prediction only		
15598146	PA2950	pfmß	proton motive force protein, PMF	1.97	6.16E-04	Glucose	4.8	43528	16	Cytoplasmic	COG3007	Function unknown		
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	2.28	6.82E-03	Oktansaeure	4.8	31423	20	Periplasmic	COG2025	Energy production and conversion		
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	1.82	7.91E-04	Oktansaeure	9.6	26377	26	Outer Membrane Vesicle	COG2086	Energy production and conversion		
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	1.28	3.17E-01	Oktansaeure	5.6	59896	9	Outer Membrane Vesicle	COG0644	Energy production and conversion		
15598150	PA2954		hypothetical protein	2.37	1.26E-02	Oktansaeure	4.9	21240	7	Cytoplasmic	COG3816	Function unknown		
15598155	PA2959		conserved hypothetical protein	1.28	7.46E-02	Glucose	5.3	28114	6	Cytoplasmic	COG0084	DNA replication, recombination, and repair		
15598157	PA2961	holB	DNA polymerase III, delta prime subunit	1.37	1.40E-01	Glucose	6.6	35746	5	Cytoplasmic	COG0470	DNA replication, recombination, and repair		
15598158	PA2962	tmk	thymidylate kinase	1.65	1.34E-01	Oktansaeure	4.9	23077	7	Cytoplasmic	COG0125	Nucleotide transport and metabolism		
15598160	PA2964	pabC	4-amino-4-deoxychorismate lyase	1.12	2.90E-01	Glucose	5.7	29886	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism	
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.04	6.86E-01	Oktansaeure	5.8	43465	9	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15598162	PA2966	acpP	acyl carrier protein	1.03	8.50E-01	Oktansaeure	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	1.29	3.23E-01	Glucose	6.6	25585	16	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	3.17	5.50E-04	Glucose	4.8	32444	15	Periplasmic	COG0331	Lipid metabolism		
15598168	PA2972		conserved hypothetical protein	1.46	6.79E-02	Oktansaeure	6.0	21054	10	Cytoplasmic	COG0424	Cell division and chromosome partitioning		
15598170	PA2974		probable hydrolase	2.04	6.72E-03	Glucose	5.4	25322	4	Cytoplasmic	COG0546	General function prediction only		
15598172	PA2976	rne	ribonuclease E	1.05	8.16E-01	Oktansaeure	4.6	117463	41	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis		
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	1.02	8.50E-01	Oktansaeure	6.7	37595	4	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane		
15598174	PA2978	ptpA	phosphotyrosine protein phosphatase	1.64	7.04E-02	Glucose	6.1	17152	8	Cytoplasmic	COG0394	Signal transduction mechanisms		
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.13	5.19E-01	Glucose	5.4	27646	12	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane		
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	1.46	4.47E-02	Glucose	6.7	51161	13	Cytoplasmic	COG1249	Energy production and conversion		
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	1.17	4.86E-01	Glucose	5.7	128763	32	Periplasmic	COG1197	DNA replication, recombination, and repair	Transcription	
15598199	PA3003		hypothetical protein	1.55	3.18E-02	Oktansaeure	4.5	22474	8	Periplasmic				
15598200	PA3004		5'-methylthioinosine phosphorylase	1.24	1.27E-01	Glucose	6.6	26266	6	Cytoplasmic	COG0005	Nucleotide transport and metabolism		
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.16	1.27E-01	Glucose	6.2	36101	11	Cytoplasmic	COG1472	Carbohydrate transport and metabolism		
15598202	PA3006	psrA	transcriptional regulator PsrA	2.8	4.66E-02	Oktansaeure	9.9	25784	4	Cytoplasmic	COG1309	Transcription		
15598207	PA3011	topA	DNA topoisomerase I	1.77	1.43E-01	Glucose	8.7	97282	55	Cytoplasmic	COG0550	DNA replication, recombination, and repair		
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	9.17	5.63E-04	Oktansaeure	6.8	41643	26	Cytoplasmic	COG0183	Lipid metabolism		
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	5.57	1.25E-04	Oktansaeure	5.6	76954	43	Periplasmic	COG1250	Lipid metabolism		
15598215	PA3019		probable ATP-binding component of ABC transporter	1.34	6.41E-02	Glucose	5.0	71155	19	Cytoplasmic	COG0488	General function prediction only		
15598217	PA3021		hypothetical protein	1.85	4.32E-02	Oktansaeure	7.8	14206	7	Unknown	COG3755	Function unknown		
15598218	PA3022		hypothetical protein	1.12	7.39E-01	Oktansaeure	5.9	29579	15	Cytoplasmic	COG3217	General function prediction only		
15598219	PA3023		conserved hypothetical protein	5.51	2.22E-03	Oktansaeure	4.7	31504	6	Cytoplasmic	COG1597	Lipid metabolism	General function prediction only	
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.01	9.63E-01	Oktansaeure	5.0	43359	4	Cytoplasmic	COG0303	Coenzyme metabolism		
15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	1.2	1.44E-01	Oktansaeure	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism		
15598226	PA3030	mobA	molybdopterin-guanine dinucleotide biosynthesis protein MobA	2.12	2.31E-02	Oktansaeure	7.6	21870	8	Cytoplasmic	COG0746	Coenzyme metabolism		
15598227	PA3031		hypothetical protein	1.4	4.74E-01	Glucose	4.7	8012	2	Outer Membrane Vesicle				
15598230	PA3034		probable transcriptional regulator	2.96	8.80E-04	Oktansaeure	8.5	20988	2	Cytoplasmic				
15598239	PA3043		conserved hypothetical protein	1.46	6.03E-02	Oktansaeure	6.5	50083	3	Cytoplasmic	COG0232	Nucleotide transport and metabolism		
15598244	PA3048		conserved hypothetical protein	1.24	5.37E-02	Oktansaeure	8.0	81155	11	Cytoplasmic	COG0116	DNA replication, recombination, and repair		
15598249	PA3053		probable hydrolytic enzyme	1.18	3.67E-01	Oktansaeure	8.0	37485	4	Periplasmic	COG0596	General function prediction only		
15598250	PA3054		hypothetical protein	2.45	5.77E-04	Oktansaeure	6.6	71165	6	Periplasmic	COG2866	Amino acid transport and metabolism		
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	4.72	9.20E-01	Oktansaeure	6.1	182637	5	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism		
15598277	PA3081		conserved hypothetical protein	5.55	2.68E-02	Oktansaeure	9.2	50680	4	Periplasmic				
15598278	PA3082	gbt	glycine betaine transmethylase	4.36	1.14E-02	Oktansaeure	4.5	71403	6	Periplasmic				
15598279	PA3083	pepN	aminopeptidase N	1.21	3.51E-01	Glucose	4.9	100046	48	Periplasmic	COG0308	Amino acid transport and metabolism		
15598280	PA3084		hypothetical protein	1.29	2.17E-01	Glucose	7.6	29990	2	Cytoplasmic				
15598283	PA3087		hypothetical protein	1.73	1.24E-01	Glucose	6.3	37211	2	Cytoplasmic				
15598284	PA3088		conserved hypothetical protein	1.5	2.63E-01	Oktansaeure	7.3	32140	7	Cytoplasmic	COG0061	Coenzyme metabolism		
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	1.61	5.31E-01	Oktansaeure	7.2	72969	4	Cytoplasmic	COG1902	Energy production and conversion		
15598297	PA3101	xcpT	general secretion pathway protein G	1.18	3.41E-01	Oktansaeure	8.8	16112	2	Cytoplasmic Membrane	COG2165	Cell motility and secretion	Intracellular trafficking and secretion	
15598302	PA3106		probable short-chain dehydrogenase	1.65	2.83E-03	Glucose	4.6	26997	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598303	PA3107	metZ	o-succinylhomoserine sulfhydrylase	1.06	4.87E-01	Glucose	6.3	43185	11	Periplasmic	COG0626	Amino acid transport and metabolism		
15598304	PA3108	purF	amidophosphoribosyltransferase	2.01	8.47E-03	Glucose	6.8	55370	14	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism		
15598307	PA3111	folC	folylpolyglutamate synthetase	1.82	2.37E-01	Glucose	5.0	46505	4	Cytoplasmic	COG0285	Coenzyme metabolism		
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	1.11	6.11E-01	Glucose	7.1	31843	14	Periplasmic	COG0777	Lipid metabolism		
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	116.22	1.16E-02	Glucose	6.8	22280	3	Cytoplasmic	COG0135	Amino acid transport and metabolism		
15598311	PA3115	fimV	Motility protein FimV	4.31	3.13E-01	Oktansaeure	4.0	96928	2	Outer Membrane Vesicle	COG3170	Cell motility and secretion	Intracellular trafficking and secretion	
15598312	PA3116		probable aspartate-semialdehyde dehydrogenase	1.93	2.51E-01	Glucose	4.5	35349	4	Cytoplasmic	COG0136	Amino acid transport and metabolism		
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	1.02	8.47E-01	Glucose	5.5	40494	23	Periplasmic	COG0136	Amino acid transport and metabolism		
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.38	6.98E-02	Oktansaeure	4.8	39120	12	Cytoplasmic	COG0473	Amino acid transport and metabolism		
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	1.58	3.79E-02	Glucose	4.7	24011	16	Cytoplasmic	COG0066	Amino acid transport and metabolism		
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	2.09	2.40E-03	Glucose	6.3	51042	14	Cytoplasmic	COG0065	Amino acid transport and metabolism		
15598318	PA3122		probable transcriptional regulator	1.09	5.52E-01	Glucose	6.4	32835	6	Cytoplasmic	COG0583	Transcription		
15598319	PA3123		conserved hypothetical protein	1.5	4.11E-01	Oktansaeure	4.6	13516	5	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis		
15598322	PA3126	ibpA	heat-shock protein IbpA	2.37	7.95E-02	Glucose	6.1	16583	4	Cytoplasmic	COG0071	Posttranslational modification, protein turnover, chaperones		
15598323	PA3127		hypothetical protein	1.58	9.81E-02	Oktansaeure	5.0	29403	8	Unknown				
15598324	PA3128		probable short-chain dehydrogenase	1.75	7.73E-03	Oktansaeure	6.8	26219	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598326	PA3130		hypothetical protein	1.03	8.18E-01	Glucose	5.2	16555	9	Unknown	COG0824	General function prediction only		
15598327	PA3131		probable aldolase	1.56	2.22E-02	Oktansaeure	5.3	22852	9	Cytoplasmic	COG0800	Carbohydrate transport and metabolism		
15598330	PA3134	gltX	glutamyl-tRNA synthetase	1.42	9.19E-03	Glucose	6.7	56749	17	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis		
15598334	PA3138	uvrB	excinuclease ABC subunit B	1.19	3.15E-01	Glucose	5.1	76067	14	Cytoplasmic	COG0556	DNA replication, recombination, and repair		
15598335	PA3139		probable amino acid aminotransferase	1.44	1.93E-02	Glucose	6.6	43319	21	Periplasmic	COG1448	Amino acid transport and metabolism		
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	1.44	1.02E-03	Glucose	5.8	38907	19	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane		
15598346	PA3150	wbpG	LPS biosynthesis protein WbpG	1.09	8.94E-01	Glucose	8.3	43471	2	Outer Membrane Vesicle	COG0037	Cell cycle control, cell division, chromosome partitioning		
15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	1.19	1.89E-01	Glucose	5.7	27448	9	Cytoplasmic	COG0107	Amino acid transport and metabolism		
15598348	PA3152	hisH2	glutamine amidotransferase	1.24	4.49E-01	Oktansaeure	7.1	22663	10	Cytoplasmic	COG0118	Amino acid transport and metabolism		
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase, wbpE	1.28	7.73E-02	Oktansaeure	6.0	38924	16	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane		
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-acetyltransferase, WbpD	1.26	3.97E-01	Glucose	7.8	20562	5	Cytoplasmic	COG1045	Amino acid transport and metabolism		
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	1.54	1.44E-01	Glucose	6.6	35717	20	Cytoplasmic	COG0673	General function prediction only		
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.21	2.44E-02	Glucose	5.2	48155	29	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane		
15598358	PA3162	rpsA	30S ribosomal protein S1	1.19	2.83E-01	Oktansaeure	4.6	61869	32	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis		
15598359	PA3163	cmk	cytidylate kinase	1.15	3.89E-01	Glucose	4.8	24637	11	Cytoplasmic	COG0283	Nucleotide transport and metabolism		
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	1.42	1.03E-02	Glucose	4.8	39483	12	Cytoplasmic	COG0079	Amino acid transport and metabolism		
15598362	PA3166	pheA	chorismate mutase	1.1	4.79E-01	Oktansaeure	6.3	40632	9	Cytoplasmic	COG0077	Amino acid transport and metabolism		
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.17	2.45E-01	Glucose	4.7	39917	10	Periplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism	
15598364	PA3168	gyrA	DNA gyrase subunit A	1.61	4.04E-02	Glucose	4.6	101134	52	Cytoplasmic	COG0188	DNA replication, recombination, and repair		

15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.12	3.08E-01	Glucose	5.1	39425	8	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis		
15598366	PA3170		conserved hypothetical protein	1.15	4.94E-01	Glucose	5.5	48493	4	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only	
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	1.05	9.23E-01	Oktansaeure	6.3	25860	9	Cytoplasmic	COG2227	Coenzyme metabolism		
15598368	PA3172		probable hydrolase	1.85	3.51E-02	Oktansaeure	5.0	24944	12	Cytoplasmic	COG0546	General function prediction only		
15598369	PA3173		probable short-chain dehydrogenase	1.03	8.06E-01	Glucose	4.9	26332	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598376	PA3180		hypothetical protein	1.78	9.81E-02	Oktansaeure	4.7	16863	3	Unknown	COG1051	Nucleotide transport and metabolism		
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	57.93	9.34E-06	Glucose	7.6	23953	14	Cytoplasmic	COG0800	Carbohydrate transport and metabolism		
15598378	PA3182	pgl	6-phosphogluconolactonase	63.47	6.16E-06	Glucose	6.5	25571	13	Unknown	COG0363	Carbohydrate transport and metabolism		
15598379	PA3183	zwf	glucose-6-phosphate 1-dehydrogenase	15.55	1.32E-03	Glucose	5.7	55620	22	Cytoplasmic	COG0364	Carbohydrate transport and metabolism		
15598382	PA3186	oprB	Glucose/carbohydrate outer membrane porin OprB precursor	13.11	1.12E-01	Glucose	5.5	50753	5	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane		
15598383	PA3187		probable ATP-binding component of ABC transporter	5.41	5.04E-04	Glucose	7.5	42240	4	Outer Membrane Vesicle	COG3839	Carbohydrate transport and metabolism		
15598386	PA3190		probable binding protein component of ABC sugar transporter	19.31	6.98E-06	Glucose	5.8	45131	29	Periplasmic	COG1653	Carbohydrate transport and metabolism		
15598388	PA3192	gltR	two-component response regulator GltR	13.1	1.37E-03	Glucose	5.7	27381	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15598389	PA3193	glk	glucokinase	10.46	5.70E-05	Glucose	5.0	34606	10	Cytoplasmic	COG0837	Carbohydrate transport and metabolism		
15598390	PA3194	edd	phosphogluconate dehydratase	3.07	5.13E-02	Glucose	6.7	65182	26	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism	
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	41.12	6.40E-05	Glucose	6.6	36170	22	Cytoplasmic	COG0057	Carbohydrate transport and metabolism		
15598392	PA3196		hypothetical protein	1.26	4.31E-01	Glucose	3.9	19293	2	Unknown				
15598395	PA3199		conserved hypothetical protein	1.17	6.56E-01	Oktansaeure	6.7	23144	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis		
15598404	PA3208		conserved hypothetical protein	2.48	3.74E-02	Oktansaeure	6.5	19948	12	Cytoplasmic Membrane	COG0778	Energy production and conversion		
15598410	PA3214		hypothetical protein	2.53	7.44E-02	Oktansaeure	10.4	23214	4	Unknown	COG3218	General function prediction only		
15598421	PA3225		probable transcriptional regulator	2.33	1.60E-02	Oktansaeure	7.4	34098	6	Cytoplasmic	COG0583	Transcription		
15598422	PA3226		probable hydrolase	1.22	3.88E-01	Oktansaeure	7.8	30473	2	Cytoplasmic	COG0596	General function prediction only		
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.31	2.44E-01	Glucose	8.5	20104	12	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones		
15598439	PA3243	minC	cell division inhibitor MinC	1.2	2.23E-01	Oktansaeure	6.5	28124	10	Cytoplasmic	COG0850	Cell division and chromosome partitioning		
15598440	PA3244	minD	cell division inhibitor MinD	1.05	8.46E-01	Oktansaeure	5.5	29617	22	Periplasmic	COG2894	Cell division and chromosome partitioning		
15598442	PA3246	rluA	pseudouridine synthase RluA	1.26	2.00E-01	Glucose	7.0	24339	5	Cytoplasmic	COG0564	Translation, ribosomal structure and biogenesis		
15598443	PA3247		hypothetical protein	1.05	6.72E-01	Oktansaeure	6.0	46658	6	Cytoplasmic	COG1362	Amino acid transport and metabolism		
15598446	PA3250		hypothetical protein	8.71	1.56E-02	Oktansaeure	6.2	38285	7	Periplasmic	COG1840	Inorganic ion transport and metabolism		
15598451	PA3255		hypothetical protein	1.37	1.22E-01	Glucose	4.4	21635	9	Cytoplasmic	COG0560	Amino acid transport and metabolism		
15598452	PA3256		probable oxidoreductase	1.01	9.03E-01	Glucose	5.2	33387	11	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only	
15598453	PA3257	prc	periplasmic tail-specific protease	1.05	7.04E-01	Oktansaeure	6.6	78182	34	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane		
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.36	1.67E-01	Glucose	4.8	26845	11	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones		
15598459	PA3263		conserved hypothetical protein	1.24	1.35E-01	Glucose	4.7	34015	20	Cytoplasmic	COG2974	DNA replication, recombination, and repair		
15598466	PA3270		hypothetical protein	1.4	4.49E-01	Glucose	9.9	21901	3	Unknown	COG1670	Translation, ribosomal structure and biogenesis		
15598473	PA3277		probable short-chain dehydrogenase	1.39	7.84E-02	Oktansaeure	6.5	29251	3	Cytoplasmic	COG0300	General function prediction only		
15598482	PA3286		hypothetical protein	1.31	7.19E-02	Oktansaeure	6.4	38139	14	Periplasmic	COG0332	acyl-carrier-protein		
15598483	PA3287		conserved hypothetical protein	1.67	1.06E-01	Oktansaeure	5.5	18194	3	Periplasmic	COG0666	General function prediction only		
15598493	PA3297		probable ATP-dependent helicase	2.06	5.37E-02	Oktansaeure	8.5	149907	2	Cytoplasmic Membrane	COG1643	DNA replication, recombination, and repair		
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	3.29	1.28E-03	Oktansaeure	7.5	61654	10	Outer Membrane Vesicle	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	1.11	7.40E-01	Oktansaeure	7.2	61736	4	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15598498	PA3302		conserved hypothetical protein	1.87	8.71E-02	Oktansaeure	5.0	16901	7	Unknown	COG2030	Lipid metabolism		
15598504	PA3308	hepA	RNA helicase HepA	1.49	1.07E-02	Glucose	4.8	106839	25	Periplasmic	COG0553	Transcription	DNA replication, recombination, and repair	
15598505	PA3309		conserved hypothetical protein	20.4	1.69E-03	Oktansaeure	5.4	16496	16	Periplasmic	COG0589	Signal transduction mechanisms		
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.65	9.68E-02	Glucose	5.5	30908	9	Cytoplasmic	COG2084	Lipid metabolism		
15598509	PA3313		hypothetical protein	1.09	5.52E-01	Glucose	10.2	36539	23	Periplasmic	COG3221	Inorganic ion transport and metabolism		
15598522	PA3326	clpP2	ClpP2	17.05	5.05E-05	Oktansaeure	5.4	22142	14	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion	
15598523	PA3327		probable non-ribosomal peptide synthetase	33.4	7.90E-04	Oktansaeure	5.5	259403	97	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism		
15598524	PA3328		probable FAD-dependent monooxygenase	72.91	2.43E-05	Oktansaeure	8.3	42498	4	Unknown	COG0654	Coenzyme metabolism	Energy production and conversion	
15598525	PA3329		hypothetical protein	8.13	6.25E-05	Oktansaeure	6.2	49134	7	Cytoplasmic				
15598526	PA3330		probable short chain dehydrogenase	30.77	1.09E-04	Oktansaeure	8.8	32031	10	Cytoplasmic	COG4221	General function prediction only		
15598527	PA3331		cytochrome P450	26.79	4.82E-05	Oktansaeure	5.7	46345	8	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism		
15598528	PA3332		conserved hypothetical protein	26.16	1.33E-04	Oktansaeure	5.5	15920	8	Cytoplasmic	COG3631	General function prediction only		
15598529	PA3333	fabH2	3-oxoacyl-[acyl-carrier-protein] synthase III	37.18	4.00E-06	Oktansaeure	5.0	34003	10	Cytoplasmic	COG0332	acyl-carrier-protein		
15598531	PA3335		hypothetical protein	48.33	2.20E-04	Oktansaeure	5.2	27632	6	Cytoplasmic				
15598533	PA3337	rfaD	ADP-L-glycero-D-mannoheptose 6-epimerase	57.43	3.91E-03	Oktansaeure	6.5	37384	4	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15598537	PA3341		probable transcriptional regulator	2.93	1.14E-01	Oktansaeure	8.6	16071	3	Cytoplasmic	COG1846	Transcription		
15598540	PA3344	recQ	ATP-dependent DNA helicase RecQ	1.2	4.24E-01	Glucose	5.8	79449	6	Cytoplasmic	COG0514	DNA replication, recombination, and repair		
15598544	PA3348		probable chemotaxis protein methyltransferase	1.13	8.70E-01	Oktansaeure	9.6	30615	7	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms	
15598545	PA3349		probable chemotaxis protein	1.52	1.27E-01	Oktansaeure	6.1	34402	10	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms	
15598549	PA3353		hypothetical protein	1.4	2.07E-01	Glucose	6.8	29852	12	Cytoplasmic	COG5581	Signal transduction mechanisms		
15598553	PA3357	dsdA	D-serine dehydratase	1.35	6.95E-02	Glucose	6.0	48200	7	Cytoplasmic	COG3048	Amino acid transport and metabolism		
15598593	PA3397	fpr	NADP+-dependent ferredoxin reductase	1.6	2.08E-01	Oktansaeure	5.9	29518	23	Periplasmic	COG1018	Energy production and conversion		
15598611	PA3415		probable dihydrolipoamide acetyltransferase	12.87	3.02E-02	Oktansaeure	5.5	39521	7	Cytoplasmic	COG0508	Energy production and conversion		
15598612	PA3416		probable pyruvate dehydrogenase E1 component, beta chain	73.4	1.16E-01	Oktansaeure	5.7	36143	4	Unknown	COG0022	Energy production and conversion		
15598613	PA3417		probable pyruvate dehydrogenase E1 component, alpha subunit	68.08	3.76E-03	Oktansaeure	5.2	40414	4	Cytoplasmic	COG1071	Energy production and conversion		
15598614	PA3418	ldh	leucine dehydrogenase	8.6	1.54E-02	Oktansaeure	5.9	35633	4	Cytoplasmic	COG0334	Amino acid transport and metabolism		
15598623	PA3427		probable short-chain dehydrogenases	2.16	7.72E-02	Oktansaeure	5.8	32323	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598626	PA3430		probable aldolase	7.5	4.81E-02	Oktansaeure	6.6	27993	3	Cytoplasmic	COG0235	Carbohydrate transport and metabolism		
15598633	PA3437	folM	dihydromonapterin reductase, FolM	1.28	3.19E-01	Oktansaeure	7.0	25403	2	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	2.25	5.24E-03	Oktansaeure	7.6	20833	7	Cytoplasmic	COG0302	Coenzyme metabolism		
15598640	PA3444		conserved hypothetical protein	17.48	1.58E-02	Oktansaeure	6.1	41567	2	Cytoplasmic	COG2141	Energy production and conversion		
15598641	PA3445		conserved hypothetical protein	9.07	2.01E-03	Oktansaeure	9.0	35184	4	Unknown	COG0715	Inorganic ion transport and metabolism		
15598646	PA3450		probable antioxidant protein	2.93	6.50E-03	Oktansaeure	5.2	24164	14	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones		
15598649	PA3453		conserved hypothetical protein	2.11	4.76E-02	Oktansaeure	5.4	24160	10	Unknown	COG3132	Function unknown		
15598652	PA3456		hypothetical protein	2.04	4.20E-03	Oktansaeure	7.2	70517	6	Cytoplasmic	COG4121	Function unknown		
15598654	PA3458		probable transcriptional regulator	1.87	4.40E-02	Oktansaeure	5.6	17599	3	Unknown	COG1846	Transcription		
15598657	PA3461		conserved hypothetical protein	2.28	3.06E-03	Oktansaeure	5.1	43294	2	Cytoplasmic	COG1363	Carbohydrate transport and metabolism		
15598666	PA3470		hypothetical protein	3.11	1.10E-02	Glucose	5.2	16673	3	Unknown	COG0494	DNA replication, recombination, and repair	General function prediction only	
15598667	PA3471		probable malic enzyme	2.21	7.98E-03	Glucose	5.2	62420	25	Periplasmic	COG0281	Energy production and conversion		
15598672	PA3476	rhlI	autoinducer synthesis protein RhlI	2.3	7.95E-01	Oktansaeure	5.3	22630	4	Unknown	COG3916	Signal transduction mechanisms	Secondary metabolites biosynthesis, transport, and catabolism	
15598673	PA3477	rhlR	transcriptional regulator RhlR	1.05	9.58E-01	Oktansaeure	7.2	27577	3	Cytoplasmic	COG2771	Transcription		
15598676	PA3480		probable deoxycytidine triphosphate deaminase	1.71	1.52E-01	Oktansaeure	6.3	21154	8	Cytoplasmic	COG0717	Nucleotide transport and metabolism		
15598677	PA3481		conserved hypothetical protein	1.49	1.84E-02	Oktansaeure	5.1	38889	9	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning		
15598678	PA3482	metG	methionyl-tRNA synthetase	1.16	1.46E-01	Glucose	5.4	74903	32	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis		
15598682	PA3486		conserved hypothetical protein	24.94	1.89E-04	Oktansaeure	6.3	90635	6	Cytoplasmic	COG3501	Function unknown		
15598683	PA3487	pldA	phospholipase D	6.17	1.76E-03	Oktansaeure	6.7	122340	8	Periplasmic	COG1502	Lipid metabolism		
15598720	PA3524	gloA1	lactoylglutathione lyase	2.16	1.08E-01	Glucose	4.7	14251	2	Cytoplasmic	COG0346	Amino acid transport and metabolism		
15598721	PA3525	argG	argininosuccinate synthase	1.22	4.61E-02	Glucose	5.3	45297	18	Periplasmic	COG0137	Amino acid transport and metabolism		
15598723	PA3527	pyrC	dihydroorotase	1.36	3.95E-01	Oktansaeure	6.6	38406	10	Cytoplasmic	COG0418	Nucleotide transport and metabolism		
15598724	PA3528	rnt	ribonuclease T	1.37	1.57E-01	Glucose	4.8	24723	9	Cytoplasmic	COG0847	DNA replication, recombination, and repair		
15598725	PA3529		alkylhydroperoxide reductase C	1.4	2.00E-01	Oktansaeure	5.3	21822	17	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones		

15598727	PA3531	bfrB	bacterioferritin	3.18	1.63E-01	Oktansaeure	4.8	18553	4	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.57	7.02E-02	Glucose	5.7	33924	14	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15598735	PA3539		conserved hypothetical protein	1.11	4.14E-01	Glucose	6.7	29560	13	Cytoplasmic	COG3022	Function unknown	
15598748	PA3552	arnB	ArnB	4.04	3.28E-03	Oktansaeure	8.0	41867	2	Cytoplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598750	PA3554	arnA	ArnA	2.88	1.96E-02	Oktansaeure	6.7	74360	9	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis	
15598759	PA3563	fruR	fructose transport system repressor FruR	1.25	1.81E-01	Oktansaeure	6.4	36369	3	Cytoplasmic	COG1609	Transcription	
15598763	PA3567		probable oxidoreductase	1.77	2.89E-01	Glucose	6.6	36678	5	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15598764	PA3568		probable acetyl-coa synthetase	4.66	3.44E-02	Oktansaeure	6.7	68990	5	Cytoplasmic	COG0365	Lipid metabolism	
15598765	PA3569	mmsB	3-hydroxyisobutyrate dehydrogenase	2.84	4.30E-01	Oktansaeure	6.2	30486	2	Cytoplasmic	COG2084	Lipid metabolism	
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	17.03	1.18E-02	Oktansaeure	6.4	53663	4	Cytoplasmic	COG1012	Energy production and conversion	
15598774	PA3578		conserved hypothetical protein	1.26	3.00E-01	Oktansaeure	4.9	28906	5	Cytoplasmic Membrane	COG0384	General function prediction only	
15598775	PA3579		probable carbohydrate kinase	1.35	3.60E-01	Oktansaeure	5.6	54207	2	Cytoplasmic	COG0554	Energy production and conversion	
15598776	PA3580		conserved hypothetical protein	5.25	1.82E-02	Oktansaeure	10.1	16493	4	Cytoplasmic	COG2606	Function unknown	
15598778	PA3582	glpK	glycerol kinase	2.65	1.63E-02	Oktansaeure	5.9	55966	16	Cytoplasmic	COG0554	Energy production and conversion	
15598783	PA3587	metR	transcriptional regulator MetR	1.83	1.42E-02	Oktansaeure	5.6	34216	3	Cytoplasmic	COG0583	Transcription	
15598800	PA3604	erdR	response regulator ErdR	1.01	8.97E-01	Oktansaeure	4.8	23531	10	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598806	PA3610	potD	polyamine transport protein PotD	2.54	1.91E-01	Glucose	5.5	39260	5	Periplasmic	COG0687	Amino acid transport and metabolism	
15598809	PA3613		hypothetical protein	10.71	3.93E-04	Oktansaeure	6.4	88379	24	Periplasmic	COG3957	Carbohydrate transport and metabolism	
15598810	PA3614		hypothetical protein	3.09	2.79E-03	Oktansaeure	7.0	51921	4	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
15598811	PA3615		hypothetical protein	2.1	4.09E-03	Oktansaeure	6.0	40465	4	Cytoplasmic	COG1611	General function prediction only	
15598813	PA3617	recA	RecA protein	1.32	3.53E-01	Oktansaeure	5.2	36879	12	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
15598814	PA3618		conserved hypothetical protein	1.17	6.09E-01	Oktansaeure	5.0	17715	4	Unknown	COG1546	General function prediction only	
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.44	2.30E-01	Glucose	6.1	94977	27	Cytoplasmic	COG0249	DNA replication, recombination, and repair	
15598817	PA3621	fdxA	ferredoxin I	1.23	4.49E-01	Glucose	3.7	12159	3	Cytoplasmic	COG1146	Energy production and conversion	
15598818	PA3622	rpoS	sigma factor RpoS	3.39	1.06E-02	Oktansaeure	5.1	38235	3	Cytoplasmic	COG0568	Transcription	
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	1	8.42E-01	Oktansaeure	6.1	23407	7	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones	
15598821	PA3625	surE	survival protein SurE	1.54	1.46E-02	Glucose	5.2	26368	5	Unknown	COG0496	General function prediction only	
15598823	PA3627	ygbB	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	45.2	1.36E-01	Glucose	7.1	16662	3	Cytoplasmic	COG0245	Lipid metabolism	
15598824	PA3628		probable esterase	1.39	5.42E-02	Oktansaeure	6.3	31243	5	Unknown	COG0627	General function prediction only	
15598825	PA3629	adhC	alcohol dehydrogenase class III	1.16	6.86E-01	Oktansaeure	5.4	39208	3	Cytoplasmic	COG1062	Energy production and conversion	
15598829	PA3633	ygbP	4-diphosphocytidyl-2-C-methylerythritol synthase	1.48	7.83E-02	Glucose	5.2	25613	2	Cytoplasmic	COG1211	Lipid metabolism	
15598831	PA3635	eno	enolase	1.44	4.58E-03	Glucose	4.8	45195	17	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	1.62	3.68E-02	Glucose	6.5	31143	18	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
15598833	PA3637	pyrG	CTP synthase	1.68	2.60E-02	Glucose	5.4	59617	33	Periplasmic	COG0504	Nucleotide transport and metabolism	
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)	1.16	4.20E-01	Glucose	5.2	34947	23	Outer Membrane Vesicle	COG0825	Lipid metabolism	
15598836	PA3640	dnaE	DNA polymerase III, alpha chain	1.3	1.65E-01	Glucose	5.1	130904	47	Cytoplasmic	COG0587	DNA replication, recombination, and repair	
15598838	PA3642	rnhB	ribonuclease HII	3.06	5.49E-02	Glucose	6.5	21771	4	Cytoplasmic	COG0164	DNA replication, recombination, and repair	
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase	1.29	2.09E-01	Glucose	7.1	28010	6	Cytoplasmic	COG1043	acyl carrier protein	
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	1.4	3.77E-01	Oktansaeure	7.6	16774	5	Cytoplasmic	COG0764	Lipid metabolism	
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase	1.13	2.81E-01	Oktansaeure	6.2	36191	2	Cytoplasmic	COG1044	3-hydroxymyristoyl	
15598843	PA3647		probable outer membrane protein precursor	1.01	9.39E-01	Glucose	10.0	19058	6	Unknown	COG2825	Cell envelope biogenesis, outer membrane	
15598844	PA3648	opr86	outer membrane protein Opr86	1.73	1.47E-01	Glucose	4.8	88286	6	Periplasmic	COG4775	Cell envelope biogenesis, outer membrane	
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase	1.01	9.10E-01	Oktansaeure	5.7	42508	4	Unknown	COG0743	Lipid metabolism	
15598849	PA3653	frr	ribosome recycling factor	2.13	5.35E-02	Oktansaeure	5.9	20485	18	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis	
15598850	PA3654	pyrH	uridylate kinase	1.68	6.97E-02	Glucose	5.4	26272	14	Periplasmic	COG0528	Nucleotide transport and metabolism	
15598851	PA3655	tsf	elongation factor Ts	1.53	7.59E-02	Glucose	5.0	30653	33	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis	
15598852	PA3656	rpsB	30S ribosomal protein S2	1.13	6.36E-01	Oktansaeure	9.0	27336	15	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis	
15598853	PA3657	map	methionine aminopeptidase	1.65	9.80E-02	Oktansaeure	6.3	29086	10	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis	
15598854	PA3658	glnD	protein-PII uridylyltransferase	1.08	6.45E-01	Oktansaeure	5.5	103403	3	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones	
15598855	PA3659		probable aminotransferase	1.03	7.48E-01	Glucose	5.5	44544	10	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase	1.16	2.69E-01	Oktansaeure	6.0	35973	9	Periplasmic	COG2171	Amino acid transport and metabolism	
15598871	PA3675		hypothetical protein	1.45	1.97E-01	Glucose	9.4	23645	6	Unknown			
15598874	PA3678		probable transcriptional regulator	2.84	9.66E-02	Oktansaeure	6.3	23150	10	Cytoplasmic	COG1309	Transcription	
15598878	PA3682		hypothetical protein	1.3	1.96E-01	Oktansaeure	5.0	29150	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15598881	PA3685		conserved hypothetical protein	1.41	1.57E-01	Glucose	4.8	24180	5	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones	
15598882	PA3686	adk	adenylate kinase	1.43	1.65E-01	Oktansaeure	6.4	23107	18	Cytoplasmic	COG0563	Nucleotide transport and metabolism	
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase	1.69	8.61E-02	Oktansaeure	6.2	97839	21	Cytoplasmic	COG2352	Energy production and conversion	
15598888	PA3692	lptF	Lipotoxon F, LptF	4.56	2.10E-02	Oktansaeure	9.9	28514	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
15598889	PA3693		conserved hypothetical protein	1.13	5.90E-01	Glucose	7.0	18219	4	Unknown	COG2110	General function prediction only	
15598892	PA3696		conserved hypothetical protein	1.01	8.85E-01	Glucose	5.4	26551	4	Unknown	COG2013	Function unknown	
15598894	PA3698		hypothetical protein	1.07	6.50E-01	Oktansaeure	4.5	20351	4	Unknown			
15598896	PA3700	lysS	lysyl-tRNA synthetase	1.39	1.69E-01	Glucose	5.0	57329	36	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis	
15598911	PA3716		hypothetical protein	1.55	2.74E-01	Oktansaeure	4.1	60503	9	Outer Membrane Vesicle			
15598918	PA3723		probable FMN oxidoreductase	10.58	1.08E-02	Oktansaeure	6.3	40319	9	Cytoplasmic	COG1902	Energy production and conversion	
15598921	PA3726		conserved hypothetical protein	1.44	2.49E-01	Glucose	4.8	20596	6	Cytoplasmic	COG4681	Function unknown	
15598922	PA3727		hypothetical protein	1.42	2.65E-01	Oktansaeure	4.9	26461	4	Cytoplasmic	COG1502	Lipid metabolism	
15598923	PA3728		hypothetical protein	1.61	2.74E-01	Oktansaeure	4.9	197133	67	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning	
15598924	PA3729		conserved hypothetical protein	1.1	6.12E-01	Oktansaeure	4.9	75882	4	Outer Membrane Vesicle	COG2268	Function unknown	
15598926	PA3731		conserved hypothetical protein	1.54	1.25E-01	Oktansaeure	7.5	24893	9	Cytoplasmic	COG1842	Transcription	Signal transduction mechanisms
15598927	PA3732		conserved hypothetical protein	1.06	6.54E-01	Glucose	4.0	15959	2	Unknown	COG3789	Function unknown	
15598928	PA3733		hypothetical protein	1.34	4.08E-01	Oktansaeure	5.9	44766	2	Cytoplasmic	COG1804	Energy production and conversion	
15598930	PA3735	thrC	threonine synthase	1.14	1.73E-02	Glucose	6.6	51795	21	Periplasmic	COG0498	Amino acid transport and metabolism	
15598931	PA3736	hom	homoserine dehydrogenase	1.49	1.47E-02	Glucose	5.1	46192	15	Cytoplasmic	COG0460	Amino acid transport and metabolism	
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC	1.4	2.32E-02	Glucose	8.8	26095	9	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15598937	PA3742	rplS	50S ribosomal protein L19	2.35	1.94E-01	Glucose	11.1	13032	3	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis	
15598938	PA3743	trmD	tRNA (guanine-N1)-methyltransferase	1.39	8.33E-02	Glucose	4.9	28359	3	Cytoplasmic	COG0336	Translation, ribosomal structure and biogenesis	
15598941	PA3746	ffh	signal recognition particle protein Ffh	1.65	2.52E-01	Oktansaeure	10.3	49359	5	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2	1.44	1.46E-02	Oktansaeure	6.1	42342	13	Periplasmic	COG0027	Nucleotide transport and metabolism	
15598948	PA3753		conserved hypothetical protein	1.73	1.69E-01	Glucose	7.0	18509	5	Cytoplasmic	COG0663	General function prediction only	
15598949	PA3754		hypothetical protein	1.23	9.55E-01	Oktansaeure	4.5	22855	2	Cytoplasmic			
15598950	PA3755		conserved hypothetical protein	1.72	9.57E-01	Oktansaeure	4.6	20829	2	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15598955	PA3760		N-Acetyl-D-Glucosamine phosphotransferase system transporter	1.36	5.98E-01	Glucose	5.4	89195	2	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase	1.57	4.22E-02	Glucose	4.8	140646	63	Periplasmic	COG0046	Nucleotide transport and metabolism	
15598960	PA3765		hypothetical protein	1.71	1.03E-02	Oktansaeure	6.3	20903	3	Unknown	COG3644	Function unknown	
15598962	PA3767		conserved hypothetical protein	1.2	4.54E-01	Oktansaeure	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15598964	PA3769	guaA	GMP synthase	1.97	6.53E-03	Glucose	5.6	57959	31	Periplasmic	COG0519	Nucleotide transport and metabolism	
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase	1.52	2.22E-02	Glucose	6.7	51707	26	Periplasmic	COG0516	Nucleotide transport and metabolism	
15598978	PA3783		hypothetical protein	1.99	6.08E-02	Oktansaeure	6.4	23091	8	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15598980	PA3785		conserved hypothetical protein	4.86	5.07E-03	Oktansaeure	6.8	17000	11	Periplasmic	COG2847	Inorganic ion transport and metabolism	
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precursor	3.65	1.61E-02	Oktansaeure	6.4	79303	15	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15598990	PA3795		probable oxidoreductase	1.62	2.96E-03	Oktansaeure	5.3	34803	6	Cytoplasmic	COG0667	Energy production and conversion	

15598992	PA3797		conserved hypothetical protein		1.19	3.16E-01	Glucose	5.8	29996	4	Cytoplasmic	COG0388	General function prediction only	
15598993	PA3798		probable aminotransferase		1.23	1.51E-01	Oktansaeure	6.2	42594	6	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598996	PA3801		conserved hypothetical protein		2.13	1.85E-01	Oktansaeure	4.8	23108	4	Outer Membrane Vesicle	COG2976	Function unknown	
15598997	PA3802	hisS	histidyl-tRNA synthetase		1.46	1.67E-02	Glucose	5.0	47480	14	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE		1.19	3.68E-01	Glucose	6.4	40056	12	Cytoplasmic	COG0821	Lipid metabolism	
15599000	PA3805	pilF	type 4 fimbrial biogenesis protein PilF		1.34	3.53E-01	Glucose	7.3	28537	2	Periplasmic	COG3063	Cell motility and secretion	Intracellular trafficking and secretion
15599001	PA3806		conserved hypothetical protein		2.65	8.41E-01	Glucose	8.4	41700	2	Cytoplasmic	COG0820	General function prediction only	
15599002	PA3807	ndk	nucleoside diphosphate kinase		1.66	1.62E-01	Glucose	5.3	15592	12	Cytoplasmic	COG0105	Nucleotide transport and metabolism	
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]		1.37	2.35E-01	Glucose	4.0	12241	5	Cytoplasmic	COG0633	Energy production and conversion	
15599005	PA3810	hscA	heat shock protein HscA		1.37	2.37E-02	Glucose	4.6	66446	18	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599006	PA3811	hscB	heat shock protein HscB		2.56	3.41E-02	Oktansaeure	4.6	20203	3	Cytoplasmic	COG1076	Posttranslational modification, protein turnover, chaperones	
15599008	PA3813	iscU	probable iron-binding protein IscU		3.65	3.47E-02	Glucose	5.8	13753	4	Cytoplasmic	COG0822	Energy production and conversion	
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)		1.7	4.08E-03	Glucose	5.9	44666	22	Cytoplasmic	COG1104	Amino acid transport and metabolism	
15599010	PA3815	iscR	IscR		1.7	5.97E-02	Glucose	6.9	17853	7	Unknown	COG1959	Transcription	
15599012	PA3817		probable methyltransferase		1.29	1.54E-01	Glucose	6.2	28493	7	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis	
15599013	PA3818		extragenic suppressor protein SuhB		1.53	1.94E-02	Glucose	6.6	29521	10	Periplasmic	COG0483	Carbohydrate transport and metabolism	
15599014	PA3819		conserved hypothetical protein		2.13	1.21E-01	Oktansaeure	9.4	18941	2	Outer Membrane	COG3134	Function unknown	
15599017	PA3822		conserved hypothetical protein		1.77	5.91E-03	Glucose	9.6	11862	2	Outer Membrane Vesicle	COG1862	Intracellular trafficking and secretion	
15599018	PA3823	tgt	queuine tRNA-ribosyltransferase		1.18	3.67E-01	Glucose	6.9	41205	3	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis	
15599029	PA3834	valS	valyl-tRNA synthetase		1.68	9.52E-02	Glucose	5.2	107707	47	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis	
15599031	PA3836		hypothetical protein		1.34	2.32E-01	Oktansaeure	8.7	34220	19	Periplasmic	COG2984	General function prediction only	
15599039	PA3844		hypothetical protein		2.57	7.06E-03	Oktansaeure	4.8	22795	5	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599041	PA3846		hypothetical protein		4.19	1.09E-02	Oktansaeure	5.1	19892	6	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15599044	PA3849		conserved hypothetical protein		1.61	1.79E-01	Oktansaeure	5.1	37930	3	Cytoplasmic	COG3081	General function prediction only	
15599045	PA3850		hypothetical protein		1.02	8.45E-01	Glucose	4.4	33613	2	Unknown			
15599047	PA3852		hypothetical protein		2.7	8.77E-04	Oktansaeure	5.4	33979	3	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599050	PA3855		hypothetical protein		1.61	1.05E-01	Oktansaeure	7.9	26286	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599053	PA3858		probable amino acid-binding protein		3.17	1.50E-02	Oktansaeure	7.9	37043	10	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599054	PA3859		carboxylesterase		2.27	2.13E-03	Oktansaeure	4.9	23420	7	Unknown	COG0400	General function prediction only	
15599055	PA3860		probable AMP-binding enzyme		9.86	1.50E-05	Oktansaeure	6.2	68986	17	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599060	PA3865		probable amino acid binding protein		1.17	5.89E-01	Oktansaeure	6.1	28433	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599061	PA3866		pyocin protein		2.58	1.40E-01	Glucose	8.8	80731	5	Extracellular			
15599074	PA3879	narL	two-component response regulator NarL		3.15	7.05E-02	Oktansaeure	4.8	24255	2	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599077	PA3882		hypothetical protein		1.11	5.51E-01	Glucose	7.5	28238	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15599081	PA3886		hypothetical protein		1.22	1.93E-01	Glucose	4.9	32290	4	Cytoplasmic	COG0647	Carbohydrate transport and metabolism	
15599091	PA3896		probable 2-hydroxyacid dehydrogenase		1.06	6.43E-01	Glucose	8.2	35632	9	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599098	PA3903	prfC	peptide chain release factor 3		1.33	6.35E-01	Oktansaeure	5.7	59865	13	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
15599100	PA3905		hypothetical protein		1.17	5.96E-01	Glucose	7.7	20024	5	Unknown			
15599103	PA3908		hypothetical protein		1.31	1.28E-01	Oktansaeure	5.0	27294	9	Cytoplasmic			
15599113	PA3918	moaC	molybdopterin biosynthetic protein C		1.38	3.08E-01	Glucose	7.0	17306	13	Cytoplasmic	COG0315	Coenzyme metabolism	
15599114	PA3919		conserved hypothetical protein		5.43	1.97E-04	Oktansaeure	6.3	51700	15	Cytoplasmic	COG1875	General function prediction only	
15599117	PA3922		conserved hypothetical protein		1.98	1.18E-01	Oktansaeure	9.0	51229	17	Periplasmic			
15599118	PA3923		hypothetical protein		2.14	4.76E-02	Oktansaeure	4.7	69590	5	Outer Membrane			
15599119	PA3924		probable medium-chain acyl-CoA ligase		1.34	4.13E-01	Oktansaeure	6.0	62315	22	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599120	PA3925		probable acyl-CoA thiolase		6.23	1.01E-04	Oktansaeure	6.4	40553	27	Cytoplasmic	COG0183	Lipid metabolism	
15599126	PA3931		conserved hypothetical protein		1.76	3.36E-02	Oktansaeure	8.6	28101	13	Periplasmic	COG1464	Inorganic ion transport and metabolism	
15599133	PA3938		probable periplasmic taurine-binding protein precursor		5.62	3.43E-03	Oktansaeure	7.9	35859	11	Unknown	COG4521	Inorganic ion transport and metabolism	
15599135	PA3940		probable DNA binding protein		1.45	5.75E-01	Oktansaeure	9.2	9892	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
15599136	PA3941		hypothetical protein		2.04	1.48E-01	Oktansaeure	5.8	22025	4	Cytoplasmic	COG0546	General function prediction only	
15599137	PA3942	tesB	acyl-CoA thioesterase II		1.2	3.13E-01	Glucose	5.8	32934	5	Cytoplasmic	COG1946	Lipid metabolism	
15599139	PA3944		conserved hypothetical protein		2.07	9.00E-04	Oktansaeure	5.3	21857	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15599140	PA3945		conserved hypothetical protein	Infinity		4.08E-04	Oktansaeure	5.7	22403	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
15599143	PA3948	rocA1	Two-component response regulator RocA1		1.69	1.58E-01	Oktansaeure	6.8	22996	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599146	PA3951		conserved hypothetical protein		1.37	1.87E-01	Glucose	7.5	18088	3	Unknown	COG1432	Function unknown	
15599151	PA3956		hypothetical protein		1.81	1.33E-02	Oktansaeure	5.1	15453	2	Unknown	COG0346	Amino acid transport and metabolism	
15599156	PA3961		probable ATP-dependent helicase		1.48	5.30E-02	Oktansaeure	7.5	91833	2	Cytoplasmic	COG1643	DNA replication, recombination, and repair	
15599160	PA3965		probable transcriptional regulator		1.11	6.55E-01	Glucose	5.7	19289	8	Cytoplasmic	COG1522	Transcription	
15599165	PA3970	amn	AMP nucleosidase		1.13	8.01E-01	Oktansaeure	6.8	56225	11	Cytoplasmic	COG0775	Nucleotide transport and metabolism	
15599167	PA3972		probable acyl-CoA dehydrogenase		3.81	2.05E-03	Oktansaeure	6.4	60338	14	Cytoplasmic	COG1960	Lipid metabolism	
15599170	PA3975	thiD	phosphomethylpyrimidine kinase		1.88	3.06E-02	Glucose	6.2	27979	3	Periplasmic	COG0351	Coenzyme metabolism	
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase		1.07	6.57E-01	Oktansaeure	7.1	22146	6	Unknown	COG0352	Coenzyme metabolism	
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase		1.13	3.65E-01	Oktansaeure	5.6	45398	16	Cytoplasmic	COG0001	Coenzyme metabolism	
15599173	PA3978		hypothetical protein		1.24	1.43E-01	Glucose	4.3	19636	2	Unknown	COG0790	General function prediction only	
15599175	PA3980		conserved hypothetical protein		19.8	1.12E-03	Glucose	5.8	49978	3	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis	
15599178	PA3983		conserved hypothetical protein		1.09	3.57E-01	Glucose	4.6	31549	5	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism	
15599182	PA3987	leuS	leucyl-tRNA synthetase		1.51	1.97E-01	Glucose	5.5	97647	42	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis	
15599183	PA3988		hypothetical protein		1.12	7.32E-01	Oktansaeure	5.0	22884	8	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane	
15599184	PA3989	holA	DNA polymerase III, delta subunit		1.92	2.82E-01	Glucose	6.9	37378	3	Unknown	COG1466	DNA replication, recombination, and repair	
15599191	PA3996	lis	lipoate synthase		3.58	9.56E-03	Glucose	6.9	36733	7	Cytoplasmic	COG0320	Coenzyme metabolism	
15599192	PA3997	lipB	lipoate-protein ligase B		1.31	1.93E-01	Glucose	6.0	23856	4	Cytoplasmic	COG0321	Coenzyme metabolism	
15599199	PA4004		conserved hypothetical protein		1.28	1.53E-01	Glucose	9.2	17791	4	Cytoplasmic	COG1576	Function unknown	
15599201	PA4006	nadD	nicotinic acid mononucleotide adenylyltransferase		1.3	3.04E-01	Glucose	6.4	23801	3	Cytoplasmic	COG1057	Coenzyme metabolism	
15599202	PA4007	proA	gamma-glutamyl phosphate reductase		1.07	4.73E-01	Oktansaeure	5.2	45044	12	Periplasmic	COG0014	Amino acid transport and metabolism	
15599205	PA4010		hypothetical protein		1.16	3.64E-01	Glucose	8.8	26949	5	Cytoplasmic	COG2094	DNA replication, recombination, and repair	
15599210	PA4015		conserved hypothetical protein		1.33	3.89E-01	Oktansaeure	5.6	16700	12	Cytoplasmic	COG2030	Lipid metabolism	
15599212	PA4017		conserved hypothetical protein		2.51	2.97E-02	Oktansaeure	7.1	23164	6	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599214	PA4019		probable aromatic acid decarboxylase		12.45	7.40E-03	Glucose	4.8	22367	2	Cytoplasmic	COG0163	Coenzyme metabolism	
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase		1.41	1.31E-01	Oktansaeure	6.4	48469	6	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599217	PA4022	hdhA	hydrazone dehydrogenase, HdhA		1.72	5.79E-01	Oktansaeure	5.5	54979	17	Outer Membrane Vesicle	COG1012	Energy production and conversion	
15599221	PA4026		probable acetyltransferase		1.44	2.23E-01	Oktansaeure	7.0	18049	10	Cytoplasmic	COG0456	General function prediction only	
15599226	PA4031	ppa	inorganic pyrophosphatase		1.81	1.45E-01	Oktansaeure	4.9	19396	12	Cytoplasmic	COG0221	Energy production and conversion	
15599227	PA4032		probable two-component response regulator		1.11	3.89E-01	Oktansaeure	5.7	27422	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599230	PA4035		hypothetical protein		1.01	8.92E-01	Oktansaeure	6.3	35895	5	Periplasmic	COG4254	Function unknown	
15599238	PA4043	ispA	geranyltranstransferase		1.69	2.46E-01	Glucose	5.1	31464	6	Cytoplasmic	COG0142	Coenzyme metabolism	
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase		1.5	3.59E-02	Oktansaeure	5.5	68049	9	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism
15599243	PA4048		hypothetical protein		2.68	6.13E-02	Oktansaeure	9.4	23085	2	Unknown	COG3577	General function prediction only	
15599247	PA4052	nusB	NusB protein		1	9.65E-01	Oktansaeure	8.5	17675	4	Unknown	COG0781	Transcription	
15599248	PA4053	ribE	6,7-dimethyl-8-ribityllumazine synthase		6.75	2.58E-01	Glucose	5.8	16413	4	Cytoplasmic	COG0054	Coenzyme metabolism	
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase		2.4	7.61E-04	Oktansaeure	5.1	39438	11	Cytoplasmic	COG0108	Coenzyme metabolism	
15599250	PA4055	ribC	riboflavin synthase alpha chain		1.73	6.52E-02	Oktansaeure	6.4	23469	5	Cytoplasmic	COG0307	Coenzyme metabolism	
15599251	PA4056	ribD	riboflavin-specific deaminase/reductase		2.19	5.30E-01	Glucose	7.3	39764	2	Cytoplasmic	COG0117	Coenzyme metabolism	

15599252	PA4057	nrdR	NrdR	1.09	5.55E-01	Oktansaeure	8.0	17925	6	Cytoplasmic	COG1327	Transcription	
15599256	PA4061		probable thioredoxin	1.29	2.74E-01	Oktansaeure	4.4	31878	14	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15599258	PA4063		hypothetical protein	3.25	8.66E-02	Glucose	6.4	21235	2	Periplasmic			
15599262	PA4067	oprG	Outer membrane protein OprG precursor	22.88	1.67E-02	Oktansaeure	4.7	25193	5	Periplasmic	COG3047	Cell envelope biogenesis, outer membrane	
15599263	PA4068		probable epimerase	1.13	3.58E-01	Glucose	5.7	33310	13	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599264	PA4069		hypothetical protein	1.02	9.29E-01	Glucose	6.3	32939	5	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15599274	PA4079		probable dehydrogenase	1.02	9.70E-01	Oktansaeure	5.1	24319	9	Extracellular	COG0300	General function prediction only	
15599305	PA4110	ampC	beta-lactamase precursor	1.86	9.64E-01	Oktansaeure	8.8	43401	2	Periplasmic	COG1680	Defense mechanisms	
15599310	PA4115		conserved hypothetical protein	2.13	2.72E-04	Oktansaeure	7.1	51130	6	Cytoplasmic	COG1611	General function prediction only	
15599311	PA4116	bphO	heme oxygenase, BphO	6.74	9.77E-02	Glucose	4.9	21464	2	Cytoplasmic	COG3230	Inorganic ion transport and metabolism	
15599312	PA4117	bphP	bacterial phytochrome, BphP	1.75	2.98E-01	Glucose	5.7	80930	2	Cytoplasmic Membrane	COG4251	Signal transduction mechanisms	
15599324	PA4129		hypothetical protein	12.86	6.15E-03	Oktansaeure	5.3	18122	6	Unknown	COG3749	Function unknown	
15599357	PA4162		probable short-chain dehydrogenase	2.44	6.78E-02	Oktansaeure	8.0	24857	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599358	PA4163		hypothetical protein	1.2	4.70E-01	Glucose	4.7	60494	20	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599375	PA4180		probable acetolactate synthase large subunit	1.5	1.18E-01	Oktansaeure	6.3	59806	8	Cytoplasmic	COG0028		
15599385	PA4190	pqsL	probable FAD-dependent monooxygenase	3.03	9.27E-02	Oktansaeure	6.3	43975	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15599386	PA4191		probable iron/ascorbate oxidoreductase	1.24	4.41E-01	Oktansaeure	5.8	37441	2	Cytoplasmic	COG3491	General function prediction only	
15599390	PA4195		probable binding protein component of ABC transporter	1.75	1.26E-02	Oktansaeure	7.9	29539	8	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599394	PA4199		probable acyl-CoA dehydrogenase	1.31	1.99E-01	Oktansaeure	5.0	63926	9	Cytoplasmic	COG1960	Lipid metabolism	
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	1.19	3.73E-01	Glucose	4.9	36533	7	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599397	PA4202		hypothetical protein	1.11	4.38E-01	Glucose	8.1	36782	7	Cytoplasmic	COG2070	General function prediction only	
15599399	PA4204	ppgL	periplasmic gluconolactonase, PpgL	1.19	8.16E-01	Oktansaeure	7.4	41616	5	Periplasmic	COG2706	Carbohydrate transport and metabolism	
15599406	PA4211	phzB1	probable phenazine biosynthesis protein	31.27	3.27E-04	Oktansaeure	5.9	18888	5	Cytoplasmic			
15599413	PA4217	phzS	flavin-containing monooxygenase	10.07	5.77E-03	Oktansaeure	5.9	43644	2	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15599423	PA4227	pchR	transcriptional regulator PchR	2.47	1.02E-02	Glucose	7.4	32339	3	Cytoplasmic	COG2207	Transcription	
15599428	PA4232	ssb	single-stranded DNA-binding protein	1.76	1.06E-02	Oktansaeure	5.3	18557	9	Cytoplasmic	COG0629	DNA replication, recombination, and repair	
15599430	PA4234	uvrA	excinuclease ABC subunit A	1.15	6.24E-01	Glucose	6.6	104456	35	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
15599431	PA4235	bfrA	bacterioferritin	1.33	4.99E-01	Oktansaeure	4.8	17940	10	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15599432	PA4236	katA	catalase	2.65	3.54E-02	Oktansaeure	6.7	55589	20	Periplasmic	COG0753	Inorganic ion transport and metabolism	
15599433	PA4237	rplQ	50S ribosomal protein L17	1.17	6.79E-01	Glucose	11.1	14504	3	Outer Membrane Vesicle	COG0203	Translation, ribosomal structure and biogenesis	
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.2	2.80E-01	Oktansaeure	4.6	36649	15	Outer Membrane Vesicle	COG0202	Transcription	
15599435	PA4239	rpsD	30S ribosomal protein S4	1.16	6.63E-01	Oktansaeure	10.5	23277	15	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis	
15599436	PA4240	rpsK	30S ribosomal protein S11	1.46	2.19E-01	Glucose	11.5	13630	5	Outer Membrane Vesicle	COG0100	Translation, ribosomal structure and biogenesis	
15599437	PA4241	rpsM	30S ribosomal protein S13	2.24	2.12E-01	Glucose	11.5	13265	9	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
15599440	PA4244	rplO	50S ribosomal protein L15	1.28	5.49E-01	Glucose	11.6	15174	6	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
15599442	PA4246	rpsE	30S ribosomal protein S5	1.53	4.05E-01	Glucose	10.6	17625	14	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
15599443	PA4247	rplR	50S ribosomal protein L18	7.81	3.99E-02	Glucose	10.9	12662	2	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis	
15599444	PA4248	rplF	50S ribosomal protein L6	1.79	3.01E-01	Oktansaeure	10.5	19099	9	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
15599445	PA4249	rpsH	30S ribosomal protein S8	1.74	2.18E-01	Glucose	10.2	14171	8	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
15599446	PA4250	rpsN	30S ribosomal protein S14	1.93	1.78E-01	Glucose	11.9	11565	4	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
15599447	PA4251	rplE	50S ribosomal protein L5	1.05	7.09E-01	Oktansaeure	10.3	20392	18	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis	
15599448	PA4252	rplX	50S ribosomal protein L24	2.64	2.00E-01	Glucose	11.0	11470	5	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis	
15599449	PA4253	rplN	50S ribosomal protein L14	1.5	1.57E-01	Glucose	11.4	13412	7	Outer Membrane Vesicle	COG0093	Translation, ribosomal structure and biogenesis	
15599452	PA4256	rplP	50S ribosomal protein L16	1.03	9.48E-01	Glucose	11.8	15401	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
15599453	PA4257	rpsC	30S ribosomal protein S3	1.29	4.89E-01	Glucose	10.8	25838	14	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis	
15599454	PA4258	rplV	50S ribosomal protein L22	2.84	1.70E-01	Glucose	10.9	11911	2	Cytoplasmic	COG0091	Translation, ribosomal structure and biogenesis	
15599456	PA4260	rplB	50S ribosomal protein L2	1.27	6.61E-01	Glucose	11.8	29579	4	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
15599457	PA4261	rplW	50S ribosomal protein L23	2.14	3.92E-02	Glucose	10.8	10950	2	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis	
15599458	PA4262	rplD	50S ribosomal protein L4	1.83	3.45E-01	Oktansaeure	10.6	21640	4	Outer Membrane Vesicle	COG0088	Translation, ribosomal structure and biogenesis	
15599459	PA4263	rplC	50S ribosomal protein L3	1.13	8.04E-01	Glucose	10.6	22592	5	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis	
15599461	PA4265	tufA	elongation factor Tu	1.03	7.42E-01	Glucose	5.0	43337	51	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
15599462	PA4266	fusA1	elongation factor G	1.89	3.34E-02	Glucose	4.8	77752	77	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15599463	PA4267	rpsG	30S ribosomal protein S7	1.39	3.14E-01	Glucose	10.9	17504	18	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis	
15599464	PA4268	rpsL	30S ribosomal protein S12	1.36	3.74E-01	Glucose	11.6	13799	6	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	1.16	1.02E-01	Glucose	7.1	154364	109	Outer Membrane Vesicle	COG0086	Transcription	
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	1.43	1.66E-01	Glucose	5.6	150837	117	Periplasmic	COG0085	Transcription	
15599468	PA4272	rplJ	50S ribosomal protein L10	1.06	9.79E-01	Glucose	9.5	17602	10	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
15599469	PA4273	rplA	50S ribosomal protein L1	1.29	3.37E-01	Oktansaeure	10.3	24234	15	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis	
15599470	PA4274	rplK	50S ribosomal protein L11	1.89	5.11E-02	Glucose	10.4	14907	5	Outer Membrane Vesicle	COG0080	Translation, ribosomal structure and biogenesis	
15599471	PA4275	nusG	transcription antitermination protein NusG	1.51	1.89E-01	Oktansaeure	5.8	20130	13	Cytoplasmic	COG0250	Transcription	
15599474	PA4278		hypothetical protein	1.45	1.21E-01	Oktansaeure	5.9	26077	4	Unknown			
15599475	PA4279		hypothetical protein	1.52	4.66E-02	Glucose	5.4	26758	7	Cytoplasmic	COG1521	Transcription	
15599478	PA4282		probable exonuclease	1.07	6.85E-01	Oktansaeure	5.5	138959	8	Extracellular	COG0419	DNA replication, recombination, and repair	
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	1.18	9.50E-02	Oktansaeure	6.7	79084	7	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	1.53	3.78E-01	Glucose	5.5	139379	6	Unknown	COG1074	DNA replication, recombination, and repair	
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	1.2	4.79E-01	Glucose	5.3	132646	6	Cytoplasmic	COG1330	DNA replication, recombination, and repair	
15599482	PA4286		hypothetical protein	1.12	4.84E-01	Glucose	5.2	24815	2	Unknown	COG0095	Coenzyme metabolism	
15599492	PA4296	pprB	two-component response regulator, PprB	12.6	1.53E-02	Oktansaeure	6.7	30557	7	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599504	PA4308		conserved hypothetical protein	1.4	1.43E-02	Oktansaeure	6.5	53246	9	Unknown	COG0433	Replication, recombination, and repair	
15599506	PA4310	pctB	chemotactic transducer PctB	1	6.22E-01	Oktansaeure	4.8	68076	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	1.18	1.97E-01	Glucose	6.5	32410	10	Periplasmic	COG0788	Nucleotide transport and metabolism	
15599511	PA4315	mvaT	transcriptional regulator MvaT, P16 subunit	1.61	2.03E-01	Oktansaeure	10.1	14180	3	Cytoplasmic			
15599512	PA4316	sbcB	exodeoxyribonuclease I	2.57	9.00E-03	Glucose	5.4	55449	5	Cytoplasmic	COG2925	DNA replication, recombination, and repair	
15599518	PA4322		conserved hypothetical protein	1.03	9.15E-01	Oktansaeure	6.2	36661	5	Cytoplasmic	COG0714	General function prediction only	
15599525	PA4329	pykA	pyruvate kinase II	2.54	4.01E-03	Glucose	6.7	52252	30	Periplasmic	COG0469	Carbohydrate transport and metabolism	
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	1.85	2.18E-04	Oktansaeure	6.7	28152	5	Cytoplasmic	COG1024	Lipid metabolism	
15599529	PA4333		probable fumarase	5.11	9.80E-03	Glucose	5.2	54763	25	Periplasmic	COG1951	Energy production and conversion	
15599532	PA4336		conserved hypothetical protein	1.06	9.95E-01	Oktansaeure	6.0	20993	6	Cytoplasmic	COG0693	General function prediction only	
15599536	PA4340		hypothetical protein	2.4	4.14E-02	Oktansaeure	6.1	20988	6	Periplasmic			
15599541	PA4345		hypothetical protein	1.82	8.76E-01	Oktansaeure	4.8	22161	2	Unknown	COG2353	Function unknown	
15599545	PA4349		hypothetical protein	1.75	3.92E-03	Oktansaeure	6.2	31671	8	Unknown	COG1960	Lipid metabolism	
15599548	PA4352		conserved hypothetical protein	18.47	2.22E-03	Oktansaeure	6.2	30972	14	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms	
15599549	PA4353		conserved hypothetical protein	3.19	1.31E-01	Oktansaeure	8.5	22029	2	Cytoplasmic	COG3124	Function unknown	
15599552	PA4356	xenB	xenobiotic reductase	1.97	4.25E-04	Oktansaeure	4.9	37796	20	Periplasmic	COG1902	Energy production and conversion	
15599562	PA4366	sodB	superoxide dismutase	1.19	3.47E-01	Glucose	5.2	21351	7	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein precursor	1.02	8.49E-01	Oktansaeure	4.5	47230	21	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
15599568	PA4372		hypothetical protein	2.09	2.79E-02	Glucose	6.0	38323	8	Outer Membrane Vesicle	COG3489	General function prediction only	
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	1.25	1.98E-02	Oktansaeure	6.7	45690	3	Cytoplasmic	COG1488	Coenzyme metabolism	
15599577	PA4381		probable two-component response regulator	1.04	9.12E-01	Oktansaeure	5.9	25235	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599581	PA4385	groEL	GroEL protein	1.04	7.75E-01	Glucose	4.8	57086	61	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
15599582	PA4386	groES	GroES protein	1.47	8.85E-02	Glucose	4.9	10267	7	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	

15599584	PA4388		hypothetical protein	1.33	6.37E-02	Glucose	6.4	26982	6	Cytoplasmic	COG0748	Inorganic ion transport and metabolism			
15599585	PA4389		probable short-chain dehydrogenase	3.44	1.55E-02	Oktansaeure	7.3	26720	26	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only		
15599591	PA4395		conserved hypothetical protein	1.4	2.22E-01	Oktansaeure	8.2	18044	14	Cytoplasmic	COG1666	Function unknown			
15599595	PA4399		conserved hypothetical protein	1.34	2.87E-01	Oktansaeure	6.1	21065	5	Cytoplasmic	COG2096	Coenzyme transport and metabolism			
15599596	PA4400		probable pyrophosphohydrolase	1.26	1.31E-01	Oktansaeure	5.1	34022	3	Cytoplasmic	COG0352	Coenzyme metabolism			
15599597	PA4401		probable glutathione S-transferase	1.54	2.79E-01	Oktansaeure	5.4	23789	15	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones			
15599598	PA4402	argJ	glutamate N-acetyltransferase	1.31	1.47E-01	Glucose	5.3	41762	22	Cytoplasmic	COG1364	Amino acid transport and metabolism			
15599599	PA4403	secA	secretion protein SecA	1.1	3.62E-01	Glucose	5.4	103854	39	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion			
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.69	1.08E-02	Glucose	5.0	33435	14	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane			
15599603	PA4407	ftsZ	cell division protein FtsZ	1.36	4.73E-02	Glucose	4.7	41218	10	Periplasmic	COG0206	Cell division and chromosome partitioning			
15599604	PA4408	ftsA	cell division protein FtsA	1.33	2.36E-02	Oktansaeure	5.0	44646	13	Cytoplasmic	COG0849	Cell division and chromosome partitioning			
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.08	6.26E-01	Glucose	4.7	34363	12	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane			
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.39	1.54E-01	Glucose	6.1	51949	8	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane			
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.08	4.67E-01	Glucose	5.7	48080	14	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane			
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.32	4.52E-02	Oktansaeure	6.5	47412	14	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane			
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1.11	6.40E-01	Glucose	5.1	51263	12	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane			
15599616	PA4420		conserved hypothetical protein	1.32	3.57E-01	Oktansaeure	7.7	34640	9	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane			
15599619	PA4423		conserved hypothetical protein	2.33	1.45E-01	Glucose	7.2	65629	6	Periplasmic	COG3107	General function prediction only			
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	2.87	3.72E-03	Oktansaeure	4.7	21413	9	Cytoplasmic	COG0279	Carbohydrate transport and metabolism			
15599622	PA4426		conserved hypothetical protein	1.93	1.09E-01	Glucose	9.8	20619	3	Outer Membrane Vesicle	COG2823	General function prediction only			
15599623	PA4427	sspB	stringent starvation protein B	1.57	3.50E-01	Glucose	4.3	14548	3	Unknown	COG2969	General function prediction only			
15599624	PA4428	sspA	stringent starvation protein A	1.01	8.74E-01	Oktansaeure	6.1	23615	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones			
15599625	PA4429		probable cytochrome c1 precursor	1.16	7.20E-01	Glucose	7.5	28993	4	Outer Membrane Vesicle	COG2857	Energy production and conversion			
15599627	PA4431		probable iron-sulfur protein	1.19	5.86E-01	Glucose	6.5	20828	4	Outer Membrane Vesicle	COG0723	Energy production and conversion			
15599628	PA4432	rpsI	30S ribosomal protein S9	1.44	2.30E-01	Glucose	11.8	14615	5	Outer Membrane Vesicle	COG0103	Translation, ribosomal structure and biogenesis			
15599629	PA4433	rplM	50S ribosomal protein L13	1.06	9.04E-01	Glucose	10.4	16029	5	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis			
15599630	PA4434		probable oxidoreductase	2.3	2.78E-03	Oktansaeure	5.7	38644	8	Periplasmic	COG0667	Energy production and conversion			
15599631	PA4435		probable acyl-CoA dehydrogenase	7.99	1.59E-03	Oktansaeure	6.1	42128	5	Cytoplasmic	COG1960	Lipid metabolism			
15599634	PA4438		conserved hypothetical protein	1.53	2.79E-02	Oktansaeure	6.2	41993	4	Cytoplasmic	COG1485	General function prediction only			
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.01	5.91E-01	Glucose	5.8	48961	16	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis			
15599636	PA4440		hypothetical protein	1.41	2.48E-01	Oktansaeure	6.2	22315	7	Unknown	COG2945	General function prediction only			
15599637	PA4441		hypothetical protein	1.97	1.41E-02	Glucose	6.3	16386	3	Outer Membrane Vesicle	COG3105	Function unknown			
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	1.09	2.25E-01	Glucose	5.6	69268	30	Periplasmic	COG2895	Inorganic ion transport and metabolism			
15599639	PA4443	cysD	ATP sulfurylase small subunit	1.19	3.73E-01	Glucose	7.1	35478	15	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism		
15599641	PA4445		conserved hypothetical protein	1.47	7.48E-02	Glucose	5.3	27360	8	Cytoplasmic	COG0327	Function unknown			
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	1.39	5.51E-02	Glucose	6.0	38655	12	Periplasmic	COG0079	Amino acid transport and metabolism			
15599644	PA4448	hisD	histidinol dehydrogenase	1.61	8.57E-03	Glucose	4.9	47179	16	Periplasmic	COG0141	Amino acid transport and metabolism			
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	1.18	6.28E-01	Oktansaeure	9.3	22844	16	Cytoplasmic	COG0040	Amino acid transport and metabolism			
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.03	5.51E-01	Oktansaeure	5.5	44645	20	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane			
15599649	PA4453		conserved hypothetical protein	1.87	1.60E-01	Oktansaeure	9.7	23760	14	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism			
15599650	PA4454		conserved hypothetical protein	2.05	3.14E-01	Glucose	4.7	16557	3	Outer Membrane Vesicle	COG1463	Secondary metabolites biosynthesis, transport, and catabolism			
15599653	PA4457		arabinose-5-phosphate isomerase KdsD	1.26	1.60E-01	Glucose	5.6	34179	13	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane			
15599654	PA4458		conserved hypothetical protein	1.49	1.02E-01	Glucose	5.6	19334	10	Cytoplasmic	COG1778	General function prediction only			
15599656	PA4460		conserved hypothetical protein	1.25	3.72E-01	Glucose	9.6	19126	10	Periplasmic	COG1934	Function unknown			
15599657	PA4461		probable ATP-binding component of ABC transporter	1.2	4.38E-01	Glucose	6.7	26450	2	Outer Membrane Vesicle	COG1137	General function prediction only			
15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.26	1.20E-01	Glucose	4.4	56054	7	Cytoplasmic	COG1508	Transcription			
15599660	PA4464	ptsN	nitrogen regulatory IIA protein	4.75	3.09E-01	Glucose	4.7	16730	3	Cytoplasmic	COG1762	Carbohydrate transport and metabolism	Signal transduction mechanisms		
15599661	PA4465		conserved hypothetical protein	1.26	6.20E-02	Oktansaeure	5.7	32218	5	Cytoplasmic	COG1660	General function prediction only			
15599664	PA4468	sodM	superoxide dismutase	4.89	1.83E-02	Oktansaeure	6.2	22506	7	Periplasmic	COG0605	Inorganic ion transport and metabolism			
15599665	PA4469		hypothetical protein	7.85	1.37E-02	Glucose	6.9	17141	2	Cytoplasmic					
15599666	PA4470	fumC1	fumarate hydratase	4.27	3.65E-03	Oktansaeure	5.9	48695	20	Cytoplasmic	COG0114	Energy production and conversion			
15599668	PA4472	pmbA	PmbA protein	1.49	1.08E-01	Oktansaeure	5.5	47908	8	Cytoplasmic	COG0312	General function prediction only			
15599670	PA4474		conserved hypothetical protein	1.28	4.00E-02	Oktansaeure	5.0	50266	3	Cytoplasmic	COG0312	General function prediction only			
15599671	PA4475		conserved hypothetical protein	1.1	2.68E-01	Oktansaeure	6.8	30724	10	Cytoplasmic	COG0388	General function prediction only			
15599673	PA4477	cafA	cytoplasmic axial filament protein	1.1	6.31E-01	Oktansaeure	5.0	54665	7	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis			
15599674	PA4478		conserved hypothetical protein	1.28	4.50E-01	Oktansaeure	4.7	20974	9	Cytoplasmic	COG0424	Cell division and chromosome partitioning			
15599677	PA4481	mreB	rod shape-determining protein MreB	1.36	2.63E-01	Glucose	5.1	36976	15	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning			
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.66	2.95E-02	Glucose	5.5	51862	19	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis			
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.35	6.64E-02	Glucose	5.1	53081	25	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis			
15599685	PA4489		conserved hypothetical protein	1.49	2.44E-02	Oktansaeure	5.3	167428	23	Outer Membrane Vesicle	COG2373	General function prediction only			
15599686	PA4490		conserved hypothetical protein	4.05	2.10E-03	Oktansaeure	10.3	23969	5	Cytoplasmic Membrane	COG3234	Function unknown			
15599689	PA4493	roxR	RoxR	3.9	1.16E-02	Oktansaeure	5.3	20616	9	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription		
15599691	PA4495		hypothetical protein	2.29	6.13E-03	Oktansaeure	5.9	24879	12	Periplasmic	COG3471	Function unknown			
15599692	PA4496		probable binding protein component of ABC transporter	1.58	1.70E-01	Oktansaeure	7.6	60077	13	Periplasmic	COG0747	Amino acid transport and metabolism			
15599695	PA4499		probable transcriptional regulator	2.91	2.10E-02	Oktansaeure	6.2	20435	4	Cytoplasmic	COG1396	Transcription			
15599698	PA4502		probable binding protein component of ABC transporter	2.35	8.29E-02	Oktansaeure	6.6	58611	2	Periplasmic	COG0747	Amino acid transport and metabolism			
15599704	PA4508		probable transcriptional regulator	1.06	6.56E-01	Oktansaeure	6.7	17334	2	Cytoplasmic	COG1522	Transcription			
15599711	PA4515		conserved hypothetical protein	1.28	2.87E-01	Glucose	6.6	25616	2	Cytoplasmic	COG3128	Function unknown			
15599715	PA4519	speC	ornithine decarboxylase	1.36	4.47E-02	Glucose	4.7	43559	15	Cytoplasmic	COG0019	Amino acid transport and metabolism			
15599718	PA4522	ampD	beta-lactamase expression regulator AmpD	1.53	2.73E-01	Oktansaeure	5.5	21028	3	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane			
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	1.01	9.06E-01	Glucose	5.1	30552	15	Cytoplasmic	COG0157	Coenzyme metabolism			
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	1.61	2.24E-02	Oktansaeure	6.6	15512	6	Outer Membrane Vesicle	COG4969	Cell motility and secretion	Intracellular trafficking and secretion		
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	2.3	1.56E-04	Oktansaeure	5.7	62328	6	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion		
15599725	PA4529	coaE	dephosphocoenzyme A kinase	1.61	1.34E-01	Oktansaeure	6.8	22843	10	Cytoplasmic	COG0237	Coenzyme metabolism			
15599729	PA4533		hypothetical protein	1.31	7.03E-01	Glucose	9.5	17613	3	Periplasmic					
15599738	PA4542	clpB	ClpB protein	1.16	3.73E-01	Oktansaeure	5.1	95005	44	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones			
15599739	PA4543		conserved hypothetical protein	1.29	2.13E-01	Glucose	7.5	26047	5	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism			
15599743	PA4547	pilR	two-component response regulator PilR	1.09	7.18E-01	Glucose	5.9	49737	2	Cytoplasmic	COG2204	Signal transduction mechanisms			
15599744	PA4548		probable D-amino acid oxidase	1.55	1.21E-02	Oktansaeure	6.5	39413	4	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism			
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	1.03	9.80E-01	Glucose	6.4	126583	6	Periplasmic	COG3419	Cell motility and secretion	Intracellular trafficking and secretion		
15599753	PA4557	lytB	LytB protein	2.65	7.10E-02	Glucose	5.2	34762	6	Cytoplasmic	COG0761	Lipid metabolism			
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.55	3.92E-03	Glucose	4.3	15984	8	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones			
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	1.69	5.56E-03	Glucose	6.1	105464	45	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis			
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	1.15	3.14E-01	Glucose	9.1	34340	8	Cytoplasmic	COG0196	Coenzyme metabolism			
15599760	PA4564		conserved hypothetical protein	2.41	6.49E-02	Glucose	9.2	16724	5	Periplasmic	COG3045	Function unknown			
15599761	PA4565	proB	glutamate 5-kinase	1.03	7.71E-01	Glucose	7.3	39845	5	Cytoplasmic	COG0263	Amino acid transport and metabolism			
15599762	PA4566	obg	GTP-binding protein Obg	1.31	1.02E-01	Oktansaeure	4.5	44338	4	Cytoplasmic	COG0536	General function prediction only			
15599764	PA4568	rplU	50S ribosomal protein L21	3.69	1.38E-01	Glucose	10.6	11654	2	Outer Membrane Vesicle	COG0261	Translation, ribosomal structure and biogenesis			
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.21	2.73E-01	Glucose	4.6	34851	15	Cytoplasmic	COG0142	Coenzyme metabolism			
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	1.36	2.93E-01	Oktansaeure	4.5	21795	9	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones			
15599772	PA4576		probable ATP-dependent protease	1.22	2.65E-01	Glucose	4.7	90222	38	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones			

15599776	PA4580		conserved hypothetical protein	1.68	8.33E-02	Oktansaeure	8.2	20498	2	Cytoplasmic	COG3236	Function unknown	
15599783	PA4587	ccpR	cytochrome c551 peroxidase precursor	26.91	1.83E-01	Oktansaeure	6.7	37403	3	Periplasmic	COG1858	Inorganic ion transport and metabolism	
15599784	PA4588	gdhA	glutamate dehydrogenase	1.17	2.35E-01	Glucose	6.0	48856	22	Unknown	COG0334	Amino acid transport and metabolism	
15599791	PA4595		probable ATP-binding component of ABC transporter	1.27	1.01E-01	Oktansaeure	5.4	61302	31	Periplasmic	COG0488	General function prediction only	
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.44	3.81E-02	Glucose	6.0	45157	19	Periplasmic	COG0112	Amino acid transport and metabolism	
15599800	PA4604		conserved hypothetical protein	1.6	2.83E-01	Glucose	4.5	37256	3	Cytoplasmic	COG0523	General function prediction only	
15599804	PA4608		hypothetical protein	3.95	1.44E-01	Oktansaeure	4.5	14573	2	Cytoplasmic			
15599805	PA4609	radA	DNA repair protein RadA	2.72	8.89E-02	Oktansaeure	6.9	48411	2	Unknown	COG1066	Posttranslational modification, protein turnover, chaperones	
15599810	PA4614	mscL	conductance mechanosensitive channel	1.18	6.40E-01	Oktansaeure	4.6	14432	4	Outer Membrane Vesicle	COG1970	Cell envelope biogenesis, outer membrane	
15599811	PA4615		probable oxidoreductase	1.27	4.90E-01	Oktansaeure	5.2	29377	11	Cytoplasmic	COG1018	Energy production and conversion	
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	1.09	7.66E-01	Oktansaeure	4.7	219755	2	Extracellular			
15599822	PA4626	hprA	glycerate dehydrogenase	1.22	3.28E-01	Glucose	6.7	34285	9	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599823	PA4627		conserved hypothetical protein	1.23	9.60E-02	Glucose	8.1	35937	2	Cytoplasmic	COG2813	Translation, ribosomal structure and biogenesis	
15599828	PA4632		hypothetical protein	1.03	7.64E-01	Glucose	7.6	29159	3	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15599829	PA4633		probable chemotaxis transducer	1.56	2.99E-01	Oktansaeure	4.5	76623	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15599830	PA4634		hypothetical protein	4.53	7.27E-02	Glucose	8.7	22996	3	Unknown	COG2135	Function unknown	
15599835	PA4639		hypothetical protein	1.46	1.24E-01	Glucose	9.8	20736	9	Outer Membrane Vesicle			
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.01	9.71E-01	Glucose	7.0	55498	7	Cytoplasmic	COG0579	General function prediction only	
15599839	PA4644		hypothetical protein	1.32	4.26E-01	Oktansaeure	5.9	17109	2	Unknown			
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	1.47	3.39E-01	Oktansaeure	5.6	20639	14	Cytoplasmic	COG0634	Nucleotide transport and metabolism	
15599841	PA4646	upp	uracil phosphoribosyltransferase	1.56	1.85E-01	Oktansaeure	7.0	22938	18	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
15599851	PA4656		conserved hypothetical protein	2.47	2.58E-02	Oktansaeure	8.3	33852	5	Cytoplasmic	COG1090	General function prediction only	
15599852	PA4657		hypothetical protein	2.16	4.16E-02	Oktansaeure	6.8	35913	10	Unknown	COG3380	General function prediction only	
15599856	PA4661	pagL	Lipid A 3-O-deacylase	1.02	9.20E-01	Oktansaeure	6.3	18393	10	Periplasmic			
15599857	PA4662	murI	glutamate racemase	1.45	4.74E-02	Glucose	5.2	28274	4	Cytoplasmic	COG0796	Cell envelope biogenesis, outer membrane	
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	1.21	3.62E-01	Glucose	5.6	26686	6	Cytoplasmic	COG0476	Coenzyme metabolism	
15599860	PA4665	prfA	peptide chain release factor 1	1.09	5.01E-01	Glucose	4.8	40040	3	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis	
15599864	PA4669	ipk	isopentenyl monophosphate kinase	1.64	1.74E-02	Glucose	6.6	30843	7	Unknown	COG1947	Lipid metabolism	
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.52	9.54E-02	Glucose	6.5	34008	21	Periplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
15599866	PA4671		probable ribosomal protein L25	1.3	3.48E-01	Oktansaeure	6.2	21962	12	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis	
15599867	PA4672		peptidyl-tRNA hydrolase	1.01	9.74E-01	Glucose	9.8	20772	6	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis	
15599868	PA4673		conserved hypothetical protein	1.69	8.88E-03	Glucose	4.8	40078	11	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
15599870	PA4675		probable TonB-dependent receptor	1.06	9.01E-01	Glucose	5.2	80952	10	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599871	PA4676		probable carbonic anhydrase	1.51	2.76E-01	Oktansaeure	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15599873	PA4678	rimI	peptide n-acetyltransferase RimI	1.53	2.79E-01	Glucose	6.2	17095	4	Cytoplasmic	COG0456	General function prediction only	
15599874	PA4679		hypothetical protein	1.08	6.80E-01	Glucose	5.0	24841	3	Unknown			
15599881	PA4686		hypothetical protein	5.8	2.69E-02	Glucose	5.3	106827	25	Periplasmic	COG1196	Cell division and chromosome partitioning	
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	1.02	8.09E-01	Glucose	5.5	36149	18	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.04	7.77E-01	Glucose	5.7	36424	31	Periplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	1.15	4.00E-01	Oktansaeure	6.3	17784	10	Cytoplasmic	COG0440	Amino acid transport and metabolism	
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.09	6.58E-01	Oktansaeure	6.8	62986	35	Cytoplasmic	COG0028		
15599895	PA4701		conserved hypothetical protein	1.39	1.58E-01	Glucose	6.0	58344	20	Periplasmic	COG2187	Function unknown	
15599902	PA4708	phuT	Heme-transport protein, PhuT	1.31	1.26E-01	Oktansaeure	7.8	31037	16	Periplasmic	COG4558	Inorganic ion transport and metabolism	
15599903	PA4709		probable hemin degrading factor	1.09	6.06E-01	Oktansaeure	5.6	39057	7	Cytoplasmic	COG3720	Inorganic ion transport and metabolism	
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR precursor	1.61	3.56E-01	Oktansaeure	5.9	84724	11	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599909	PA4715		probable aminotransferase	1.43	2.75E-02	Oktansaeure	8.1	46064	4	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599910	PA4716		hypothetical protein	1.15	4.78E-01	Oktansaeure	5.0	30850	4	Cytoplasmic	COG0384	General function prediction only	
15599911	PA4717		conserved hypothetical protein	4.39	1.26E-02	Oktansaeure	6.1	31861	2	Unknown	COG2321	General function prediction only	
15599914	PA4720	trmA	tRNA (uracil-5-)-methyltransferase	1.29	2.31E-01	Glucose	7.0	41206	2	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis	
15599916	PA4722		probable aminotransferase	1.24	7.18E-02	Oktansaeure	5.7	42567	6	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599917	PA4723	dksA	suppressor protein DksA	1.21	1.94E-01	Oktansaeure	4.8	17344	10	Periplasmic	COG1734	Signal transduction mechanisms	
15599920	PA4726	cbrB	two-component response regulator CbrB	1.21	4.15E-02	Oktansaeure	5.5	52286	22	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	1.1	8.35E-01	Glucose	4.6	18014	3	Cytoplasmic	COG0801	Coenzyme metabolism	
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.43	1.17E-02	Glucose	5.8	27874	11	Periplasmic	COG0413	Coenzyme metabolism	
15599924	PA4730	panC	pantoate--beta-alanine ligase	1.31	1.15E-01	Glucose	6.5	30836	9	Cytoplasmic	COG0414	Coenzyme metabolism	
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.05	5.96E-01	Glucose	6.6	61944	15	Periplasmic	COG0166	Carbohydrate transport and metabolism	
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	1.77	1.57E-01	Oktansaeure	6.2	71624	10	Cytoplasmic	COG0365	Lipid metabolism	
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.24	1.75E-01	Glucose	4.8	75421	54	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis	
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	1.5	6.11E-03	Glucose	6.9	33378	9	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis	
15599938	PA4744	infB	translation initiation factor IF-2	1.22	3.51E-01	Glucose	6.0	90912	44	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis	
15599939	PA4745	nusA	N utilization substance protein A	1.28	2.60E-01	Oktansaeure	4.3	54658	27	Periplasmic	COG0195	Transcription	
15599940	PA4746		conserved hypothetical protein	3.26	1.03E-01	Oktansaeure	4.3	17139	2	Cytoplasmic	COG0779	Function unknown	
15599941	PA4747	secG	secretion protein SecG	1.42	3.24E-01	Oktansaeure	5.1	13207	2	Outer Membrane Vesicle	COG1314	Intracellular trafficking and secretion	
15599942	PA4748	tpiA	triosephosphate isomerase	1.09	5.00E-01	Oktansaeure	5.3	25621	8	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
15599943	PA4749	glmM	phosphoglucosamine mutase	1.65	4.28E-02	Glucose	6.0	47796	5	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15599944	PA4750	folP	dihydropteroate synthase	1.5	5.41E-03	Glucose	5.4	30490	5	Cytoplasmic	COG0294	Coenzyme metabolism	
15599945	PA4751	ftsH	cell division protein FtsH	1.31	1.54E-01	Glucose	5.6	69955	3	Outer Membrane Vesicle	COG0465	Posttranslational modification, protein turnover, chaperones	
15599949	PA4755	greA	transcription elongation factor GreA	2.36	2.60E-03	Oktansaeure	4.7	17158	11	Periplasmic	COG0782	Function unknown	
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	1.43	2.53E-01	Glucose	4.8	117330	77	Periplasmic	COG0458	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.06	4.75E-01	Glucose	5.2	40810	9	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.4	8.43E-02	Glucose	6.0	28324	15	Periplasmic	COG0289	Amino acid transport and metabolism	
15599954	PA4760	dnaJ	DnaJ protein	1.01	9.72E-01	Glucose	7.4	40260	6	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
15599955	PA4761	dnaK	DnaK protein	1.03	7.28E-01	Oktansaeure	4.5	68403	56	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599956	PA4762	grpE	heat shock protein GrpE	1.24	6.65E-01	Oktansaeure	4.2	20702	12	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
15599958	PA4764	fur	ferric uptake regulation protein	1.06	6.73E-01	Oktansaeure	5.9	15234	9	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15599962	PA4768	smpB	SmpB protein	1.05	7.73E-01	Glucose	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones	
15599980	PA4786		probable short-chain dehydrogenase	2.91	3.37E-02	Oktansaeure	9.9	47182	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599987	PA4793		hypothetical protein	1.63	6.52E-02	Oktansaeure	8.4	21281	2	Periplasmic			
15599990	PA4796		hypothetical protein	1.07	6.40E-01	Oktansaeure	4.8	17129	3	Unknown	COG0509	Amino acid transport and metabolism	
15600003	PA4809	fdhE	FdhE protein	1.3	2.53E-01	Oktansaeure	5.8	33830	2	Cytoplasmic	COG3058	Posttranslational modification, protein turnover, chaperones	
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.22	2.26E-02	Glucose	5.2	70667	16	Periplasmic	COG1166	Amino acid transport and metabolism	
15600034	PA4841		conserved hypothetical protein	2.87	3.13E-02	Oktansaeure	4.4	19733	4	Unknown	COG1443	Lipid metabolism	
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	1.25	2.60E-01	Oktansaeure	4.7	16455	10	Unknown	COG0511	Lipid metabolism	
15600041	PA4848	accC	biotin carboxylase	1.76	4.21E-03	Glucose	6.3	48888	18	Periplasmic	COG0439	Lipid metabolism	
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	1.44	6.08E-04	Glucose	4.2	32000	3	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis	
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	2.33	7.46E-03	Glucose	6.5	57665	29	Periplasmic	COG0138	Nucleotide transport and metabolism	
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	1.55	4.02E-03	Glucose	4.7	45212	15	Periplasmic	COG0151	Nucleotide transport and metabolism	
15600059	PA4866		conserved hypothetical protein	1.34	1.56E-01	Oktansaeure	6.3	18743	3	Unknown	COG1247	Cell envelope biogenesis, outer membrane	
15600061	PA4868	ureC	urease alpha subunit	1.92	3.30E-02	Oktansaeure	6.2	60611	13	Cytoplasmic	COG0804	Amino acid transport and metabolism	
15600065	PA4872		hypothetical protein	1.72	2.49E-03	Glucose	5.4	31320	10	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15600073	PA4880		probable bacterioferritin	1.31	4.38E-01	Oktansaeure	4.4	20217	4	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	

15600077	PA4884		hypothetical protein	3.3	1.67E-01	Oktansaeure	9.7	21561	3	Periplasmic				
15600083	PA4890	desT	DesT	3.5	4.30E-03	Oktansaeure	9.1	22899	4	Cytoplasmic	COG1309	Transcription		
15600086	PA4893	ureG	urease accessory protein UreG	4.14	9.66E-04	Oktansaeure	4.6	21991	7	Cytoplasmic	COG0378	Posttranslational modification, protein turnover, chaperones	Transcription	
15600100	PA4907		probable short-chain dehydrogenase	1.54	2.17E-02	Glucose	5.1	27384	12	Cytoplasmic	COG4221	General function prediction only		
15600106	PA4913		probable binding protein component of ABC transporter	9.92	1.63E-02	Oktansaeure	6.6	39798	6	Periplasmic	COG0683	Amino acid transport and metabolism		
15600109	PA4916		hypothetical protein	1.4	2.94E-01	Glucose	6.5	25457	2	Unknown	COG1051	Nucleotide transport and metabolism		
15600111	PA4918		hypothetical protein	2.91	7.60E-03	Glucose	4.7	23821	11	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	2.2	3.55E-04	Glucose	6.3	46095	12	Cytoplasmic	COG1488	Coenzyme metabolism		
15600113	PA4920	nadE	NH3-dependent NAD synthetase	2.75	2.91E-03	Glucose	5.4	29696	17	Periplasmic	COG0171	Coenzyme metabolism		
15600115	PA4922	azu	azurin precursor	1.68	6.88E-03	Oktansaeure	6.9	16008	18	Periplasmic	COG3241	Energy production and conversion		
15600116	PA4923		conserved hypothetical protein	1.18	9.24E-01	Oktansaeure	5.2	20725	4	Unknown	COG1611	General function prediction only		
15600124	PA4931	dnaB	replicative DNA helicase	1.38	1.09E-01	Glucose	4.7	51589	6	Cytoplasmic	COG0305	DNA replication, recombination, and repair		
15600125	PA4932	rplI	50S ribosomal protein L9	1.04	7.94E-01	Glucose	5.3	15532	6	Periplasmic	COG0359	Translation, ribosomal structure and biogenesis		
15600128	PA4935	rpsF	30S ribosomal protein S6	1.01	8.39E-01	Oktansaeure	4.6	16165	16	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis		
15600129	PA4936		probable rRNA methylase	1.37	1.73E-01	Oktansaeure	7.2	27081	2	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis		
15600131	PA4938	purA	adenylosuccinate synthetase	1.98	3.75E-03	Glucose	6.0	46814	21	Periplasmic	COG0104	Nucleotide transport and metabolism		
15600132	PA4939		conserved hypothetical protein	1.26	2.31E-01	Glucose	4.8	42546	8	Cytoplasmic	COG3705	Amino acid transport and metabolism		
15600139	PA4946	mutL	DNA mismatch repair protein MutL	2.02	9.42E-02	Oktansaeure	6.5	69748	4	Cytoplasmic	COG0323	DNA replication, recombination, and repair		
15600141	PA4948		conserved hypothetical protein	1.34	1.30E-01	Oktansaeure	4.7	16463	3	Cytoplasmic	COG0802	General function prediction only		
15600142	PA4949		conserved hypothetical protein	1.07	7.43E-01	Glucose	7.6	51550	4	Unknown	COG0063	Carbohydrate transport and metabolism		
15600144	PA4951	orn	oligoribonuclease	1.3	5.90E-01	Oktansaeure	5.6	20826	3	Cytoplasmic	COG1949	RNA processing and modification		
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	1.09	3.21E-01	Glucose	5.3	29391	9	Cytoplasmic	COG2897	Inorganic ion transport and metabolism		
15600150	PA4957	psd	phosphatidylserine decarboxylase	1.71	1.08E-01	Glucose	7.9	32001	2	Outer Membrane Vesicle	COG0688	Lipid metabolism		
15600152	PA4959	fimX	FimX	1.03	7.58E-01	Glucose	4.9	75992	16	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms		
15600153	PA4960		probable phosphoserine phosphatase	1.37	1.04E-02	Oktansaeure	4.9	46438	7	Cytoplasmic	COG0560	Amino acid transport and metabolism		
15600157	PA4964	parC	topoisomerase IV subunit A	1.21	3.34E-01	Oktansaeure	5.9	83364	16	Cytoplasmic	COG0188	DNA replication, recombination, and repair		
15600160	PA4967	parE	topoisomerase IV subunit B	1.52	4.59E-02	Oktansaeure	5.9	69178	9	Cytoplasmic	COG0187	DNA replication, recombination, and repair		
15600161	PA4968		conserved hypothetical protein	1.42	3.86E-02	Glucose	6.8	22645	4	Unknown	COG3150	General function prediction only		
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	1.23	1.67E-01	Oktansaeure	4.8	30498	3	Cytoplasmic	COG1409	General function prediction only		
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.16	4.00E-01	Glucose	4.7	23133	6	Cytoplasmic				
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	3.18	3.33E-03	Glucose	5.8	69784	20	Cytoplasmic	COG0422	Coenzyme metabolism		
15600167	PA4974		probable outer membrane protein precursor	1.06	9.76E-01	Glucose	5.9	53405	7	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion	
15600180	PA4987		probable transcriptional regulator	1.87	1.64E-01	Oktansaeure	5.6	22368	2	Cytoplasmic	COG1917	Function unknown		
15600185	PA4992		hypothetical protein	1.34	9.66E-03	Glucose	6.4	29030	8	Cytoplasmic	COG0667	Energy production and conversion		
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.01	8.68E-01	Oktansaeure	6.2	50348	15	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane		
15600194	PA5001		hypothetical protein	1.14	2.01E-01	Glucose	8.7	36625	6	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane		
15600198	PA5005		probable carbamoyl transferase	1.06	9.54E-01	Oktansaeure	6.9	66047	10	Outer Membrane Vesicle	COG2192	Posttranslational modification, protein turnover, chaperones		
15600205	PA5012	waaF	heptosyltransferase II	2.53	1.71E-01	Glucose	8.0	38409	4	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane		
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.1	5.16E-01	Glucose	6.2	34084	23	Periplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism	
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	1.12	5.72E-01	Oktansaeure	5.2	110102	25	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms	
15600208	PA5015	aceE	pyruvate dehydrogenase	2.56	1.25E-01	Glucose	5.6	99563	61	Periplasmic	COG2609	Energy production and conversion		
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	1.66	2.78E-01	Glucose	5.0	56676	30	Periplasmic	COG0508	Energy production and conversion		
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	1.12	7.95E-01	Oktansaeure	5.0	23517	7	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones		
15600212	PA5019		conserved hypothetical protein	2.17	8.97E-02	Oktansaeure	6.0	31882	8	Cytoplasmic	COG2961	General function prediction only		
15600213	PA5020		probable acyl-CoA dehydrogenase	1.3	2.85E-01	Glucose	6.2	66235	2	Cytoplasmic	COG1960	Lipid metabolism		
15600218	PA5025	metY	homocysteine synthase	2.35	6.69E-04	Oktansaeure	6.5	45177	10	Cytoplasmic	COG2873	Amino acid transport and metabolism		
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	1.1	7.86E-01	Oktansaeure	6.3	38792	10	Cytoplasmic	COG0407	Coenzyme metabolism		
15600228	PA5035	gltD	glutamate synthase small chain	2.39	1.11E-02	Glucose	6.4	52625	21	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only	
15600229	PA5036	gltB	glutamate synthase large chain precursor	2.06	2.92E-03	Glucose	6.0	161607	77	Cytoplasmic	COG0069	Amino acid transport and metabolism		
15600231	PA5038	aroB	3-dehydroquinate synthase	1.43	1.01E-01	Oktansaeure	5.6	40109	10	Cytoplasmic	COG0337	Amino acid transport and metabolism		
15600232	PA5039	aroK	shikimate kinase	1.1	7.34E-01	Glucose	8.8	19205	2	Cytoplasmic	COG0703	Amino acid transport and metabolism		
15600233	PA5040	pilQ	Type 4 fimbrial biogenesis outer membrane protein PilQ precursor	1.94	1.23E-02	Glucose	5.2	77378	3	Periplasmic	COG4796	Intracellular trafficking and secretion		
15600239	PA5046		malic enzyme	1.87	1.24E-03	Glucose	4.8	45428	34	Periplasmic	COG0281	Energy production and conversion		
15600244	PA5051	argS	arginyl-tRNA synthetase	1.45	9.41E-02	Glucose	5.2	65199	19	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis		
15600246	PA5053	hslV	heat shock protein HslV	1.31	4.28E-01	Glucose	6.7	18767	8	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones		
15600247	PA5054	hslU	heat shock protein HslU	1.5	1.21E-02	Glucose	5.4	50082	14	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones		
15600253	PA5060	phaF	polyhydroxyalkanoate synthesis protein PhaF	18.02	2.07E-01	Oktansaeure	11.1	30577	2	Cytoplasmic	COG3937	Function unknown		
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	1.04	9.18E-01	Oktansaeure	9.5	28254	14	Cytoplasmic	COG2226	Coenzyme metabolism		
15600257	PA5064		hypothetical protein	1.79	1.85E-02	Oktansaeure	6.0	22767	7	Cytoplasmic	COG3165	Function unknown		
15600259	PA5066	hisI	phosphoribosyl-AMP cyclohydrolase	1.07	9.20E-01	Glucose	6.0	15375	6	Cytoplasmic	COG0139	Amino acid transport and metabolism		
15600264	PA5071		conserved hypothetical protein	1.41	5.46E-02	Glucose	9.1	26065	4	Cytoplasmic	COG1385	Function unknown		
15600269	PA5076		probable binding protein component of ABC transporter	1.61	3.07E-02	Glucose	7.6	29736	19	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15600270	PA5077	mdoH	periplasmic glucans biosynthesis protein MdoH	2.63	2.57E-01	Oktansaeure	8.9	96994	2	Outer Membrane Vesicle	COG2943	Cell envelope biogenesis, outer membrane		
15600271	PA5078		conserved hypothetical protein	1.03	7.93E-01	Oktansaeure	7.0	59444	16	Periplasmic	COG3131	Inorganic ion transport and metabolism		
15600272	PA5079		conserved hypothetical protein	1.04	9.10E-01	Glucose	6.3	15530	4	Unknown	COG1490	Translation, ribosomal structure and biogenesis		
15600273	PA5080		prolyl aminopeptidase	1.17	3.95E-01	Oktansaeure	6.2	36515	16	Cytoplasmic	COG0596	General function prediction only		
15600274	PA5081		hypothetical protein	1.44	2.47E-01	Oktansaeure	4.7	17918	3	Cytoplasmic	COG1051	Nucleotide transport and metabolism		
15600283	PA5090		conserved hypothetical protein	440.96	9.45E-03	Oktansaeure	5.8	87821	5	Cytoplasmic	COG3501	Function unknown		
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	1.81	8.48E-02	Oktansaeure	5.9	29791	4	Cytoplasmic	COG3741	Amino acid transport and metabolism		
15600289	PA5096		probable binding protein component of ABC transporter	4.52	4.89E-02	Oktansaeure	5.2	35496	3	Periplasmic	COG2113	Amino acid transport and metabolism		
15600291	PA5098	hutH	histidine ammonia-lyase	4.31	3.24E-02	Oktansaeure	5.8	53779	3	Cytoplasmic	COG2986	Amino acid transport and metabolism		
15600296	PA5103		hypothetical protein	1.15	4.91E-01	Oktansaeure	6.2	37890	2	Periplasmic	COG2113	Amino acid transport and metabolism		
15600297	PA5104		conserved hypothetical protein	4.5	5.66E-02	Oktansaeure	5.6	21415	5	Unknown	COG3758	Function unknown		
15600298	PA5105	hutC	histidine utilization repressor HutC	2.32	1.59E-01	Oktansaeure	7.4	27779	2	Cytoplasmic	COG2188	Transcription		
15600302	PA5109		hypothetical protein	1.82	6.43E-02	Oktansaeure	5.1	22697	7	Cytoplasmic	COG3803	Function unknown		
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	1.57	1.07E-01	Glucose	5.9	37216	10	Periplasmic	COG0158	Carbohydrate transport and metabolism		
15600304	PA5111	gloA3	lactoylglutathione lyase	1.18	6.54E-01	Oktansaeure	4.8	20215	6	Cytoplasmic	COG0346	Amino acid transport and metabolism		
15600305	PA5112	estA	esterase EstA	1.48	2.23E-01	Oktansaeure	4.5	69608	2	Periplasmic	COG3240	Lipid metabolism	General function prediction only	
15600308	PA5115		conserved hypothetical protein	5.6	9.89E-03	Oktansaeure	5.2	20998	5	Cytoplasmic				
15600310	PA5117	typA	regulatory protein TypA	1.65	2.29E-02	Glucose	5.0	66903	21	Periplasmic	COG1217	Signal transduction mechanisms		
15600311	PA5118	thiI	thiazole biosynthesis protein ThiI	1.38	1.34E-01	Glucose	6.7	54849	2	Cytoplasmic	COG0301	Coenzyme metabolism		
15600312	PA5119	glnA	glutamine synthetase	1.14	7.57E-01	Oktansaeure	5.0	51944	24	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism		
15600318	PA5125	ntrC	two-component response regulator NtrC	1.26	3.79E-01	Glucose	5.8	52753	3	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600320	PA5127		probable rRNA methylase	1.34	4.44E-01	Glucose	8.3	17458	2	Unknown	COG0219	Translation, ribosomal structure and biogenesis		
15600321	PA5128	secB	secretion protein SecB	1.16	2.80E-01	Glucose	4.2	18146	11	Periplasmic	COG1952	Intracellular trafficking and secretion		
15600324	PA5131	pgm	phosphoglycerate mutase	1.21	4.23E-01	Glucose	4.9	55601	25	Periplasmic	COG0696	Carbohydrate transport and metabolism		
15600327	PA5134		probable carboxyl-terminal protease	1.32	1.59E-01	Oktansaeure	5.4	46018	6	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane		
15600330	PA5137		hypothetical protein	1.71	2.19E-02	Glucose	7.5	27991	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15600331	PA5138		hypothetical protein	1.16	4.10E-01	Glucose	4.9	27915	11	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15600332	PA5139		hypothetical protein	1.12	9.15E-01	Oktansaeure	5.8	27565	6	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	1.39	6.29E-02	Glucose	4.7	25938	3	Cytoplasmic	COG0106	Amino acid transport and metabolism		

15600335	PA5142	hisH1	glutamine amidotransferase	1.08	8.24E-01	Oktansaeure	6.3	23666	12	Cytoplasmic	COG0118	Amino acid transport and metabolism		
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	1.62	1.01E-01	Oktansaeure	6.5	21937	7	Cytoplasmic	COG0131	Amino acid transport and metabolism		
15600339	PA5146		hypothetical protein	1.12	8.13E-01	Glucose	8.3	80849	6	Outer Membrane Vesicle	COG2982	Cell envelope biogenesis, outer membrane		
15600343	PA5150		probable short-chain dehydrogenase	2.42	9.23E-03	Oktansaeure	6.2	26191	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic binding protein	1.54	2.73E-01	Oktansaeure	4.9	27561	22	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms	
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	1.1	1.55E-01	Oktansaeure	5.9	39542	13	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane		
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	1.02	8.35E-01	Glucose	6.1	33106	9	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane		
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	1.14	4.05E-01	Oktansaeure	5.0	32457	16	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane		
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.22	5.73E-01	Glucose	6.0	20766	11	Unknown	COG1898	Cell envelope biogenesis, outer membrane		
15600359	PA5166	dctD	DctD	1.91	8.96E-03	Glucose	5.5	50864	4	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600360	PA5167	dctP	DctP	3.1	2.44E-02	Oktansaeure	8.8	37051	14	Periplasmic	COG1638	Carbohydrate transport and metabolism		
15600364	PA5171	arcA	arginine deiminase	23.32	9.16E-04	Oktansaeure	5.5	46436	27	Cytoplasmic	COG2235	Amino acid transport and metabolism		
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	17.75	3.25E-03	Oktansaeure	6.6	38108	19	Cytoplasmic	COG0078	Amino acid transport and metabolism		
15600366	PA5173	arcC	carbamate kinase	23.99	3.18E-04	Oktansaeure	5.0	33080	18	Cytoplasmic	COG0549	Amino acid transport and metabolism		
15600367	PA5174		probable beta-ketoacyl synthase	8.85	2.80E-04	Glucose	6.0	68763	28	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism	
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	1.28	2.75E-01	Oktansaeure	4.8	29779	5	Cytoplasmic	COG1218	Inorganic ion transport and metabolism		
15600369	PA5176		conserved hypothetical protein	1.1	8.82E-01	Oktansaeure	4.5	20983	8	Cytoplasmic	COG1051	Nucleotide transport and metabolism		
15600370	PA5177		probable hydrolase	1.22	3.79E-01	Glucose	5.9	25629	5	Cytoplasmic	COG1011	General function prediction only		
15600372	PA5179		probable transcriptional regulator	1.4	3.78E-01	Oktansaeure	6.4	32533	2	Cytoplasmic	COG0583	Transcription		
15600377	PA5184		hypothetical protein	1.1	5.46E-01	Oktansaeure	8.8	20417	10	Periplasmic	COG1605	Amino acid transport and metabolism		
15600379	PA5186		probable iron-containing alcohol dehydrogenase	13.78	8.95E-05	Oktansaeure	5.4	40354	4	Cytoplasmic	COG1454	Energy production and conversion		
15600380	PA5187		probable acyl-CoA dehydrogenase	8.64	1.51E-03	Oktansaeure	5.3	64558	7	Cytoplasmic	COG1960	Lipid metabolism		
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	12.06	1.49E-05	Oktansaeure	5.2	44810	7	Cytoplasmic	COG1250	Lipid metabolism		
15600383	PA5190		probable nitroreductase	1.35	1.62E-01	Oktansaeure	6.0	22450	11	Cytoplasmic	COG0778	Energy production and conversion		
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.02	8.11E-01	Oktansaeure	5.1	55732	32	Periplasmic	COG1866	Energy production and conversion		
15600386	PA5193	yrfI	heat shock protein HSP33	1.26	1.33E-02	Glucose	4.5	32834	9	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones		
15600393	PA5200	amgR	AmgR	1.3	1.00E-01	Oktansaeure	6.6	27924	12	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15600394	PA5201		conserved hypothetical protein	1.36	1.38E-01	Glucose	6.3	84963	38	Periplasmic	COG2183	Transcription		
15600396	PA5203	gshA	glutamate--cysteine ligase	1.28	3.61E-01	Oktansaeure	4.9	59205	16	Cytoplasmic	COG2918	Coenzyme metabolism		
15600397	PA5204	argA	N-acetylglutamate synthase	1.55	5.01E-02	Oktansaeure	6.5	47858	12	Cytoplasmic	COG0548	Amino acid transport and metabolism		
15600401	PA5208		conserved hypothetical protein	11.71	8.95E-04	Oktansaeure	5.2	25644	3	Cytoplasmic	COG1392	Inorganic ion transport and metabolism		
15600403	PA5210		probable secretion pathway ATPase	1.95	1.51E-01	Oktansaeure	6.5	65981	7	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion	
15600406	PA5213	gcvP1	glycine cleavage system protein P1	6.96	2.56E-02	Oktansaeure	6.5	104710	7	Cytoplasmic	COG1003	Amino acid transport and metabolism		
15600407	PA5214	gcvH1	glycine cleavage system protein H1	3.74	4.24E-01	Glucose	3.9	13642	3	Unknown	COG0509	Amino acid transport and metabolism		
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	1.08	7.21E-01	Glucose	5.4	38907	8	Periplasmic	COG0404	Amino acid transport and metabolism		
15600410	PA5217		probable binding protein component of ABC iron transporter	2.62	5.20E-03	Oktansaeure	6.4	36292	4	Periplasmic	COG1840	Inorganic ion transport and metabolism		
15600413	PA5220		hypothetical protein	6.1	7.75E-01	Oktansaeure	6.2	30542	2	Unknown				
15600417	PA5224	pepP	aminopeptidase P	1.14	2.32E-01	Oktansaeure	5.1	49710	12	Cytoplasmic	COG0006	Amino acid transport and metabolism		
15600418	PA5225		hypothetical protein	2.92	1.47E-02	Glucose	4.0	19358	5	Unknown	COG3079	Function unknown		
15600421	PA5228		conserved hypothetical protein	2.9	1.27E-02	Oktansaeure	12.0	23077	3	Unknown	COG0212	Coenzyme metabolism		
15600422	PA5229		conserved hypothetical protein	1.21	3.58E-01	Oktansaeure	7.5	16871	7	Unknown	COG2947	Function unknown		
15600427	PA5234		probable oxidoreductase	1.24	4.15E-01	Glucose	7.0	34011	10	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only	
15600430	PA5237		conserved hypothetical protein	1.65	3.64E-03	Glucose	6.5	54621	3	Cytoplasmic	COG0043	Coenzyme metabolism		
15600432	PA5239	rho	transcription termination factor Rho	1.43	8.00E-03	Oktansaeure	6.8	47069	13	Periplasmic	COG1158	Transcription		
15600433	PA5240	trxA	thioredoxin	1.22	2.63E-01	Glucose	4.5	11870	9	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones		
15600434	PA5241	ppx	exopolyphosphatase	1.08	5.64E-01	Glucose	6.7	56419	9	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism	
15600435	PA5242	ppk	polyphosphate kinase	1.99	1.05E-02	Oktansaeure	7.7	83151	22	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism		
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	2.45	1.43E-02	Oktansaeure	4.8	37005	6	Cytoplasmic	COG0113	Coenzyme metabolism		
15600438	PA5245		conserved hypothetical protein	1.47	3.80E-01	Oktansaeure	4.7	23426	11	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism		
15600445	PA5252		probable ATP-binding component of ABC transporter	1.11	2.99E-01	Glucose	5.9	70871	14	Cytoplasmic	COG0488	General function prediction only		
15600447	PA5254		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	2.28	2.17E-02	Oktansaeure	5.4	23047	2	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones		
15600448	PA5255	algQ	Alginate regulatory protein AlgQ	1.52	3.50E-01	Glucose	4.6	18011	2	Cytoplasmic	COG3160	Transcription		
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	1.25	2.98E-01	Glucose	4.8	27247	4	Unknown	COG1587	Coenzyme metabolism		
15600453	PA5260	hemC	porphobilinogen deaminase	1.08	5.06E-01	Oktansaeure	5.3	33641	5	Cytoplasmic	COG0181	Coenzyme metabolism		
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	3.74	1.17E-02	Oktansaeure	7.3	27608	10	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms	
15600456	PA5263	argH	argininosuccinate lyase	1.15	1.26E-01	Glucose	5.5	51640	14	Periplasmic	COG0165	Amino acid transport and metabolism		
15600459	PA5266		conserved hypothetical protein	125.71	2.73E-04	Oktansaeure	6.4	76707	10	Cytoplasmic	COG3501	Function unknown		
15600467	PA5274	rnk	nucleoside diphosphate kinase regulator	3.03	7.23E-01	Glucose	4.2	14405	2	Cytoplasmic	COG0782	Function unknown		
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.2	1.06E-01	Oktansaeure	5.4	45490	14	Periplasmic	COG0019	Amino acid transport and metabolism		
15600471	PA5278	dapF	diaminopimelate epimerase	1.08	5.57E-01	Oktansaeure	7.7	30320	7	Cytoplasmic	COG0253	Amino acid transport and metabolism		
15600472	PA5279		conserved hypothetical protein	1.05	6.95E-01	Glucose	5.3	25767	5	Cytoplasmic	COG3159	Function unknown		
15600474	PA5281		probable hydrolase	1.01	9.04E-01	Oktansaeure	5.9	25852	3	Cytoplasmic	COG1011	General function prediction only		
15600485	PA5292	pchP	phosphorylcholine phosphatase	1.14	5.67E-01	Glucose	5.8	39117	2	Periplasmic				
15600489	PA5296	rep	ATP-dependent DNA helicase Rep	1.57	2.89E-02	Glucose	6.0	77041	2	Cytoplasmic	COG0210	DNA replication, recombination, and repair		
15600490	PA5297	poxB	pyruvate dehydrogenase (cytochrome)	26.21	1.22E-03	Oktansaeure	6.0	62320	3	Cytoplasmic Membrane	COG0028			
15600491	PA5298		xanthine phosphoribosyltransferase	1.44	1.53E-01	Oktansaeure	6.6	20575	8	Cytoplasmic	COG0503	Nucleotide transport and metabolism		
15600492	PA5299		hypothetical protein	2.16	3.27E-02	Oktansaeure	5.7	68673	3	Cytoplasmic	COG0427	Energy production and conversion		
15600494	PA5301	pauR	probable transcriptional regulator	1.9	1.19E-01	Oktansaeure	5.3	19944	4	Cytoplasmic	COG1396	Transcription		
15600505	PA5312	pauC	Aldehyde dehydrogenase	1.46	3.64E-02	Oktansaeure	5.3	53143	19	Periplasmic	COG1012	Energy production and conversion		
15600506	PA5313	gabT2	Transaminase	8.73	4.37E-02	Oktansaeure	6.7	48347	2	Cytoplasmic	COG0161	Coenzyme metabolism		
15600510	PA5317		probable binding protein component of ABC dipeptide transporter	1.26	1.19E-01	Oktansaeure	7.0	57880	6	Periplasmic	COG0747	Amino acid transport and metabolism		
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine decarboxylase	1.11	2.06E-01	Oktansaeure	6.3	43133	11	Cytoplasmic	COG0452	Coenzyme metabolism		
15600515	PA5322	algC	phosphomannomutase AlgC	1.33	6.40E-02	Glucose	5.0	50295	26	Cytoplasmic	COG1109	Carbohydrate transport and metabolism		
15600516	PA5323	argB	acetylglutamate kinase	1.18	4.08E-01	Glucose	6.8	31849	22	Cytoplasmic	COG0548	Amino acid transport and metabolism		
15600522	PA5329		conserved hypothetical protein	1.33	1.70E-01	Oktansaeure	5.0	17712	5	Cytoplasmic	COG0824	General function prediction only		
15600523	PA5330		hypothetical protein	1.69	2.15E-01	Glucose	9.4	22434	10	Unknown				
15600524	PA5331	pyrE	orotate phosphoribosyltransferase	1.22	5.08E-01	Oktansaeure	5.1	23320	12	Cytoplasmic	COG0461	Nucleotide transport and metabolism		
15600525	PA5332	crc	catabolite repression control protein	1.18	2.90E-01	Glucose	5.2	29844	11	Cytoplasmic	COG0708	DNA replication, recombination, and repair		
15600527	PA5334	rph	ribonuclease PH	1.17	5.28E-01	Oktansaeure	5.9	25654	7	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis		
15600528	PA5335		conserved hypothetical protein	1.21	3.36E-01	Glucose	5.8	31708	13	Cytoplasmic	COG1561	Function unknown		
15600529	PA5336	gmk	guanylate kinase	1.3	4.59E-01	Oktansaeure	5.3	23102	12	Cytoplasmic	COG0194	Nucleotide transport and metabolism		
15600530	PA5337	rpoZ	RNA polymerase omega subunit	1.77	7.58E-02	Glucose	4.0	9775	2	Unknown	COG1758	Transcription		
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.3	1.27E-01	Oktansaeure	9.4	78861	20	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription	
15600532	PA5339		conserved hypothetical protein	1.83	4.53E-01	Glucose	4.8	13610	7	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis		
15600536	PA5343		hypothetical protein	1.18	4.86E-01	Oktansaeure	6.2	30778	4	Unknown	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15600537	PA5344	oxyR	OxyR	1.47	6.95E-02	Oktansaeure	6.7	34295	10	Cytoplasmic	COG0583	Transcription		
15600538	PA5345	recG	ATP-dependent DNA helicase RecG	1.67	2.14E-01	Oktansaeure	7.3	76178	5	Cytoplasmic	COG1200	DNA replication, recombination, and repair	Transcription	
15600539	PA5346	sadB	SadB	1.12	4.00E-01	Glucose	6.0	51427	4	Cytoplasmic	COG1639	Signal transduction mechanisms		
15600540	PA5347		hypothetical protein	2.33	3.49E-02	Oktansaeure	11.1	14726	6	Unknown				
15600542	PA5349		probable rubredoxin reductase	1.03	6.97E-01	Glucose	5.5	40617	11	Cytoplasmic	COG1251	Energy production and conversion		
15600550	PA5357		hypothetical protein	1.17	3.18E-01	Oktansaeure	4.7	19512	9	Cytoplasmic	COG3161	Coenzyme metabolism		

15600552	PA5359		hypothetical protein	3.13	8.98E-02	Oktansaeure	8.0	16472	2	Periplasmic	COG4315	Function unknown		
15600553	PA5360	phoB	two-component response regulator PhoB	1.28	2.39E-01	Oktansaeure	5.1	25711	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription	
15600557	PA5364		probable two-component response regulator	1.8	3.28E-02	Oktansaeure	9.4	32401	4	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU	1.22	2.68E-01	Oktansaeure	5.0	27487	5	Cytoplasmic	COG0704	Inorganic ion transport and metabolism		
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding protein, PstS	1.47	9.10E-02	Glucose	9.5	34473	7	Periplasmic	COG0226	Inorganic ion transport and metabolism		
15600564	PA5371		conserved hypothetical protein	1.22	4.09E-01	Glucose	4.5	14555	2	Unknown	COG1607	Lipid metabolism		
15600566	PA5373	betB	betaine aldehyde dehydrogenase	1.1	7.13E-01	Glucose	5.0	53332	8	Cytoplasmic	COG1012	Energy production and conversion		
15600567	PA5374	betI	transcriptional regulator BetI	1.8	3.49E-01	Oktansaeure	9.0	21861	3	Unknown	COG1309	Transcription		
15600571	PA5378		hypothetical protein	1.29	1.41E-01	Glucose	7.3	34427	9	Periplasmic	COG2113	Amino acid transport and metabolism		
15600588	PA5395		conserved hypothetical protein	1.86	6.30E-02	Oktansaeure	7.8	18513	3	Unknown	COG3558	Function unknown		
15600606	PA5413	ltaA	low specificity l-threonine aldolase	1.64	5.96E-02	Glucose	5.0	38213	7	Cytoplasmic	COG2008	Amino acid transport and metabolism		
15600616	PA5423		hypothetical protein	1.28	2.09E-01	Oktansaeure	5.7	20002	3	Periplasmic	COG3495	Function unknown		
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase	1	9.86E-01	Glucose	5.4	38496	8	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism		
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.03	5.65E-03	Glucose	6.2	16889	10	Unknown	COG0041	Nucleotide transport and metabolism		
15600620	PA5427	adhA	alcohol dehydrogenase	54.94	2.71E-04	Oktansaeure	5.8	35911	10	Outer Membrane Vesicle	COG1064	General function prediction only		
15600622	PA5429	aspA	aspartate ammonia-lyase	4.31	1.05E-02	Oktansaeure	5.6	51069	7	Periplasmic	COG1027	Amino acid transport and metabolism		
15600628	PA5435		probable transcarboxylase subunit	5.65	1.52E-03	Glucose	5.7	66095	50	Cytoplasmic	COG5016	Energy production and conversion		
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase	6.3	3.38E-05	Glucose	6.6	51816	21	Cytoplasmic	COG0439	Lipid metabolism		
15600631	PA5438		probable transcriptional regulator	9.98	5.28E-03	Oktansaeure	7.2	31648	3	Cytoplasmic	COG1737	Transcription		
15600632	PA5439		probable glucose-6-phosphate dehydrogenase	1.43	1.88E-01	Oktansaeure	7.2	54573	2	Cytoplasmic	COG0364	Carbohydrate transport and metabolism		
15600634	PA5441		hypothetical protein	1.21	3.29E-01	Oktansaeure	4.6	80036	34	Periplasmic				
15600636	PA5443	uvrD	DNA helicase II	1.01	9.39E-01	Glucose	5.7	81494	17	Cytoplasmic	COG0210	DNA replication, recombination, and repair		
15600645	PA5452	wbpW	phosphomannose isomerase/GDP-mannose WbpW	3.13	1.66E-04	Oktansaeure	6.4	52574	2	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane		
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase	1.89	1.70E-02	Oktansaeure	6.5	36399	9	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane		
15600647	PA5454	rmd	oxidoreductase Rmd	2.68	1.01E-02	Oktansaeure	6.7	33910	6	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism	
15600650	PA5457		hypothetical protein	5.09	1.15E-01	Oktansaeure	6.2	31744	2	Cytoplasmic	COG2227	Coenzyme metabolism		
15600652	PA5459		hypothetical protein	1.68	1.13E-01	Oktansaeure	4.7	30701	7	Cytoplasmic	COG2226	Coenzyme metabolism		
15600668	PA5475		hypothetical protein	78.56	3.33E-04	Oktansaeure	4.8	21000	7	Cytoplasmic				
15600674	PA5481		hypothetical protein	4.93	2.19E-04	Oktansaeure	5.2	17366	4	Periplasmic				
15600676	PA5483	algB	two-component response regulator AlgB	1.2	1.45E-01	Oktansaeure	5.2	49323	7	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA	1.71	6.71E-02	Oktansaeure	6.4	23375	12	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones		
15600683	PA5490	cc4	cytochrome c4 precursor	1.18	5.99E-01	Glucose	7.6	20735	5	Outer Membrane Vesicle	COG2863	Energy production and conversion		
15600685	PA5492		conserved hypothetical protein	1.86	1.92E-02	Oktansaeure	7.1	23786	8	Unknown	COG0218	General function prediction only		
15600686	PA5493	polA	DNA polymerase I	1.39	2.47E-01	Glucose	4.8	99792	47	Periplasmic	COG0749	DNA replication, recombination, and repair		
15600689	PA5496	nrdJb	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, NrdJb	5.07	1.25E-02	Oktansaeure	6.4	24886	3	Cytoplasmic	COG0209	Nucleotide transport and metabolism		
15600690	PA5497	nrdJa	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, NrdJa	4.16	2.05E-02	Oktansaeure	6.0	82741	7	Cytoplasmic	COG0209	Nucleotide transport and metabolism		
15600692	PA5499	np20	transcriptional regulator np20	1.25	4.81E-01	Glucose	6.9	18216	2	Cytoplasmic	COG0735	Inorganic ion transport and metabolism		
15600698	PA5505		probable TonB-dependent receptor	1.32	7.22E-02	Glucose	8.7	28065	17	Periplasmic	COG1464	Inorganic ion transport and metabolism		
15600700	PA5507		hypothetical protein	1.24	2.93E-01	Oktansaeure	6.4	24262	7	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15600709	PA5516	pdxY	pyridoxamine kinase	1.03	7.48E-01	Glucose	6.0	31285	5	Cytoplasmic	COG2240	Coenzyme metabolism		
15600712	PA5519		conserved hypothetical protein	2.07	9.85E-03	Glucose	7.5	21215	4	Unknown	COG1607	Lipid metabolism		
15600713	PA5520		hypothetical protein	1.09	6.96E-01	Glucose	5.1	26250	2	Unknown				
15600714	PA5521		probable short-chain dehydrogenase	1.03	9.83E-01	Oktansaeure	5.8	26894	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15600717	PA5524		probable short-chain dehydrogenase	1.09	5.10E-01	Glucose	5.0	27158	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only	
15600735	PA5542		hypothetical protein	1	9.27E-01	Glucose	6.3	45872	3	Unknown	COG1680	Defense mechanisms		
15600738	PA5545		conserved hypothetical protein	2.29	2.05E-01	Oktansaeure	7.8	33627	13	Periplasmic	COG2358	General function prediction only		
15600739	PA5546		conserved hypothetical protein	9.38	3.54E-04	Oktansaeure	5.7	44096	9	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane		
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.16	1.21E-01	Oktansaeure	5.9	66294	27	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane		
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	1.06	6.35E-01	Glucose	6.2	48851	8	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane		
15600747	PA5554	atpD	ATP synthase beta chain	1.16	5.94E-02	Glucose	4.7	49499	33	Periplasmic	COG0055	Energy production and conversion		
15600748	PA5555	atpG	ATP synthase gamma chain	1.19	3.16E-01	Glucose	8.1	31553	13	Outer Membrane Vesicle	COG0224	Energy production and conversion		
15600749	PA5556	atpA	ATP synthase alpha chain	1.25	1.41E-01	Glucose	5.1	55393	23	Periplasmic	COG0056	Energy production and conversion		
15600750	PA5557	atpH	ATP synthase delta chain	1.57	1.69E-01	Oktansaeure	5.9	19260	10	Outer Membrane Vesicle	COG0712	Energy production and conversion		
15600751	PA5558	atpF	ATP synthase B chain	1.72	1.14E-02	Glucose	5.8	16924	11	Outer Membrane Vesicle	COG0711	Energy production and conversion		
15600753	PA5560	atpB	ATP synthase A chain	1.07	8.28E-01	Oktansaeure	6.5	31921	2	Outer Membrane Vesicle	COG0356	Energy production and conversion		
15600755	PA5562	spoOJ	chromosome partitioning protein Spo0J	1.46	1.39E-01	Oktansaeure	10.0	31969	4	Cytoplasmic	COG1475	Transcription		
15600756	PA5563	soj	chromosome partitioning protein Soj	1.44	1.33E-01	Oktansaeure	6.1	28609	2	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning		
15600757	PA5564	gidB	glucose inhibited division protein B	1.82	1.32E-01	Oktansaeure	6.3	23735	5	Unknown	COG0357	Cell envelope biogenesis, outer membrane		
15600758	PA5565	gidA	glucose-inhibited division protein A	1.84	2.33E-03	Glucose	6.5	69605	8	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning		
15600760	PA5567		conserved hypothetical protein	2.3	1.01E-01	Oktansaeure	4.9	48744	2	Cytoplasmic	COG0486	General function prediction only		
15600761	PA5568		conserved hypothetical protein	2.79	7.23E-02	Glucose	8.0	64074	2	Outer Membrane Vesicle	COG0706	Intracellular trafficking and secretion		
15600762	PA5569	rnpA	ribonuclease P protein component	1.14	6.90E-01	Glucose	11.5	15282	5	Unknown	COG0594	Translation, ribosomal structure and biogenesis		
375041995				1.3	4.54E-01	Oktansaeure			91					
22001796				1.1	5.99E-01	Glucose			32					
313111914				9.71	1.55E-03	Oktansaeure			23					
313110180				1.45	6.70E-02	Glucose			25					
375044686				1.11	6.53E-01	Oktansaeure			20					
107100513				1.18	6.20E-02	Oktansaeure			17					
296388504				1.07	4.96E-01	Oktansaeure			23					
347307435				1.51	2.34E-03	Oktansaeure			14					
239949862				1.39	5.91E-02	Oktansaeure			16					
239949861				1.06	6.67E-01	Glucose			14					
308154506				1.96	6.36E-01	Oktansaeure			11					
107104524				1.19	3.77E-01	Oktansaeure			11					
375041918				2.36	2.23E-02	Oktansaeure			11					
308198348				1.01	9.86E-01	Oktansaeure			10					
282403589				1.2	4.89E-01	Oktansaeure			9					
346058454				2.59	1.44E-01	Oktansaeure			8					
344189438				1.71	1.77E-01	Oktansaeure			8					
296389665				1.17	4.83E-01	Glucose			7					
107104196				6.51	9.42E-02	Oktansaeure			7					
107102694				1.1	5.37E-01	Oktansaeure			7					
107099078				4.85	6.61E-02	Oktansaeure			6					
15826101				43.12	1.17E-02	Oktansaeure			6					
107101116				1.56	1.42E-01	Oktansaeure			7					
107100575				3.38	4.78E-04	Oktansaeure			6					
313112332				2	3.01E-02	Glucose			6					
107099288				3.17	2.02E-03	Oktansaeure			5					
359783701				1.12	5.36E-01	Oktansaeure			2					
107102668				1.15	3.73E-01	Oktansaeure			4					
107103573				1.2	1.82E-01	Glucose			4					

254236426		1.28	2.80E-01	Glucose	4
107102551		1.43	2.13E-01	Oktansaeure	4
289625348		11.02	2.05E-03	Oktansaeure	2
107102888		1.98	7.62E-04	Oktansaeure	3
149194851		1.96	3.20E-01	Oktansaeure	3
107101938		2.22	6.58E-03	Oktansaeure	3
355639818		2	2.08E-01	Oktansaeure	3
254244230		1.34	5.14E-01	Glucose	3
359782167		1.31	2.66E-01	Oktansaeure	3
107102789		1.08	9.41E-01	Glucose	3
107104298		1.54	5.81E-02	Oktansaeure	3
295698607		1.41	5.39E-01	Glucose	2
258591310		3.06	7.75E-01	Oktansaeure	2
347305107		1.79	2.39E-01	Oktansaeure	2
254240896		3.17	4.45E-02	Oktansaeure	2
222477179		5.11	5.52E-01	Oktansaeure	1
312386137	Infinity		1.76E-01	Glucose	2
56459460		1.66	9.33E-02	Glucose	2
330505329		5.81	5.55E-04	Oktansaeure	2
379708778		6.12	1.05E-03	Oktansaeure	3
70732985		12.45	2.37E-04	Oktansaeure	2
339494273		13.65	1.03E-03	Oktansaeure	3
157830859		2.54	3.13E-01	Glucose	1
327479614		1.12	4.56E-01	Glucose	2
182677049		18.4	1.28E-02	Oktansaeure	3
226944916		10.19	4.45E-03	Oktansaeure	3
88798958		1.36	3.66E-01	Oktansaeure	2
374702386		11.76	1.10E-02	Oktansaeure	2
344942279		1		-	0
254481764		1.38	2.79E-01	Oktansaeure	2
116052531		2.96	2.34E-02	Oktansaeure	2
226946604		4.36	3.06E-04	Oktansaeure	2
330502104		10.57	1.60E-04	Oktansaeure	2
218891628		2.47	5.02E-02	Oktansaeure	2
359782718		5.23	9.31E-03	Oktansaeure	2
374702598		12.89	2.18E-02	Glucose	2
104781332		1.7	1.04E-01	Glucose	3

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.0	8.40E-01	Citronellsäure	4.9	40694	20	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	2.4	2.81E-03	Citronellsäure	5.7	90188	34	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	1.0	8.57E-01	Citronellsäure	4.5	19115	3	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	1.4	2.02E-01	Citronellol	7.9	61755	18	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.4	1.58E-01	Citronellsäure	4.8	73973	27	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	2.2	1.79E-01	Citronellsäure	4.7	36109	10	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	25.3	2.46E-03	Citronellsäure	7.0	33028	7	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	2.2	4.27E-01	Citronellol	4.7	19365	4	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	5.0	2.11E-02	Citronellol	9.4	37586	3	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	10.8	5.08E-02	Citronellsäure	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	5.0	3.23E-03	Citronellsäure	6.3	35095	11	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	8.5	1.06E-03	Citronellsäure	5.8	34774	5	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	14.7	8.88E-03	Citronellsäure	5.5	29484	6	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	2.5	2.85E-02	Citronellsäure	5.0	28488	9	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	1.9	4.57E-02	Citronellsäure	6.3	43680	13	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	1.6	3.13E-01	Citronellsäure	7.1	7863	4	Unknown	COG3360	Function unknown	
15595253	PA0055		hypothetical protein	2.2	4.55E-03	Citronellol	5.7	18433	9	Cytoplasmic	COG3812	Function unknown	
15595263	PA0065		hypothetical protein	19.5	1.59E-01	Citronellsäure	6.1	24951	4	Cytoplasmic	COG0546	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.1	8.83E-02	Citronellsäure	4.9	76011	26	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	6.0	8.89E-03	Citronellol	8.9	31716	4	Periplasmic			
15595273	PA0075	pppA	PppA	4.0	1.16E-01	Citronellsäure	6.2	25904	6	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	3.7	6.79E-02	Citronellsäure	4.4	23856	3	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	1.0	8.02E-01	Citronellsäure	6.1	48275	6	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	1.7	1.37E-01	Citronellsäure	4.9	18785	14	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.6	7.43E-03	Citronellsäure	5.0	55771	26	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	11.3	5.65E-02	Citronellol	6.8	17415	7	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	1.4	6.18E-02	Citronellol	4.4	30361	5	Cytoplasmic	COG4455	General function prediction only	
15595288	PA0090	clpV1	ClpV1	3.3	1.09E-02	Citronellsäure	5.3	98737	31	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	1.0	8.48E-01	Citronellsäure	6.4	72012	16	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	1.1	9.85E-01	Citronellsäure	8.9	44738	5	Cytoplasmic Membrane	COG4104	Function unknown	
15595298	PA0100		hypothetical protein	1.0	9.45E-01	Citronellol	4.1	33723	5	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.6	1.59E-02	Citronellol	6.7	26622	6	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595316	PA0118		hypothetical protein	67.7	9.54E-04	Citronellsäure	6.8	21473	7	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.3	9.04E-02	Citronellol	6.0	53323	8	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	1.9	1.57E-02	Citronellol	6.3	20541	12	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	1.3	2.44E-01	Citronellsäure	5.0	55835	8	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
15595342	PA0144		hypothetical protein	1.6	2.36E-01	Citronellsäure	8.4	22431	6	Unknown	COG3613	Nucleotide transport and metabolism	
15595343	PA0145		hypothetical protein	4.8	2.43E-01	Citronellsäure	4.4	18448	2	Cytoplasmic	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.1	8.31E-01	Citronellol	4.9	36163	5	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595362	PA0164		probable gamma-glutamyltranspeptidase	1.3	4.19E-01	Citronellsäure	6.5	58453	2	Periplasmic	COG0405	Amino acid transport and metabolism	
15595367	PA0169	siaD	SiaD	1.5	3.89E-01	Citronellsäure	9.5	26792	2	Cytoplasmic	COG2199	Signal transduction mechanisms	
15595369	PA0171		hypothetical protein	2.5	1.35E-02	Citronellsäure	7.1	19800	10	Cytoplasmic			
15595372	PA0174		conserved hypothetical protein	6.6	3.26E-02	Citronellol	8.5	22206	2	Cytoplasmic	COG1871	Cell motility and secretion	Signal transduction mechanisms
15595374	PA0176	aer2	aerotaxis transducer Aer2	1.4	2.20E-01	Citronellsäure	4.8	72591	30	Cytoplasmic	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595375	PA0177		probable purine-binding chemotaxis protein	1.3	4.18E-01	Citronellol	4.3	17487	4	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595376	PA0178		probable two-component sensor	2.1	2.65E-01	Citronellsäure	4.5	68931	7	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	1.6	6.18E-02	Citronellsäure	5.9	38650	20	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595405	PA0208	mdcA	malonate decarboxylase alpha subunit	1.1	6.75E-01	Citronellol	6.4	61424	6	Cytoplasmic	COG4670	Lipid metabolism	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	1.5	1.02E-02	Citronellol	4.5	30343	10	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	1.8	1.10E-02	Citronellol	7.1	28496	9	Cytoplasmic			
15595420	PA0223		probable dihydrodipicolinate synthetase	15.4	7.48E-04	Citronellsäure	5.2	31652	2	Cytoplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
15595423	PA0226		probable CoA transferase, subunit A	1.3	1.61E-01	Citronellol	6.2	30920	3	Cytoplasmic	COG1788	Lipid metabolism	
15595424	PA0227		probable CoA transferase, subunit B	3.1	1.22E-01	Citronellsäure	5.4	27314	4	Cytoplasmic	COG2057	Lipid metabolism	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	2.5	5.97E-03	Citronellol	6.2	49121	4	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	30.2	5.68E-03	Citronellsäure	5.1	27985	4	Unknown	COG0596	General function prediction only	
15595444	PA0247	pobA	p-hydroxybenzoate hydroxylase	1.4	2.45E-02	Citronellsäure	6.8	44323	6	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15595456	PA0259		hypothetical protein	1.1	7.56E-01	Citronellol	5.0	52444	4	Unknown			
15595460	PA0263	hcpC	secreted protein Hcp	56.0	1.68E-05	Citronellsäure	5.8	19091	6	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.0	7.73E-01	Citronellsäure	5.4	51622	29	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	1.4	5.48E-03	Citronellsäure	6.4	45220	20	Periplasmic	COG0160	Amino acid transport and metabolism	
15595471	PA0274		hypothetical protein	27.3	1.14E-01	Citronellsäure	8.8	28498	2	Outer Membrane			
15595474	PA0277		conserved hypothetical protein	7.6	2.02E-03	Citronellsäure	6.5	26626	7	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	3.8	7.72E-02	Citronellsäure	9.0	36433	13	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	1.1	7.94E-01	Citronellsäure	9.1	49667	4	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.1	8.07E-01	Citronellol	4.6	41191	3	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595491	PA0294	aguR	transcriptional regulator AguR	6.4	1.53E-02	Citronellsäure	6.4	24424	2	Cytoplasmic	COG1309	Transcription	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	2.3	1.93E-02	Citronellsäure	4.6	50907	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595494	PA0297	spuA	probable glutamine amidotransferase	41.3	1.42E-04	Citronellsäure	6.4	26477	3	Unknown	COG2071	General function prediction only	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	1.5	2.82E-01	Citronellsäure	5.0	50965	6	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595496	PA0299	spuC	Polyamine:pyruvate transaminase	1.1	6.03E-01	Citronellsäure	6.0	50453	22	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	22.8	1.42E-04	Citronellsäure	7.6	40629	17	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	8.2	1.56E-02	Citronellsäure	5.5	40069	15	Periplasmic	COG0687	Amino acid transport and metabolism	
15595506	PA0309		hypothetical protein	24.4	2.10E-03	Citronellsäure	7.6	27021	4	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	39.0	2.75E-05	Citronellsäure	9.7	28005	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15595512	PA0315		hypothetical protein	3.1	1.29E-01	Citronellol	7.2	15463	7	Unknown			
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.2	3.19E-01	Citronellsäure	6.5	44216	18	Periplasmic	COG0111	Amino acid transport and metabolism	
15595514	PA0317		hypothetical protein	1.9	2.16E-02	Citronellol	4.9	51286	15	Periplasmic	COG0277	Energy production and conversion	
15595515	PA0318		conserved hypothetical protein	56.5	1.17E-03	Citronellsäure	5.3	23843	5	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15595520	PA0323		probable binding protein component of ABC transporter	2.4	2.25E-01	Citronellol	6.8	38901	2	Periplasmic	COG0687	Amino acid transport and metabolism	
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	9.0	1.05E-02	Citronellsäure	5.3	23721	10	Cytoplasmic	COG0120	Carbohydrate transport and metabolism	
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	1.7	2.25E-02	Citronellsäure	6.5	55351	6	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15595532	PA0335		hypothetical protein	1.2	3.45E-01	Citronellsäure	4.5	24353	7	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.4	2.31E-01	Citronellsäure	9.5	18726	7	Cytoplasmic	COG0494	DNA replication, recombination, and repair	General function prediction only
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.2	3.26E-01	Citronellol	5.6	83606	19	Cytoplasmic	COG3605	Signal transduction mechanisms	
15595536	PA0339		hypothetical protein	1.2	4.83E-01	Citronellsäure	6.7	26527	8	Unknown	COG3332	Function unknown	
15595539	PA0342	thyA	thymidylate synthase	2.6	7.75E-03	Citronellol	6.5	30016	3	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
15595547	PA0350	folA	dihydrofolate reductase	2.0	2.97E-01	Citronellsäure	5.3	18203	4	Unknown	COG0262	Coenzyme metabolism	
15595548	PA0351		conserved hypothetical protein	3.7	2.84E-01	Citronellol	6.7	17217	2	Cytoplasmic	COG0622	General function prediction only	
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.5	9.22E-03	Citronellsäure	6.0	65160	28	Periplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15595552	PA0355	pfpI	protease PfpI	2.6	1.68E-01	Citronellol	5.0	19246	8	Cytoplasmic	COG0693	General function prediction only	
15595553	PA0356		hypothetical protein	1.3	3.13E-01	Citronellsäure	5.3	30360	3	Unknown	COG1639	Signal transduction mechanisms	
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	4.0	1.91E-01	Citronellol	9.0	17771	5	Cytoplasmic	COG0669	Coenzyme metabolism	
15595561	PA0364		probable oxidoreductase	11.0	1.03E-03	Citronellol	7.0	57805	9	Unknown	COG2303	Amino acid transport and metabolism	
15595563	PA0366		probable aldehyde dehydrogenase	13.1	1.83E-05	Citronellol	9.2	52876	15	Cytoplasmic	COG1012	Energy production and conversion	
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	3.8	3.67E-02	Citronellsäure	4.5	48391	10	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.2	5.13E-01	Citronellsäure	4.8	28234	9	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
15595579	PA0382	micA	DNA mismatch repair protein MicA	3.8	7.79E-02	Citronellsäure	8.3	25331	3	Cytoplasmic	COG0220	General function prediction only	
15595580	PA0383		conserved hypothetical protein	1.6	7.22E-03	Citronellsäure	8.3	50243	9	Unknown			
15595584	PA0387		conserved hypothetical protein	2.8	6.83E-02	Citronellol	6.1	21242	7	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	5.2	5.55E-02	Citronellsäure	4.5	28094	7	Cytoplasmic	COG0345	Amino acid transport and metabolism	
15595591	PA0394		conserved hypothetical protein	2.9	4.77E-01	Citronellol	6.7	24505	6	Cytoplasmic	COG0325	General function prediction only	
15595592	PA0395	pilT	twitching motility protein PilT	2.9	1.23E-01	Citronellsäure	6.9	38021	4	Cytoplasmic	COG2805	Cell motility and secretion	Intracellular trafficking and secretion
15595596	PA0399		cystathionine beta-synthase	1.1	6.36E-02	Citronellol	5.5	49170	16	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15595597	PA0400		probable cystathionine gamma-lyase	1.3	4.79E-01	Citronellsäure	6.6	42786	10	Cytoplasmic	COG0626	Amino acid transport and metabolism	
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.1	5.01E-01	Citronellol	5.8	44150	8	Periplasmic	COG0044	Nucleotide transport and metabolism	
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.0	5.57E-01	Citronellsäure	6.8	36629	9	Periplasmic	COG0540	Nucleotide transport and metabolism	
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.8	3.25E-02	Citronellol	5.7	18676	8	Cytoplasmic	COG2065	Nucleotide transport and metabolism	
15595604	PA0407	gshB	glutathione synthetase	1.0	7.76E-01	Citronellsäure	5.8	35705	13	Periplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
15595610	PA0413	chpA	component of chemotactic signal transduction system	4.2	3.11E-02	Citronellsäure	4.2	268573	27	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595612	PA0415	chpC	probable chemotaxis protein	3.4	5.66E-02	Citronellsäure	4.7	17625	6	Unknown			

15595615	PA0418		hypothetical protein	2.2	1.79E-01	Citronellol	5.6	52140	2	Cytoplasmic			
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1.3	2.07E-01	Citronellol	6.3	52478	8	Cytoplasmic	COG0161	Coenzyme metabolism	
15595620	PA0423	pasP	PasP	7.9	3.99E-03	Citronellsäure	6.5	20776	17	Periplasmic	COG2353	Function unknown	
15595622	PA0425	mexA	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexA precursor	1.4	2.45E-01	Citronellol	9.2	40969	3	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15595623	PA0426	mexB	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB	8.1	5.90E-03	Citronellol	5.4	112790	4	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15595624	PA0427	oprM	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	8.9	3.15E-04	Citronellol	5.3	52598	3	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15595626	PA0429		hypothetical protein	5.7	8.30E-03	Citronellsäure	7.0	40872	4	Cytoplasmic			
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	2.5	1.42E-01	Citronellsäure	6.5	32196	16	Periplasmic	COG0685	Amino acid transport and metabolism	
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	1.0	6.86E-01	Citronellsäure	6.0	51400	36	Periplasmic	COG0499	Coenzyme metabolism	
15595631	PA0434		hypothetical protein	46.3	9.94E-03	Citronellol	5.8	81304	6	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15595634	PA0437	codA	cytosine deaminase	1.3	6.05E-02	Citronellol	6.0	47074	5	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15595643	PA0446		conserved hypothetical protein	1.5	1.72E-01	Citronellsäure	5.3	43847	2	Cytoplasmic	COG1804	Energy production and conversion	
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	1.3	1.44E-01	Citronellol	6.1	43311	5	Cytoplasmic	COG1960	Lipid metabolism	
15595656	PA0459		probable ClpA/B protease ATP binding subunit	1.0	9.49E-01	Citronellol	6.7	94143	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595659	PA0462		hypothetical protein	2.0	2.63E-01	Citronellol	10.6	26230	6	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15595664	PA0467		conserved hypothetical protein	2.0	2.85E-01	Citronellol	7.5	23301	5	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15595666	PA0469		hypothetical protein	5.7	4.86E-02	Citronellsäure	4.7	32137	3	Cytoplasmic			
15595670	PA0473		probable glutathione S-transferase	1.1	5.76E-01	Citronellsäure	5.8	28294	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15595679	PA0482	glcB	malate synthase G	1.2	6.30E-01	Citronellol	5.5	78659	66	Periplasmic	COG2225	Energy production and conversion	
15595681	PA0484		conserved hypothetical protein	1.8	2.55E-02	Citronellol	4.5	18553	3	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15595697	PA0500	bioB	biotin synthase	3.2	1.13E-01	Citronellsäure	6.0	39113	2	Cytoplasmic	COG0502	Coenzyme metabolism	
15595698	PA0501	bioF	8-amino-7-oxononanoate synthase	32.4	4.04E-03	Citronellsäure	5.9	42237	3	Cytoplasmic	COG0156	Coenzyme metabolism	
15595699	PA0502		probable biotin biosynthesis protein bioH	5.9	1.72E-01	Citronellsäure	4.3	26494	2	Cytoplasmic	COG0596	General function prediction only	
15595700	PA0503		probable biotin synthesis protein BioC	3.0	1.18E-02	Citronellsäure	9.0	29712	2	Unknown	COG2226	Coenzyme metabolism	
15595701	PA0504	bioD	dethiobiotin synthase	3.2	2.72E-03	Citronellol	5.3	23337	8	Cytoplasmic	COG0132	Coenzyme metabolism	
15595703	PA0506		probable acyl-CoA dehydrogenase	1.5	6.28E-02	Citronellsäure	5.8	65358	49	Periplasmic	COG1960	Lipid metabolism	
15595704	PA0507		probable acyl-CoA dehydrogenase	18.9	4.40E-02	Citronellol	6.4	64349	2	Cytoplasmic	COG1960	Lipid metabolism	
15595705	PA0508		probable acyl-CoA dehydrogenase	1.2	1.79E-01	Citronellsäure	5.1	63628	55	Cytoplasmic	COG1960	Lipid metabolism	
15595743	PA0546	metK	methionine adenosyltransferase	1.2	1.03E-01	Citronellsäure	5.2	42709	26	Cytoplasmic	COG0192	Coenzyme metabolism	
15595745	PA0548	tktA	transketolase	1.2	2.18E-01	Citronellsäure	5.0	72220	31	Periplasmic	COG0021	Carbohydrate transport and metabolism	
15595747	PA0550		conserved hypothetical protein	1.1	8.97E-01	Citronellol	5.4	29834	5	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	5.7	1.61E-02	Citronellsäure	5.8	38743	3	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15595749	PA0552	pgk	phosphoglycerate kinase	10.4	8.47E-04	Citronellsäure	5.1	40404	18	Periplasmic	COG0126	Carbohydrate transport and metabolism	
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	2.2	4.87E-03	Citronellsäure	5.3	38574	25	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
15595755	PA0558		conserved hypothetical protein	13.2	5.44E-03	Citronellsäure	6.2	27987	6	Cytoplasmic	COG2226	Coenzyme metabolism	
15595759	PA0562		probable hydrolase	4.2	1.23E-01	Citronellsäure	5.4	24232	4	Cytoplasmic	COG0637	General function prediction only	
15595768	PA0571		hypothetical protein	81.7	5.68E-05	Citronellsäure	5.0	22501	4	Unknown			
15595773	PA0576	rpoD	sigma factor RpoD	1.6	3.23E-01	Citronellsäure	4.6	69643	23	Outer Membrane Vesicle	COG0568	Transcription	
15595775	PA0578		conserved hypothetical protein	1.4	5.96E-01	Citronellol	6.0	16842	2	Cytoplasmic	COG1610	Function unknown	
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	2.8	2.97E-02	Citronellsäure	6.2	36561	2	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
15595780	PA0583		hypothetical protein	120.6	1.85E-03	Citronellsäure	5.6	20091	3	Cytoplasmic	COG0801	Coenzyme metabolism	
15595783	PA0586		conserved hypothetical protein	1.7	9.84E-03	Citronellsäure	5.1	60814	17	Cytoplasmic	COG2719	Function unknown	
15595784	PA0587		conserved hypothetical protein	1.0	9.47E-01	Citronellsäure	7.8	48742	11	Cytoplasmic	COG2718	Function unknown	
15595785	PA0588		conserved hypothetical protein	1.7	2.77E-02	Citronellsäure	5.5	73722	44	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms	
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	25.1	1.49E-02	Citronellsäure	7.2	32019	4	Cytoplasmic			
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.0	8.00E-01	Citronellsäure	6.6	34891	8	Cytoplasmic	COG1995	Coenzyme metabolism	
15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.1	4.10E-01	Citronellsäure	5.6	48441	23	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15595793	PA0596		hypothetical protein	18.5	7.71E-05	Citronellsäure	5.1	38185	3	Cytoplasmic	COG3178	General function prediction only	
15595794	PA0597		probable nucleotidyl transferase	389.1	2.15E-02	Citronellsäure	6.1	24149	2	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
15595801	PA0604		probable binding protein component of ABC transporter	1.1	5.02E-01	Citronellsäure	5.6	38167	9	Periplasmic	COG0687	Amino acid transport and metabolism	
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.4	3.05E-01	Citronellsäure	5.1	24096	9	Cytoplasmic	COG0036	Carbohydrate transport and metabolism	
15595806	PA0609	trpE	anthranilate synthetase component I	1.1	2.22E-01	Citronellol	4.7	54555	16	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
15595846	PA0649	trpG	anthranilate synthase component II	27.8	9.32E-03	Citronellsäure	6.0	22046	4	Cytoplasmic	COG0512	Amino acid transport and metabolism	Coenzyme metabolism
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	1.8	3.54E-02	Citronellsäure	5.6	37384	5	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	4.3	1.25E-02	Citronellsäure	4.6	30315	8	Cytoplasmic	COG0134	Amino acid transport and metabolism	
15595850	PA0653		conserved hypothetical protein	1.7	3.02E-01	Citronellol	6.4	15237	4	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones	
15595851	PA0654	speD	S-adenosylmethionine decarboxylase proenzyme	38.5	2.52E-02	Citronellsäure	4.5	30446	2	Cytoplasmic	COG1586	Amino acid transport and metabolism	
15595852	PA0655		hypothetical protein	2.4	1.23E-01	Citronellsäure	5.3	23644	3	Unknown	COG2941	Coenzyme metabolism	
15595857	PA0660		hypothetical protein	2.5	5.67E-04	Citronellol	6.2	34814	13	Cytoplasmic	COG2070	General function prediction only	
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	20.2	1.74E-05	Citronellsäure	6.7	36684	16	Cytoplasmic	COG0002	Amino acid transport and metabolism	
15595863	PA0666		conserved hypothetical protein	7.6	4.51E-04	Citronellsäure	5.2	39087	4	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.2	3.24E-01	Citronellol	5.6	44129	23	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis	
15595869	PA0672	hemO	heme oxygenase	1.7	2.07E-01	Citronellsäure	4.8	21953	6	Unknown	COG3230	Inorganic ion transport and metabolism	
15595901	PA0704		probable amidase	1.8	9.05E-01	Citronellol	6.9	50605	2	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15595903	PA0706	cat	chloramphenicol acetyltransferase	875.5	1.27E-02	Citronellsäure	6.1	23524	2	Unknown	COG0110	General function prediction only	
15595912	PA0715		hypothetical protein	1.5	5.42E-02	Citronellol	9.9	36589	4	Cytoplasmic	COG3344	DNA replication, recombination, and repair	
15595938	PA0741		conserved hypothetical protein	8.3	2.50E-04	Citronellol	6.6	22687	5	Unknown	COG2910	General function prediction only	
15595941	PA0744		probable enoyl-CoA hydratase/isomerase	9.9	2.42E-03	Citronellsäure	5.1	40589	4	Cytoplasmic	COG1024	Lipid metabolism	
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	1.1	4.93E-01	Citronellsäure	6.4	29904	7	Cytoplasmic	COG1024	Lipid metabolism	
15595944	PA0747		probable aldehyde dehydrogenase	1.9	1.51E-02	Citronellol	6.1	54564	3	Cytoplasmic	COG1012	Energy production and conversion	
15595947	PA0750	ung	uracil-DNA glycosylase	68.7	3.18E-04	Citronellsäure	8.2	26010	5	Cytoplasmic	COG0692	DNA replication, recombination, and repair	
15595951	PA0754		hypothetical protein	5.0	6.57E-02	Citronellsäure	5.5	34918	17	Unknown	COG3181	Function unknown	
15595953	PA0756		probable two-component response regulator	4.0	2.02E-01	Citronellsäure	5.2	24431	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595955	PA0758		hypothetical protein	5.5	6.12E-04	Citronellsäure	4.7	30875	8	Cytoplasmic	COG1639	Signal transduction mechanisms	
15595956	PA0759		conserved hypothetical protein	2.0	5.02E-03	Citronellol	5.2	33667	8	Unknown	COG0354	General function prediction only	
15595958	PA0761	nadB	L-aspartate oxidase	1.6	1.03E-01	Citronellsäure	6.3	60004	5	Cytoplasmic	COG0029	Coenzyme metabolism	
15595959	PA0762	algU	sigma factor AlgU	24.8	1.00E-03	Citronellsäure	5.4	22196	7	Cytoplasmic	COG1595	Transcription	
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	19.4	1.91E-03	Citronellsäure	6.1	34572	3	Periplasmic	COG3302	Signal transduction mechanisms	
15595963	PA0766	mucD	serine protease MucD precursor	1.2	5.73E-01	Citronellol	7.8	50321	6	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
15595964	PA0767	lepA	GTP-binding protein LepA	3.0	5.94E-02	Citronellsäure	5.3	66263	3	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
15595968	PA0771	era	GTP-binding protein Era	2.9	2.56E-01	Citronellol	6.6	34550	2	Cytoplasmic Membrane	COG1159	General function prediction only	
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	2.3	1.44E-01	Citronellsäure	5.6	27228	4	Cytoplasmic	COG0854	Coenzyme metabolism	
15595972	PA0775		conserved hypothetical protein	2.3	1.25E-01	Citronellsäure	5.3	27608	2	Cytoplasmic	COG4106	General function prediction only	
15595976	PA0779		probable ATP-dependent protease	1.4	4.65E-01	Citronellol	6.8	88574	10	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15595979	PA0782	putA	proline dehydrogenase PutA	1.6	2.78E-01	Citronellsäure	6.0	115630	25	Periplasmic	COG4230	Energy production and conversion	
15595989	PA0792	prpD	propionate catabolic protein PrpD	3.4	9.27E-03	Citronellol	6.6	54881	3	Cytoplasmic	COG2079	General function prediction only	
15595991	PA0794		probable aconitate hydratase	2.5	6.89E-03	Citronellsäure	5.3	94890	22	Cytoplasmic	COG1048	Energy production and conversion	
15595992	PA0795	prpC	citrate synthase 2	4.6	5.43E-05	Citronellsäure	6.4	41689	18	Cytoplasmic	COG0372	Energy production and conversion	
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.0	9.77E-01	Citronellsäure	5.2	32137	9	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15596005	PA0808		hypothetical protein	4.9	7.29E-02	Citronellol	4.8	17551	3	Cytoplasmic	COG3832	Function unknown	
15596030	PA0833		hypothetical protein	1.6	1.73E-01	Citronellol	9.0	24713	3	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596032	PA0835	pta	phosphate acetyltransferase	1.8	6.28E-02	Citronellol	5.0	75696	12	Periplasmic	COG0280	Energy production and conversion	
15596033	PA0836	ackA	acetate kinase	1.6	9.94E-01	Citronellsäure	7.1	42421	6	Cytoplasmic	COG0282	Energy production and conversion	
15596035	PA0838		probable glutathione peroxidase	2.4	6.27E-02	Citronellol	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596037	PA0840		probable oxidoreductase	1.2	5.11E-01	Citronellsäure	5.5	40334	6	Cytoplasmic	COG1902	Energy production and conversion	
15596045	PA0848		probable alkyl hydroperoxide reductase	4.4	6.42E-01	Citronellol	5.1	21814	2	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15596048	PA0851		hypothetical protein	1.6	2.43E-01	Citronellsäure	6.8	34024	4	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15596050	PA0853		probable oxidoreductase	1.1	7.67E-01	Citronellol	8.3	23485	3	Cytoplasmic	COG2249	General function prediction only	
15596051	PA0854	fumC2	fumarate hydratase	1.6	1.37E-02	Citronellol	6.1	49122	17	Cytoplasmic	COG0114	Energy production and conversion	
15596055	PA0858		conserved hypothetical protein	24.8	1.03E-01	Citronellsäure	5.7	35420	2	Cytoplasmic	COG1054	General function prediction only	
15596056	PA0859		hypothetical protein	3.7	6.88E-02	Citronellsäure	4.6	21466	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
15596059	PA0862		hypothetical protein	1.9	1.01E-01	Citronellol	6.5	29845	4	Cytoplasmic	COG5424	Coenzyme metabolism	
15596062	PA0865	hpd	4-hydroxyphenylpyruvate dioxygenase	231.5	4.30E-02	Citronellsäure	4.9	39913	2	Periplasmic	COG3185	Amino acid transport and metabolism	General function prediction only
15596067	PA0870	phhC	aromatic amino acid aminotransferase	19.8	1.69E-04	Citronellsäure	6.2	43273	7	Cytoplasmic	COG1448	Amino acid transport and metabolism	
15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	6.2	1.34E-01	Citronellol	6.4	13333	4	Cytoplasmic	COG2154	Coenzyme metabolism	
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	1.7	6.20E-03	Citronellsäure	6.3	71762	39	Cytoplasmic	COG0365	Lipid metabolism	
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.0	9.24E-01	Citronellsäure	6.8	28010	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596088	PA0891		hypothetical protein	1.3	2.03E-01	Citronellol	4.9	40214	3	Cytoplasmic	COG3608	General function prediction only	
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.2	4.66E-01	Citronellol	5.8	43747	24	Periplasmic	COG4992	Amino acid transport and metabolism	
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	1.1	5.71E-01	Citronellol	4.7	36930	3	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	6.2	9.93E-03	Citronellsäure	6.5	37245	8	Cytoplasmic	COG3138	Amino acid transport and metabolism	

15596095	PA0898	aruD	succinylglutamate 5-semialdehyde dehydrogenase	1.1	5.35E-01	Citronellol	6.2	51510	14	Periplasmic	COG1012	Energy production and conversion	
15596096	PA0899	aruB	succinylarginine dihydrolase	2.3	6.82E-03	Citronellol	6.2	48875	10	Periplasmic	COG3724	Amino acid transport and metabolism	
15596098	PA0901	aruE	succinylglutamate desuccinylase	1.7	2.01E-01	Citronellsäure	6.0	36909	7	Cytoplasmic	COG2988	Amino acid transport and metabolism	
15596099	PA0902		hypothetical protein	2.1	1.61E-01	Citronellsäure	6.4	35430	6	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15596100	PA0903	alaS	alanyl-tRNA synthetase	1.4	3.15E-01	Citronellsäure	5.2	94701	49	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.8	3.69E-02	Citronellol	5.0	44388	26	Cytoplasmic	COG0527	Amino acid transport and metabolism	
15596124	PA0927	ldhA	D-lactate dehydrogenase (fermentative)	4.8	7.24E-02	Citronellsäure	6.1	35756	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15596129	PA0932	cysM	cysteine synthase B	15.3	2.28E-03	Citronellsäure	5.5	32448	10	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596131	PA0934	relA	GTP pyrophosphokinase	4.7	2.10E-02	Citronellsäure	7.6	83815	13	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15596132	PA0935		conserved hypothetical protein	7.2	2.28E-01	Citronellsäure	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only	
15596140	PA0943		hypothetical protein	1.2	6.11E-01	Citronellol	8.7	27183	8	Periplasmic			
15596141	PA0944	purN	phosphoribosylaminoimidazole synthetase	134.7	1.14E-03	Citronellsäure	7.2	24734	2	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	2.6	1.24E-01	Citronellsäure	4.5	37122	10	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
15596144	PA0947		conserved hypothetical protein	10.2	2.29E-02	Citronellsäure	6.0	26843	2	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	9.8	7.18E-03	Citronellol	6.8	20744	7	Unknown	COG0655	General function prediction only	
15596153	PA0956	proS	prolyl-tRNA synthetase	1.7	1.44E-03	Citronellsäure	5.1	63103	25	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis	
15596154	PA0957		hypothetical protein	1.3	1.87E-01	Citronellol	6.3	14622	4	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	5.5	5.17E-03	Citronellol	4.8	48360	10	Periplasmic			
15596159	PA0962		probable dna-binding stress protein	4.0	1.96E-01	Citronellol	4.7	17493	9	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.3	1.88E-01	Citronellsäure	5.2	66207	36	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis	
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.1	8.43E-01	Citronellol	6.1	21927	5	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
15596165	PA0968		conserved hypothetical protein	49.3	1.86E-03	Citronellsäure	8.7	16672	2	Cytoplasmic	COG0824	General function prediction only	
15596169	PA0972	tolB	TolB protein	1.0	9.97E-01	Citronellol	9.2	47720	12	Periplasmic	COG0823	Intracellular trafficking and secretion	
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	2.2	9.47E-02	Citronellol	6.3	17925	4	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596171	PA0974		conserved hypothetical protein	8.3	2.90E-02	Citronellsäure	8.7	29097	8	Outer Membrane Vesicle	COG1729	Function unknown	
15596173	PA0976		conserved hypothetical protein	1.6	1.67E-01	Citronellsäure	4.7	23900	4	Unknown	COG0603	General function prediction only	
15596194	PA0997	pqsB	PqsB	28.2	1.85E-03	Citronellsäure	4.6	30501	2	Cytoplasmic	COG0332	acyl-carrier-protein	
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	17.3	1.03E-01	Citronellsäure	5.3	36378	2	Cytoplasmic	COG0332	acyl-carrier-protein	
15596201	PA1004	nadA	quinolinate synthetase A	1.0	9.29E-01	Citronellol	5.4	38418	5	Cytoplasmic	COG0379	Coenzyme metabolism	
15596202	PA1005		conserved hypothetical protein	29.6	1.97E-03	Citronellol	8.4	52994	2	Periplasmic	COG4783	General function prediction only	
15596205	PA1008	bcp	bacterioferritin comigratory protein	3.3	1.32E-01	Citronellol	7.3	17352	8	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones	
15596206	PA1009		hypothetical protein	2.9	1.58E-01	Citronellol	5.6	20585	2	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15596207	PA1010	dapA	dihydrodipicolinate synthase	4.8	4.33E-02	Citronellsäure	6.4	31449	17	Periplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
15596208	PA1011		hypothetical protein	1.4	1.58E-01	Citronellol	4.7	43055	3	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane	
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	2.9	2.09E-03	Citronellsäure	5.1	26831	19	Periplasmic	COG0152	Nucleotide transport and metabolism	
15596220	PA1023		probable short-chain dehydrogenase	126.8	7.57E-06	Citronellsäure	6.7	32821	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596224	PA1027		probable aldehyde dehydrogenase	2.7	1.52E-01	Citronellsäure	6.8	57291	2	Cytoplasmic	COG1012	Energy production and conversion	
15596233	PA1036		hypothetical protein	12.7	8.97E-03	Citronellol	4.6	19537	2	Unknown			
15596236	PA1039		conserved hypothetical protein	1.2	7.57E-01	Citronellol	6.7	17189	4	Unknown	COG3012	Function unknown	
15596237	PA1040		hypothetical protein	1.4	1.17E-01	Citronellol	6.0	18721	5	Unknown			
15596244	PA1047		probable esterase	25.1	5.91E-03	Citronellsäure	6.1	42335	3	Periplasmic	COG1680	Defense mechanisms	
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	1.2	7.07E-01	Citronellol	6.8	24860	6	Cytoplasmic	COG0259	Coenzyme metabolism	
15596258	PA1061		conserved hypothetical protein	16.3	1.97E-03	Citronellsäure	6.6	39952	12	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596259	PA1062		hypothetical protein	2.0	1.73E-02	Citronellsäure	6.5	19155	3	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane	
15596263	PA1066		probable short-chain dehydrogenase	2.0	5.10E-01	Citronellol	7.6	23376	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596265	PA1068		probable heat shock protein (hsp90 family)	2.6	8.70E-03	Citronellsäure	5.7	70659	9	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596266	PA1069		hypothetical protein	2.4	4.18E-02	Citronellsäure	4.3	86114	26	Cytoplasmic			
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	1.1	5.43E-01	Citronellsäure	5.5	39769	30	Periplasmic	COG0683	Amino acid transport and metabolism	
15596287	PA1090		hypothetical protein	17.3	7.14E-03	Citronellsäure	5.3	24703	5	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane	
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	1.7	7.18E-01	Citronellol	5.2	187155	31	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane	
15596289	PA1092	fliC	flagellin type B	2.9	1.57E-03	Citronellol	5.2	49242	19	Periplasmic	COG1344	Cell motility and secretion	
15596291	PA1094	fliD	flagellar capping protein FliD	1.3	2.96E-01	Citronellol	7.1	49449	10	Periplasmic	COG1345	Cell motility and secretion	
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.2	7.19E-01	Citronellol	5.0	55277	8	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596324	PA1127		probable oxidoreductase	1.3	3.08E-01	Citronellsäure	5.2	36474	2	Cytoplasmic	COG0667	Energy production and conversion	
15596332	PA1135		conserved hypothetical protein	2.3	3.87E-04	Citronellol	6.4	31898	9	Cytoplasmic	COG0693	General function prediction only	
15596336	PA1139		hypothetical protein	57.4	8.47E-02	Citronellsäure	5.1	29336	3	Periplasmic	COG2340	Function unknown	
15596337	PA1140		conserved hypothetical protein	860.4	1.55E-02	Citronellsäure	6.3	31614	3	Cytoplasmic	COG3257	General function prediction only	
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucleotide reductase	1.9	2.76E-03	Citronellsäure	4.5	47386	6	Periplasmic	COG0208	Nucleotide transport and metabolism	
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	2.3	2.04E-03	Citronellsäure	5.7	107105	45	Periplasmic	COG0209	Nucleotide transport and metabolism	
15596354	PA1157		probable two-component response regulator	1.0	7.90E-01	Citronellsäure	4.7	26373	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	2.9	1.96E-02	Citronellsäure	5.0	41077	7	Cytoplasmic	COG0624	Amino acid transport and metabolism	
15596363	PA1166		hypothetical protein	36.5	3.40E-03	Citronellsäure	7.3	28156	8	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596368	PA1171		probable transglycolase	9.0	1.97E-03	Citronellsäure	9.3	42682	12	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane	
15596370	PA1173	napB	cytochrome c-type protein NapB precursor	4.0	2.38E-03	Citronellol	8.3	17918	4	Periplasmic	COG3043	Energy production and conversion	
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	2.8	2.91E-02	Citronellol	8.6	92942	27	Periplasmic	COG0243	Energy production and conversion	
15596376	PA1179	phoP	two-component response regulator PhoP	14.1	4.76E-05	Citronellsäure	5.2	25650	11	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596384	PA1187		probable acyl-CoA dehydrogenase	9.8	1.24E-05	Citronellsäure	6.5	42350	16	Cytoplasmic	COG1960	Lipid metabolism	
15596385	PA1188		hypothetical protein	27.0	4.27E-03	Citronellsäure	6.0	42128	5	Cytoplasmic	COG1804	Energy production and conversion	
15596389	PA1192		conserved hypothetical protein	2.0	1.46E-01	Citronellsäure	6.5	31260	2	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
15596390	PA1193		hypothetical protein	1.8	6.85E-01	Citronellol	9.1	25292	4	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15596397	PA1200		conserved hypothetical protein	1.6	3.02E-01	Citronellsäure	5.1	24597	5	Cytoplasmic	COG4122	General function prediction only	
15596399	PA1202		probable hydrolase	2.5	1.58E-01	Citronellsäure	4.8	22471	11	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596401	PA1204		conserved hypothetical protein	37.0	9.10E-03	Citronellsäure	6.5	20224	5	Cytoplasmic	COG0431	General function prediction only	
15596403	PA1206		hypothetical protein	3.8	3.68E-02	Citronellsäure	4.4	17690	6	Cytoplasmic			
15596413	PA1216		hypothetical protein	5.7	1.70E-02	Citronellol	6.1	28573	4	Cytoplasmic	COG4976	General function prediction only	
15596457	PA1260		amino acid ABC transporter periplasmic binding protein	3.4	1.45E-01	Citronellsäure	5.2	29142	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596477	PA1280		hypothetical protein	63.1	3.95E-04	Citronellsäure	6.7	21591	2	Cytoplasmic	COG0406	General function prediction only	
15596480	PA1283		probable transcriptional regulator	19.9	6.21E-02	Citronellsäure	4.9	20307	2	Unknown	COG1309	Transcription	
15596484	PA1287		probable glutathione peroxidase	1.0	9.10E-01	Citronellol	8.3	20217	12	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596485	PA1288		probable outer membrane protein precursor	1.4	3.70E-01	Citronellsäure	6.0	45561	12	Periplasmic	COG2067	Lipid metabolism	
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	8.6	1.03E-02	Citronellsäure	5.3	30597	9	Periplasmic	COG2897	Inorganic ion transport and metabolism	
15596491	PA1294	rnd	ribonuclease D	20.3	8.36E-04	Citronellsäure	4.8	43066	5	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
15596501	PA1304		probable oligopeptidase	1.1	8.14E-01	Citronellol	4.7	75881	18	Periplasmic	COG1770	Amino acid transport and metabolism	
15596504	PA1307		conserved hypothetical protein	1.5	1.91E-01	Citronellsäure	5.7	28544	3	Cytoplasmic	COG0121	General function prediction only	
15596521	PA1324		hypothetical protein	3.0	4.14E-02	Citronellol	5.8	18303	2	Unknown			
15596532	PA1335		probable two-component response regulator	3.8	2.74E-01	Citronellol	6.9	46687	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596534	PA1337	ansB	glutaminase-asparaginase	2.1	2.32E-02	Citronellsäure	7.3	38644	15	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	1.1	7.72E-01	Citronellol	6.2	59874	18	Periplasmic	COG0405	Amino acid transport and metabolism	
15596539	PA1342		probable binding protein component of ABC transporter	10.0	4.64E-04	Citronellsäure	8.6	33054	44	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596541	PA1344		probable short-chain dehydrogenase	3.2	8.06E-02	Citronellsäure	4.9	27397	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596568	PA1371		hypothetical protein	1.4	2.30E-01	Citronellol	5.2	27419	2	Unknown	COG5619	Function unknown	
15596569	PA1372		hypothetical protein	1.6	4.69E-02	Citronellol	5.5	79820	18	Cytoplasmic	COG3972	General function prediction only	
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	1.1	5.12E-01	Citronellsäure	5.0	66760	19	Cytoplasmic	COG4579	Signal transduction mechanisms	
15596599	PA1402		hypothetical protein	3.2	5.45E-02	Citronellsäure	4.7	23753	7	Cytoplasmic	COG4122	General function prediction only	
15596627	PA1430	lasR	transcriptional regulator LasR	138.9	1.19E-03	Citronellsäure	6.5	26618	10	Cytoplasmic	COG2771	Transcription	
15596637	PA1440		hypothetical protein	7.5	3.96E-02	Citronellsäure	3.9	22382	3	Cytoplasmic	COG3318	General function prediction only	
15596640	PA1443	fliM	flagellar motor switch protein FliM	53.2	6.27E-04	Citronellsäure	5.0	36282	5	Cytoplasmic	COG1868	Cell motility and secretion	
15596641	PA1444	fliN	flagellar motor switch protein FliN	1.6	2.17E-01	Citronellsäure	4.0	16620	2	Cytoplasmic Membrane	COG1886	Cell motility and secretion	Intracellular trafficking and secretion
15596652	PA1455	fliA	sigma factor FliA	63.4	6.74E-04	Citronellsäure	5.9	27522	6	Cytoplasmic	COG1191	Transcription	
15596654	PA1457	cheZ	chemotaxis protein CheZ	2.2	4.10E-03	Citronellsäure	4.6	29622	12	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
15596655	PA1458		probable two-component sensor	3.5	1.87E-02	Citronellsäure	4.3	79737	16	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15596656	PA1459		probable methyltransferase	4.0	3.11E-02	Citronellsäure	8.6	39004	6	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
15596661	PA1464		probable purine-binding chemotaxis protein	1.2	3.94E-01	Citronellol	4.1	17536	11	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15596667	PA1470		probable short-chain dehydrogenase	1.4	4.95E-01	Citronellol	4.9	25365	7	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	26.2	1.33E-04	Citronellsäure	8.6	36485	13	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15596711	PA1514		ureidoglycolate hydrolaseYbbT	1.5	3.04E-01	Citronellsäure	5.6	18983	2	Unknown	COG3194	Nucleotide transport and metabolism	
15596713	PA1516		hypothetical protein	155.9	5.52E-02	Citronellsäure	4.8	18896	5	Cytoplasmic	COG3195	Function unknown	
15596718	PA1521		probable guanine deaminase	25.6	2.93E-03	Citronellol	5.2	48311	2	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15596724	PA1527		conserved hypothetical protein	2.7	6.92E-01	Citronellol	4.8	131580	17	Cytoplasmic	COG1196	Cell division and chromosome partitioning	
15596726	PA1529	lig	DNA ligase	1.0	8.82E-01	Citronellol	5.1	86767	20	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	7.5	1.01E-02	Citronellsäure	4.4	73309	9	Cytoplasmic	COG2812	DNA replication, recombination, and repair	

15596731	PA1534	recR	recombination protein RecR	5.2	5.14E-02	Citronellol	6.0	21173	3	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
15596732	PA1535		citronellyl-CoA dehydrogenase	1.9	2.06E-02	Citronellsäure	5.6	42041	20	Cytoplasmic	COG1960	Lipid metabolism	
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.4	9.06E-02	Citronellol	4.6	19804	2	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15596741	PA1544	anr	transcriptional regulator Anr	33.4	2.55E-05	Citronellsäure	5.2	27129	7	Cytoplasmic	COG0664	Signal transduction mechanisms	
15596759	PA1562	acnA	aconitate hydratase 1	1.3	2.30E-01	Citronellsäure	5.4	99147	47	Cytoplasmic	COG1048	Energy production and conversion	
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	1.6	9.28E-02	Citronellol	5.2	30777	3	Cytoplasmic	COG2084	Lipid metabolism	
15596776	PA1579		hypothetical protein	15.4	3.35E-03	Citronellsäure	8.2	22110	8	Periplasmic			
15596777	PA1580	gltA	citrate synthase	1.0	8.05E-01	Citronellsäure	7.0	47695	37	Periplasmic	COG0372	Energy production and conversion	
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	1.8	9.46E-03	Citronellsäure	6.5	63532	22	Periplasmic	COG1053	Energy production and conversion	
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	15.2	4.54E-03	Citronellsäure	6.9	26155	6	Outer Membrane Vesicle	COG0479	Energy production and conversion	
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	6.0	2.67E-05	Citronellol	6.5	105877	38	Outer Membrane Vesicle	COG0567	Energy production and conversion	
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	13.7	1.45E-03	Citronellol	5.2	42887	18	Periplasmic	COG0508	Energy production and conversion	
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.1	5.53E-01	Citronellol	7.0	50165	27	Periplasmic	COG1249	Energy production and conversion	
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	1.7	4.45E-02	Citronellsäure	6.1	41542	28	Periplasmic	COG0045	Energy production and conversion	
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	3.7	6.67E-03	Citronellol	6.0	30266	9	Periplasmic	COG0074	Energy production and conversion	
15596793	PA1596	htpG	heat shock protein HtpG	2.2	6.30E-03	Citronellsäure	4.9	71667	49	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596794	PA1597		hypothetical protein	1.2	4.70E-01	Citronellsäure	5.9	25791	6	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.2	4.61E-01	Citronellsäure	5.3	42806	17	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	5.2	8.17E-02	Citronellol	6.9	18747	6	Cytoplasmic	COG0764	Lipid metabolism	
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.7	6.29E-02	Citronellol	6.2	36773	6	Cytoplasmic	COG0240	Energy production and conversion	
15596814	PA1617		probable AMP-binding enzyme	3.1	9.12E-03	Citronellsäure	7.2	61370	25	Cytoplasmic	COG1022	Lipid metabolism	
15596819	PA1622		probable hydrolase	1.3	4.72E-01	Citronellol	7.1	31290	7	Cytoplasmic	COG0596	General function prediction only	
15596820	PA1623		conserved hypothetical protein	1.1	6.95E-02	Citronellsäure	6.1	24924	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596836	PA1639		hypothetical protein	1.4	2.59E-01	Citronellol	5.4	22457	7	Periplasmic			
15596839	PA1642	selD	selenophosphate synthetase	2.0	1.74E-01	Citronellsäure	4.7	36354	9	Cytoplasmic	COG0709	Amino acid transport and metabolism	
15596841	PA1644		conserved hypothetical protein	23.7	1.48E-02	Citronellsäure	5.5	21838	5	Unknown	COG1853	General function prediction only	
15596851	PA1654		probable aminotransferase	2.0	1.25E-01	Citronellsäure	5.3	43311	4	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
15596852	PA1655		probable glutathione S-transferase	1.8	6.32E-01	Citronellol	5.3	22738	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596854	PA1657		conserved hypothetical protein	3.2	1.30E-01	Citronellsäure	4.5	18165	2	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15596855	PA1658		conserved hypothetical protein	58.9	3.79E-03	Citronellsäure	5.1	55560	2	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.2	7.82E-01	Citronellol	7.6	20236	6	Outer Membrane Vesicle	COG0302	Coenzyme metabolism	
15596874	PA1677		conserved hypothetical protein	2.6	1.08E-03	Citronellol	6.5	21034	11	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596878	PA1681	aroC	chorismate synthase	22.7	1.34E-03	Citronellsäure	6.6	38987	6	Cytoplasmic	COG0082	Amino acid transport and metabolism	
15596880	PA1683		probable sugar aldolase	12.5	2.38E-03	Citronellsäure	6.5	22868	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	6.9	1.17E-02	Citronellsäure	5.0	20552	6	Cytoplasmic	COG1791	Function unknown	
15596884	PA1687	speE	spermidine synthase	2.7	4.41E-02	Citronellsäure	4.9	32238	4	Periplasmic	COG0421	Amino acid transport and metabolism	
15596886	PA1689		conserved hypothetical protein	98.8	5.88E-04	Citronellol	6.5	77984	7	Outer Membrane Vesicle	COG1368	Cell envelope biogenesis, outer membrane	
15596923	PA1726	bglX	periplasmic beta-glucosidase	1.7	3.33E-01	Citronellol	7.1	83003	5	Periplasmic	COG1472	Carbohydrate transport and metabolism	
15596930	PA1733		conserved hypothetical protein	21.8	6.56E-05	Citronellsäure	5.3	26467	5	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones	
15596933	PA1736		probable acyl-CoA thiolase	1.2	7.96E-02	Citronellsäure	5.3	42102	26	Cytoplasmic	COG0183	Lipid metabolism	
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	1.2	2.50E-01	Citronellsäure	6.7	76666	47	Cytoplasmic	COG1250	Lipid metabolism	
15596939	PA1742	pauD2	Glutamine amidotransferase class I	84.2	1.02E-02	Citronellsäure	5.0	27361	7	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	5.2	8.05E-02	Citronellsäure	7.8	24412	13	Cytoplasmic	COG1024	Lipid metabolism	
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.0	9.75E-01	Citronellol	6.5	39132	10	Cytoplasmic	COG0722	Amino acid transport and metabolism	
15596949	PA1752		hypothetical protein	3.2	1.21E-01	Citronellsäure	6.7	34141	8	Cytoplasmic	COG1893	Coenzyme metabolism	
15596950	PA1753		conserved hypothetical protein	3.2	9.54E-02	Citronellsäure	4.7	18372	5	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596951	PA1754	cysB	transcriptional regulator CysB	1.1	5.52E-01	Citronellsäure	7.0	36110	8	Periplasmic	COG0583	Transcription	
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	1.2	1.83E-01	Citronellsäure	6.4	30215	4	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15596954	PA1757	thrH	homoserine kinase	2.8	1.18E-01	Citronellsäure	5.0	23501	7	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596956	PA1759		probable transcriptional regulator	1.4	5.39E-01	Citronellsäure	6.3	101111	15	Unknown	COG2909	Transcription	
15596957	PA1760		probable transcriptional regulator	2.7	5.45E-02	Citronellsäure	6.8	101628	10	Cytoplasmic	COG2909	Transcription	
15596965	PA1768		hypothetical protein	2.7	2.44E-02	Citronellol	9.6	19720	7	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15596966	PA1769		conserved hypothetical protein	3.0	1.21E-01	Citronellsäure	6.1	31074	8	Cytoplasmic	COG1806	Function unknown	
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.1	9.43E-01	Citronellsäure	4.8	85798	59	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
15596969	PA1772		probable methyltransferase	3.2	1.53E-03	Citronellol	4.6	17404	6	Cytoplasmic	COG0684	Coenzyme metabolism	
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precursor	1.3	3.11E-01	Citronellol	4.8	37639	9	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596984	PA1787	acnB	aconitate hydratase 2	1.5	1.99E-01	Citronellsäure	5.0	93595	84	Periplasmic	COG1049	Energy production and conversion	
15596987	PA1790		hypothetical protein	2.8	1.18E-01	Citronellsäure	6.7	23312	2	Cytoplasmic	COG4445	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	2.2	5.62E-03	Citronellol	6.2	18126	10	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.0	7.89E-01	Citronellol	5.6	62912	26	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	1.2	3.42E-02	Citronellsäure	5.4	51245	19	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis	
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase	15.5	1.25E-03	Citronellsäure	5.8	30549	6	Periplasmic	COG0190	Coenzyme metabolism	
15596997	PA1800	tig	trigger factor	1.3	1.89E-02	Citronellol	4.5	48582	30	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
15596998	PA1801	clpP	ClpP	4.2	1.49E-02	Citronellol	6.4	23502	13	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15596999	PA1802	clpX	ClpX	1.3	2.09E-01	Citronellol	4.8	46991	25	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
15597000	PA1803	lon	Lon protease	1.8	1.09E-01	Citronellol	6.0	88647	23	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	1.1	7.98E-01	Citronellol	4.7	68741	2	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	28.4	9.93E-04	Citronellsäure	5.7	28006	8	Cytoplasmic Membrane	COG0623	acyl-carrier-protein	
15597007	PA1810		probable binding protein component of ABC transporter	1.3	1.05E-01	Citronellsäure	6.5	70473	11	Periplasmic	COG4166	Amino acid transport and metabolism	
15597010	PA1813		probable hydroxyacylglutathione hydrolase	1.7	2.42E-01	Citronellsäure	6.3	28865	3	Cytoplasmic	COG0491	General function prediction only	
15597012	PA1815	rnhA	ribonuclease H	7.3	2.15E-01	Citronellsäure	8.7	16697	3	Unknown	COG0328	DNA replication, recombination, and repair	
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	1.3	2.23E-01	Citronellol	6.1	82757	17	Cytoplasmic	COG1982	Amino acid transport and metabolism	
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	1.8	2.01E-01	Citronellsäure	5.4	29957	7	Cytoplasmic	COG1024	Lipid metabolism	
15597020	PA1823		conserved hypothetical protein	9.7	6.51E-02	Citronellol	4.9	31356	3	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
15597025	PA1828		probable short-chain dehydrogenase	1.9	8.35E-02	Citronellol	7.4	26919	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597026	PA1829		hypothetical protein	3.8	8.21E-03	Citronellsäure	5.9	40833	8	Cytoplasmic	COG3173	General function prediction only	
15597028	PA1831		hypothetical protein	3.2	1.02E-01	Citronellsäure	6.3	26378	6	Cytoplasmic	COG0406	General function prediction only	
15597030	PA1833		probable oxidoreductase	11.4	2.94E-05	Citronellsäure	5.2	34552	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597034	PA1837		hypothetical protein	1.8	1.44E-01	Citronellsäure	4.7	18765	6	Cytoplasmic	COG3749	Function unknown	
15597035	PA1838	cysI	sulfite reductase	1.8	7.28E-03	Citronellsäure	5.9	62132	27	Periplasmic	COG0155	Inorganic ion transport and metabolism	
15597040	PA1843	metH	methionine synthase	1.1	6.87E-01	Citronellol	4.6	135062	49	Periplasmic	COG1410	Amino acid transport and metabolism	
15597042	PA1845		hypothetical protein	1.3	7.98E-01	Citronellol	4.6	18757	2	Unknown			
15597043	PA1846	cti	cis/trans isomerase	14.4	1.71E-02	Citronellsäure	6.0	86517	3	Periplasmic			
15597044	PA1847	nfuA	NfuA	1.2	9.69E-01	Citronellol	4.2	21136	8	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	54.0	1.56E-03	Citronellsäure	6.8	26377	5	Periplasmic	COG0725	Inorganic ion transport and metabolism	
15597071	PA1874		hypothetical protein	2.4	1.53E-01	Citronellsäure	3.1	238414	5	Unknown			
15597077	PA1880		probable oxidoreductase	2.7	4.09E-04	Citronellol	7.4	77656	23	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597084	PA1887		hypothetical protein	2.5	7.38E-01	Citronellol	8.0	24376	2	Unknown			
15597087	PA1890		probable glutathione S-transferase	1.1	6.98E-01	Citronellol	7.0	23440	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597091	PA1894		hypothetical protein	3.8	8.86E-03	Citronellsäure	5.3	26179	7	Unknown			
15597109	PA1913		hypothetical protein	2.3	2.74E-01	Citronellsäure	8.4	25410	2	Unknown			
15597110	PA1914		conserved hypothetical protein	1.5	7.31E-02	Citronellol	6.9	46125	9	Extracellular			
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	3.1	4.20E-02	Citronellsäure	5.7	86211	13	Cytoplasmic	COG0620	Amino acid transport and metabolism	
15597126	PA1930		probable chemotaxis transducer	2.8	2.07E-02	Citronellsäure	6.5	47801	6	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	29.2	1.40E-04	Citronellsäure	8.4	33860	10	Periplasmic	COG1879	Carbohydrate transport and metabolism	
15597145	PA1949	rbsR	ribose operon repressor RbsR	1.7	1.30E-02	Citronellol	7.2	36446	4	Cytoplasmic	COG1609	Transcription	
15597146	PA1950	rbsK	ribokinase	2.3	1.51E-02	Citronellol	4.9	31846	7	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597160	PA1964		probable ATP-binding component of ABC transporter	2.7	3.94E-01	Citronellsäure	4.8	57917	5	Cytoplasmic	COG0488	General function prediction only	
15597170	PA1974		hypothetical protein	673.7	1.38E-02	Citronellsäure	4.3	43218	3	Outer Membrane			
15597177	PA1981		hypothetical protein	19.9	3.83E-04	Citronellsäure	5.8	22869	8	Extracellular	COG1357	Function unknown	
15597178	PA1982	exaA	quinoprotein ethanol dehydrogenase	19.4	7.45E-03	Citronellsäure	7.1	68123	29	Periplasmic	COG4993	Carbohydrate transport and metabolism	
15597179	PA1983	exaB	cytochrome c550	8.6	1.28E-02	Citronellsäure	5.6	15850	2	Unknown	COG2010	Energy production and conversion	
15597180	PA1984	exaC	NAD+ dependent aldehyde dehydrogenase ExaC	18.7	6.38E-03	Citronellsäure	5.4	54892	34	Periplasmic	COG1012	Energy production and conversion	
15597182	PA1986	pqqB	pyrroloquinoline quinone biosynthesis protein B	1.6	5.88E-01	Citronellsäure	5.5	33018	9	Cytoplasmic	COG1235	General function prediction only	
15597183	PA1987	pqqC	pyrroloquinoline quinone biosynthesis protein C	3.7	7.80E-05	Citronellsäure	7.4	29449	9	Cytoplasmic	COG5424	Coenzyme metabolism	
15597185	PA1989	pqqE	pyrroloquinoline quinone biosynthesis protein E	14.9	3.43E-02	Citronellsäure	6.1	42549	2	Cytoplasmic	COG0535	General function prediction only	
15597190	PA1994		hypothetical protein	13.6	2.22E-03	Citronellol	4.7	21561	3	Cytoplasmic	COG3554	Function unknown	
15597193	PA1997		probable AMP-binding enzyme	1.4	1.61E-01	Citronellsäure	6.5	71929	11	Cytoplasmic	COG0365	Lipid metabolism	
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	1.3	3.14E-01	Citronellol	5.0	25244	5	Cytoplasmic	COG1788	Lipid metabolism	
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	4.1	5.97E-02	Citronellsäure	4.6	23187	17	Cytoplasmic	COG2057	Lipid metabolism	
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	2.4	6.92E-03	Citronellsäure	6.4	40405	29	Cytoplasmic	COG0183	Lipid metabolism	

15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase		2.7	1.28E-02	Citronellol	5.6	26727	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597203	PA2007	maiA	maleylacetoacetate isomerase		48.8	1.07E-01	Citronellsäure	6.9	23685	6	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597204	PA2008	fahA	fumarylacetoacetase		1.0	8.21E-01	Citronellol	6.0	46341	5	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase		1.3	3.74E-01	Citronellsäure	6.0	31837	12	Cytoplasmic	COG0119	Amino acid transport and metabolism	
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containing)		1.9	5.65E-03	Citronellol	5.6	71282	32	Cytoplasmic	COG4770	Lipid metabolism	
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase		2.5	2.11E-03	Citronellol	5.2	28947	13	Cytoplasmic	COG1024	Lipid metabolism	
15597210	PA2014	liuB	methylcrotonyl-CoA carboxylase, beta-subunit		1.8	1.29E-03	Citronellol	6.7	57433	30	Cytoplasmic	COG4799	Lipid metabolism	
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase		1.1	7.58E-01	Citronellol	5.5	42209	33	Cytoplasmic	COG1960	Lipid metabolism	
15597216	PA2020		probable transcriptional regulator		2.5	1.23E-01	Citronellsäure	7.1	23695	2	Cytoplasmic	COG1309	Transcription	
15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase		7.3	1.70E-02	Citronellsäure	5.1	31236	14	Periplasmic	COG1210	Cell envelope biogenesis, outer membrane	
15597221	PA2025	gor	glutathione reductase		1.4	1.09E-01	Citronellol	6.3	49237	12	Cytoplasmic	COG1249	Energy production and conversion	
15597240	PA2044		hypothetical protein		1.6	4.40E-02	Citronellsäure	6.1	70083	4	Periplasmic	COG1305	Amino acid transport and metabolism	
15597267	PA2071	fusA2	elongation factor G		1.4	2.62E-01	Citronellol	4.9	77574	24	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15597276	PA2080	kynU	kynureninase KynU		1.1	5.19E-01	Citronellsäure	5.3	46294	11	Cytoplasmic	COG3844	Amino acid transport and metabolism	
15597277	PA2081	kynB	kynurenine formamidase, KynB		4.0	2.58E-02	Citronellsäure	5.2	23152	8	Cytoplasmic	COG1878	Amino acid transport and metabolism	
15597315	PA2119		alcohol dehydrogenase (Zn-dependent)		2.9	5.34E-02	Citronellsäure	5.4	38561	3	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
15597348	PA2152		probable trehalose synthase		5.8	2.08E-01	Citronellsäure	5.7	124521	3	Cytoplasmic	COG3281	Carbohydrate transport and metabolism	
15597372	PA2176		hypothetical protein		1.6	5.25E-02	Citronellol	4.9	20943	4	Unknown	COG2910	General function prediction only	
15597380	PA2184		conserved hypothetical protein		2.5	2.46E-01	Citronellol	4.7	18990	2	Cytoplasmic	COG3685	Function unknown	
15597393	PA2197		conserved hypothetical protein		1.3	6.91E-01	Citronellol	6.3	37135	11	Cytoplasmic	COG2130	General function prediction only	
15597395	PA2199		probable dehydrogenase		1.9	2.77E-02	Citronellol	5.4	30886	5	Cytoplasmic	COG2084	Lipid metabolism	
15597400	PA2204		probable binding protein component of ABC transporter		11.6	3.43E-03	Citronellsäure	9.7	29309	13	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15597418	PA2222		hypothetical protein		26.7	4.32E-03	Citronellsäure	5.0	23441	5	Unknown			
15597425	PA2229		conserved hypothetical protein		1.7	3.38E-02	Citronellol	6.5	26560	3	Cytoplasmic	COG2258	Function unknown	
15597428	PA2232	pslB	PslB		1.4	6.42E-02	Citronellsäure	6.0	53515	12	Periplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15597449	PA2253	ansA	L-asparaginase I		2.1	4.83E-03	Citronellol	5.3	34755	2	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15597467	PA2271		probable acetyltransferase		1.3	3.54E-01	Citronellsäure	6.2	19165	4	Cytoplasmic			
15597497	PA2301		hypothetical protein		2.2	4.35E-02	Citronellsäure	6.5	19330	6	Cytoplasmic	COG2606	Function unknown	
15597498	PA2302	ambE	AmbE		2.3	1.34E-02	Citronellol	4.8	229041	81	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597500	PA2304	ambC	AmbC		2.7	1.86E-02	Citronellol	6.8	40696	7	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597501	PA2305	ambB	AmbB		3.4	3.63E-01	Citronellol	6.3	134446	28	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597559	PA2363		hypothetical protein		69.3	7.62E-02	Citronellol	5.2	47778	2	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15597561	PA2365		conserved hypothetical protein		1.2	9.36E-01	Citronellol	4.4	20177	3	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15597562	PA2366		uricase PuuD		5.8	3.18E-03	Citronellsäure	5.7	55042	18	Cytoplasmic Membrane	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15597563	PA2367		hypothetical protein		1.9	2.20E-02	Citronellol	4.6	17636	13	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15597567	PA2371		probable ClpA/B-type protease		4.0	2.50E-02	Citronellsäure	5.1	92424	9	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597568	PA2372		hypothetical protein		9.9	1.32E-02	Citronellsäure	8.4	21241	3	Unknown			
15597574	PA2378		probable aldehyde dehydrogenase		2.1	8.91E-03	Citronellol	8.4	83665	27	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ		5.2	1.10E-02	Citronellol	7.1	84039	27	Periplasmic	COG2366	General function prediction only	
15597582	PA2386	pvdA	L-ornithine N5-oxygenase		2.2	1.64E-01	Citronellol	6.5	49478	6	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
15597590	PA2394	pvdN	PvdN		1.3	4.78E-01	Citronellol	7.3	47981	4	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
15597591	PA2395	pvdO	PvdO		3.4	8.16E-02	Citronellsäure	5.4	31070	9	Periplasmic	COG1262	Function unknown	
15597592	PA2396	pvdF	pyoverdine synthetase F		13.3	9.29E-04	Citronellsäure	5.0	31039	15	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15597594	PA2398	fpvA	ferrypyoverdine receptor		1.4	3.10E-01	Citronellol	5.3	91167	19	Periplasmic	COG4773	Inorganic ion transport and metabolism	
15597595	PA2399	pvdD	pyoverdine synthetase D		1.5	1.02E-01	Citronellsäure	5.0	273645	52	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597598	PA2402		probable non-ribosomal peptide synthetase		1.5	2.05E-01	Citronellsäure	5.1	569179	132	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597603	PA2407		probable adhesion protein		1.1	5.56E-01	Citronellol	9.6	34309	5	Periplasmic	COG0803	Inorganic ion transport and metabolism	
15597606	PA2410		hypothetical protein		3.5	1.46E-02	Citronellol	5.0	31732	4	Unknown	COG0803	Inorganic ion transport and metabolism	
15597607	PA2411		probable thioesterase		6.6	2.50E-02	Citronellsäure	5.4	27846	6	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	
15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, PvdH		4.8	1.12E-02	Citronellsäure	6.5	50215	2	Cytoplasmic	COG0160	Amino acid transport and metabolism	
15597620	PA2424	pvdL	PvdL		1.5	1.95E-01	Citronellsäure	5.1	480292	95	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597638	PA2442	gcvT2	glycine cleavage system protein T2		5.7	1.42E-03	Citronellsäure	6.4	39882	17	Periplasmic	COG0404	Amino acid transport and metabolism	
15597640	PA2444	glyA2	serine hydroxymethyltransferase		1.9	2.85E-02	Citronellol	6.5	44974	3	Periplasmic	COG0112	Amino acid transport and metabolism	
15597641	PA2445	gcvP2	glycine cleavage system protein P2		2.2	1.98E-02	Citronellsäure	6.0	103918	33	Periplasmic	COG1003	Amino acid transport and metabolism	
15597646	PA2450		hypothetical protein		96.0	1.04E-02	Citronellsäure	6.4	34331	3	Periplasmic			
15597651	PA2455		hypothetical protein		21.7	1.26E-01	Citronellsäure	5.6	20332	2	Cytoplasmic	COG3153	General function prediction only	
15597655	PA2459		hypothetical protein		2.7	1.24E-01	Citronellsäure	5.6	23801	2	Cytoplasmic			
15597658	PA2462		hypothetical protein		6.2	4.73E-03	Citronellol	5.1	573168	28	Outer Membrane Vesicle	COG3210	Intracellular trafficking and secretion	
15597660	PA2464		hypothetical protein		4.0	1.11E-01	Citronellol	4.6	17626	4	Periplasmic			
15597671	PA2475		probable cytochrome P450		139.4	2.67E-02	Citronellol	6.4	49401	2	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG		44.6	5.14E-02	Citronellsäure	7.1	28053	3	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15597679	PA2483		conserved hypothetical protein		6.7	5.03E-02	Citronellsäure	6.2	36102	3	Cytoplasmic	COG2141	Energy production and conversion	
15597687	PA2491		probable oxidoreductase		19.8	1.72E-04	Citronellsäure	5.3	36832	9	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexE precursor		2.9	1.12E-01	Citronellsäure	8.8	45031	3	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15597690	PA2494	mexF	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF		14.0	6.08E-03	Citronellol	5.4	115509	8	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15597691	PA2495	oprN	Multidrug efflux outer membrane protein OprN precursor		330.4	3.51E-02	Citronellol	5.1	51165	2	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15597699	PA2503		hypothetical protein		1.0	9.24E-01	Citronellol	4.6	45895	3	Cytoplasmic			
15597700	PA2504		hypothetical protein		5.1	4.51E-02	Citronellsäure	4.3	22822	3	Cytoplasmic	COG4859	Function unknown	
15597703	PA2507	catA	catechol 1,2-dioxygenase		10.8	2.27E-04	Citronellsäure	5.1	34160	7	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
15597725	PA2529		hypothetical protein		2.9	1.80E-01	Citronellol	5.6	52681	2	Cytoplasmic	COG0312	General function prediction only	
15597726	PA2530		hypothetical protein		3.2	1.06E-01	Citronellsäure	5.7	48959	3	Unknown	COG0312	General function prediction only	
15597727	PA2531		probable aminotransferase		13.6	2.41E-02	Citronellsäure	9.4	40715	2	Unknown	COG0079	Amino acid transport and metabolism	
15597728	PA2532	tpx	thiol peroxidase		1.1	8.57E-01	Citronellsäure	4.9	17234	14	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
15597741	PA2545	xthA	exodeoxyribonuclease III		1.8	3.08E-04	Citronellol	6.4	31003	6	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15597746	PA2550		probable acyl-CoA dehydrogenase		1.7	8.23E-01	Citronellol	6.6	45482	2	Cytoplasmic	COG1960	Lipid metabolism	
15597747	PA2551		probable transcriptional regulator		23.1	7.72E-03	Citronellsäure	9.9	35144	2	Cytoplasmic	COG0583	Transcription	
15597748	PA2552		probable acyl-CoA dehydrogenase		2.6	1.14E-01	Citronellsäure	5.6	40908	6	Cytoplasmic	COG1960	Lipid metabolism	
15597749	PA2553		probable acyl-CoA thiolase		1.2	1.75E-01	Citronellol	5.9	41400	16	Cytoplasmic	COG0183	Lipid metabolism	
15597750	PA2554		probable short-chain dehydrogenase		14.8	3.03E-03	Citronellsäure	6.6	26394	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597751	PA2555		probable AMP-binding enzyme		1.7	1.19E-01	Citronellsäure	6.1	60159	6	Cytoplasmic	COG0365	Lipid metabolism	
15597753	PA2557		probable AMP-binding enzyme		1.1	2.94E-01	Citronellsäure	6.1	62629	30	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15597768	PA2572		probable two-component response regulator		1.3	5.28E-01	Citronellol	5.4	50757	2	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15597771	PA2575		hypothetical protein		7.0	2.18E-01	Citronellol	6.4	22222	11	Unknown	COG3560	General function prediction only	
15597778	PA2582		hypothetical protein		1.0	5.84E-01	Citronellol	10.5	19446	4	Unknown	COG3109	Signal transduction mechanisms	
15597782	PA2586	gacA	response regulator GacA		11.9	1.17E-02	Citronellsäure	6.1	23576	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15597788	PA2592		probable periplasmic spermidine/putrescine-binding protein		6.0	1.63E-02	Citronellsäure	6.7	40725	8	Periplasmic	COG0687	Amino acid transport and metabolism	
15597790	PA2594		conserved hypothetical protein		1.2	6.49E-01	Citronellol	9.2	34686	3	Periplasmic	COG0715	Inorganic ion transport and metabolism	
15597797	PA2601		probable transcriptional regulator		2.3	1.45E-01	Citronellsäure	5.5	32375	2	Cytoplasmic	COG0583	Transcription	
15597799	PA2603		probable thiosulfate sulfurtransferase	Infinity		1.16E-01	Citronellol	5.0	57285	2	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15597807	PA2611	cysG	siroheme synthase		5.3	7.47E-02	Citronellsäure	6.3	50370	3	Cytoplasmic	COG0007	Coenzyme metabolism	
15597808	PA2612	serS	seryl-tRNA synthetase		1.3	3.46E-01	Citronellol	5.3	47231	13	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis	
15597810	PA2614	lolA	periplasmic chaperone LolA		76.5	8.76E-05	Citronellsäure	5.8	23072	11	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane	
15597812	PA2616	trxB1	thioredoxin reductase 1		1.1	9.25E-01	Citronellol	5.2	33818	8	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones	
15597816	PA2620	clpA	ATP-binding protease component ClpA		1.1	6.16E-01	Citronellsäure	5.9	84010	24	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597819	PA2623	icd	isocitrate dehydrogenase		2.0	1.18E-02	Citronellsäure	4.9	45577	46	Periplasmic	COG0538	Energy production and conversion	
15597820	PA2624	idh	isocitrate dehydrogenase		1.2	4.73E-01	Citronellsäure	6.1	81633	31	Periplasmic	COG2838	Energy production and conversion	
15597821	PA2625		conserved hypothetical protein		2.9	4.47E-03	Citronellol	5.2	17525	4	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15597822	PA2626	trmU	tRNA methyltransferase		1.0	3.83E-01	Citronellsäure	5.9	41886	2	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
15597823	PA2627		conserved hypothetical protein		14.5	6.34E-04	Citronellsäure	10.9	23030	2	Unknown	COG2915	General function prediction only	
15597825	PA2629	purB	adenylosuccinate lyase		1.0	9.18E-01	Citronellol	5.7	50500	20	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15597826	PA2630		conserved hypothetical protein		14.7	1.11E-02	Citronellol	4.1	44057	2	Cytoplasmic	COG2850	Function unknown	
15597827	PA2631		probable acetyl transferase		4.0	5.36E-03	Citronellsäure	4.8	16040	3	Cytoplasmic	COG2153	General function prediction only	
15597830	PA2634	aceA	isocitrate lyase AceA		1.5	1.92E-02	Citronellsäure	5.9	58886	57	Periplasmic	COG2224	Energy production and conversion	
15597836	PA2640	nuoE	NADH dehydrogenase I chain E		1.5	5.21E-02	Citronellol	4.8	18088	4	Cytoplasmic	COG1905	Energy production and conversion	
15597838	PA2642	nuoG	NADH dehydrogenase I chain G		6.1	2.23E-02	Citronellsäure	6.0	98999	3	Outer Membrane Vesicle	COG1034	Energy production and conversion	
15597853	PA2657		probable two-component response regulator	Infinity		4.49E-09	Citronellsäure	5.9	24729	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15597875	PA2679		hypothetical protein		9.3	8.61E-03	Citronellsäure	5.2	27641	5	Cytoplasmic	COG2226	Coenzyme metabolism	
15597880	PA2684		conserved hypothetical protein		1.1	8.92E-01	Citronellol	6.6	145819	8	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane	
15597895	PA2699		hypothetical protein		21.0	4.81E-02	Citronellol	6.2	67906	2	Unknown	COG1574	General function prediction only	
15597901	PA2705		hypothetical protein		7.5	6.08E-02	Citronellsäure	7.1	45584	2	Cytoplasmic	COG3825	Function unknown	
15597902	PA2706		hypothetical protein		2.1	1.07E-01	Citronellsäure	6.6	14228	3	Unknown	COG3791	Function unknown	

15597903	PA2707		hypothetical protein	1.0	8.11E-01	Citronellsäure	6.1	32205	19	Cytoplasmic	COG0714	General function prediction only	
15597905	PA2709	cysK	cysteine synthase A	2.1	1.78E-01	Citronellol	6.6	34309	11	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15597913	PA2717	cpo	chloroperoxidase precursor	1.3	3.25E-01	Citronellsäure	5.9	30435	8	Cytoplasmic	COG0596	General function prediction only	
15597916	PA2720		hypothetical protein	12.3	2.11E-02	Citronellsäure	4.7	23816	7	Cytoplasmic			
15597921	PA2725		probable chaperone	2.8	2.76E-01	Citronellsäure	6.2	68829	7	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597928	PA2732		hypothetical protein	1.7	7.48E-01	Citronellol	6.2	128671	29	Cytoplasmic	COG0610	Defense mechanisms	
15597930	PA2734		hypothetical protein	1.5	1.87E-01	Citronellol	6.1	48703	4	Cytoplasmic	COG0732	Defense mechanisms	
15597931	PA2735		probable restriction-modification system protein	1.5	4.03E-01	Citronellsäure	5.4	89570	24	Cytoplasmic	COG0286	Defense mechanisms	
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit	1.6	1.17E-01	Citronellsäure	5.1	86799	39	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis	
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit	25.6	9.31E-05	Citronellsäure	5.8	38063	16	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis	
15597939	PA2743	infC	translation initiation factor IF-3	1.4	3.17E-01	Citronellsäure	10.3	20864	4	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
15597940	PA2744	thrS	threonyl-tRNA synthetase	1.7	6.01E-03	Citronellsäure	6.3	73080	34	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis	
15597951	PA2755	eco	ecotin precursor	8.3	1.25E-02	Citronellol	6.5	17228	5	Periplasmic	COG4574	General function prediction only	
15597956	PA2760	oprQ	OprQ	1.0	8.78E-01	Citronellsäure	5.5	46850	12	Periplasmic			
15597960	PA2764		hypothetical protein	2.9	3.44E-02	Citronellol	6.0	24519	4	Cytoplasmic			
15597961	PA2765		hypothetical protein	195.5	2.18E-05	Citronellsäure	4.5	32396	11	Unknown	COG2837	Inorganic ion transport and metabolism	
15597966	PA2770		hypothetical protein	24.3	1.16E-04	Citronellsäure	4.7	28258	6	Cytoplasmic	COG0384	General function prediction only	
15597988	PA2792		hypothetical protein	22.7	1.47E-01	Citronellsäure	6.4	22070	2	Unknown			
15597990	PA2794		pseudaminidase	26.5	1.48E-04	Citronellol	6.2	47151	5	Unknown			
15597992	PA2796	tal	transaldolase	2.0	5.02E-04	Citronellol	4.9	33946	17	Cytoplasmic	COG0176	Carbohydrate transport and metabolism	
15597993	PA2797		hypothetical protein	4.8	2.11E-02	Citronellsäure	4.6	17710	6	Cytoplasmic	COG1366	Signal transduction mechanisms	
15597994	PA2798		probable two-component response regulator	3.9	4.50E-04	Citronellsäure	4.6	43485	6	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription
15598002	PA2806		conserved hypothetical protein	7.3	8.16E-02	Citronellsäure	5.4	30848	5	Cytoplasmic	COG2904	Function unknown	
15598003	PA2807		hypothetical protein	45.4	4.20E-03	Citronellsäure	7.9	22458	5	Unknown	COG4454	Inorganic ion transport and metabolism	
15598005	PA2809	copR	two-component response regulator, CopR	3.1	1.10E-01	Citronellsäure	4.6	25716	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15598009	PA2813		probable glutathione S-transferase	8.9	7.68E-03	Citronellol	4.8	23405	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598010	PA2814		hypothetical protein	8.7	1.21E-02	Citronellsäure	6.9	25274	5	Cytoplasmic	COG1305	Amino acid transport and metabolism	
15598017	PA2821		probable glutathione S-transferase	18.8	2.32E-04	Citronellsäure	6.1	24716	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598018	PA2822		conserved hypothetical protein	2.5	2.34E-01	Citronellol	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms	
15598019	PA2823		conserved hypothetical protein	1.5	3.30E-01	Citronellsäure	5.7	33760	5	Cytoplasmic	COG2607	General function prediction only	
15598022	PA2826		probable glutathione peroxidase	3.6	3.03E-03	Citronellol	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15598024	PA2828		probable aminotransferase	1.7	3.47E-01	Citronellsäure	6.1	44799	6	Periplasmic	COG0436	Amino acid transport and metabolism	
15598027	PA2831		conserved hypothetical protein	1.4	2.01E-01	Citronellol	5.3	42933	5	Cytoplasmic	COG2866	Amino acid transport and metabolism	
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	51.3	2.31E-02	Citronellsäure	5.4	28612	6	Cytoplasmic	COG1024	Lipid metabolism	
15598039	PA2843		probable aldolase	1.2	4.73E-01	Citronellol	6.1	49851	4	Cytoplasmic	COG3200	Amino acid transport and metabolism	
15598047	PA2851	efp	translation elongation factor P	1.2	4.71E-01	Citronellol	4.5	20985	7	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis	
15598049	PA2853	oprI	Outer membrane lipoprotein OprI precursor	19.1	1.31E-02	Citronellol	8.5	8835	2	Outer Membrane			
15598050	PA2854		conserved hypothetical protein	1.4	2.31E-01	Citronellol	5.6	34799	8	Periplasmic	COG1376	Function unknown	
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	1.2	4.22E-01	Citronellol	5.9	21037	9	Periplasmic	COG2755	Amino acid transport and metabolism	
15598067	PA2871		hypothetical protein	1.6	4.84E-02	Citronellol	5.4	28695	8	Unknown	COG1946	Lipid metabolism	
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	7.5	5.02E-03	Citronellsäure	5.3	24394	9	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
15598081	PA2885	atuR	putative repressor of atu genes	6.1	1.90E-03	Citronellsäure	4.9	22057	8	Unknown	COG1309	Transcription	
15598082	PA2886	atuA	expressed protein with apparent function in citronellol catabolism	1.1	5.44E-01	Citronellol	5.1	64435	30	Cytoplasmic			
15598083	PA2887	atuB	putative dehydrogenase involved in catabolism of citronellol	1.7	2.22E-01	Citronellsäure	7.3	30751	19	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598084	PA2888	atuC	geranyl-CoA carboxylase, beta-subunit	1.3	1.06E-01	Citronellol	6.5	57328	29	Cytoplasmic	COG4799	Lipid metabolism	
15598085	PA2889	atuD	citronellyl-CoA dehydrogenase, AtuD	1.4	8.80E-02	Citronellol	6.3	42714	36	Cytoplasmic	COG1960	Lipid metabolism	
15598086	PA2890	atuE	putative isohexenylglutaconyl-CoA hydratase	2.7	3.28E-03	Citronellol	5.2	27717	12	Cytoplasmic	COG1024	Lipid metabolism	
15598087	PA2891	atuF	geranyl-CoA carboxylase, alpha-subunit (biotin-containing)	1.6	1.25E-01	Citronellol	6.1	71747	37	Cytoplasmic	COG4770	Lipid metabolism	
15598088	PA2892	atuG	GCase, alpha-subunit (biotin-containing)	3.2	7.51E-02	Citronellsäure	7.2	29631	19	Cytoplasmic	COG4221	General function prediction only	
15598095	PA2899		probable transcriptional regulator	1.3	2.85E-01	Citronellsäure	7.6	23250	4	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	3667.1	4.12E-03	Citronellsäure	6.3	27275	2	Cytoplasmic	COG2243	Coenzyme metabolism	
15598101	PA2905	cobH	precorrin isomerase CobH	2.6	1.87E-01	Citronellsäure	5.7	21650	7	Cytoplasmic	COG2082	Coenzyme metabolism	
15598114	PA2918		probable short-chain dehydrogenase	29.8	4.89E-03	Citronellsäure	7.2	26738	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598135	PA2939		probable aminopeptidase	49.5	7.16E-05	Citronellol	4.8	57511	20	Extracellular	COG2234	General function prediction only	
15598136	PA2940		probable acyl-CoA thiolase	2.8	1.43E-01	Citronellsäure	5.5	39211	2	Cytoplasmic	COG0183	Lipid metabolism	
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	6.8	2.34E-01	Citronellsäure	5.2	138499	9	Cytoplasmic	COG1429	Coenzyme metabolism	
15598141	PA2945		conserved hypothetical protein	2.2	6.97E-02	Citronellsäure	4.9	41175	6	Cytoplasmic	COG0523	General function prediction only	
15598146	PA2950	pfmß	proton motive force protein, PMF	1.1	5.87E-01	Citronellol	4.8	43528	18	Cytoplasmic	COG3007	Function unknown	
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	1.3	9.40E-02	Citronellol	4.8	31423	16	Periplasmic	COG2025	Energy production and conversion	
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	1.2	3.93E-01	Citronellol	9.6	26377	22	Outer Membrane Vesicle	COG2086	Energy production and conversion	
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	1.5	1.50E-02	Citronellsäure	5.6	59896	17	Outer Membrane Vesicle	COG0644	Energy production and conversion	
15598150	PA2954		hypothetical protein	2.7	1.16E-03	Citronellol	4.9	21240	5	Cytoplasmic	COG3816	Function unknown	
15598155	PA2959		conserved hypothetical protein	1.1	5.33E-01	Citronellsäure	5.3	28114	4	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598158	PA2962	tmk	thymidylate kinase	2.0	1.70E-01	Citronellsäure	4.9	23077	4	Cytoplasmic	COG0125	Nucleotide transport and metabolism	
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.3	1.31E-02	Citronellsäure	5.8	43465	9	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598162	PA2966	acpP	acyl carrier protein	1.1	7.60E-01	Citronellsäure	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	1.1	7.73E-01	Citronellol	6.6	25585	12	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	25.1	9.80E-04	Citronellsäure	4.8	32444	8	Periplasmic	COG0331	Lipid metabolism	
15598168	PA2972		conserved hypothetical protein	2.5	2.65E-02	Citronellsäure	6.0	21054	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15598172	PA2976	rne	ribonuclease E	1.0	8.62E-01	Citronellol	4.6	117463	23	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis	
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	13.2	8.69E-04	Citronellsäure	6.7	37595	4	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.2	6.81E-01	Citronellol	5.4	27646	6	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	1.7	1.15E-01	Citronellol	6.7	51161	13	Cytoplasmic	COG1249	Energy production and conversion	
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	1.3	9.93E-01	Citronellol	5.7	128763	41	Periplasmic	COG1197	DNA replication, recombination, and repair	Transcription
15598199	PA3003		hypothetical protein	2.0	1.08E-02	Citronellol	4.5	22474	6	Periplasmic			
15598200	PA3004		5'-methylthioinosine phosphorylase	64.2	1.39E-03	Citronellsäure	6.6	26266	4	Cytoplasmic	COG0005	Nucleotide transport and metabolism	
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.3	3.00E-01	Citronellol	6.2	36101	8	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
15598202	PA3006	psrA	transcriptional regulator PsrA	4.5	1.96E-01	Citronellsäure	9.9	25784	3	Cytoplasmic	COG1309	Transcription	
15598206	PA3010		hypothetical protein	2.8	1.15E-01	Citronellsäure	4.6	19071	2	Unknown			
15598207	PA3011	topA	DNA topoisomerase I	1.1	9.81E-01	Citronellsäure	8.7	97282	54	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	1.8	9.47E-02	Citronellsäure	6.8	41643	25	Cytoplasmic	COG0183	Lipid metabolism	
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	1.0	9.80E-01	Citronellol	5.6	76954	58	Periplasmic	COG1250	Lipid metabolism	
15598211	PA3015		hypothetical protein	2.5	6.03E-02	Citronellsäure	5.9	30469	7	Unknown			
15598215	PA3019		probable ATP-binding component of ABC transporter	3.9	1.33E-02	Citronellsäure	5.0	71155	10	Cytoplasmic	COG0488	General function prediction only	
15598218	PA3022		hypothetical protein	14.8	3.63E-06	Citronellsäure	5.9	29579	8	Cytoplasmic	COG3217	General function prediction only	
15598219	PA3023		conserved hypothetical protein	17.0	2.28E-03	Citronellsäure	4.7	31504	9	Cytoplasmic	COG1597	Lipid metabolism	General function prediction only
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.5	2.84E-02	Citronellol	5.0	43359	7	Cytoplasmic	COG0303	Coenzyme metabolism	
15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	1.6	2.00E-02	Citronellol	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism	
15598228	PA3032	snr1	cytochrome c Snr1	5.2	1.80E-03	Citronellol	6.8	52500	9	Cytoplasmic	COG1858	Inorganic ion transport and metabolism	
15598234	PA3038		probable porin	2.2	3.29E-02	Citronellol	7.1	46712	6	Periplasmic			
15598244	PA3048		conserved hypothetical protein	1.2	4.96E-01	Citronellsäure	8.0	81155	9	Cytoplasmic	COG0116	DNA replication, recombination, and repair	
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	1.3	4.35E-01	Citronellsäure	6.1	182637	24	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism	
15598275	PA3079		hypothetical protein	27.5	6.50E-01	Citronellol	7.1	87351	2	Cytoplasmic Membrane	COG1033	General function prediction only	
15598276	PA3080		hypothetical protein	6.4	4.31E-02	Citronellsäure	4.8	38479	4	Unknown	COG4447	General function prediction only	
15598277	PA3081		conserved hypothetical protein	1.4	3.32E-02	Citronellol	9.2	50680	10	Periplasmic			
15598278	PA3082	gbt	glycine betaine transmethylase	1.7	2.45E-01	Citronellsäure	4.5	71403	6	Periplasmic			
15598279	PA3083	pepN	aminopeptidase N	1.1	9.96E-01	Citronellsäure	4.9	100046	55	Periplasmic	COG0308	Amino acid transport and metabolism	
15598284	PA3088		conserved hypothetical protein	14.2	8.04E-03	Citronellsäure	7.3	32140	5	Cytoplasmic	COG0061	Coenzyme metabolism	
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	2.6	1.50E-03	Citronellsäure	7.2	72969	29	Cytoplasmic	COG1902	Energy production and conversion	
15598302	PA3106		probable short-chain dehydrogenase	5.1	9.78E-02	Citronellsäure	4.6	26997	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598303	PA3107	metZ	o-succinylhomoserine sulfhydrylase	1.1	4.57E-01	Citronellsäure	6.3	43185	7	Periplasmic	COG0626	Amino acid transport and metabolism	
15598304	PA3108	purF	amidophosphoribosyltransferase	1.5	3.22E-02	Citronellsäure	6.8	55370	17	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism	
15598307	PA3111	folC	folylpolyglutamate synthetase	1.1	4.92E-01	Citronellol	5.0	46505	3	Cytoplasmic	COG0285	Coenzyme metabolism	
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	3.0	2.64E-02	Citronellsäure	7.1	31843	7	Periplasmic	COG0777	Lipid metabolism	
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	1.3	8.23E-01	Citronellol	6.8	22280	3	Cytoplasmic	COG0135	Amino acid transport and metabolism	
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	13.5	8.68E-03	Citronellsäure	5.5	40494	21	Periplasmic	COG0136	Amino acid transport and metabolism	
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.0	9.82E-01	Citronellol	4.8	39120	14	Cytoplasmic	COG0473	Amino acid transport and metabolism	
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	5.1	2.10E-02	Citronellsäure	4.7	24011	14	Cytoplasmic	COG0066	Amino acid transport and metabolism	
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	1.1	4.91E-01	Citronellsäure	6.3	51042	16	Cytoplasmic	COG0065	Amino acid transport and metabolism	
15598318	PA3122		probable transcriptional regulator	1.1	4.90E-01	Citronellol	6.4	32835	2	Cytoplasmic	COG0583	Transcription	
15598323	PA3127		hypothetical protein	1.9	5.68E-01	Citronellol	5.0	29403	5	Unknown			

15598324	PA3128		probable short-chain dehydrogenase	1.5	5.80E-03	Citronellol	6.8	26219	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598327	PA3131		probable aldolase	1.1	7.91E-01	Citronellol	5.3	22852	6	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598330	PA3134	gltX	glutamyl-tRNA synthetase	1.2	2.69E-01	Citronellol	6.7	56749	25	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15598334	PA3138	uvrB	excinuclease ABC subunit B	1.3	4.15E-01	Citronellol	5.1	76067	10	Cytoplasmic	COG0556	DNA replication, recombination, and repair	
15598335	PA3139		probable amino acid aminotransferase	18.6	1.55E-05	Citronellsäure	6.6	43319	22	Periplasmic	COG1448	Amino acid transport and metabolism	
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	2.5	4.95E-02	Citronellsäure	5.8	38907	19	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane	
15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	21.2	3.25E-04	Citronellsäure	5.7	27448	4	Cytoplasmic	COG0107	Amino acid transport and metabolism	
15598348	PA3152	hisH2	glutamine amidotransferase	1.2	1.00E+00	Citronellol	7.1	22663	5	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase, wbpE	2.9	4.61E-04	Citronellsäure	6.0	38924	17	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-acetyltransferase, WbpD	54.1	5.22E-04	Citronellsäure	7.8	20562	4	Cytoplasmic	COG1045	Amino acid transport and metabolism	
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	2.7	1.86E-03	Citronellsäure	6.6	35717	17	Cytoplasmic	COG0673	General function prediction only	
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.0	9.41E-01	Citronellol	5.2	48155	32	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane	
15598358	PA3162	rpsA	30S ribosomal protein S1	1.0	9.24E-01	Citronellsäure	4.6	61869	32	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis	
15598359	PA3163	cmk	cytidylate kinase	1.3	2.57E-01	Citronellol	4.8	24637	7	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	175.7	1.85E-03	Citronellsäure	4.8	39483	3	Cytoplasmic	COG0079	Amino acid transport and metabolism	
15598362	PA3166	pheA	chorismate mutase	1.2	1.38E-01	Citronellol	6.3	40632	10	Cytoplasmic	COG0077	Amino acid transport and metabolism	
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.2	3.90E-01	Citronellol	4.7	39917	13	Periplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
15598364	PA3168	gyrA	DNA gyrase subunit A	1.8	5.17E-02	Citronellsäure	4.6	101134	45	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.5	3.49E-02	Citronellsäure	5.1	39425	8	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis	
15598366	PA3170		conserved hypothetical protein	4.8	1.33E-01	Citronellol	5.5	48493	4	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	1.3	5.38E-01	Citronellol	6.3	25860	2	Cytoplasmic	COG2227	Coenzyme metabolism	
15598368	PA3172		probable hydrolase	2.0	2.02E-01	Citronellsäure	5.0	24944	10	Cytoplasmic	COG0546	General function prediction only	
15598369	PA3173		probable short-chain dehydrogenase	2.8	1.14E-02	Citronellsäure	4.9	26332	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	21.8	1.72E-02	Citronellsäure	7.6	23953	4	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598378	PA3182	pgl	6-phosphogluconolactonase	176.0	4.80E-02	Citronellsäure	6.5	25571	2	Unknown	COG0363	Carbohydrate transport and metabolism	
15598386	PA3190		probable binding protein component of ABC sugar transporter	41.1	5.45E-05	Citronellsäure	5.8	45131	9	Periplasmic	COG1653	Carbohydrate transport and metabolism	
15598389	PA3193	glk	glucokinase	14.1	8.09E-05	Citronellsäure	5.0	34606	3	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
15598390	PA3194	edd	phosphogluconate dehydratase	3.0	1.25E-02	Citronellol	6.7	65182	7	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	1.2	4.84E-01	Citronellsäure	6.6	36170	6	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15598404	PA3208		conserved hypothetical protein	7.6	1.04E-02	Citronellol	6.5	19948	8	Cytoplasmic Membrane	COG0778	Energy production and conversion	
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.9	4.19E-02	Citronellol	8.5	20104	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15598429	PA3233		hypothetical protein	5.9	1.99E-01	Citronellol	6.3	66563	2	Cytoplasmic	COG2905	Signal transduction mechanisms	
15598439	PA3243	minC	cell division inhibitor MinC	5.4	1.39E-01	Citronellol	6.5	28124	5	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
15598440	PA3244	minD	cell division inhibitor MinD	3.9	8.68E-02	Citronellsäure	5.5	29617	18	Periplasmic	COG2894	Cell division and chromosome partitioning	
15598442	PA3246	rluA	pseudouridine synthase RluA	82.0	6.22E-03	Citronellsäure	7.0	24339	2	Cytoplasmic	COG0564	Translation, ribosomal structure and biogenesis	
15598443	PA3247		hypothetical protein	3.9	7.21E-04	Citronellol	6.0	46658	10	Cytoplasmic	COG1362	Amino acid transport and metabolism	
15598444	PA3248		hypothetical protein	3.4	7.60E-02	Citronellsäure	8.0	20759	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
15598446	PA3250		hypothetical protein	3.5	4.43E-02	Citronellsäure	6.2	38285	11	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15598451	PA3255		hypothetical protein	1.4	5.07E-02	Citronellol	4.4	21635	6	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15598452	PA3256		probable oxidoreductase	2.0	7.41E-03	Citronellol	5.2	33387	6	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15598453	PA3257	prc	periplasmic tail-specific protease	1.5	1.04E-01	Citronellol	6.6	78182	33	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	9.5	7.26E-06	Citronellsäure	4.8	26845	9	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones	
15598459	PA3263		conserved hypothetical protein	1.1	3.20E-01	Citronellsäure	4.7	34015	16	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
15598473	PA3277		probable short-chain dehydrogenase	8.1	3.37E-02	Citronellsäure	6.5	29251	2	Cytoplasmic	COG0300	General function prediction only	
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	1.5	6.38E-03	Citronellol	7.5	61654	23	Outer Membrane Vesicle	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	4.1	1.28E-02	Citronellol	7.2	61736	12	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598498	PA3302		conserved hypothetical protein	8.6	1.19E-02	Citronellsäure	5.0	16901	6	Unknown	COG2030	Lipid metabolism	
15598504	PA3308	hepA	RNA helicase HepA	1.4	2.01E-01	Citronellsäure	4.8	106839	20	Periplasmic	COG0553	Transcription	DNA replication, recombination, and repair
15598505	PA3309		conserved hypothetical protein	3.6	2.02E-02	Citronellol	5.4	16496	8	Periplasmic	COG0589	Signal transduction mechanisms	
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.8	2.03E-01	Citronellsäure	5.5	30908	4	Cytoplasmic	COG2084	Lipid metabolism	
15598509	PA3313		hypothetical protein	22.5	5.38E-05	Citronellsäure	10.2	36539	20	Periplasmic	COG3221	Inorganic ion transport and metabolism	
15598522	PA3326	clpP2	ClpP2	1.8	1.36E-01	Citronellol	5.4	22142	10	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15598523	PA3327		probable non-ribosomal peptide synthetase	4.0	3.19E-03	Citronellol	5.5	259403	53	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15598525	PA3329		hypothetical protein	27.9	4.62E-04	Citronellol	6.2	49134	9	Cytoplasmic			
15598527	PA3331		cytochrome P450	10.0	1.48E-03	Citronellol	5.7	46345	3	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
15598528	PA3332		conserved hypothetical protein	35.0	5.34E-03	Citronellol	5.5	15920	2	Cytoplasmic	COG3631	General function prediction only	
15598544	PA3348		probable chemotaxis protein methyltransferase	2.3	2.52E-03	Citronellol	9.6	30615	2	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
15598545	PA3349		probable chemotaxis protein	1.6	7.85E-02	Citronellsäure	6.1	34402	15	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15598549	PA3353		hypothetical protein	1.2	3.51E-01	Citronellsäure	6.8	29852	5	Cytoplasmic	COG5581	Signal transduction mechanisms	
15598550	PA3354		hypothetical protein	15.1	2.31E-03	Citronellsäure	5.6	22398	3	Cytoplasmic	COG3222	Function unknown	
15598553	PA3357	dsdA	D-serine dehydratase	1.1	6.24E-01	Citronellol	6.0	48200	5	Cytoplasmic	COG3048	Amino acid transport and metabolism	
15598593	PA3397	fpr	NADPH-dependent ferredoxin reductase	1.3	1.84E-01	Citronellol	5.9	29518	18	Periplasmic	COG1018	Energy production and conversion	
15598611	PA3415		probable dihydrolipoamide acetyltransferase	4.1	3.86E-02	Citronellsäure	5.5	39521	3	Cytoplasmic	COG0508	Energy production and conversion	
15598614	PA3418	ldh	leucine dehydrogenase	8.1	1.60E-04	Citronellsäure	5.9	35633	6	Cytoplasmic	COG0334	Amino acid transport and metabolism	
15598617	PA3421		conserved hypothetical protein	14.5	2.24E-02	Citronellol	9.2	50690	2	Unknown			
15598623	PA3427		probable short-chain dehydrogenases	5.6	1.08E-02	Citronellsäure	5.8	32323	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598626	PA3430		probable aldolase	2.3	1.74E-01	Citronellol	6.6	27993	3	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15598633	PA3437	folM	dihydromonapterin reductase, FolM	5.4	3.65E-02	Citronellsäure	7.0	25403	2	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	9.5	7.49E-03	Citronellsäure	7.6	20833	4	Cytoplasmic	COG0302	Coenzyme metabolism	
15598646	PA3450		probable antioxidant protein	1.4	1.54E-01	Citronellsäure	5.2	24164	4	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598649	PA3453		conserved hypothetical protein	1.5	7.87E-01	Citronellol	5.4	24160	7	Unknown	COG3132	Function unknown	
15598654	PA3458		probable transcriptional regulator	9.7	1.93E-01	Citronellol	5.6	17599	2	Unknown	COG1846	Transcription	
15598657	PA3461		conserved hypothetical protein	1.3	1.73E-01	Citronellol	5.1	43294	8	Cytoplasmic	COG1363	Carbohydrate transport and metabolism	
15598667	PA3471		probable malic enzyme	2.8	1.89E-02	Citronellol	5.2	62420	12	Periplasmic	COG0281	Energy production and conversion	
15598671	PA3475	pheC	cyclohexadienyl dehydratase precursor	1.5	2.75E-01	Citronellsäure	6.9	30448	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598673	PA3477	rhlR	transcriptional regulator RhlR	15.5	1.15E-03	Citronellsäure	7.2	27577	5	Cytoplasmic	COG2771	Transcription	
15598676	PA3480		probable deoxycytidine triphosphate deaminase	1.7	4.87E-01	Citronellol	6.3	21154	5	Cytoplasmic	COG0717	Nucleotide transport and metabolism	
15598677	PA3481		conserved hypothetical protein	12.3	3.74E-04	Citronellsäure	5.1	38889	8	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
15598678	PA3482	metG	methionyl-tRNA synthetase	1.1	2.96E-01	Citronellsäure	5.4	74903	30	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis	
15598711	PA3515		hypothetical protein	40.4	9.51E-05	Citronellsäure	4.9	39764	33	Cytoplasmic	COG2227	Coenzyme metabolism	
15598712	PA3516		probable lyase	118.2	2.85E-05	Citronellsäure	6.3	52927	23	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15598713	PA3517		probable lyase	40.4	3.85E-04	Citronellsäure	6.4	52228	20	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15598715	PA3519		hypothetical protein	58.7	2.41E-04	Citronellsäure	5.9	39369	11	Cytoplasmic			
15598721	PA3525	argG	argininosuccinate synthase	1.5	1.63E-02	Citronellsäure	5.3	45297	19	Periplasmic	COG0137	Amino acid transport and metabolism	
15598723	PA3527	pyrC	dihydroorotase	19.6	2.41E-05	Citronellsäure	6.6	38406	12	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
15598724	PA3528	rnt	ribonuclease T	1.0	8.24E-01	Citronellol	4.8	24723	6	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15598725	PA3529		alkylhydroperoxide reductase C	1.3	6.51E-01	Citronellol	5.3	21822	15	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598730	PA3534		probable oxidoreductase	4.8	2.92E-01	Citronellol	6.9	76766	2	Cytoplasmic	COG0243	Energy production and conversion	
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.3	1.07E-01	Citronellol	5.7	33924	9	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15598735	PA3539		conserved hypothetical protein	5.6	3.69E-02	Citronellsäure	6.7	29560	9	Cytoplasmic	COG3022	Function unknown	
15598748	PA3552	arnB	ArnB	10.4	3.68E-02	Citronellsäure	8.0	41867	3	Cytoplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598750	PA3554	arnA	ArnA	2.0	1.07E-01	Citronellsäure	6.7	74360	5	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis	
15598758	PA3562	fruI	phosphotransferase system transporter enzyme I, FruI	1.1	4.87E-01	Citronellsäure	4.8	101572	4	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598759	PA3563	fruR	fructose transport system repressor FruR	3.4	9.87E-02	Citronellsäure	6.4	36369	2	Cytoplasmic	COG1609	Transcription	
15598763	PA3567		probable oxidoreductase	1.4	6.49E-01	Citronellol	6.6	36678	3	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15598764	PA3568		probable acetyl-coa synthetase	1.1	7.80E-01	Citronellol	6.7	68990	8	Cytoplasmic	COG0365	Lipid metabolism	
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	3.2	1.77E-03	Citronellol	6.4	53663	6	Cytoplasmic	COG1012	Energy production and conversion	
15598774	PA3578		conserved hypothetical protein	95.7	1.42E-04	Citronellsäure	4.9	28906	4	Cytoplasmic Membrane	COG0384	General function prediction only	
15598778	PA3582	glpK	glycerol kinase	1.0	9.65E-01	Citronellol	5.9	55966	32	Cytoplasmic	COG0554	Energy production and conversion	
15598783	PA3587	metR	transcriptional regulator MetR	17.7	1.12E-02	Citronellsäure	5.6	34216	2	Cytoplasmic	COG0583	Transcription	
15598800	PA3604	erdR	response regulator ErdR	5.4	1.64E-03	Citronellsäure	4.8	23531	9	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598806	PA3610	potD	polyamine transport protein PotD	17.3	3.17E-02	Citronellsäure	5.5	39260	3	Periplasmic	COG0687	Amino acid transport and metabolism	
15598809	PA3613		hypothetical protein	1.9	1.41E-01	Citronellol	6.4	88379	13	Periplasmic	COG3957	Carbohydrate transport and metabolism	
15598810	PA3614		hypothetical protein	1.4	2.11E-01	Citronellol	7.0	51921	7	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
15598811	PA3615		hypothetical protein	2.0	1.72E-01	Citronellsäure	6.0	40465	5	Cytoplasmic	COG1611	General function prediction only	
15598813	PA3617	recA	RecA protein	1.9	4.13E-02	Citronellol	5.2	36879	13	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.3	5.41E-01	Citronellsäure	6.1	94977	21	Cytoplasmic	COG0249	DNA replication, recombination, and repair	
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	44.6	4.11E-05	Citronellsäure	6.1	23407	4	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones	
15598821	PA3625	surE	survival protein SurE	49.1	1.10E-02	Citronellsäure	5.2	26368	4	Unknown	COG0496	General function prediction only	
15598822	PA3626		conserved hypothetical protein	7.8	3.12E-02	Citronellsäure	6.8	38782	2	Cytoplasmic	COG0585	Function unknown	
15598825	PA3629	adhC	alcohol dehydrogenase class III	1.8	9.77E-03	Citronellol	5.4	39208	5	Cytoplasmic	COG1062	Energy production and conversion	

15598831	PA3635	eno	enolase		1.1	6.60E-01	Citronellol	4.8	45195	20	Cytoplasmic	COG0148	Carbohydrate transport and metabolism		
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase		29.1	9.12E-05	Citronellsäure	6.5	31143	16	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane		
15598833	PA3637	pyrG	CTP synthase		1.4	6.25E-02	Citronellsäure	5.4	59617	30	Periplasmic	COG0504	Nucleotide transport and metabolism		
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)		1.8	3.83E-02	Citronellsäure	5.2	34947	19	Outer Membrane Vesicle	COG0825	Lipid metabolism		
15598836	PA3640	dnaE	DNA polymerase III, alpha chain		1.5	2.82E-01	Citronellsäure	5.1	130904	52	Cytoplasmic	COG0587	DNA replication, recombination, and repair		
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase		1.6	1.23E-02	Citronellol	7.1	28010	6	Cytoplasmic	COG1043	acyl carrier protein		
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase		3.0	8.26E-03	Citronellsäure	7.6	16774	8	Cytoplasmic	COG0764	Lipid metabolism		
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase		9.4	3.99E-03	Citronellsäure	6.2	36191	2	Cytoplasmic	COG1044	3-hydroxymyristoyl		
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase		1.1	4.30E-01	Citronellsäure	5.7	42508	2	Unknown	COG0743	Lipid metabolism		
15598849	PA3653	frr	ribosome recycling factor		38.8	2.43E-05	Citronellsäure	5.9	20485	15	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis		
15598850	PA3654	pyrH	uridylate kinase		1.4	1.11E-01	Citronellol	5.4	26272	6	Periplasmic	COG0528	Nucleotide transport and metabolism		
15598851	PA3655	tsf	elongation factor Ts		1.2	1.19E-01	Citronellsäure	5.0	30653	27	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis		
15598852	PA3656	rpsB	30S ribosomal protein S2		1.6	2.59E-01	Citronellsäure	9.0	27336	9	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis		
15598853	PA3657	map	methionine aminopeptidase		1.4	3.42E-02	Citronellol	6.3	29086	5	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis		
15598854	PA3658	glnD	protein-PII uridylyltransferase		3.1	7.78E-01	Citronellol	5.5	103403	2	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones		
15598855	PA3659		probable aminotransferase		1.8	2.78E-02	Citronellsäure	5.5	44544	6	Cytoplasmic	COG0436	Amino acid transport and metabolism		
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase		16.9	1.77E-04	Citronellsäure	6.0	35973	10	Periplasmic	COG2171	Amino acid transport and metabolism		
15598871	PA3675		hypothetical protein		1.5	7.03E-01	Citronellol	9.4	23645	5	Unknown				
15598874	PA3678		probable transcriptional regulator		20.6	5.44E-03	Citronellol	6.3	23150	2	Cytoplasmic	COG1309	Transcription		
15598878	PA3682		hypothetical protein		28.1	1.92E-04	Citronellsäure	5.0	29150	5	Cytoplasmic	COG2513	Carbohydrate transport and metabolism		
15598881	PA3685		conserved hypothetical protein		16.0	1.24E-02	Citronellsäure	4.8	24180	5	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones		
15598882	PA3686	adk	adenylate kinase		1.1	5.49E-01	Citronellol	6.4	23107	16	Cytoplasmic	COG0563	Nucleotide transport and metabolism		
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase		1.1	5.75E-01	Citronellol	6.2	97839	24	Cytoplasmic	COG2352	Energy production and conversion		
15598888	PA3692	lptF	Lipotoxon F, LptF		1.6	2.84E-01	Citronellsäure	9.9	28514	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane		
15598889	PA3693		conserved hypothetical protein		1.1	6.75E-01	Citronellol	7.0	18219	2	Unknown	COG2110	General function prediction only		
15598894	PA3698		hypothetical protein		1.9	2.21E-01	Citronellsäure	4.5	20351	5	Unknown				
15598896	PA3700	lysS	lysyl-tRNA synthetase		1.1	2.30E-01	Citronellsäure	5.0	57329	30	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis		
15598897	PA3702	wspR	WspR		151.5	4.97E-02	Citronellsäure	5.6	37887	2	Cytoplasmic	COG3706	Signal transduction mechanisms		
15598918	PA3723		probable FMN oxidoreductase		1.8	1.21E-01	Citronellsäure	6.3	40319	15	Cytoplasmic	COG1902	Energy production and conversion		
15598921	PA3726		conserved hypothetical protein		1.1	8.49E-01	Citronellol	4.8	20596	6	Cytoplasmic	COG4681	Function unknown		
15598923	PA3728		hypothetical protein		2.0	2.17E-01	Citronellsäure	4.9	197133	52	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning		
15598926	PA3731		conserved hypothetical protein		1.3	3.44E-01	Citronellsäure	7.5	24893	5	Cytoplasmic	COG1842	Transcription		Signal transduction mechanisms
15598927	PA3732		conserved hypothetical protein		1.4	9.13E-02	Citronellol	4.0	15959	2	Unknown	COG3789	Function unknown		
15598928	PA3733		hypothetical protein		116.7	5.52E-02	Citronellsäure	5.9	44766	2	Cytoplasmic	COG1804	Energy production and conversion		
15598930	PA3735	thrC	threonine synthase		1.2	2.70E-01	Citronellol	6.6	51795	23	Periplasmic	COG0498	Amino acid transport and metabolism		
15598931	PA3736	hom	homoserine dehydrogenase		1.0	8.33E-01	Citronellsäure	5.1	46192	12	Cytoplasmic	COG0460	Amino acid transport and metabolism		
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC		7.7	3.24E-02	Citronellsäure	8.8	26095	5	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones		
15598935	PA3740		hypothetical protein	Infinity		7.43E-08	Citronellsäure	10.0	24754	2	Unknown				
15598941	PA3746	ffh	signal recognition particle protein Ffh		1.5	3.49E-01	Citronellol	10.3	49359	3	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion		
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2		1.0	4.61E-01	Citronellsäure	6.1	42342	20	Periplasmic	COG0027	Nucleotide transport and metabolism		
15598948	PA3753		conserved hypothetical protein		1.5	1.61E-01	Citronellol	7.0	18509	5	Cytoplasmic	COG0663	General function prediction only		
15598949	PA3754		hypothetical protein		102.7	3.57E-02	Citronellsäure	4.5	22855	3	Cytoplasmic				
15598950	PA3755		conserved hypothetical protein		7.2	7.22E-03	Citronellsäure	4.6	20829	2	Cytoplasmic	COG1051	Nucleotide transport and metabolism		
15598954	PA3759		probable aminotransferase		14.4	1.42E-01	Citronellsäure	5.7	36123	2	Cytoplasmic	COG2222	Cell envelope biogenesis, outer membrane		
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase		1.1	6.00E-01	Citronellsäure	4.8	140646	60	Periplasmic	COG0046	Nucleotide transport and metabolism		
15598962	PA3767		conserved hypothetical protein		1.9	3.09E-01	Citronellol	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism		Translation, ribosomal structure and biogenesis
15598964	PA3769	guaA	GMP synthase		1.3	3.89E-02	Citronellsäure	5.6	57959	27	Periplasmic	COG0519	Nucleotide transport and metabolism		
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase		1.0	8.71E-01	Citronellol	6.7	51707	29	Periplasmic	COG0516	Nucleotide transport and metabolism		
15598974	PA3779		hypothetical protein		15.2	5.34E-03	Citronellsäure	5.3	37696	5	Periplasmic	COG1638	Carbohydrate transport and metabolism		
15598978	PA3783		hypothetical protein		1.3	3.63E-01	Citronellol	6.4	23091	5	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15598980	PA3785		conserved hypothetical protein		32.6	7.97E-04	Citronellol	6.8	17000	4	Periplasmic	COG2847	Inorganic ion transport and metabolism		
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precursor		79.6	2.84E-05	Citronellol	6.4	79303	5	Periplasmic	COG1629	Inorganic ion transport and metabolism		
15598990	PA3795		probable oxidoreductase		1.7	4.10E-01	Citronellol	5.3	34803	5	Cytoplasmic	COG0667	Energy production and conversion		
15598992	PA3797		conserved hypothetical protein		1.8	1.88E-01	Citronellsäure	5.8	29996	5	Cytoplasmic	COG0388	General function prediction only		
15598993	PA3798		probable aminotransferase		1.3	2.47E-01	Citronellol	6.2	42594	4	Cytoplasmic	COG0436	Amino acid transport and metabolism		
15598997	PA3802	hisS	histidyl-tRNA synthetase		1.2	2.14E-01	Citronellsäure	5.0	47480	14	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis		
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE		1.3	9.51E-02	Citronellol	6.4	40056	10	Cytoplasmic	COG0821	Lipid metabolism		
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]		3.4	9.89E-03	Citronellol	4.0	12241	2	Cytoplasmic	COG0633	Energy production and conversion		
15599005	PA3810	hscA	heat shock protein HscA		2.1	3.99E-03	Citronellsäure	4.6	66446	14	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones		
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)		1.7	9.42E-03	Citronellsäure	5.9	44666	29	Cytoplasmic	COG1104	Amino acid transport and metabolism		
15599010	PA3815	iscR	IscR		2.0	1.07E-01	Citronellol	6.9	17853	7	Unknown	COG1959	Transcription		
15599012	PA3817		probable methyltransferase		1.3	3.77E-02	Citronellol	6.2	28493	6	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis		
15599013	PA3818		extragenic suppressor protein SuhB		1.7	2.28E-01	Citronellsäure	6.6	29521	3	Periplasmic	COG0483	Carbohydrate transport and metabolism		
15599014	PA3819		conserved hypothetical protein		10.3	6.80E-03	Citronellsäure	9.4	18941	3	Outer Membrane	COG3134	Function unknown		
15599018	PA3823	tgt	queuine tRNA-ribosyltransferase		2.6	3.12E-03	Citronellsäure	6.9	41205	2	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis		
15599029	PA3834	valS	valyl-tRNA synthetase		1.2	2.22E-01	Citronellsäure	5.2	107707	46	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis		
15599031	PA3836		hypothetical protein		5.4	6.38E-04	Citronellsäure	8.7	34220	22	Periplasmic	COG2984	General function prediction only		
15599041	PA3846		hypothetical protein		27.4	2.85E-03	Citronellsäure	5.1	19892	7	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15599044	PA3849		conserved hypothetical protein		27.6	2.75E-06	Citronellol	5.1	37930	6	Cytoplasmic	COG3081	General function prediction only		
15599045	PA3850		hypothetical protein		7.5	2.32E-02	Citronellsäure	4.4	33613	2	Unknown				
15599047	PA3852		hypothetical protein		1.1	1.45E-01	Citronellol	5.4	33979	7	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones		
15599053	PA3858		probable amino acid-binding protein		3.2	2.37E-03	Citronellsäure	7.9	37043	9	Periplasmic	COG0834	Amino acid transport and metabolism		Signal transduction mechanisms
15599054	PA3859		carboxylesterase		4.6	1.01E-01	Citronellsäure	4.9	23420	5	Unknown	COG0400	General function prediction only		
15599055	PA3860		probable AMP-binding enzyme		2.0	9.47E-04	Citronellsäure	6.2	68986	30	Cytoplasmic	COG0318	Lipid metabolism		Secondary metabolites biosynthesis, transport, and catabolism
15599060	PA3865		probable amino acid binding protein		29.1	1.29E-03	Citronellsäure	6.1	28433	5	Periplasmic	COG0834	Amino acid transport and metabolism		Signal transduction mechanisms
15599061	PA3866		pyocin protein		1.0	9.02E-01	Citronellol	8.8	80731	7	Extracellular				
15599074	PA3879	narL	two-component response regulator NarL		76.4	3.69E-02	Citronellsäure	4.8	24255	3	Cytoplasmic	COG2197	Signal transduction mechanisms		Transcription
15599081	PA3886		hypothetical protein		3.4	1.67E-01	Citronellsäure	4.9	32290	3	Cytoplasmic	COG0647	Carbohydrate transport and metabolism		
15599091	PA3896		probable 2-hydroxyacid dehydrogenase		1.6	2.27E-01	Citronellsäure	8.2	35632	4	Cytoplasmic	COG1052	Energy production and conversion		Coenzyme metabolism
15599098	PA3903	prfC	peptide chain release factor 3		1.1	6.47E-01	Citronellol	5.7	59865	9	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis		
15599100	PA3905		hypothetical protein		4.9	1.72E-02	Citronellsäure	7.7	20024	3	Unknown				
15599103	PA3908		hypothetical protein		1.6	6.65E-02	Citronellsäure	5.0	27294	8	Cytoplasmic				
15599113	PA3918	moaC	molybdopterin biosynthetic protein C		4.1	1.94E-01	Citronellol	7.0	17306	5	Cytoplasmic	COG0315	Coenzyme metabolism		
15599114	PA3919		conserved hypothetical protein		3.0	1.94E-05	Citronellsäure	6.3	51700	19	Cytoplasmic	COG1875	General function prediction only		
15599115	PA3920		probable metal transporting P-type ATPase		64.2	1.13E-01	Citronellsäure	6.9	83437	2	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism		
15599117	PA3922		conserved hypothetical protein		1.6	3.11E-02	Citronellol	9.0	51229	36	Periplasmic				
15599118	PA3923		hypothetical protein		1.4	8.54E-02	Citronellsäure	4.7	69590	15	Outer Membrane				
15599119	PA3924		probable medium-chain acyl-CoA ligase		1.6	5.18E-02	Citronellol	6.0	62315	26	Cytoplasmic	COG0318	Lipid metabolism		Secondary metabolites biosynthesis, transport, and catabolism
15599120	PA3925		probable acyl-CoA thiolase		1.7	3.21E-02	Citronellsäure	6.4	40553	34	Cytoplasmic	COG0183	Lipid metabolism		
15599126	PA3931		conserved hypothetical protein		6.7	4.14E-03	Citronellsäure	8.6	28101	9	Periplasmic	COG1464	Inorganic ion transport and metabolism		
15599136	PA3941		hypothetical protein		9.7	7.07E-03	Citronellol	5.8	22025	3	Cytoplasmic	COG0546	General function prediction only		
15599137	PA3942	tesB	acyl-CoA thioesterase II		1.2	4.94E-01	Citronellol	5.8	32934	3	Cytoplasmic	COG1946	Lipid metabolism		
15599143	PA3948	rocA1	Two-component response regulator RocA1		8.9	3.83E-03	Citronellsäure	6.8	22996	2	Cytoplasmic	COG2197	Signal transduction mechanisms		Transcription
15599146	PA3951		conserved hypothetical protein		1.2	7.25E-01	Citronellsäure	7.5	18088	2	Unknown	COG1432	Function unknown		
15599151	PA3956		hypothetical protein		5.2	1.37E-01	Citronellol	5.1	15453	4	Unknown	COG0346	Amino acid transport and metabolism		
15599160	PA3965		probable transcriptional regulator		3.1	5.13E-02	Citronellol	5.7	19289	5	Cytoplasmic	COG1522	Transcription		
15599165	PA3970	amn	AMP nucleosidase		29.9	2.74E-03	Citronellsäure	6.8	56225	5	Cytoplasmic	COG0775	Nucleotide transport and metabolism		
15599167	PA3972		probable acyl-CoA dehydrogenase		1.0	9.60E-01	Citronellsäure	6.4	60338	30	Cytoplasmic	COG1960	Lipid metabolism		
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase		13.4	9.04E-02	Citronellsäure	7.1	22146	5	Unknown	COG0352	Coenzyme metabolism		
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase		1.0	6.73E-01	Citronellsäure	5.6	45398	21	Cytoplasmic	COG0001	Coenzyme metabolism		
15599177	PA3982		conserved hypothetical protein		5.6	2.30E-02	Citronellsäure	4.1	17981	2	Cytoplasmic	COG0319	General function prediction only		
15599178	PA3983		conserved hypothetical protein		1.3	9.51E-01	Citronellol	4.6	31549	2	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism		
15599182	PA3987	leuS	leucyl-tRNA synthetase		1.4	3.58E-01	Citronellsäure	5.5	97647	42	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis		
15599183	PA3988		hypothetical protein		4.5	1.21E-03	Citronellol	5.0	22884	2	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane		
15599192	PA3997	lipB	lipoate-protein ligase B		24.0	3.58E-03	Citronellsäure	6.0	23856	4	Cytoplasmic	COG0321	Coenzyme metabolism		
15599199	PA4004		conserved hypothetical protein		1.7	3.57E-01	Citronellol	9.2	17791	2	Cytoplasmic	COG1576	Function unknown		
15599201	PA4006	nadD	nicotinic acid mononucleotide adenylyltransferase		23.3	1.07E-01	Citronellsäure	6.4	23801	2	Cytoplasmic	COG1057	Coenzyme metabolism		
15599202	PA4007	proA	gamma-glutamyl phosphate reductase		1.0	6.66E-01	Citronellol	5.2	45044	9	Periplasmic	COG0014	Amino acid transport and metabolism		
15599207	PA4012		hypothetical protein		145.7	4.15E-02	Citronellsäure	4.3	21808	3	Cytoplasmic	COG2802	General function prediction only		
15599212	PA4017		conserved hypothetical protein		6.4	1.01E-01	Citronellsäure	7.1	23164	4	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane		Carbohydrate transport and metabolism
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase		1.7	6.93E-02	Citronellsäure	6.4	48469	5	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane		

15599217	PA4022	hdhA	hydrazone dehydrogenase, HdhA	8.6	2.50E-01	Citronellol	5.5	54979	16	Outer Membrane Vesicle	COG1012	Energy production and conversion	
15599220	PA4025		probable ethanolamine ammonia-lyase light chain	20.8	1.22E-01	Citronellsäure	6.6	30144	2	Cytoplasmic	COG4302	Amino acid transport and metabolism	
15599221	PA4026		probable acetyltransferase	3.5	1.21E-01	Citronellol	7.0	18049	8	Cytoplasmic	COG0456	General function prediction only	
15599226	PA4031	ppa	inorganic pyrophosphatase	2.1	1.89E-02	Citronellol	4.9	19396	13	Cytoplasmic	COG0221	Energy production and conversion	
15599230	PA4035		hypothetical protein	2.0	4.27E-02	Citronellol	6.3	35895	5	Periplasmic	COG4254	Function unknown	
15599238	PA4043	ispA	geranyltranstransferase	2.1	1.63E-01	Citronellsäure	5.1	31464	2	Cytoplasmic	COG0142	Coenzyme metabolism	
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase	1.7	7.52E-01	Citronellsäure	5.5	68049	3	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism
15599242	PA4047	ribA	GTP cyclohydrolase II	3.3	2.07E-01	Citronellsäure	6.6	22067	3	Cytoplasmic	COG0807	Coenzyme metabolism	
15599243	PA4048		hypothetical protein	52.5	4.54E-02	Citronellsäure	9.4	23085	2	Unknown	COG3577	General function prediction only	
15599247	PA4052	nusB	NusB protein	6.0	3.42E-03	Citronellsäure	8.5	17675	2	Unknown	COG0781	Transcription	
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	1.1	5.85E-01	Citronellsäure	5.1	39438	14	Cytoplasmic	COG0108	Coenzyme metabolism	
15599250	PA4055	ribC	riboflavin synthase alpha chain	5.6	5.26E-02	Citronellsäure	6.4	23469	5	Cytoplasmic	COG0307	Coenzyme metabolism	
15599251	PA4056	ribD	riboflavin-specific deaminase/reductase	9.7	1.98E-04	Citronellsäure	7.3	39764	3	Cytoplasmic	COG0117	Coenzyme metabolism	
15599256	PA4061		probable thioredoxin	4.9	4.02E-02	Citronellsäure	4.4	31878	12	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15599258	PA4063		hypothetical protein	107.5	5.89E-02	Citronellsäure	6.4	21235	2	Periplasmic			
15599263	PA4068		probable epimerase	7.8	1.08E-03	Citronellsäure	5.7	33310	9	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599264	PA4069		hypothetical protein	39.7	9.29E-05	Citronellsäure	6.3	32939	4	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15599274	PA4079		probable dehydrogenase	54.6	2.79E-02	Citronellsäure	5.1	24319	8	Extracellular	COG0300	General function prediction only	
15599310	PA4115		conserved hypothetical protein	1.8	1.19E-01	Citronellsäure	7.1	51130	10	Cytoplasmic	COG1611	General function prediction only	
15599357	PA4162		probable short-chain dehydrogenase	5.4	2.65E-02	Citronellol	8.0	24857	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599358	PA4163		hypothetical protein	1.0	7.03E-01	Citronellol	4.7	60494	15	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599375	PA4180		probable acetolactate synthase large subunit	3.4	1.12E-01	Citronellsäure	6.3	59806	3	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
15599390	PA4195		probable binding protein component of ABC transporter	25.3	7.29E-03	Citronellsäure	7.9	29539	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599393	PA4198		probable AMP-binding enzyme	2.1	1.37E-02	Citronellsäure	6.2	59548	3	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599394	PA4199		probable acyl-CoA dehydrogenase	1.0	9.91E-01	Citronellol	5.0	63926	9	Cytoplasmic	COG1960	Lipid metabolism	
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	2.7	8.92E-02	Citronellsäure	4.9	36533	4	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599397	PA4202		hypothetical protein	1.7	2.75E-01	Citronellol	8.1	36782	4	Cytoplasmic	COG2070	General function prediction only	
15599399	PA4204	pgl	periplasmic gluconolactonase, PpgL	1.5	2.53E-01	Citronellsäure	7.4	41616	6	Periplasmic	COG2706	Carbohydrate transport and metabolism	
15599428	PA4232	ssb	single-stranded DNA-binding protein	10.4	2.74E-04	Citronellsäure	5.3	18557	7	Cytoplasmic	COG0629	DNA replication, recombination, and repair	
15599430	PA4234	uvrA	excinuclease ABC subunit A	1.3	4.42E-01	Citronellsäure	6.6	104456	31	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
15599431	PA4235	bfrA	bacterioferritin	5.3	5.63E-06	Citronellol	4.8	17940	2	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15599432	PA4236	katA	catalase	1.6	1.98E-04	Citronellol	6.7	55589	23	Periplasmic	COG0753	Inorganic ion transport and metabolism	
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.1	8.56E-02	Citronellol	4.6	36649	18	Outer Membrane Vesicle	COG0202	Transcription	
15599435	PA4239	rpsD	30S ribosomal protein S4	3.5	4.76E-01	Citronellol	10.5	23277	7	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis	
15599442	PA4246	rpsE	30S ribosomal protein S5	2.0	9.47E-02	Citronellol	10.6	17625	8	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
15599447	PA4251	rplE	50S ribosomal protein L5	1.5	8.53E-02	Citronellsäure	10.3	20392	14	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis	
15599453	PA4257	rpsC	30S ribosomal protein S3	3.2	3.90E-02	Citronellsäure	10.8	25838	14	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis	
15599461	PA4265	tufA	elongation factor Tu	1.2	2.38E-01	Citronellsäure	5.0	43337	52	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
15599462	PA4266	fusA1	elongation factor G	1.5	2.35E-01	Citronellsäure	4.8	77752	76	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15599463	PA4267	rpsG	30S ribosomal protein S7	8.0	7.91E-02	Citronellol	10.9	17504	8	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis	
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	1.7	7.70E-01	Citronellol	7.1	154364	94	Outer Membrane Vesicle	COG0086	Transcription	
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	1.6	9.89E-01	Citronellol	5.6	150837	104	Periplasmic	COG0085	Transcription	
15599469	PA4273	rplA	50S ribosomal protein L1	3.1	3.57E-02	Citronellsäure	10.3	24234	12	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis	
15599471	PA4275	nusG	transcription antitermination protein NusG	33.9	7.08E-05	Citronellsäure	5.8	20130	12	Cytoplasmic	COG0250	Transcription	
15599475	PA4279		hypothetical protein	1.6	9.67E-02	Citronellol	5.4	26758	2	Cytoplasmic	COG1521	Transcription	
15599478	PA4282		probable exonuclease	1.2	3.88E-01	Citronellsäure	5.5	138959	13	Extracellular	COG0419	DNA replication, recombination, and repair	
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	5.9	1.15E-01	Citronellol	6.7	79084	3	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	2.0	6.27E-01	Citronellol	5.5	139379	21	Unknown	COG1074	DNA replication, recombination, and repair	
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	2.1	1.76E-01	Citronellsäure	5.3	132646	9	Cytoplasmic	COG1330	DNA replication, recombination, and repair	
15599482	PA4286		hypothetical protein	4.7	8.44E-02	Citronellol	5.2	24815	3	Unknown	COG0095	Coenzyme metabolism	
15599504	PA4308		conserved hypothetical protein	2.5	1.57E-02	Citronellol	6.5	53246	16	Unknown	COG0433	Replication, recombination, and repair	
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	67.2	9.96E-04	Citronellsäure	6.5	32410	6	Periplasmic	COG0788	Nucleotide transport and metabolism	
15599512	PA4316	sbcB	exodeoxyribonuclease I	1.2	5.52E-01	Citronellol	5.4	55449	3	Cytoplasmic	COG2925	DNA replication, recombination, and repair	
15599525	PA4329	pykA	pyruvate kinase II	1.0	9.68E-01	Citronellol	6.7	52252	25	Periplasmic	COG0469	Carbohydrate transport and metabolism	
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	44.0	8.16E-04	Citronellsäure	6.7	28152	16	Cytoplasmic	COG1024	Lipid metabolism	
15599529	PA4333		probable fumarase	1.9	1.69E-01	Citronellsäure	5.2	54763	16	Periplasmic	COG1951	Energy production and conversion	
15599532	PA4336		conserved hypothetical protein	6.5	1.55E-02	Citronellol	6.0	20993	5	Cytoplasmic	COG0693	General function prediction only	
15599536	PA4340		hypothetical protein	10.8	6.77E-03	Citronellol	6.1	20988	2	Periplasmic			
15599545	PA4349		hypothetical protein	2.0	1.71E-01	Citronellsäure	6.2	31671	4	Unknown	COG1960	Lipid metabolism	
15599548	PA4352		conserved hypothetical protein	6.5	1.86E-02	Citronellsäure	6.2	30972	5	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms	
15599552	PA4356	xenB	xenobiotic reductase	1.1	8.55E-01	Citronellol	4.9	37796	14	Periplasmic	COG1902	Energy production and conversion	
15599562	PA4366	sodB	superoxide dismutase	1.6	2.87E-01	Citronellsäure	5.2	21351	8	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein precursor	2.1	3.88E-02	Citronellol	4.5	47230	23	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
15599568	PA4372		hypothetical protein	2.1	1.52E-01	Citronellsäure	6.0	38323	3	Outer Membrane Vesicle	COG3489	General function prediction only	
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	3.4	8.16E-03	Citronellsäure	6.7	45690	3	Cytoplasmic	COG1488	Coenzyme metabolism	
15599577	PA4381		probable two-component response regulator	3.0	3.81E-02	Citronellsäure	5.9	25235	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599581	PA4385	groEL	GroEL protein	1.1	2.16E-01	Citronellsäure	4.8	57086	56	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
15599582	PA4386	groES	GroES protein	231.8	9.65E-04	Citronellol	4.9	10267	4	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
15599584	PA4388		hypothetical protein	3.2	9.48E-03	Citronellsäure	6.4	26982	7	Cytoplasmic	COG0748	Inorganic ion transport and metabolism	
15599585	PA4389		probable short-chain dehydrogenase	8.8	3.58E-04	Citronellsäure	7.3	26720	24	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599591	PA4395		conserved hypothetical protein	1.1	7.61E-01	Citronellol	8.2	18044	14	Cytoplasmic	COG1666	Function unknown	
15599595	PA4399		conserved hypothetical protein	9.0	3.32E-04	Citronellsäure	6.1	21065	3	Cytoplasmic	COG2096	Coenzyme transport and metabolism	
15599596	PA4400		probable pyrophosphohydrolase	1.3	2.01E-01	Citronellol	5.1	34022	7	Cytoplasmic	COG0352	Coenzyme metabolism	
15599597	PA4401		probable glutathione S-transferase	1.2	2.97E-01	Citronellsäure	5.4	23789	15	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599598	PA4402	argJ	glutamate N-acetyltransferase	7.9	1.60E-02	Citronellsäure	5.3	41762	15	Cytoplasmic	COG1364	Amino acid transport and metabolism	
15599599	PA4403	secA	secretion protein SecA	1.7	2.80E-02	Citronellsäure	5.4	103854	39	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion	
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	2.7	8.27E-02	Citronellsäure	5.0	33435	12	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane	
15599603	PA4407	ftsZ	cell division protein FtsZ	6.3	1.18E-03	Citronellsäure	4.7	41218	15	Periplasmic	COG0206	Cell division and chromosome partitioning	
15599604	PA4408	ftsA	cell division protein FtsA	5.9	4.33E-02	Citronellsäure	5.0	44646	7	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.2	2.05E-01	Citronellol	4.7	34363	7	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.9	3.79E-02	Citronellol	6.1	51949	10	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599608	PA4412	murG	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	29.5	8.83E-02	Citronellsäure	10.0	37799	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.7	4.26E-02	Citronellol	5.7	48080	17	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane	
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase	1.0	7.20E-01	Citronellol	6.5	47412	19	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1.2	2.39E-01	Citronellol	5.1	51263	16	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
15599616	PA4420		conserved hypothetical protein	1.7	1.36E-01	Citronellsäure	7.7	34640	6	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane	
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	5.7	3.57E-02	Citronellsäure	4.7	21413	8	Cytoplasmic	COG0279	Carbohydrate transport and metabolism	
15599622	PA4426		conserved hypothetical protein	15.8	4.07E-03	Citronellol	9.8	20619	2	Outer Membrane Vesicle	COG2823	General function prediction only	
15599624	PA4428	sspA	stringent starvation protein A	6.5	4.45E-02	Citronellsäure	6.1	23615	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599627	PA4431		probable iron-sulfur protein	5.7	1.67E-04	Citronellol	6.5	20828	2	Outer Membrane Vesicle	COG0723	Energy production and conversion	
15599629	PA4433	rplM	50S ribosomal protein L13	4.6	2.81E-02	Citronellol	10.4	16029	2	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis	
15599630	PA4434		probable oxidoreductase	14.0	2.01E-03	Citronellsäure	5.7	38644	5	Periplasmic	COG0667	Energy production and conversion	
15599631	PA4435		probable acyl-CoA dehydrogenase	1.0	9.08E-01	Citronellol	6.1	42128	22	Cytoplasmic	COG1960	Lipid metabolism	
15599634	PA4438		conserved hypothetical protein	35.0	3.16E-04	Citronellsäure	6.2	41993	3	Cytoplasmic	COG1485	General function prediction only	
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.4	1.52E-02	Citronellol	5.8	48961	13	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis	
15599636	PA4440		hypothetical protein	1.9	1.27E-01	Citronellsäure	6.2	22315	5	Unknown	COG2945	General function prediction only	
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	2.8	6.16E-03	Citronellsäure	5.6	69268	25	Periplasmic	COG2895	Inorganic ion transport and metabolism	
15599639	PA4443	cysD	ATP sulfurylase small subunit	1.7	5.78E-03	Citronellsäure	7.1	35478	9	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15599641	PA4445		conserved hypothetical protein	92.2	5.67E-04	Citronellsäure	5.3	27360	4	Cytoplasmic	COG0327	Function unknown	
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	2.0	7.47E-03	Citronellol	6.0	38655	6	Periplasmic	COG0079	Amino acid transport and metabolism	
15599644	PA4448	hisD	histidinol dehydrogenase	2.1	3.10E-03	Citronellol	4.9	47179	21	Periplasmic	COG0141	Amino acid transport and metabolism	
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	3.0	6.42E-02	Citronellsäure	9.3	22844	14	Cytoplasmic	COG0040	Amino acid transport and metabolism	
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.0	7.82E-01	Citronellsäure	5.5	44645	13	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane	
15599649	PA4453		conserved hypothetical protein	1.2	2.90E-01	Citronellsäure	9.7	23760	13	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
15599654	PA4458		conserved hypothetical protein	1.6	3.24E-02	Citronellol	5.6	19334	8	Cytoplasmic	COG1778	General function prediction only	
15599656	PA4460		conserved hypothetical protein	2.0	9.74E-02	Citronellol	9.6	19126	8	Periplasmic	COG1934	Function unknown	
15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.5	3.83E-01	Citronellsäure	4.4	56054	8	Cytoplasmic	COG1508	Transcription	
15599661	PA4465		conserved hypothetical protein	24.1	5.97E-05	Citronellsäure	5.7	32218	6	Cytoplasmic	COG1660	General function prediction only	
15599664	PA4468	sodM	superoxide dismutase	1.3	3.15E-01	Citronellsäure	6.2	22506	6	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599666	PA4470	fumC1	fumarate hydratase	2.7	6.09E-02	Citronellol	5.9	48695	19	Cytoplasmic	COG0114	Energy production and conversion	
15599668	PA4472	pmbA	PmbA protein	1.5	1.49E-02	Citronellol	5.5	47908	13	Cytoplasmic	COG0312	General function prediction only	

15599670	PA4474		conserved hypothetical protein	1.6	2.04E-03	Citronellol	5.0	50266	8	Cytoplasmic	COG0312	General function prediction only	
15599671	PA4475		conserved hypothetical protein	2.0	1.60E-01	Citronellsäure	6.8	30724	9	Cytoplasmic	COG0388	General function prediction only	
15599673	PA4477	cafA	cytoplasmic axial filament protein	1.3	1.30E-01	Citronellol	5.0	54665	10	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
15599674	PA4478		conserved hypothetical protein	2.2	4.22E-02	Citronellol	4.7	20974	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15599677	PA4481	mreB	rod shape-determining protein MreB	3.1	8.91E-02	Citronellsäure	5.1	36976	13	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning	
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.1	7.88E-01	Citronellol	5.5	51862	23	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.0	8.58E-01	Citronellol	5.1	53081	23	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis	
15599685	PA4489		conserved hypothetical protein	4.0	2.81E-02	Citronellol	5.3	167428	21	Outer Membrane Vesicle	COG2373	General function prediction only	
15599689	PA4493	roxR	RoxR	1.5	1.85E-01	Citronellol	5.3	20616	8	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription
15599691	PA4495		hypothetical protein	1.5	7.17E-02	Citronellsäure	5.9	24879	10	Periplasmic	COG3471	Function unknown	
15599692	PA4496		probable binding protein component of ABC transporter	1.1	7.25E-01	Citronellol	7.6	60077	26	Periplasmic	COG0747	Amino acid transport and metabolism	
15599694	PA4498		probable metallopeptidase	1.6	3.38E-01	Citronellsäure	6.2	44126	2	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15599695	PA4499		probable transcriptional regulator	1.5	9.96E-01	Citronellol	6.2	20435	2	Cytoplasmic	COG1396	Transcription	
15599698	PA4502		probable binding protein component of ABC transporter	1.2	2.99E-01	Citronellsäure	6.6	58611	6	Periplasmic	COG0747	Amino acid transport and metabolism	
15599715	PA4519	speC	ornithine decarboxylase	1.0	8.26E-01	Citronellol	4.7	43559	15	Cytoplasmic	COG0019	Amino acid transport and metabolism	
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	8.2	4.86E-02	Citronellsäure	5.1	30552	9	Cytoplasmic	COG0157	Coenzyme metabolism	
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	49.9	4.53E-04	Citronellol	6.6	15512	4	Outer Membrane Vesicle	COG4969	Cell motility and secretion	Intracellular trafficking and secretion
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	2.1	2.78E-01	Citronellsäure	5.7	62328	5	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15599725	PA4529	coaE	dephosphocoenzyme A kinase	2.6	1.37E-01	Citronellsäure	6.8	22843	7	Cytoplasmic	COG0237	Coenzyme metabolism	
15599738	PA4542	clpB	ClpB protein	1.5	4.47E-02	Citronellsäure	5.1	95005	43	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15599739	PA4543		conserved hypothetical protein	6.1	7.76E-03	Citronellsäure	7.5	26047	2	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
15599743	PA4547	pilR	two-component response regulator PilR	1.4	2.66E-01	Citronellsäure	5.9	49737	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599744	PA4548		probable D-amino acid oxidase	29.4	9.82E-03	Citronellsäure	6.5	39413	2	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism	
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	1.6	2.79E-01	Citronellol	6.4	126583	7	Periplasmic	COG3419	Cell motility and secretion	Intracellular trafficking and secretion
15599753	PA4557	lytB	LytB protein	1.1	5.59E-01	Citronellsäure	5.2	34762	4	Cytoplasmic	COG0761	Lipid metabolism	
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	7.9	4.83E-02	Citronellol	4.3	15984	3	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	1.8	1.84E-02	Citronellsäure	6.1	105464	42	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	14.5	4.63E-02	Citronellsäure	9.1	34340	4	Cytoplasmic	COG0196	Coenzyme metabolism	
15599761	PA4565	proB	glutamate 5-kinase	1.7	5.86E-03	Citronellsäure	7.3	39845	8	Cytoplasmic	COG0263	Amino acid transport and metabolism	
15599762	PA4566	obg	GTP-binding protein Obg	1.3	5.13E-01	Citronellsäure	4.5	44338	6	Cytoplasmic	COG0536	General function prediction only	
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.5	3.29E-02	Citronellol	4.6	34851	13	Cytoplasmic	COG0142	Coenzyme metabolism	
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	1.0	5.08E-01	Citronellol	4.5	21795	5	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15599772	PA4576		probable ATP-dependent protease	1.1	6.79E-01	Citronellol	4.7	90222	36	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
15599783	PA4587	ccpR	cytochrome c551 peroxidase precursor	73.5	9.60E-02	Citronellsäure	6.7	37403	2	Periplasmic	COG1858	Inorganic ion transport and metabolism	
15599784	PA4588	gdhA	glutamate dehydrogenase	1.3	1.44E-02	Citronellsäure	6.0	48856	20	Unknown	COG0334	Amino acid transport and metabolism	
15599791	PA4595		probable ATP-binding component of ABC transporter	1.6	1.34E-03	Citronellsäure	5.4	61302	29	Periplasmic	COG0488	General function prediction only	
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.3	3.38E-02	Citronellsäure	6.0	45157	18	Periplasmic	COG0112	Amino acid transport and metabolism	
15599800	PA4604		conserved hypothetical protein	2.8	1.53E-02	Citronellsäure	4.5	37256	5	Cytoplasmic	COG0523	General function prediction only	
15599809	PA4613	katB	catalase	13.7	1.41E-04	Citronellol	8.6	57131	3	Cytoplasmic	COG0753	Inorganic ion transport and metabolism	
15599811	PA4615		probable oxidoreductase	1.2	7.15E-01	Citronellol	5.2	29377	7	Cytoplasmic	COG1018	Energy production and conversion	
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	2.0	2.72E-01	Citronellsäure	4.7	219755	2	Extracellular			
15599828	PA4632		hypothetical protein	22.0	5.29E-04	Citronellsäure	7.6	29159	6	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15599835	PA4639		hypothetical protein	4.0	1.98E-02	Citronellol	9.8	20736	3	Outer Membrane Vesicle			
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.3	3.78E-01	Citronellsäure	7.0	55498	4	Cytoplasmic	COG0579	General function prediction only	
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	4.4	3.24E-02	Citronellol	5.6	20639	11	Cytoplasmic	COG0634	Nucleotide transport and metabolism	
15599841	PA4646	upp	uracil phosphoribosyltransferase	3.2	1.00E-01	Citronellsäure	7.0	22938	10	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
15599846	PA4651	cupE4	Pilin assembly chaperone CupE4	62.5	5.25E-04	Citronellsäure	9.7	28981	2	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
15599852	PA4657		hypothetical protein	1.9	3.21E-03	Citronellol	6.8	35913	6	Unknown	COG3380	General function prediction only	
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	11.4	1.87E-01	Citronellsäure	5.6	26686	2	Cytoplasmic	COG0476	Coenzyme metabolism	
15599860	PA4665	prfA	peptide chain release factor 1	1.9	1.69E-02	Citronellol	4.8	40040	4	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis	
15599864	PA4669	ipk	isopentenyl monophosphate kinase	1.8	2.06E-01	Citronellsäure	6.6	30843	3	Unknown	COG1947	Lipid metabolism	
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.3	4.27E-01	Citronellol	6.5	34008	16	Periplasmic	COG0462	Nucleotide transport and metabolism	Amino acid transport and metabolism
15599866	PA4671		probable ribosomal protein L25	1.1	6.27E-01	Citronellsäure	6.2	21962	10	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis	
15599868	PA4673		conserved hypothetical protein	1.4	7.28E-02	Citronellol	4.8	40078	13	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis	
15599870	PA4675		probable TonB-dependent receptor	1.1	8.32E-01	Citronellsäure	5.2	80952	10	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599871	PA4676		probable carbonic anhydrase	1.3	3.03E-01	Citronellsäure	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	2.4	5.73E-02	Citronellsäure	5.5	36149	16	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.9	1.27E-01	Citronellsäure	5.7	36424	28	Periplasmic	COG0059	Amino acid transport and metabolism	Coenzyme metabolism
15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	2.6	2.47E-01	Citronellol	6.3	17784	8	Cytoplasmic	COG0440	Amino acid transport and metabolism	
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.8	1.68E-03	Citronellsäure	6.8	62986	24	Cytoplasmic	COG0028	Acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
15599895	PA4701		conserved hypothetical protein	1.0	9.95E-01	Citronellol	6.0	58344	30	Periplasmic	COG2187	Function unknown	
15599902	PA4708	phuT	Heme-transport protein, PhuT	1.1	5.61E-01	Citronellol	7.8	31037	9	Periplasmic	COG4558	Inorganic ion transport and metabolism	
15599903	PA4709		probable hemin degrading factor	1.4	3.03E-01	Citronellsäure	5.6	39057	5	Cytoplasmic	COG3720	Inorganic ion transport and metabolism	
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR precursor	3.9	2.92E-01	Citronellol	5.9	84724	2	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15599909	PA4715		probable aminotransferase	1.5	4.00E-02	Citronellol	8.1	46064	4	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599916	PA4722		probable aminotransferase	1.5	2.18E-01	Citronellol	5.7	42567	2	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15599917	PA4723	dksA	suppressor protein DksA	1.2	4.84E-01	Citronellol	4.8	17344	10	Periplasmic	COG1734	Signal transduction mechanisms	
15599920	PA4726	cbrB	two-component response regulator CbrB	2.1	6.36E-03	Citronellsäure	5.5	52286	9	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	5.8	7.66E-02	Citronellsäure	4.6	18014	3	Cytoplasmic	COG0801	Coenzyme metabolism	
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.1	7.40E-01	Citronellsäure	5.8	27874	6	Periplasmic	COG0413	Coenzyme metabolism	
15599924	PA4730	panC	pantoate--beta-alanine ligase	15.1	1.84E-04	Citronellsäure	6.5	30836	6	Cytoplasmic	COG0414	Coenzyme metabolism	
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.1	2.81E-01	Citronellsäure	6.6	61944	15	Periplasmic	COG0166	Carbohydrate transport and metabolism	
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	2.3	1.41E-02	Citronellol	6.2	71624	25	Cytoplasmic	COG0365	Lipid metabolism	
15599929	PA4735		hypothetical protein	4.4	1.18E-01	Citronellsäure	5.1	118589	2	Outer Membrane Vesicle			
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.4	9.76E-02	Citronellol	4.8	75421	58	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis	
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	1.7	1.38E-01	Citronellsäure	6.9	33378	6	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis	
15599938	PA4744	infB	translation initiation factor IF-2	1.3	2.09E-01	Citronellsäure	6.0	90912	27	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis	
15599939	PA4745	nusA	N utilization substance protein A	1.4	1.18E-01	Citronellol	4.3	54658	21	Periplasmic	COG0195	Transcription	
15599942	PA4748	tpiA	triosephosphate isomerase	18.1	1.73E-03	Citronellsäure	5.3	25621	6	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
15599943	PA4749	glmM	phosphoglucosamine mutase	1.4	2.90E-01	Citronellol	6.0	47796	7	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15599944	PA4750	folP	dihydropteroate synthase	1.8	1.85E-01	Citronellsäure	5.4	30490	3	Cytoplasmic	COG0294	Coenzyme metabolism	
15599949	PA4755	greA	transcription elongation factor GreA	7.6	3.34E-05	Citronellsäure	4.7	17158	8	Periplasmic	COG0782	Function unknown	
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	1.1	7.82E-01	Citronellol	4.8	117330	71	Periplasmic	COG0458	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.1	4.63E-01	Citronellsäure	5.2	40810	7	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.1	4.48E-01	Citronellsäure	6.0	28324	10	Periplasmic	COG0289	Amino acid transport and metabolism	
15599954	PA4760	dnaJ	DnaJ protein	10.9	1.90E-02	Citronellsäure	7.4	40260	3	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
15599955	PA4761	dnaK	DnaK protein	1.2	3.78E-01	Citronellsäure	4.5	68403	51	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599956	PA4762	grpE	heat shock protein GrpE	4.3	1.21E-02	Citronellsäure	4.2	20702	11	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
15599958	PA4764	fur	ferric uptake regulation protein	3.9	1.30E-01	Citronellol	5.9	15234	8	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15599962	PA4768	smpB	SmpB protein	2.7	2.46E-01	Citronellsäure	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones	
15599975	PA4781		cyclic di-GMP phosphodiesterase	3.4	1.72E-02	Citronellol	5.0	43628	3	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.1	5.16E-01	Citronellol	5.2	70667	8	Periplasmic	COG1166	Amino acid transport and metabolism	
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	2.4	7.20E-02	Citronellol	4.7	16455	6	Unknown	COG0511	Lipid metabolism	
15600041	PA4848	accC	biotin carboxylase	1.0	9.99E-01	Citronellsäure	6.3	48888	17	Periplasmic	COG0439	Lipid metabolism	
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	2.6	9.49E-02	Citronellsäure	4.2	32000	4	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis	
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	1.3	1.07E-01	Citronellsäure	6.5	57665	25	Periplasmic	COG0138	Nucleotide transport and metabolism	
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	1.2	2.61E-01	Citronellol	4.7	45212	19	Periplasmic	COG0151	Nucleotide transport and metabolism	
15600061	PA4868	ureC	urease alpha subunit	1.8	1.52E-02	Citronellol	6.2	60611	2	Cytoplasmic	COG0804	Amino acid transport and metabolism	
15600065	PA4872		hypothetical protein	1.3	3.70E-01	Citronellsäure	5.4	31320	5	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15600071	PA4878		probable transcriptional regulator	128.6	2.51E-04	Citronellsäure	6.9	31168	4	Cytoplasmic	COG3708	Function unknown	
15600073	PA4880		probable bacterioferritin	1.6	5.78E-02	Citronellsäure	4.4	20217	12	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
15600092	PA4899		probable aldehyde dehydrogenase	1.6	8.16E-02	Citronellol	5.8	52697	6	Cytoplasmic	COG1012	Energy production and conversion	
15600100	PA4907		probable short-chain dehydrogenase	1.4	5.38E-02	Citronellol	5.1	27384	12	Cytoplasmic	COG4221	General function prediction only	
15600106	PA4913		probable binding protein component of ABC transporter	1.2	5.61E-01	Citronellsäure	6.6	39798	17	Periplasmic	COG0683	Amino acid transport and metabolism	
15600111	PA4918		hypothetical protein	16.9	3.05E-04	Citronellsäure	4.7	23821	9	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	1.7	3.91E-02	Citronellsäure	6.3	46095	5	Cytoplasmic	COG1488	Coenzyme metabolism	
15600113	PA4920	nadE	NH3-dependent NAD synthetase	29.2	1.20E-05	Citronellsäure	5.4	29696	16	Periplasmic	COG0171	Coenzyme metabolism	
15600116	PA4923		conserved hypothetical protein	1.1	8.21E-01	Citronellol	5.2	20725	3	Unknown	COG1611	General function prediction only	
15600123	PA4930	alr	biosynthetic alanine racemase	14.8	5.00E-03	Citronellsäure	6.1	38310	2	Cytoplasmic	COG0787	Cell envelope biogenesis, outer membrane	
15600124	PA4931	dnaB	replicative DNA helicase	1.1	4.34E-01	Citronellol	4.7	51589	3	Cytoplasmic	COG0305	DNA replication, recombination, and repair	
15600128	PA4935	rpsF	30S ribosomal protein S6	33.5	1.56E-02	Citronellol	4.6	16165	2	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis	

15600131	PA4938	purA	adenylosuccinate synthetase	1.3	6.17E-02	Citronellsäure	6.0	46814	21	Periplasmic	COG0104	Nucleotide transport and metabolism	
15600132	PA4939		conserved hypothetical protein	1.1	1.09E-02	Citronellsäure	4.8	42546	11	Cytoplasmic	COG3705	Amino acid transport and metabolism	
15600141	PA4948		conserved hypothetical protein	5.2	2.59E-01	Citronellsäure	4.7	16463	2	Cytoplasmic	COG0802	General function prediction only	
15600142	PA4949		conserved hypothetical protein	1.2	5.68E-01	Citronellsäure	7.6	51550	2	Unknown	COG0063	Carbohydrate transport and metabolism	
15600144	PA4951	orn	oligoribonuclease	2.7	3.40E-03	Citronellol	5.6	20826	2	Cytoplasmic	COG1949	RNA processing and modification	
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	2.1	1.63E-01	Citronellsäure	5.3	29391	9	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15600152	PA4959	fimX	FimX	1.4	2.13E-01	Citronellsäure	4.9	75992	9	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15600153	PA4960		probable phosphoserine phosphatase	1.2	1.75E-01	Citronellsäure	4.9	46438	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15600157	PA4964	parC	topoisomerase IV subunit A	2.3	2.46E-03	Citronellol	5.9	83364	8	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	17.9	1.66E-02	Citronellsäure	4.8	30498	2	Cytoplasmic	COG1409	General function prediction only	
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.0	8.22E-01	Citronellsäure	4.7	23133	6	Cytoplasmic			
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	1.2	4.10E-01	Citronellol	5.8	69784	12	Cytoplasmic	COG0422	Coenzyme metabolism	
15600167	PA4974		probable outer membrane protein precursor	2.7	1.82E-01	Citronellol	5.9	53405	4	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15600168	PA4975		NAD(P)H quinone oxidoreductase	1.4	3.93E-01	Citronellsäure	6.0	26315	2	Cytoplasmic	COG2249	General function prediction only	
15600185	PA4992		hypothetical protein	2.2	1.64E-01	Citronellsäure	6.4	29030	3	Cytoplasmic	COG0667	Energy production and conversion	
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.8	1.75E-03	Citronellol	6.2	50348	20	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane	
15600191	PA4998		conserved hypothetical protein	108.7	2.48E-02	Citronellsäure	10.0	24986	2	Cytoplasmic			
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.1	5.30E-01	Citronellol	6.2	34084	19	Periplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	2.5	2.16E-02	Citronellsäure	5.2	110102	32	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
15600208	PA5015	aceE	pyruvate dehydrogenase	1.9	1.22E-01	Citronellol	5.6	99563	41	Periplasmic	COG2609	Energy production and conversion	
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	3.5	7.96E-03	Citronellol	5.0	56676	15	Periplasmic	COG0508	Energy production and conversion	
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	1.5	8.49E-02	Citronellol	5.0	23517	6	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
15600212	PA5019		conserved hypothetical protein	12.5	1.67E-03	Citronellsäure	6.0	31882	8	Cytoplasmic	COG2961	General function prediction only	
15600218	PA5025	metY	homocysteine synthase	1.1	8.37E-03	Citronellsäure	6.5	45177	8	Cytoplasmic	COG2873	Amino acid transport and metabolism	
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	29.0	2.85E-04	Citronellsäure	6.3	38792	9	Cytoplasmic	COG0407	Coenzyme metabolism	
15600228	PA5035	gltD	glutamate synthase small chain	1.5	5.05E-02	Citronellsäure	6.4	52625	23	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
15600229	PA5036	gltB	glutamate synthase large chain precursor	1.3	3.45E-01	Citronellsäure	6.0	161607	68	Cytoplasmic	COG0069	Amino acid transport and metabolism	
15600231	PA5038	aroB	3-dehydroquinate synthase	42.6	1.29E-04	Citronellsäure	5.6	40109	12	Cytoplasmic	COG0337	Amino acid transport and metabolism	
15600232	PA5039	aroK	shikimate kinase	1.5	3.57E-01	Citronellsäure	8.8	19205	2	Cytoplasmic	COG0703	Amino acid transport and metabolism	
15600239	PA5046		malic enzyme	1.3	1.24E-01	Citronellol	4.8	45428	34	Periplasmic	COG0281	Energy production and conversion	
15600243	PA5050	priA	primosomal protein N'	2.0	2.12E-01	Citronellsäure	8.8	82120	2	Unknown	COG1198	DNA replication, recombination, and repair	
15600244	PA5051	argS	arginyl-tRNA synthetase	1.1	7.74E-01	Citronellsäure	5.2	65199	21	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis	
15600246	PA5053	hslV	heat shock protein HslV	1.5	3.57E-01	Citronellol	6.7	18767	7	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones	
15600247	PA5054	hslU	heat shock protein HslU	1.5	1.33E-01	Citronellol	5.4	50082	15	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	5.8	2.54E-03	Citronellol	9.5	28254	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15600257	PA5064		hypothetical protein	9.9	3.11E-01	Citronellol	6.0	22767	3	Cytoplasmic	COG3165	Function unknown	
15600264	PA5071		conserved hypothetical protein	22.1	2.39E-02	Citronellsäure	9.1	26065	4	Cytoplasmic	COG1385	Function unknown	
15600269	PA5076		probable binding protein component of ABC transporter	1.1	5.74E-01	Citronellsäure	7.6	29736	13	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600271	PA5078		conserved hypothetical protein	1.8	1.10E-02	Citronellol	7.0	59444	18	Periplasmic	COG3131	Inorganic ion transport and metabolism	
15600273	PA5080		prolyl aminopeptidase	2.0	1.87E-02	Citronellol	6.2	36515	12	Cytoplasmic	COG0596	General function prediction only	
15600275	PA5082		probable binding protein component of ABC transporter	16.8	1.17E-01	Citronellsäure	8.2	32866	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	2.0	2.29E-02	Citronellsäure	5.9	29791	3	Cytoplasmic	COG3741	Amino acid transport and metabolism	
15600289	PA5096		probable binding protein component of ABC transporter	3.6	1.09E-03	Citronellsäure	5.2	35496	2	Periplasmic	COG2113	Amino acid transport and metabolism	
15600293	PA5100	hutU	urocanase	3.2	1.42E-01	Citronellsäure	6.3	61161	2	Cytoplasmic	COG2987	Amino acid transport and metabolism	
15600297	PA5104		conserved hypothetical protein	1.4	1.49E-01	Citronellsäure	5.6	21415	6	Unknown	COG3758	Function unknown	
15600302	PA5109		hypothetical protein	3.4	1.29E-02	Citronellsäure	5.1	22697	5	Cytoplasmic	COG3803	Function unknown	
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	2.0	1.93E-01	Citronellsäure	5.9	37216	10	Periplasmic	COG0158	Carbohydrate transport and metabolism	
15600304	PA5111	gloA3	lactoylglutathione lyase	8.5	6.46E-04	Citronellsäure	4.8	20215	4	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15600305	PA5112	estA	esterase EstA	1.9	1.81E-01	Citronellsäure	4.5	69608	6	Periplasmic	COG3240	Lipid metabolism	General function prediction only
15600310	PA5117	typA	regulatory protein TypA	1.2	3.21E-01	Citronellsäure	5.0	66903	17	Periplasmic	COG1217	Signal transduction mechanisms	
15600312	PA5119	glnA	glutamine synthetase	1.4	3.55E-02	Citronellol	5.0	51944	20	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism	
15600318	PA5125	ntrC	two-component response regulator NtrC	2.5	3.10E-02	Citronellsäure	5.8	52753	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600321	PA5128	secB	secretion protein SecB	1.9	9.34E-02	Citronellol	4.2	18146	10	Periplasmic	COG1952	Intracellular trafficking and secretion	
15600324	PA5131	pgm	phosphoglycerate mutase	1.2	2.81E-01	Citronellsäure	4.9	55601	19	Periplasmic	COG0696	Carbohydrate transport and metabolism	
15600330	PA5137		hypothetical protein	7.0	1.19E-03	Citronellsäure	7.5	27991	7	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600331	PA5138		hypothetical protein	64.5	1.29E-03	Citronellsäure	4.9	27915	9	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600332	PA5139		hypothetical protein	5.7	6.65E-02	Citronellsäure	5.8	27565	9	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	5.8	3.13E-02	Citronellsäure	4.7	25938	3	Cytoplasmic	COG0106	Amino acid transport and metabolism	
15600335	PA5142	hisH1	glutamine amidotransferase	1.1	3.67E-01	Citronellsäure	6.3	23666	12	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	2.6	1.23E-01	Citronellsäure	6.5	21937	7	Cytoplasmic	COG0131	Amino acid transport and metabolism	
15600343	PA5150		probable short-chain dehydrogenase	1.5	9.36E-02	Citronellol	6.2	26191	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic binding protein	4.8	6.66E-03	Citronellsäure	4.9	27561	25	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	2.0	1.96E-02	Citronellsäure	5.9	39542	14	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	79.2	2.29E-03	Citronellsäure	6.1	33106	7	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	20.0	1.57E-03	Citronellsäure	5.0	32457	11	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.1	9.08E-01	Citronellol	6.0	20766	8	Unknown	COG1898	Cell envelope biogenesis, outer membrane	
15600359	PA5166	dctD	DctD	1.6	1.63E-02	Citronellsäure	5.5	50864	5	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600360	PA5167	dctP	DctP	16.0	7.07E-04	Citronellsäure	8.8	37051	17	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15600364	PA5171	arcA	arginine deiminase	5.3	3.00E-03	Citronellol	5.5	46436	32	Cytoplasmic	COG2235	Amino acid transport and metabolism	
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	2.1	1.36E-02	Citronellol	6.6	38108	18	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15600366	PA5173	arcC	carbamate kinase	2.2	2.28E-03	Citronellol	5.0	33080	12	Cytoplasmic	COG0549	Amino acid transport and metabolism	
15600367	PA5174		probable beta-ketoacyl synthase	1.2	6.01E-02	Citronellsäure	6.0	68763	3	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	24.2	1.26E-02	Citronellsäure	4.8	29779	7	Cytoplasmic	COG1218	Inorganic ion transport and metabolism	
15600369	PA5176		conserved hypothetical protein	21.3	2.06E-03	Citronellsäure	4.5	20983	9	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600370	PA5177		probable hydrolase	127.3	1.38E-03	Citronellsäure	5.9	25629	2	Cytoplasmic	COG1011	General function prediction only	
15600377	PA5184		hypothetical protein	3.3	1.43E-01	Citronellol	8.8	20417	9	Periplasmic	COG1605	Amino acid transport and metabolism	
15600379	PA5186		probable iron-containing alcohol dehydrogenase	30.8	1.91E-03	Citronellsäure	5.4	40354	3	Cytoplasmic	COG1454	Energy production and conversion	
15600380	PA5187		probable acyl-CoA dehydrogenase	1.1	4.97E-01	Citronellol	5.3	64558	8	Cytoplasmic	COG1960	Lipid metabolism	
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	1.5	3.07E-01	Citronellol	5.2	44810	6	Cytoplasmic	COG1250	Lipid metabolism	
15600383	PA5190		probable nitroreductase	1.1	6.50E-01	Citronellsäure	6.0	22450	7	Cytoplasmic	COG0778	Energy production and conversion	
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.4	1.05E-01	Citronellsäure	5.1	55732	32	Periplasmic	COG1866	Energy production and conversion	
15600386	PA5193	yrfI	heat shock protein HSP33	1.0	8.85E-01	Citronellsäure	4.5	32834	6	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
15600393	PA5200	amgR	AmgR	1.1	5.06E-01	Citronellsäure	6.6	27924	9	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600394	PA5201		conserved hypothetical protein	1.7	1.53E-01	Citronellol	6.3	84963	27	Periplasmic	COG2183	Transcription	
15600396	PA5203	gshA	glutamate--cysteine ligase	1.1	4.78E-01	Citronellol	4.9	59205	18	Cytoplasmic	COG2918	Coenzyme metabolism	
15600397	PA5204	argA	N-acetylglutamate synthase	1.1	6.52E-01	Citronellsäure	6.5	47858	9	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600403	PA5210		probable secretion pathway ATPase	1.4	4.45E-01	Citronellol	6.5	65981	2	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15600406	PA5213	gcvP1	glycine cleavage system protein P1	1.1	6.86E-01	Citronellol	6.5	104710	21	Cytoplasmic	COG1003	Amino acid transport and metabolism	
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	9.6	4.53E-05	Citronellsäure	5.4	38907	7	Periplasmic	COG0404	Amino acid transport and metabolism	
15600417	PA5224	pepP	aminopeptidase P	1.6	5.99E-02	Citronellol	5.1	49710	15	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15600418	PA5225		hypothetical protein	2.0	2.81E-01	Citronellsäure	4.0	19358	6	Unknown	COG3079	Function unknown	
15600422	PA5229		conserved hypothetical protein	1.1	6.75E-01	Citronellsäure	7.5	16871	6	Unknown	COG2947	Function unknown	
15600427	PA5234		probable oxidoreductase	2.2	1.63E-01	Citronellsäure	7.0	34011	9	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15600432	PA5239	rho	transcription termination factor Rho	1.7	8.98E-02	Citronellol	6.8	47069	16	Periplasmic	COG1158	Transcription	
15600433	PA5240	trxA	thioredoxin	214.1	2.59E-03	Citronellol	4.5	11870	2	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15600434	PA5241	ppx	exopolyphosphatase	1.8	2.60E-01	Citronellol	6.7	56419	10	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
15600435	PA5242	ppk	polyphosphate kinase	1.4	4.42E-01	Citronellol	7.7	83151	23	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	1.4	1.11E-02	Citronellol	4.8	37005	6	Cytoplasmic	COG0113	Coenzyme metabolism	
15600438	PA5245		conserved hypothetical protein	1.4	3.57E-01	Citronellol	4.7	23426	14	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
15600445	PA5252		probable ATP-binding component of ABC transporter	16.2	1.80E-05	Citronellsäure	5.9	70871	4	Cytoplasmic	COG0488	General function prediction only	
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	3.1	2.83E-02	Citronellol	4.8	27247	2	Unknown	COG1587	Coenzyme metabolism	
15600453	PA5260	hemC	porphobilinogen deaminase	7.1	5.33E-03	Citronellsäure	5.3	33641	7	Cytoplasmic	COG0181	Coenzyme metabolism	
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	2.3	1.28E-02	Citronellol	7.3	27608	11	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
15600456	PA5263	argH	argininosuccinate lyase	1.1	6.63E-01	Citronellol	5.5	51640	22	Periplasmic	COG0165	Amino acid transport and metabolism	
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.2	2.17E-01	Citronellol	5.4	45490	17	Periplasmic	COG0019	Amino acid transport and metabolism	
15600471	PA5278	dapF	diaminopimelate epimerase	36.9	3.01E-05	Citronellsäure	7.7	30320	6	Cytoplasmic	COG0253	Amino acid transport and metabolism	
15600472	PA5279		conserved hypothetical protein	1.9	1.56E-01	Citronellsäure	5.3	25767	3	Cytoplasmic	COG3159	Function unknown	
15600474	PA5281		probable hydrolase	8.8	1.65E-02	Citronellsäure	5.9	25852	4	Cytoplasmic	COG1011	General function prediction only	
15600491	PA5298		xanthine phosphoribosyltransferase	1.1	9.96E-01	Citronellol	6.6	20575	6	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15600494	PA5301	pauR	probable transcriptional regulator	4.4	4.62E-02	Citronellol	5.3	19944	2	Cytoplasmic	COG1396	Transcription	
15600506	PA5313	gabT2	Transaminase	1.2	9.45E-01	Citronellol	6.7	48347	8	Cytoplasmic	COG0161	Coenzyme metabolism	

15600510	PA5317		probable binding protein component of ABC dipeptide transporter		2.1	6.80E-02	Citronellsäure	7.0	57880	5	Periplasmic	COG0747	Amino acid transport and metabolism		
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine decarboxylase		1.3	1.52E-01	Citronellol	6.3	43133	8	Cytoplasmic	COG0452	Coenzyme metabolism		
15600515	PA5322	algC	phosphomannomutase AlgC		1.0	7.96E-01	Citronellol	5.0	50295	21	Cytoplasmic	COG1109	Carbohydrate transport and metabolism		
15600516	PA5323	argB	acetylglutamate kinase		4.3	7.17E-02	Citronellsäure	6.8	31849	15	Cytoplasmic	COG0548	Amino acid transport and metabolism		
15600523	PA5330		hypothetical protein		7.7	5.49E-04	Citronellol	9.4	22434	6	Unknown				
15600524	PA5331	pyrE	orotate phosphoribosyltransferase		1.3	3.00E-01	Citronellsäure	5.1	23320	10	Cytoplasmic	COG0461	Nucleotide transport and metabolism		
15600525	PA5332	crc	catabolite repression control protein		1.2	8.54E-01	Citronellol	5.2	29844	5	Cytoplasmic	COG0708	DNA replication, recombination, and repair		
15600527	PA5334	rph	ribonuclease PH		15.9	3.29E-02	Citronellsäure	5.9	25654	5	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis		
15600528	PA5335		conserved hypothetical protein		7.6	2.49E-02	Citronellsäure	5.8	31708	8	Cytoplasmic	COG1561	Function unknown		
15600529	PA5336	gmk	guanylate kinase		1.1	4.11E-01	Citronellol	5.3	23102	6	Cytoplasmic	COG0194	Nucleotide transport and metabolism		
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase		1.5	1.62E-01	Citronellsäure	9.4	78861	11	Cytoplasmic	COG0317	Signal transduction mechanisms		Transcription
15600536	PA5343		hypothetical protein		11.6	1.11E-04	Citronellsäure	6.2	30778	4	Unknown	COG0451	Cell envelope biogenesis, outer membrane		Carbohydrate transport and metabolism
15600537	PA5344	oxyR	OxyR		1.4	9.26E-02	Citronellol	6.7	34295	5	Cytoplasmic	COG0583	Transcription		
15600542	PA5349		probable rubredoxin reductase		1.2	2.37E-01	Citronellsäure	5.5	40617	7	Cytoplasmic	COG1251	Energy production and conversion		
15600550	PA5357		hypothetical protein		7.2	1.04E-03	Citronellol	4.7	19512	7	Cytoplasmic	COG3161	Coenzyme metabolism		
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU		26.3	1.41E-03	Citronellsäure	5.0	27487	4	Cytoplasmic	COG0704	Inorganic ion transport and metabolism		
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding protein, PstS		26.0	4.62E-04	Citronellsäure	9.5	34473	6	Periplasmic	COG0226	Inorganic ion transport and metabolism		
15600566	PA5373	betB	betaine aldehyde dehydrogenase		1.5	4.28E-02	Citronellsäure	5.0	53332	5	Cytoplasmic	COG1012	Energy production and conversion		
15600567	PA5374	betI	transcriptional regulator BetI	Infinity		1.17E-01	Citronellsäure	9.0	21861	2	Unknown	COG1309	Transcription		
15600571	PA5378		hypothetical protein		2.5	1.30E-01	Citronellsäure	7.3	34427	5	Periplasmic	COG2113	Amino acid transport and metabolism		
15600606	PA5413	ltaA	low specificity l-threonine aldolase		2.4	8.25E-02	Citronellsäure	5.0	38213	5	Cytoplasmic	COG2008	Amino acid transport and metabolism		
15600614	PA5421	fdhA	glutathione-independent formaldehyde dehydrogenase		1.9	2.76E-02	Citronellol	6.8	42008	3	Cytoplasmic	COG1063	Amino acid transport and metabolism		General function prediction only
15600616	PA5423		hypothetical protein		20.8	1.46E-02	Citronellsäure	5.7	20002	3	Periplasmic	COG3495	Function unknown		
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase		4.1	2.58E-03	Citronellsäure	5.4	38496	8	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism		
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit		43.2	3.55E-02	Citronellol	6.2	16889	3	Unknown	COG0041	Nucleotide transport and metabolism		
15600620	PA5427	adhA	alcohol dehydrogenase		17.9	1.33E-01	Citronellsäure	5.8	35911	2	Outer Membrane Vesicle	COG1064	General function prediction only		
15600622	PA5429	aspA	aspartate ammonia-lyase		1.0	8.73E-01	Citronellsäure	5.6	51069	13	Periplasmic	COG1027	Amino acid transport and metabolism		
15600626	PA5433		conserved hypothetical protein		20.6	7.87E-04	Citronellsäure	9.0	25584	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis		
15600628	PA5435		probable transcarboxylase subunit		1.1	6.88E-01	Citronellsäure	5.7	66095	28	Cytoplasmic	COG5016	Energy production and conversion		
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase		1.7	8.79E-03	Citronellol	6.6	51816	15	Cytoplasmic	COG0439	Lipid metabolism		
15600632	PA5439		probable glucose-6-phosphate dehydrogenase		1.5	9.52E-02	Citronellol	7.2	54573	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism		
15600634	PA5441		hypothetical protein		1.1	6.59E-01	Citronellsäure	4.6	80036	35	Periplasmic				
15600636	PA5443	uvrD	DNA helicase II		1.9	1.21E-01	Citronellsäure	5.7	81494	10	Cytoplasmic	COG0210	DNA replication, recombination, and repair		
15600645	PA5452	wbpW	phosphomannose isomerase/GDP-mannose WbpW		3.8	9.48E-02	Citronellsäure	6.4	52574	3	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane		
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase		2.5	1.34E-01	Citronellsäure	6.5	36399	12	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane		
15600647	PA5454	rmd	oxidoreductase Rmd		1.4	3.93E-02	Citronellol	6.7	33910	7	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane		Carbohydrate transport and metabolism
15600650	PA5457		hypothetical protein		8.0	1.09E-02	Citronellsäure	6.2	31744	4	Cytoplasmic	COG2227	Coenzyme metabolism		
15600652	PA5459		hypothetical protein		10.9	1.06E-04	Citronellsäure	4.7	30701	7	Cytoplasmic	COG2226	Coenzyme metabolism		
15600668	PA5475		hypothetical protein		1.4	5.50E-01	Citronellsäure	4.8	21000	3	Cytoplasmic				
15600676	PA5483	algB	two-component response regulator AlgB		1.2	5.62E-01	Citronellol	5.2	49323	6	Cytoplasmic	COG2204	Signal transduction mechanisms		
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA		3.7	1.10E-02	Citronellol	6.4	23375	9	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones		
15600685	PA5492		conserved hypothetical protein		12.8	1.37E-03	Citronellol	7.1	23786	2	Unknown	COG0218	General function prediction only		
15600686	PA5493	polA	DNA polymerase I		1.4	7.08E-02	Citronellsäure	4.8	99792	48	Periplasmic	COG0749	DNA replication, recombination, and repair		
15600692	PA5499	np20	transcriptional regulator np20		2.4	1.77E-01	Citronellsäure	6.9	18216	3	Cytoplasmic	COG0735	Inorganic ion transport and metabolism		
15600698	PA5505		probable TonB-dependent receptor		1.2	3.24E-01	Citronellsäure	8.7	28065	14	Periplasmic	COG1464	Inorganic ion transport and metabolism		
15600700	PA5507		hypothetical protein		14.6	1.69E-02	Citronellsäure	6.4	24262	5	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism		
15600709	PA5516	pdxY	pyridoxamine kinase		46.7	4.21E-04	Citronellsäure	6.0	31285	3	Cytoplasmic	COG2240	Coenzyme metabolism		
15600714	PA5521		probable short-chain dehydrogenase		1.5	2.19E-02	Citronellol	5.8	26894	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism		General function prediction only
15600716	PA5523		probable aminotransferase		1.2	3.08E-01	Citronellsäure	6.7	48908	3	Cytoplasmic	COG0001	Coenzyme metabolism		
15600735	PA5542		hypothetical protein		1.3	2.81E-01	Citronellol	6.3	45872	7	Unknown	COG1680	Defense mechanisms		
15600738	PA5545		conserved hypothetical protein		1.2	4.16E-01	Citronellol	7.8	33627	12	Periplasmic	COG2358	General function prediction only		
15600739	PA5546		conserved hypothetical protein		1.4	1.81E-01	Citronellol	5.7	44096	13	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane		
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase		1.9	7.10E-04	Citronellsäure	5.9	66294	24	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane		
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase		1.6	5.93E-02	Citronellol	6.2	48851	11	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane		
15600747	PA5554	atpD	ATP synthase beta chain		3.3	1.34E-03	Citronellol	4.7	49499	39	Periplasmic	COG0055	Energy production and conversion		
15600748	PA5555	atpG	ATP synthase gamma chain		11.9	2.55E-04	Citronellsäure	8.1	31553	9	Outer Membrane Vesicle	COG0224	Energy production and conversion		
15600749	PA5556	atpA	ATP synthase alpha chain		2.2	5.47E-03	Citronellol	5.1	55393	30	Periplasmic	COG0056	Energy production and conversion		
15600750	PA5557	atpH	ATP synthase delta chain		2.7	4.75E-02	Citronellsäure	5.9	19260	7	Outer Membrane Vesicle	COG0712	Energy production and conversion		
15600751	PA5558	atpF	ATP synthase B chain		54.0	8.75E-02	Citronellol	5.8	16924	2	Outer Membrane Vesicle	COG0711	Energy production and conversion		
15600756	PA5563	soj	chromosome partitioning protein Soj		4.3	9.83E-03	Citronellsäure	6.1	28609	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning		
15600757	PA5564	gidB	glucose inhibited division protein B		1.3	2.15E-01	Citronellsäure	6.3	23735	5	Unknown	COG0357	Cell envelope biogenesis, outer membrane		
15600758	PA5565	gidA	glucose-inhibited division protein A		2.2	2.12E-02	Citronellsäure	6.5	69605	5	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning		
15600762	PA5569	rnpA	ribonuclease P protein component		2.7	6.75E-02	Citronellol	11.5	15282	2	Unknown	COG0594	Translation, ribosomal structure and biogenesis		
375041995					1.3	3.75E-01	Citronellsäure			55					
313108864					15.7	1.33E-04	Citronellsäure			43					
346058816					3.1	1.24E-01	Citronellol			37					
10120672					20.5	4.47E-02	Citronellsäure			36					
296388504					15.7	5.55E-02	Citronellsäure			28					
152986613					1.1	6.70E-01	Citronellsäure			27					
22001796					1.0	5.62E-01	Citronellol			25					
375041914					2.4	2.52E-02	Citronellol			22					
4512118					17.8	1.79E-04	Citronellsäure			22					
313110180					1.2	1.00E-01	Citronellsäure			20					
282403590					2.0	1.90E-01	Citronellsäure			20					
313111914					1.7	9.21E-01	Citronellol			14					
107103312					18.7	1.64E-02	Citronellsäure			14					
296388215					8.3	5.15E-05	Citronellsäure			13					
334834247					1.1	9.65E-01	Citronellol			13					
308198348					1.7	4.44E-03	Citronellol			11					
239949862					7.1	4.43E-02	Citronellsäure			11					
107099134					2.1	1.55E-01	Citronellsäure			10					
107103488					5.9	1.63E-02	Citronellol			9					
347307435					1.4	6.82E-01	Citronellsäure			9					
239949861					1.7	2.27E-01	Citronellsäure			8					
116054234					2.5	9.15E-03	Citronellol			8					
375044686					11.8	2.52E-02	Citronellsäure			8					
254236126					1.8	2.84E-01	Citronellol			8					
355651796					3.2	2.11E-01	Citronellsäure			7					
107101116					1.7	2.00E-01	Citronellsäure			7					
344189438					3.2	3.21E-03	Citronellsäure			6					
107104524					16.6	2.83E-04	Citronellsäure			6					
107102801					1.1	4.85E-01	Citronellol			5					
107099288					1.5	2.16E-01	Citronellsäure			5					
107099958					46.2	1.85E-02	Citronellsäure			5					
375041918					2.6	4.49E-02	Citronellol			5					
107100575					27.8	5.92E-04	Citronellsäure			4					
107102888					1.5	5.42E-02	Citronellol			4					
107099096					1.1	6.36E-01	Citronellsäure			3					
152985170					2.9	2.42E-02	Citronellsäure			3					
146282899					1.0	8.10E-01	Citronellol			3					
226944916					3.8	1.22E-01	Citronellsäure			3					
107103974					1.3	9.27E-01	Citronellol			2					
107104298					1.3	4.10E-01	Citronellsäure			2					
375040819					45.3	3.82E-03	Citronellsäure			2					
107103573					1.2	6.32E-01	Citronellol			2					
107102668					11.1	1.24E-02	Citronellsäure			2					
244539066					1.3	2.93E-01	Citronellol			2					
330807576					3.2	1.38E-02	Citronellol			2					
359783701					2.1	7.23E-02	Citronellsäure			2					
104782430					16.6	1.94E-04	Citronellol			2					
116052531					33.6	1.17E-01	Citronellol			2					

296389665	1.3	4.34E-01	Citronellol	2
359394219	1.9	7.84E-01	Citronellsäure	2
152984253	1.5	3.48E-01	Citronellsäure	2
374704241	1.3	5.46E-01	Citronellol	2
359783696	12.6	7.40E-03	Citronellsäure	2
258591310	1.2	5.13E-01	Citronellsäure	2
347305107	1.3	2.81E-01	Citronellsäure	2
222478051	25.8	1.63E-01	Citronellsäure	2
146308929	9.1	2.32E-01	Citronellsäure	2

5.4.1.3 GeLCMSMS_P_aeruginosa_PAO1_Glucose_Citronellsäure_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595199	PA0001	dnaA	chromosomal replication initiator protein DnaA	1.5	1.21E-01	Glucose	8.9	57722	5	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.6	3.54E-03	Citronellsäure	4.9	40694	20	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	1.0	6.39E-01	Citronellsäure	5.7	90188	44	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	2.6	5.13E-02	Citronellsäure	4.5	19115	4	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	19.2	1.35E-04	Citronellsäure	7.9	61755	9	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.0	4.71E-01	Glucose	4.8	73973	36	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	1.2	7.55E-02	Glucose	4.7	36109	13	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	1.2	2.42E-01	Glucose	7.0	33028	12	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	1.4	1.21E-01	Glucose	4.7	19365	5	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	1.7	5.19E-02	Glucose	9.4	37586	6	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	22.1	1.57E-03	Glucose	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	4.4	1.21E-02	Citronellsäure	6.3	35095	11	Cytoplasmic	COG0604	Energy production and conversion	
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	2.2	1.38E-02	Glucose	5.8	34774	9	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	1.3	8.08E-01	Citronellsäure	5.5	29484	4	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	1.3	7.20E-02	Glucose	5.0	28488	12	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	1.1	4.69E-01	Glucose	6.3	43680	17	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	2.1	9.74E-02	Citronellsäure	7.1	7863	3	Unknown	COG3360	Function unknown	
15595243	PA0045		hypothetical protein	1.3	9.73E-01	Citronellsäure	9.6	24395	2	Periplasmic	COG1462	Cell envelope biogenesis, outer membrane	
15595252	PA0054		conserved hypothetical protein	60.9	8.71E-02	Glucose	9.6	20024	2	Unknown	COG1859	Translation, ribosomal structure and biogenesis	
15595253	PA0055		hypothetical protein	1.2	3.16E-01	Citronellsäure	5.7	18433	11	Cytoplasmic	COG3812	Function unknown	
15595263	PA0065		hypothetical protein	1.5	1.43E-02	Glucose	6.1	24951	8	Cytoplasmic	COG0546	General function prediction only	
15595264	PA0066		conserved hypothetical protein	56.9	9.30E-02	Glucose	6.6	19198	2	Cytoplasmic	COG0663	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.1	5.82E-01	Glucose	4.9	76011	29	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	3.6	5.30E-02	Glucose	8.9	31716	6	Periplasmic			
15595273	PA0075	pppA	PppA	1.7	2.90E-01	Citronellsäure	6.2	25904	6	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	2.0	3.13E-02	Citronellsäure	4.4	23856	4	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	1.4	4.89E-01	Citronellsäure	6.1	48275	4	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595280	PA0082	tssA1	TssA1	1.6	1.31E-01	Citronellsäure	4.1	36647	3	Cytoplasmic	COG3515	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	2.4	3.99E-02	Citronellsäure	4.9	18785	15	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.1	1.07E-01	Citronellsäure	5.0	55771	32	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	4.5	1.27E-01	Glucose	6.8	17415	11	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	1.8	1.78E-02	Citronellsäure	4.4	30361	8	Cytoplasmic	COG4455	General function prediction only	
15595288	PA0090	clpV1	ClpV1	1.1	6.79E-01	Citronellsäure	5.3	98737	33	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	6.3	5.04E-02	Citronellsäure	6.4	72012	14	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	27.0	3.33E-02	Citronellsäure	8.9	44738	4	Cytoplasmic Membrane	COG4104	Function unknown	
15595292	PA0094		hypothetical protein	6.5	2.04E-02	Glucose	6.8	16456	3	Unknown	COG5435	Function unknown	
15595298	PA0100		hypothetical protein	2.6	2.63E-03	Citronellsäure	4.1	33723	5	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.2	3.07E-02	Glucose	6.7	26622	10	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595313	PA0115		conserved hypothetical protein	20.9	2.05E-03	Glucose	6.3	17085	5	Cytoplasmic	COG2153	General function prediction only	
15595316	PA0118		hypothetical protein	4.8	1.61E-02	Citronellsäure	6.8	21473	5	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595320	PA0122	rahU	rahU	1.8	3.55E-01	Glucose	4.4	14579	2	Extracellular			
15595324	PA0126		hypothetical protein	2.5	4.05E-02	Glucose	8.0	22367	2	Outer Membrane Vesicle			
15595326	PA0128		conserved hypothetical protein	7.4	2.53E-03	Glucose	4.9	12132	2	Unknown	COG2824	Inorganic ion transport and metabolism	
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.1	2.95E-01	Glucose	6.0	53323	8	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	1.1	4.87E-01	Citronellsäure	6.3	20541	15	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	1.5	2.38E-02	Glucose	5.0	55835	11	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
15595342	PA0144		hypothetical protein	2.0	6.86E-02	Citronellsäure	8.4	22431	7	Unknown	COG3613	Nucleotide transport and metabolism	
15595343	PA0145		hypothetical protein	2.0	1.29E-02	Citronellsäure	4.4	18448	2	Cytoplasmic	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.5	4.68E-02	Citronellsäure	4.9	36163	5	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595357	PA0159		probable transcriptional regulator	1.0	5.95E-01	Citronellsäure	6.0	34683	2	Cytoplasmic	COG0583	Transcription	
15595362	PA0164		probable gamma-glutamyltranspeptidase	1.1	4.42E-01	Citronellsäure	6.5	58453	3	Periplasmic	COG0405	Amino acid transport and metabolism	
15595368	PA0170		hypothetical protein	5.7	6.69E-03	Glucose	4.3	14553	5	Cytoplasmic			
15595369	PA0171		hypothetical protein	1.7	1.68E-01	Citronellsäure	7.1	19800	13	Cytoplasmic			
15595372	PA0174		conserved hypothetical protein	33.7	1.11E-03	Citronellsäure	8.5	22206	2	Cytoplasmic	COG1871	Cell motility and secretion	
15595374	PA0176	aer2	aerotaxis transducer Aer2	16.0	7.13E-05	Citronellsäure	4.8	72591	29	Cytoplasmic	COG0840	Cell motility and secretion	
15595375	PA0177		probable purine-binding chemotaxis protein	64.7	3.52E-03	Citronellsäure	4.3	17487	4	Cytoplasmic	COG0835	Cell motility and secretion	
15595376	PA0178		probable two-component sensor	149.7	1.58E-04	Citronellsäure	4.5	68931	9	Cytoplasmic	COG0643	Cell motility and secretion	
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	6.6	1.23E-04	Citronellsäure	5.9	38650	20	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595405	PA0208	mdcA	malonate decarboxylase alpha subunit	219.6	1.93E-04	Citronellsäure	6.4	61424	4	Cytoplasmic	COG4670	Lipid metabolism	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	32.4	3.98E-05	Citronellsäure	4.5	30343	8	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	31.6	8.10E-05	Citronellsäure	7.1	28496	6	Cytoplasmic			
15595422	PA0225		probable transcriptional regulator	2.0	5.72E-03	Citronellsäure	6.9	19993	2	Cytoplasmic	COG1476	Transcription	
15595424	PA0227		probable CoA transferase, subunit B	17.7	1.05E-04	Citronellsäure	5.4	27314	4	Cytoplasmic	COG2057	Lipid metabolism	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	6.0	2.41E-01	Citronellsäure	6.2	49121	2	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	3.2	1.98E-02	Citronellsäure	5.1	27985	4	Unknown	COG0596	General function prediction only	
15595444	PA0247	pobA	p-hydroxybenzoate hydroxylase	149.7	4.44E-04	Citronellsäure	6.8	44323	4	Cytoplasmic	COG0654	Coenzyme metabolism	
15595456	PA0259		hypothetical protein	1.7	3.35E-01	Citronellsäure	5.0	52444	2	Unknown			
15595460	PA0263	hcpC	secreted protein Hcp	3.4	9.17E-03	Citronellsäure	5.8	19091	7	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.4	4.51E-02	Citronellsäure	5.4	51622	27	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	2.2	3.47E-04	Citronellsäure	6.4	45220	20	Periplasmic	COG0160	Amino acid transport and metabolism	
15595474	PA0277		conserved hypothetical protein	1.6	1.30E-01	Citronellsäure	6.5	26626	8	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	1.3	2.86E-02	Citronellsäure	9.0	36433	15	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	1.5	4.84E-01	Glucose	9.1	49667	7	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.6	1.39E-03	Citronellsäure	4.6	41191	6	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	2.7	1.47E-03	Citronellsäure	4.6	50907	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595494	PA0297	spuA	probable glutamine amidotransferase	19.3	1.29E-02	Citronellsäure	6.4	26477	3	Unknown	COG2071	General function prediction only	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	2.3	1.43E-03	Citronellsäure	5.0	50965	6	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595496	PA0299	spuC	Polyamine:pyruvate transaminase	2.1	2.86E-03	Citronellsäure	6.0	50453	18	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	4.9	9.47E-04	Citronellsäure	7.6	40629	16	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	4.3	2.70E-03	Citronellsäure	5.5	40069	13	Periplasmic	COG0687	Amino acid transport and metabolism	
15595506	PA0309		hypothetical protein	1.1	5.61E-01	Citronellsäure	7.6	27021	6	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	1.7	1.50E-02	Citronellsäure	9.7	28005	13	Periplasmic	COG0834	Amino acid transport and metabolism	

15595512	PA0315		hypothetical protein	1.4	9.95E-01	Citronellsäure	7.2	15463	9	Unknown		
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.5	6.63E-03	Citronellsäure	6.5	44216	20	Periplasmic	COG0111	Amino acid transport and metabolism
15595514	PA0317		hypothetical protein	1.7	1.38E-02	Glucose	4.9	51286	17	Periplasmic	COG0277	Energy production and conversion
15595515	PA0318		conserved hypothetical protein	1.4	4.04E-01	Citronellsäure	5.3	23843	5	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism
15595520	PA0323		probable binding protein component of ABC transporter	3.5	9.35E-01	Citronellsäure	6.8	38901	2	Periplasmic	COG0687	Amino acid transport and metabolism
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	1.3	1.04E-01	Citronellsäure	5.3	23721	10	Cytoplasmic	COG0120	Carbohydrate transport and metabolism
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	1.0	8.04E-01	Glucose	6.5	55351	13	Cytoplasmic	COG1171	Amino acid transport and metabolism
15595532	PA0335		hypothetical protein	1.2	5.64E-01	Glucose	4.5	24353	13	Cytoplasmic	COG0560	Amino acid transport and metabolism
15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.5	4.44E-01	Citronellsäure	9.5	18726	7	Cytoplasmic	COG0494	DNA replication, recombination, and repair
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.3	2.48E-01	Glucose	5.6	83606	25	Cytoplasmic	COG3605	Signal transduction mechanisms
15595536	PA0339		hypothetical protein	2.9	1.02E-02	Citronellsäure	6.7	26527	6	Unknown	COG3332	Function unknown
15595539	PA0342	thyA	thymidylate synthase	1.9	2.54E-04	Glucose	6.5	30016	8	Cytoplasmic	COG0207	Nucleotide transport and metabolism
15595547	PA0350	folA	dihydrofolate reductase	1.1	5.97E-01	Glucose	5.3	18203	6	Unknown	COG0262	Coenzyme metabolism
15595548	PA0351		conserved hypothetical protein	1.2	6.59E-01	Citronellsäure	6.7	17217	2	Cytoplasmic	COG0622	General function prediction only
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.1	2.62E-01	Glucose	6.0	65160	36	Periplasmic	COG0129	Amino acid transport and metabolism
15595552	PA0355	pfpI	protease PfpI	17.3	2.29E-05	Citronellsäure	5.0	19246	8	Cytoplasmic	COG0693	General function prediction only
15595553	PA0356		hypothetical protein	1.2	2.10E-01	Citronellsäure	5.3	30360	4	Unknown	COG1639	Signal transduction mechanisms
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	4.4	3.26E-02	Glucose	9.0	17771	10	Cytoplasmic	COG0669	Coenzyme metabolism
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	1.1	8.23E-01	Citronellsäure	4.5	48391	12	Cytoplasmic	COG0552	Intracellular trafficking and secretion
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.7	7.39E-03	Glucose	4.8	28234	14	Cytoplasmic	COG2022	Nucleotide transport and metabolism
15595579	PA0382	micA	DNA mismatch repair protein MicA	1.7	8.38E-03	Citronellsäure	8.3	25331	4	Cytoplasmic	COG0220	General function prediction only
15595580	PA0383		conserved hypothetical protein	8.9	1.46E-04	Citronellsäure	8.3	50243	6	Unknown		
15595584	PA0387		conserved hypothetical protein	1.2	5.00E-01	Glucose	6.1	21242	7	Cytoplasmic	COG0127	Nucleotide transport and metabolism
15595585	PA0388		hypothetical protein	28.9	1.99E-02	Glucose	7.4	15303	2	Periplasmic		
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	1.4	2.38E-02	Citronellsäure	4.5	28094	8	Cytoplasmic	COG0345	Amino acid transport and metabolism
15595591	PA0394		conserved hypothetical protein	2.8	8.20E-03	Citronellsäure	6.7	24505	6	Cytoplasmic	COG0325	General function prediction only
15595592	PA0395	pilT	twitching motility protein PilT	1.3	4.73E-01	Glucose	6.9	38021	7	Cytoplasmic	COG2805	Cell motility and secretion
15595596	PA0399		cystathionine beta-synthase	1.0	9.54E-01	Citronellsäure	5.5	49170	18	Cytoplasmic	COG0031	Amino acid transport and metabolism
15595597	PA0400		probable cystathionine gamma-lyase	1.9	9.71E-04	Citronellsäure	6.6	42786	10	Cytoplasmic	COG0626	Amino acid transport and metabolism
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.2	2.44E-01	Citronellsäure	5.8	44150	6	Periplasmic	COG0044	Nucleotide transport and metabolism
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.2	2.06E-01	Glucose	6.8	36629	13	Periplasmic	COG0540	Nucleotide transport and metabolism
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.6	1.90E-01	Citronellsäure	5.7	18676	9	Cytoplasmic	COG2065	Nucleotide transport and metabolism
15595604	PA0407	gshB	glutathione synthetase	1.4	3.86E-03	Citronellsäure	5.8	35705	16	Periplasmic	COG0189	Coenzyme metabolism
15595605	PA0408	pilG	twitching motility protein PilG	21.2	1.31E-02	Glucose	7.4	14718	3	Cytoplasmic	COG0745	Signal transduction mechanisms
15595607	PA0410	pilI	twitching motility protein PilI	1.9	3.01E-01	Citronellsäure	6.6	19934	2	Cytoplasmic	COG0835	Cell motility and secretion
15595608	PA0411	pilJ	twitching motility protein PilJ	4.1	2.93E-02	Glucose	4.4	72528	3	Outer Membrane Vesicle	COG0840	Cell motility and secretion
15595610	PA0413	chpA	component of chemotactic signal transduction system	3.8	2.79E-02	Citronellsäure	4.2	268573	26	Cytoplasmic	COG0643	Cell motility and secretion
15595612	PA0415	chpC	probable chemotaxis protein	1.5	5.35E-01	Citronellsäure	4.7	17625	7	Unknown		
15595615	PA0418		hypothetical protein	1.2	5.37E-01	Glucose	5.6	52140	3	Cytoplasmic		
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransfera	1.1	2.17E-01	Glucose	6.3	52478	10	Cytoplasmic	COG0161	Coenzyme metabolism
15595620	PA0423	pasP	PasP	2.0	2.42E-02	Citronellsäure	6.5	20776	18	Periplasmic	COG2353	Function unknown
15595625	PA0428		probable ATP-dependent RNA helicase	10.8	1.54E-02	Glucose	10.7	70112	3	Cytoplasmic	COG0513	DNA replication, recombination, and repair
15595626	PA0429		hypothetical protein	1.6	1.47E-02	Citronellsäure	7.0	40872	3	Cytoplasmic		
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	1.1	4.60E-01	Citronellsäure	6.5	32196	18	Periplasmic	COG0685	Amino acid transport and metabolism
15595628	PA0431		hypothetical protein	418.4	2.98E-02	Citronellsäure	6.8	20639	2	Unknown	COG0317	Signal transduction mechanisms
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	1.3	1.58E-02	Citronellsäure	6.0	51400	37	Periplasmic	COG0499	Coenzyme metabolism
15595634	PA0437	codA	cytosine deaminase	1.5	1.86E-01	Glucose	6.0	47074	5	Cytoplasmic	COG0402	Nucleotide transport and metabolism
15595643	PA0446		conserved hypothetical protein	5.7	6.29E-04	Citronellsäure	5.3	43847	3	Cytoplasmic	COG1804	Energy production and conversion
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	3.1	5.77E-04	Citronellsäure	6.1	43311	4	Cytoplasmic	COG1960	Lipid metabolism
15595646	PA0449		hypothetical protein	96.5	7.38E-05	Glucose	10.5	19808	10	Cytoplasmic	COG1607	Lipid metabolism
15595656	PA0459		probable ClpA/B protease ATP binding subunit	38.5	7.39E-05	Citronellsäure	6.7	94143	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
15595659	PA0462		hypothetical protein	1.5	9.59E-01	Citronellsäure	10.6	26230	8	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones
15595660	PA0463	creB	two-component response regulator CreB	1.6	1.49E-01	Glucose	5.4	25573	3	Cytoplasmic	COG0745	Signal transduction mechanisms
15595664	PA0467		conserved hypothetical protein	1.2	6.99E-02	Glucose	7.5	23301	10	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones
15595665	PA0468		hypothetical protein	1.3	3.19E-01	Glucose	4.8	33594	2	Periplasmic	COG4257	Defense mechanisms
15595666	PA0469		hypothetical protein	3.1	6.64E-03	Citronellsäure	4.7	32137	4	Cytoplasmic		
15595670	PA0473		probable glutathione S-transferase	6.7	1.46E-04	Citronellsäure	5.8	28294	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15595675	PA0478		probable N-acetyltransferase	3.5	2.38E-01	Glucose	4.6	18109	2	Cytoplasmic	COG0456	General function prediction only
15595679	PA0482	glcB	malate synthase G	2.7	5.30E-03	Citronellsäure	5.5	78659	63	Periplasmic	COG2225	Energy production and conversion
15595681	PA0484		conserved hypothetical protein	13.9	2.32E-04	Citronellsäure	4.5	18553	3	Cytoplasmic	COG2716	Amino acid transport and metabolism
15595684	PA0487		probable molybdenum transport regulator	12.8	1.97E-02	Glucose	9.2	26948	2	Cytoplasmic	COG2005	General function prediction only
15595697	PA0500	bioB	biotin synthase	3.9	1.95E-03	Glucose	6.0	39113	10	Cytoplasmic	COG0502	Coenzyme metabolism
15595698	PA0501	bioF	8-amino-7-oxononanoate synthase	407.3	3.59E-02	Citronellsäure	5.9	42237	3	Cytoplasmic	COG0156	Coenzyme metabolism
15595699	PA0502		probable biotin biosynthesis protein bioH	5.0	1.47E-02	Glucose	4.3	26494	1	Cytoplasmic	COG0596	General function prediction only
15595700	PA0503		probable biotin synthesis protein BioC	2.8	5.08E-05	Glucose	9.0	29712	6	Unknown	COG2226	Coenzyme metabolism
15595701	PA0504	bioD	dethiobiotin synthase	1.7	1.35E-02	Glucose	5.3	23337	10	Cytoplasmic	COG0132	Coenzyme metabolism
15595703	PA0506		probable acyl-CoA dehydrogenase	9.5	1.42E-04	Citronellsäure	5.8	65358	42	Periplasmic	COG1960	Lipid metabolism
15595705	PA0508		probable acyl-CoA dehydrogenase	17.4	6.91E-06	Citronellsäure	5.1	63628	44	Cytoplasmic	COG1960	Lipid metabolism
15595734	PA0537		conserved hypothetical protein	2.7	3.18E-01	Glucose	8.9	22180	6	Outer Membrane Vesicle	COG1704	Function unknown
15595743	PA0546	metK	methionine adenosyltransferase	1.7	1.23E-05	Citronellsäure	5.2	42709	24	Cytoplasmic	COG0192	Coenzyme metabolism
15595745	PA0548	tktA	transketolase	1.1	5.05E-01	Glucose	5.0	72220	39	Periplasmic	COG0021	Carbohydrate transport and metabolism
15595747	PA0550		conserved hypothetical protein	1.7	6.10E-02	Citronellsäure	5.4	29834	6	Cytoplasmic	COG3622	Carbohydrate transport and metabolism
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	1.8	2.11E-01	Citronellsäure	5.8	38743	3	Cytoplasmic	COG0057	Carbohydrate transport and metabolism
15595749	PA0552	pgk	phosphoglycerate kinase	2.8	1.96E-03	Citronellsäure	5.1	40404	21	Periplasmic	COG0126	Carbohydrate transport and metabolism
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	2.2	2.71E-02	Citronellsäure	5.3	38574	27	Cytoplasmic	COG0191	Carbohydrate transport and metabolism
15595755	PA0558		conserved hypothetical protein	1.0	8.06E-01	Glucose	6.2	27987	12	Cytoplasmic	COG2226	Coenzyme metabolism
15595759	PA0562		probable hydrolase	1.3	3.67E-02	Citronellsäure	5.4	24232	9	Cytoplasmic	COG0637	General function prediction only
15595768	PA0571		hypothetical protein	1.4	4.55E-01	Citronellsäure	5.0	22501	5	Unknown		
15595773	PA0576	rpoD	sigma factor RpoD	1.1	6.39E-01	Glucose	4.6	69643	33	Outer Membrane Vesicle	COG0568	Transcription
15595775	PA0578		conserved hypothetical protein	2.6	2.62E-02	Citronellsäure	6.0	16842	2	Cytoplasmic	COG1610	Function unknown
15595776	PA0579	rpsU	30S ribosomal protein S21	47.3	1.06E-01	Glucose	11.4	8485	2	Cytoplasmic		
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	1.2	4.57E-01	Glucose	6.2	36561	4	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones
15595780	PA0583		hypothetical protein	1.8	1.75E-01	Citronellsäure	5.6	20091	4	Cytoplasmic	COG0801	Coenzyme metabolism

15595783	PA0586		conserved hypothetical protein	15.1	1.31E-04	Citronellsäure	5.1	60814	16	Cytoplasmic	COG2719	Function unknown
15595784	PA0587		conserved hypothetical protein	27.0	1.76E-04	Citronellsäure	7.8	48742	8	Cytoplasmic	COG2718	Function unknown
15595785	PA0588		conserved hypothetical protein	15.5	1.43E-05	Citronellsäure	5.5	73722	42	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	1.8	6.29E-02	Citronellsäure	7.2	32019	6	Cytoplasmic		
15595789	PA0592	ksgA	rRNA (adenine-N6,N6)-dimethyltransferase	2.8	3.04E-02	Glucose	7.4	30058	5	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.0	7.36E-01	Glucose	6.6	34891	10	Cytoplasmic	COG1995	Coenzyme metabolism
15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.2	6.80E-02	Citronellsäure	5.6	48441	20	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones
15595792	PA0595	ostA	organic solvent tolerance protein OstA precursor	10.9	2.23E-02	Glucose	5.3	104271	6	Periplasmic	COG1452	Cell envelope biogenesis, outer membrane
15595793	PA0596		hypothetical protein	1.9	3.55E-02	Citronellsäure	5.1	38185	8	Cytoplasmic	COG3178	General function prediction only
15595794	PA0597		probable nucleotidyl transferase	4.5	2.26E-05	Citronellsäure	6.1	24149	3	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane
15595798	PA0601		probable two-component response regulator	1.3	1.15E-01	Glucose	6.5	22868	2	Cytoplasmic	COG2197	Signal transduction mechanisms
15595801	PA0604		probable binding protein component of ABC transporter	3.4	8.45E-05	Citronellsäure	5.6	38167	9	Periplasmic	COG0687	Amino acid transport and metabolism
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.2	5.82E-01	Glucose	5.1	24096	13	Cytoplasmic	COG0036	Carbohydrate transport and metabolism
15595806	PA0609	trpE	anthranilate synthetase component I	1.0	6.38E-01	Citronellsäure	4.7	54555	14	Cytoplasmic	COG0147	Amino acid transport and metabolism
15595846	PA0649	trpG	anthranilate synthase component II	1.4	2.83E-01	Citronellsäure	6.0	22046	5	Cytoplasmic	COG0512	Amino acid transport and metabolism
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	1.2	5.14E-01	Citronellsäure	5.6	37384	8	Cytoplasmic	COG0547	Amino acid transport and metabolism
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	2.4	1.12E-02	Citronellsäure	4.6	30315	11	Cytoplasmic	COG0134	Amino acid transport and metabolism
15595850	PA0653		conserved hypothetical protein	1.2	9.76E-01	Citronellsäure	6.4	15237	5	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones
15595851	PA0654	speD	S-adenosylmethionine decarboxylase proenzyme	1.5	3.78E-01	Glucose	4.5	30446	4	Cytoplasmic	COG1586	Amino acid transport and metabolism
15595852	PA0655		hypothetical protein	1.0	7.47E-01	Glucose	5.3	23644	4	Unknown	COG2941	Coenzyme metabolism
15595854	PA0657		probable ATPase	1.4	3.49E-01	Glucose	6.0	54551	2	Cytoplasmic Membrane	COG0464	Posttranslational modification, protein turnover, chaperones
15595857	PA0660		hypothetical protein	1.4	2.39E-03	Citronellsäure	6.2	34814	16	Cytoplasmic	COG2070	General function prediction only
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	2.2	3.57E-03	Citronellsäure	6.7	36684	20	Cytoplasmic	COG0002	Amino acid transport and metabolism
15595861	PA0664		hypothetical protein	4.4	7.99E-02	Glucose	5.6	14790	3	Cytoplasmic	COG1664	Cell envelope biogenesis, outer membrane
15595862	PA0665		conserved hypothetical protein	56.0	4.06E-04	Glucose	4.0	12484	2	Cytoplasmic	COG0316	Posttranslational modification, protein turnover, chaperones
15595863	PA0666		conserved hypothetical protein	1.8	3.85E-02	Citronellsäure	5.2	39087	5	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.4	8.77E-03	Citronellsäure	5.6	44129	25	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis
15595869	PA0672	hemO	heme oxygenase	3.8	8.72E-05	Glucose	4.8	21953	10	Unknown	COG3230	Inorganic ion transport and metabolism
15595903	PA0706	cat	chloramphenicol acetyltransferase	1.4	1.11E-01	Glucose	6.1	23524	2	Unknown	COG0110	General function prediction only
15595912	PA0715		hypothetical protein	1.4	6.16E-01	Citronellsäure	9.9	36589	3	Cytoplasmic	COG3344	DNA replication, recombination, and repair
15595938	PA0741		conserved hypothetical protein	3.5	1.37E-03	Citronellsäure	6.6	22687	4	Unknown	COG2910	General function prediction only
15595941	PA0744		probable enoyl-CoA hydratase/isomerase	6.6	9.98E-04	Citronellsäure	5.1	40589	4	Cytoplasmic	COG1024	Lipid metabolism
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	2.1	1.18E-03	Citronellsäure	6.4	29904	10	Cytoplasmic	COG1024	Lipid metabolism
15595947	PA0750	ung	uracil-DNA glycosylase	1.9	7.31E-03	Glucose	8.2	26010	6	Cytoplasmic	COG0692	DNA replication, recombination, and repair
15595951	PA0754		hypothetical protein	7.8	1.19E-04	Citronellsäure	5.5	34918	14	Unknown	COG3181	Function unknown
15595953	PA0756		probable two-component response regulator	1.2	9.41E-01	Glucose	5.2	24431	2	Cytoplasmic	COG0745	Signal transduction mechanisms
15595955	PA0758		hypothetical protein	1.0	9.52E-01	Citronellsäure	4.7	30875	8	Cytoplasmic	COG1639	Signal transduction mechanisms
15595956	PA0759		conserved hypothetical protein	1.8	1.02E-01	Glucose	5.2	33667	9	Unknown	COG0354	General function prediction only
15595958	PA0761	nadB	L-aspartate oxidase	1.1	5.62E-01	Glucose	6.3	60004	11	Cytoplasmic	COG0029	Coenzyme metabolism
15595959	PA0762	algU	sigma factor AlgU	1.3	2.03E-01	Glucose	5.4	22196	8	Cytoplasmic	COG1595	Transcription
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	2.0	9.13E-03	Glucose	6.1	34572	5	Periplasmic	COG3026	Signal transduction mechanisms
15595963	PA0766	mucD	serine protease MucD precursor	1.2	3.49E-01	Glucose	7.8	50321	7	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones
15595964	PA0767	lepA	GTP-binding protein LepA	1.5	2.05E-01	Glucose	5.3	66263	6	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane
15595967	PA0770	rnc	ribonuclease III	1.4	1.85E-01	Glucose	6.6	25474	3	Cytoplasmic	COG0571	Transcription
15595968	PA0771	era	GTP-binding protein Era	2.2	3.80E-02	Glucose	6.6	34550	3	Cytoplasmic Membrane	COG1159	General function prediction only
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.1	4.39E-01	Citronellsäure	5.6	27228	6	Cytoplasmic	COG0854	Coenzyme metabolism
15595971	PA0774		conserved hypothetical protein	1.8	7.66E-02	Glucose	6.4	36522	2	Cytoplasmic	COG2227	Coenzyme metabolism
15595972	PA0775		conserved hypothetical protein	1.6	1.35E-01	Glucose	5.3	27608	3	Cytoplasmic	COG4106	General function prediction only
15595976	PA0779		probable ATP-dependent protease	1.6	4.15E-01	Glucose	6.8	88574	14	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones
15595979	PA0782	putA	proline dehydrogenase PutA	4.3	6.09E-02	Citronellsäure	6.0	115630	22	Periplasmic	COG4230	Energy production and conversion
15595989	PA0792	prpD	propionate catabolic protein PrpD	1.7	2.93E-01	Glucose	6.6	54881	4	Cytoplasmic	COG2079	General function prediction only
15595991	PA0794		probable aconitate hydratase	2.9	1.31E-03	Citronellsäure	5.3	94890	19	Cytoplasmic	COG1048	Energy production and conversion
15595992	PA0795	prpC	citrate synthase 2	5.1	2.74E-04	Citronellsäure	6.4	41689	17	Cytoplasmic	COG0372	Energy production and conversion
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.6	4.57E-02	Citronellsäure	5.2	32137	12	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
15596005	PA0808		hypothetical protein	39.4	7.61E-02	Citronellsäure	4.8	17551	2	Cytoplasmic	COG3832	Function unknown
15596030	PA0833		hypothetical protein	1.4	3.99E-01	Glucose	9.0	24713	5	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane
15596032	PA0835	pta	phosphate acetyltransferase	1.2	1.70E-01	Citronellsäure	5.0	75696	10	Periplasmic	COG0280	Energy production and conversion
15596033	PA0836	ackA	acetate kinase	107.1	1.16E-01	Citronellsäure	7.1	42421	3	Cytoplasmic	COG0282	Energy production and conversion
15596034	PA0837	slyD	peptidyl-prolyl cis-trans isomerase SlyD	287.9	1.99E-03	Glucose	4.2	17010	2	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones
15596035	PA0838		probable glutathione peroxidase	2.9	3.47E-02	Citronellsäure	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones
15596037	PA0840		probable oxidoreductase	1.0	9.65E-01	Glucose	5.5	40334	10	Cytoplasmic	COG1902	Energy production and conversion
15596045	PA0848		probable alkyl hydroperoxide reductase	3.4	6.27E-03	Glucose	5.1	21814	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
15596046	PA0849	trxB2	thioredoxin reductase 2	20.2	8.02E-04	Glucose	5.4	33481	2	Cytoplasmic	COG0492	Posttranslational modification, protein turnover, chaperones
15596048	PA0851		hypothetical protein	1.8	6.04E-03	Glucose	6.8	34024	8	Cytoplasmic	COG1171	Amino acid transport and metabolism
15596050	PA0853		probable oxidoreductase	1.5	8.98E-02	Citronellsäure	8.3	23485	4	Cytoplasmic	COG2249	General function prediction only
15596051	PA0854	fumC2	fumarate hydratase	3.6	6.08E-04	Citronellsäure	6.1	49122	18	Cytoplasmic	COG0114	Energy production and conversion
15596053	PA0856		hypothetical protein	13.9	1.22E-03	Glucose	10.1	19998	10	Unknown	COG3184	Function unknown
15596055	PA0858		conserved hypothetical protein	3.5	1.28E-02	Glucose	5.7	35420	6	Cytoplasmic	COG1054	General function prediction only
15596056	PA0859		hypothetical protein	2.0	1.69E-01	Citronellsäure	4.6	21466	4	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones
15596059	PA0862		hypothetical protein	1.2	7.07E-01	Citronellsäure	6.5	29845	4	Cytoplasmic	COG5424	Coenzyme metabolism
15596060	PA0863		probable oxidoreductase	2.6	5.07E-02	Glucose	4.9	33368	3	Cytoplasmic Membrane	COG0604	Energy production and conversion
15596062	PA0865	hpd	4-hydroxyphenylpyruvate dioxygenase	16.8	5.27E-04	Citronellsäure	4.9	39913	3	Periplasmic	COG3185	Amino acid transport and metabolism
15596064	PA0867	mliC	membrane-bound lysozyme inhibitor of c-type lysozyme MliC	4.3	3.04E-03	Glucose	4.8	13695	7	Outer Membrane Vesicle	COG3895	General function prediction only
15596067	PA0870	phhC	aromatic amino acid aminotransferase	5.6	5.70E-04	Citronellsäure	6.2	43273	6	Cytoplasmic	COG1448	Amino acid transport and metabolism
15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	2.2	2.68E-01	Glucose	6.4	13333	4	Cytoplasmic	COG2154	Coenzyme metabolism
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	7.2	7.97E-06	Citronellsäure	6.3	71762	34	Cytoplasmic	COG0365	Lipid metabolism
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.7	1.08E-02	Citronellsäure	6.8	28010	17	Periplasmic	COG0834	Amino acid transport and metabolism
15596088	PA0891		hypothetical protein	6.1	1.37E-02	Citronellsäure	4.9	40214	4	Cytoplasmic	COG3608	General function prediction only
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.4	1.62E-02	Citronellsäure	5.8	43747	26	Periplasmic	COG4992	Amino acid transport and metabolism
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	1.5	5.21E-03	Citronellsäure	4.7	36930	4	Cytoplasmic	COG3138	Amino acid transport and metabolism
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	1.9	4.17E-02	Citronellsäure	6.5	37245	7	Cytoplasmic	COG3138	Amino acid transport and metabolism
15596095	PA0898	aruD	succinylglutamate 5-semialdehyde dehydrogenase	1.6	2.53E-02	Citronellsäure	6.2	51510	10	Periplasmic	COG1012	Energy production and conversion
15596096	PA0899	aruB	succinylarginine dihydrolase	1.4	2.03E-01	Glucose	6.2	48875	10	Periplasmic	COG3724	Amino acid transport and metabolism

15596098	PA0901	aruE	succinylglutamate desuccinylase	2.0	8.21E-03	Citronellsäure	6.0	36909	8	Cytoplasmic	COG2988	Amino acid transport and metabolism
15596099	PA0902		hypothetical protein	1.6	1.61E-03	Glucose	6.4	35430	11	Cytoplasmic	COG2008	Amino acid transport and metabolism
15596100	PA0903	alaS	alanyl-tRNA synthetase	1.1	6.86E-01	Citronellsäure	5.2	94701	46	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.1	5.79E-01	Glucose	5.0	44388	30	Cytoplasmic	COG0527	Amino acid transport and metabolism
15596112	PA0915		conserved hypothetical protein	15.1	1.39E-03	Glucose	6.3	17514	6	Cytoplasmic	COG4807	Function unknown
15596113	PA0916		conserved hypothetical protein	1.2	5.30E-01	Glucose	4.6	48961	3	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis
15596124	PA0927	ldhA	D-lactate dehydrogenase (fermentative)	2.7	6.79E-04	Citronellsäure	6.1	35756	2	Cytoplasmic	COG1052	Energy production and conversion
15596129	PA0932	cysM	cysteine synthase B	2.1	4.27E-02	Citronellsäure	5.5	32448	15	Cytoplasmic	COG0031	Amino acid transport and metabolism
15596131	PA0934	relA	GTP pyrophosphokinase	1.2	2.88E-01	Glucose	7.6	83815	18	Cytoplasmic	COG0317	Signal transduction mechanisms
15596132	PA0935		conserved hypothetical protein	1.1	5.20E-01	Citronellsäure	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only
15596140	PA0943		hypothetical protein	1.2	2.59E-01	Citronellsäure	8.7	27183	16	Periplasmic		
15596141	PA0944	purN	phosphoribosylaminoimidazole synthetase	1.1	5.45E-01	Glucose	7.2	24734	4	Cytoplasmic	COG0299	Nucleotide transport and metabolism
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	1.2	4.76E-01	Glucose	4.5	37122	14	Cytoplasmic	COG0150	Nucleotide transport and metabolism
15596144	PA0947		conserved hypothetical protein	3.1	5.38E-04	Glucose	6.0	26843	4	Cytoplasmic	COG0593	DNA replication, recombination, and repair
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	2.4	1.45E-02	Glucose	6.8	20744	7	Unknown	COG0655	General function prediction only
15596153	PA0956	proS	prolyl-tRNA synthetase	1.1	2.33E-01	Citronellsäure	5.1	63103	31	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis
15596154	PA0957		hypothetical protein	11.8	1.17E-04	Citronellsäure	6.3	14622	4	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane	1.5	2.89E-01	Glucose	4.8	48360	11	Periplasmic		
15596156	PA0959		hypothetical protein	5.5	2.83E-01	Glucose	6.5	23069	2	Cytoplasmic	COG0537	Nucleotide transport and metabolism
15596159	PA0962		probable dna-binding stress protein	1.4	4.33E-01	Glucose	4.7	17493	9	Cytoplasmic	COG0783	Inorganic ion transport and metabolism
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.0	6.96E-01	Citronellsäure	5.2	66207	40	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis
15596161	PA0964	pmpR	pqsR-mediated PQS regulator, PmpR	35.6	2.87E-04	Glucose	4.4	26557	2	Cytoplasmic	COG0217	Function unknown
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.0	8.65E-01	Glucose	6.1	21927	11	Cytoplasmic	COG0632	DNA replication, recombination, and repair
15596165	PA0968		conserved hypothetical protein	1.5	6.28E-01	Citronellsäure	8.7	16672	3	Cytoplasmic	COG0824	General function prediction only
15596166	PA0969	tolQ	TolQ protein	15.1	2.23E-02	Glucose	6.3	25250	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion
15596169	PA0972	tolB	TolB protein	1.5	1.09E-01	Citronellsäure	9.2	47720	17	Periplasmic	COG0823	Intracellular trafficking and secretion
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	3.8	2.58E-02	Glucose	6.3	17925	5	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane
15596171	PA0974		conserved hypothetical protein	2.2	2.14E-04	Citronellsäure	8.7	29097	7	Outer Membrane Vesicle	COG1729	Function unknown
15596173	PA0976		conserved hypothetical protein	1.0	8.73E-01	Glucose	4.7	23900	5	Unknown	COG0603	General function prediction only
15596194	PA0997	pqsB	PqsB	1.0	8.27E-01	Glucose	4.6	30501	5	Cytoplasmic	COG0332	acyl-carrier-protein
15596195	PA0998	pqsC	PqsC	1.2	2.51E-01	Glucose	4.9	38238	3	Cytoplasmic	COG0332	acyl-carrier-protein
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	2.3	1.81E-02	Glucose	5.3	36378	5	Cytoplasmic	COG0332	acyl-carrier-protein
15596201	PA1004	nadA	quinolinate synthetase A	1.2	2.96E-01	Citronellsäure	5.4	38418	6	Cytoplasmic	COG0379	Coenzyme metabolism
15596205	PA1008	bcp	bacterioferritin comigratory protein	1.2	4.84E-01	Glucose	7.3	17352	11	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones
15596206	PA1009		hypothetical protein	2.4	7.29E-02	Glucose	5.6	20585	3	Cytoplasmic	COG2716	Amino acid transport and metabolism
15596207	PA1010	dapA	dihydrodipicolinate synthase	1.1	7.63E-01	Citronellsäure	6.4	31449	24	Periplasmic	COG0329	Amino acid transport and metabolism
15596208	PA1011		hypothetical protein	1.4	3.19E-03	Glucose	4.7	43055	7	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.6	3.28E-02	Citronellsäure	5.1	26831	20	Periplasmic	COG0152	Nucleotide transport and metabolism
15596220	PA1023		probable short-chain dehydrogenase	3.9	2.73E-03	Citronellsäure	6.7	32821	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15596223	PA1026		hypothetical protein	1.0	8.91E-01	Citronellsäure	4.8	17184	2	Cytoplasmic		
15596230	PA1033		probable glutathione S-transferase	1.5	1.72E-01	Glucose	6.8	24527	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15596233	PA1036		hypothetical protein	1.1	5.98E-01	Glucose	4.6	19537	2	Unknown		
15596236	PA1039		conserved hypothetical protein	3.1	1.28E-02	Citronellsäure	6.7	17189	3	Unknown	COG3012	Function unknown
15596237	PA1040		hypothetical protein	1.2	3.38E-01	Citronellsäure	6.0	18721	5	Unknown		
15596240	PA1043		hypothetical protein	3.2	2.94E-03	Glucose	8.2	27276	3	Periplasmic		
15596244	PA1047		probable esterase	2.0	7.08E-02	Glucose	6.1	42335	5	Periplasmic	COG1680	Defense mechanisms
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	1.7	5.48E-02	Citronellsäure	6.8	24860	7	Cytoplasmic	COG0259	Coenzyme metabolism
15596250	PA1053		conserved hypothetical protein	24.3	6.67E-03	Glucose	10.1	15649	4	Outer Membrane Vesicle	COG3133	Cell envelope biogenesis, outer membrane
15596258	PA1061		conserved hypothetical protein	1.6	6.53E-02	Citronellsäure	6.6	39952	15	Cytoplasmic	COG0031	Amino acid transport and metabolism
15596259	PA1062		hypothetical protein	1.2	4.10E-01	Citronellsäure	6.5	19155	4	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane
15596261	PA1064		hypothetical protein	9.6	7.60E-03	Glucose	5.1	24172	2	Periplasmic	COG3650	Function unknown
15596263	PA1066		probable short-chain dehydrogenase	1.9	1.98E-02	Citronellsäure	7.6	23376	4	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15596266	PA1069		hypothetical protein	1.2	6.28E-01	Citronellsäure	4.3	86114	33	Cytoplasmic		
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	5.4	9.91E-06	Citronellsäure	5.5	39769	27	Periplasmic	COG0683	Amino acid transport and metabolism
15596286	PA1089		conserved hypothetical protein	2.2	2.03E-01	Glucose	5.0	22471	2	Cytoplasmic	COG0560	Amino acid transport and metabolism
15596287	PA1090		hypothetical protein	1.4	3.60E-01	Citronellsäure	5.3	24703	5	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	5.3	5.86E-03	Citronellsäure	5.2	187155	31	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane
15596289	PA1092	fliC	flagellin type B	1.7	1.48E-02	Citronellsäure	5.2	49242	12	Periplasmic	COG1344	Cell motility and secretion
15596291	PA1094	fliD	flagellar capping protein FliD	1.3	2.70E-01	Citronellsäure	7.1	49449	8	Periplasmic	COG1345	Cell motility and secretion
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.3	2.54E-02	Citronellsäure	5.0	55277	11	Cytoplasmic	COG2204	Signal transduction mechanisms
15596321	PA1124	dgt	deoxyguanosinetriphosphate triphosphohydrolase	1.2	9.36E-01	Citronellsäure	6.5	56741	2	Cytoplasmic	COG0232	Nucleotide transport and metabolism
15596324	PA1127		probable oxidoreductase	2.6	7.26E-03	Glucose	5.2	36474	5	Cytoplasmic	COG0667	Energy production and conversion
15596332	PA1135		conserved hypothetical protein	4.1	3.44E-05	Citronellsäure	6.4	31898	8	Cytoplasmic	COG0693	General function prediction only
15596336	PA1139		hypothetical protein	14.4	1.12E-04	Citronellsäure	5.1	29336	2	Periplasmic	COG2340	Function unknown
15596337	PA1140		conserved hypothetical protein	4.1	1.46E-02	Citronellsäure	6.3	31614	4	Cytoplasmic	COG3257	General function prediction only
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucle	3.3	2.03E-04	Glucose	4.5	47386	17	Periplasmic	COG0208	Nucleotide transport and metabolism
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	1.4	1.45E-01	Glucose	5.7	107105	58	Periplasmic	COG0209	Nucleotide transport and metabolism
15596354	PA1157		probable two-component response regulator	1.6	1.15E-01	Glucose	4.7	26373	4	Cytoplasmic	COG0745	Signal transduction mechanisms
15596358	PA1161	rrmA	rRNA methyltransferase	4.3	5.27E-02	Glucose	7.9	29644	5	Cytoplasmic	COG2226	Coenzyme metabolism
15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	1.1	6.72E-01	Citronellsäure	5.0	41077	9	Cytoplasmic	COG0624	Amino acid transport and metabolism
15596362	PA1165	pcpS	PcpS	1.8	7.65E-03	Citronellsäure	7.0	26715	4	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism
15596363	PA1166		hypothetical protein	36.0	8.11E-05	Citronellsäure	7.3	28156	8	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism
15596368	PA1171		probable transglycolase	2.8	2.99E-04	Citronellsäure	9.3	42682	8	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane
15596370	PA1173	napB	cytochrome c-type protein NapB precursor	25.5	2.35E-04	Citronellsäure	8.3	17918	4	Periplasmic	COG3043	Energy production and conversion
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	38.1	1.07E-04	Citronellsäure	8.6	92942	14	Periplasmic	COG0243	Energy production and conversion
15596375	PA1178	oprH	PhoP/Q and low Mg2+ inducible outer membrane protein H1 pr	2.7	2.68E-02	Citronellsäure	9.4	21574	8	Periplasmic		
15596376	PA1179	phoP	two-component response regulator PhoP	3.5	1.32E-04	Citronellsäure	5.2	25650	10	Cytoplasmic	COG0745	Signal transduction mechanisms
15596384	PA1187		probable acyl-CoA dehydrogenase	35.3	8.02E-05	Citronellsäure	6.5	42350	12	Cytoplasmic	COG1960	Lipid metabolism
15596385	PA1188		hypothetical protein	37.7	6.99E-04	Citronellsäure	6.0	42128	4	Cytoplasmic	COG1804	Energy production and conversion
15596389	PA1192		conserved hypothetical protein	2.2	8.26E-03	Glucose	6.5	31260	4	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning
15596390	PA1193		hypothetical protein	1.8	6.33E-02	Glucose	9.1	25292	6	Cytoplasmic	COG2818	DNA replication, recombination, and repair
15596397	PA1200		conserved hypothetical protein	1.7	2.77E-01	Citronellsäure	5.1	24597	6	Cytoplasmic	COG4122	General function prediction only
15596399	PA1202		probable hydrolase	2.7	6.06E-03	Citronellsäure	4.8	22471	12	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism

15596401	PA1204		conserved hypothetical protein	3.1	1.41E-03	Citronellsäure	6.5	20224	5	Cytoplasmic	COG0431	General function prediction only
15596403	PA1206		hypothetical protein	1.9	9.46E-02	Citronellsäure	4.4	17690	6	Cytoplasmic		
15596413	PA1216		hypothetical protein	1.1	6.00E-01	Glucose	6.1	28573	3	Cytoplasmic	COG4976	General function prediction only
15596422	PA1225		probable NAD(P)H dehydrogenase	9.5	1.41E-04	Glucose	7.0	22551	5	Cytoplasmic	COG2249	General function prediction only
15596431	PA1234		hypothetical protein	1.7	2.01E-01	Glucose	4.6	18460	2	Cytoplasmic		
15596457	PA1260		amino acid ABC transporter periplasmic binding protein	13.7	3.89E-04	Citronellsäure	5.2	29142	3	Periplasmic	COG0834	Amino acid transport and metabolism
15596469	PA1272	cobO	cob(I)alamin adenosyltransferase	5.1	1.18E-02	Glucose	8.0	22292	5	Cytoplasmic	COG2109	Coenzyme metabolism
15596473	PA1276	cobC	cobalamin biosynthetic protein CobC	2.9	4.36E-04	Glucose	8.0	36657	2	Cytoplasmic	COG0079	Amino acid transport and metabolism
15596475	PA1278	cobP	cobinamide kinase	2.6	2.12E-01	Glucose	5.4	18862	2	Cytoplasmic	COG2087	Coenzyme metabolism
15596476	PA1279	cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltr	1.4	1.56E-01	Citronellsäure	6.6	36531	5	Cytoplasmic	COG2038	Coenzyme metabolism
15596477	PA1280		hypothetical protein	16.6	2.19E-02	Citronellsäure	6.7	21591	2	Cytoplasmic	COG0406	General function prediction only
15596480	PA1283		probable transcriptional regulator	2.4	3.08E-01	Glucose	4.9	20307	1	Unknown	COG1309	Transcription
15596484	PA1287		probable glutathione peroxidase	3.5	5.94E-03	Citronellsäure	8.3	20217	11	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones
15596485	PA1288		probable outer membrane protein precursor	3.2	1.91E-02	Citronellsäure	6.0	45561	11	Periplasmic	COG2067	Lipid metabolism
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	1.7	1.66E-02	Citronellsäure	5.3	30597	10	Periplasmic	COG2897	Inorganic ion transport and metabolism
15596491	PA1294	rnd	ribonuclease D	6.8	4.51E-03	Glucose	4.8	43066	5	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis
15596501	PA1304		probable oligopeptidase	1.2	5.10E-01	Glucose	4.7	75881	18	Periplasmic	COG1770	Amino acid transport and metabolism
15596504	PA1307		conserved hypothetical protein	1.9	1.91E-02	Glucose	5.7	28544	5	Cytoplasmic	COG0121	General function prediction only
15596521	PA1324		hypothetical protein	4.2	4.94E-02	Citronellsäure	5.8	18303	2	Unknown		
15596523	PA1326	ilvA2	threonine dehydratase, biosynthetic	12.7	3.68E-03	Glucose	6.5	55903	2	Cytoplasmic	COG1171	Amino acid transport and metabolism
15596534	PA1337	ansB	glutaminase-asparaginase	2.3	4.13E-03	Citronellsäure	7.3	38644	15	Periplasmic	COG0252	Amino acid transport and metabolism
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	2.4	1.02E-03	Citronellsäure	6.2	59874	17	Periplasmic	COG0405	Amino acid transport and metabolism
15596539	PA1342		probable binding protein component of ABC transporter	3.4	1.81E-04	Citronellsäure	8.6	33054	43	Periplasmic	COG0834	Amino acid transport and metabolism
15596541	PA1344		probable short-chain dehydrogenase	3.3	5.23E-03	Citronellsäure	4.9	27397	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15596554	PA1357		conserved hypothetical protein	2.0	1.71E-02	Glucose	5.3	16789	2	Cytoplasmic	COG2606	Function unknown
15596567	PA1370		hypothetical protein	1.0	6.76E-01	Citronellsäure	6.3	69499	2	Cytoplasmic		
15596568	PA1371		hypothetical protein	73.6	4.40E-03	Citronellsäure	5.2	27419	2	Unknown	COG5619	Function unknown
15596569	PA1372		hypothetical protein	1.2	3.68E-01	Glucose	5.5	79820	20	Cytoplasmic	COG3972	General function prediction only
15596572	PA1375	pdxB	erythronate-4-phosphate dehydrogenase	1.1	4.85E-01	Glucose	5.5	41001	4	Cytoplasmic	COG0111	Amino acid transport and metabolism
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	3.2	1.04E-03	Citronellsäure	5.0	66760	16	Cytoplasmic	COG4579	Signal transduction mechanisms
15596574	PA1377		conserved hypothetical protein	3.4	5.22E-03	Glucose	7.9	20068	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis
15596599	PA1402		hypothetical protein	3.1	1.18E-01	Citronellsäure	4.7	23753	5	Cytoplasmic	COG4122	General function prediction only
15596627	PA1430	lasR	transcriptional regulator LasR	6.9	1.51E-04	Citronellsäure	6.5	26618	7	Cytoplasmic	COG2771	Transcription
15596637	PA1440		hypothetical protein	1.0	7.29E-01	Glucose	3.9	22382	4	Cytoplasmic	COG3318	General function prediction only
15596639	PA1442		conserved hypothetical protein	2.7	2.65E-01	Glucose	10.3	18760	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion
15596640	PA1443	fliM	flagellar motor switch protein FliM	1.4	1.58E-01	Citronellsäure	5.0	36282	5	Cytoplasmic	COG1868	Cell motility and secretion
15596641	PA1444	fliN	flagellar motor switch protein FliN	1.2	4.49E-01	Citronellsäure	4.0	16620	4	Cytoplasmic Membrane	COG1886	Cell motility and secretion
15596652	PA1455	fliA	sigma factor FliA	2.0	1.87E-03	Citronellsäure	5.9	27522	4	Cytoplasmic	COG1191	Transcription
15596654	PA1457	cheZ	chemotaxis protein CheZ	1.5	7.69E-03	Citronellsäure	4.6	29622	11	Cytoplasmic	COG3143	Cell motility and secretion
15596655	PA1458		probable two-component sensor	1.8	2.39E-02	Citronellsäure	4.3	79737	23	Cytoplasmic	COG0643	Cell motility and secretion
15596656	PA1459		probable methyltransferase	1.5	1.08E-01	Glucose	8.6	39004	9	Cytoplasmic	COG2201	Cell motility and secretion
15596659	PA1462		probable plasmid partitioning protein	1.5	7.60E-02	Glucose	10.1	28407	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning
15596661	PA1464		probable purine-binding chemotaxis protein	2.6	3.05E-02	Citronellsäure	4.1	17536	11	Cytoplasmic	COG0835	Cell motility and secretion
15596667	PA1470		probable short-chain dehydrogenase	2.7	4.93E-03	Citronellsäure	4.9	25365	8	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15596669	PA1472		conserved hypothetical protein	1.7	1.07E-01	Citronellsäure	5.8	21138	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	3.5	5.23E-03	Citronellsäure	8.6	36485	17	Periplasmic	COG1613	Inorganic ion transport and metabolism
15596711	PA1514		ureidoglycolate hydrolaseYbbT	6.2	4.35E-02	Citronellsäure	5.6	18983	2	Unknown	COG3194	Nucleotide transport and metabolism
15596713	PA1516		hypothetical protein	1.4	2.48E-01	Citronellsäure	4.8	18896	5	Cytoplasmic	COG3195	Function unknown
15596724	PA1527		conserved hypothetical protein	2.7	2.60E-02	Citronellsäure	4.8	131580	14	Cytoplasmic	COG1196	Cell division and chromosome partitioning
15596725	PA1528	zipA	cell division protein ZipA	172.4	3.70E-02	Glucose	5.7	32236	2	Outer Membrane Vesicle	COG3115	Cell division and chromosome partitioning
15596726	PA1529	lig	DNA ligase	1.4	1.65E-01	Glucose	5.1	86767	24	Cytoplasmic	COG0272	DNA replication, recombination, and repair
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	1.1	4.72E-01	Glucose	4.4	73309	16	Cytoplasmic	COG2812	DNA replication, recombination, and repair
15596731	PA1534	recR	recombination protein RecR	3.4	2.73E-02	Glucose	6.0	21173	5	Cytoplasmic	COG0353	DNA replication, recombination, and repair
15596732	PA1535		citronellyl-CoA dehydrogenase	39.4	2.37E-06	Citronellsäure	5.6	42041	18	Cytoplasmic	COG1960	Lipid metabolism
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.6	2.01E-02	Glucose	4.6	19804	9	Cytoplasmic	COG0503	Nucleotide transport and metabolism
15596741	PA1544	anr	transcriptional regulator Anr	1.2	1.94E-01	Glucose	5.2	27129	8	Cytoplasmic	COG0664	Signal transduction mechanisms
15596749	PA1552	ccoP1	Cytochrome c oxidase, cbb3-type, CcoP subunit	20.1	6.27E-03	Glucose	6.0	34644	3	Outer Membrane Vesicle	COG2010	Energy production and conversion
15596750	PA1553	ccoO1	Cytochrome c oxidase, cbb3-type, CcoO subunit	7.6	7.84E-03	Glucose	8.2	22758	4	Outer Membrane Vesicle	COG2993	Energy production and conversion
15596759	PA1562	acnA	aconitate hydratase 1	5.4	4.44E-04	Citronellsäure	5.4	99147	47	Cytoplasmic	COG1048	Energy production and conversion
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	1.3	2.38E-01	Glucose	5.2	30777	8	Cytoplasmic	COG2084	Lipid metabolism
15596776	PA1579		hypothetical protein	3.0	1.77E-02	Citronellsäure	8.2	22110	12	Periplasmic		
15596777	PA1580	gltA	citrate synthase	2.2	6.69E-04	Citronellsäure	7.0	47695	34	Periplasmic	COG0372	Energy production and conversion
15596778	PA1581	sdhC	succinate dehydrogenase (C subunit)	22.0	5.99E-03	Glucose	10.4	13738	3	Outer Membrane Vesicle	COG2009	Energy production and conversion
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	1.2	1.83E-01	Glucose	6.5	63532	24	Periplasmic	COG1053	Energy production and conversion
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	2.5	2.53E-03	Glucose	6.9	26155	9	Outer Membrane Vesicle	COG0479	Energy production and conversion
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	6.6	6.27E-03	Glucose	6.5	105877	49	Outer Membrane Vesicle	COG0567	Energy production and conversion
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	6.7	9.97E-03	Glucose	5.2	42887	24	Periplasmic	COG0508	Energy production and conversion
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.0	9.77E-01	Glucose	7.0	50165	25	Periplasmic	COG1249	Energy production and conversion
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	1.4	1.59E-02	Citronellsäure	6.1	41542	30	Periplasmic	COG0045	Energy production and conversion
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	1.1	7.33E-01	Glucose	6.0	30266	28	Periplasmic	COG0074	Energy production and conversion
15596793	PA1596	htpG	heat shock protein HtpG	1.1	4.33E-01	Citronellsäure	4.9	71667	55	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones
15596794	PA1597		hypothetical protein	1.4	4.00E-02	Citronellsäure	5.9	25791	10	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism
15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.1	3.77E-01	Glucose	5.3	42806	23	Periplasmic	COG0304	Lipid metabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	2.5	1.96E-01	Glucose	6.9	18747	10	Cytoplasmic	COG0764	Lipid metabolism
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.2	2.83E-01	Glucose	6.2	36773	15	Cytoplasmic	COG0240	Energy production and conversion
15596813	PA1616		conserved hypothetical protein	462.8	3.67E-02	Glucose	6.4	16715	4	Unknown	COG2062	Signal transduction mechanisms
15596814	PA1617		probable AMP-binding enzyme	23.6	1.41E-04	Citronellsäure	7.2	61370	21	Cytoplasmic	COG1022	Lipid metabolism
15596815	PA1618		conserved hypothetical protein	177.9	7.09E-04	Glucose	7.0	15595	7	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism
15596819	PA1622		probable hydrolase	10.7	8.47E-05	Citronellsäure	7.1	31290	7	Cytoplasmic	COG0596	General function prediction only
15596820	PA1623		conserved hypothetical protein	1.5	4.84E-02	Citronellsäure	6.1	24924	11	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15596836	PA1639		hypothetical protein	1.5	2.58E-01	Glucose	5.4	22457	7	Periplasmic		
15596839	PA1642	selD	selenophosphate synthetase	1.3	1.22E-01	Citronellsäure	4.7	36354	10	Cytoplasmic	COG0709	Amino acid transport and metabolism
15596841	PA1644		conserved hypothetical protein	1.1	7.12E-01	Citronellsäure	5.5	21838	7	Unknown	COG1853	General function prediction only

15596851	PA1654		probable aminotransferase	1.5	2.08E-01	Glucose	5.3	43311	5	Cytoplasmic	COG1167	Transcription
15596852	PA1655		probable glutathione S-transferase	1.3	4.56E-01	Glucose	5.3	22738	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15596854	PA1657		conserved hypothetical protein	3.4	2.07E-02	Citronellsäure	4.5	18165	3	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport
15596855	PA1658		conserved hypothetical protein	1.4	3.46E-01	Citronellsäure	5.1	55560	2	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.2	5.77E-01	Glucose	7.6	20236	9	Outer Membrane Vesicle	COG0302	Coenzyme metabolism
15596874	PA1677		conserved hypothetical protein	1.1	4.99E-01	Glucose	6.5	21034	11	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15596875	PA1678		probable DNA methylase	2.1	2.17E-01	Citronellsäure	4.4	34229	2	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis
15596878	PA1681	aroC	chorismate synthase	2.2	2.53E-02	Citronellsäure	6.6	38987	8	Cytoplasmic	COG0082	Amino acid transport and metabolism
15596880	PA1683		probable sugar aldolase	1.8	5.03E-02	Citronellsäure	6.5	22868	6	Cytoplasmic	COG0235	Carbohydrate transport and metabolism
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	2.0	8.15E-02	Citronellsäure	5.0	20552	7	Cytoplasmic	COG1791	Function unknown
15596883	PA1686	alkA	DNA-3-methyladenine glycosidase II	1.5	1.45E-01	Citronellsäure	6.9	32211	2	Unknown	COG0122	DNA replication, recombination, and repair
15596884	PA1687	speE	spermidine synthase	1.0	9.81E-01	Citronellsäure	4.9	32238	8	Periplasmic	COG0421	Amino acid transport and metabolism
15596923	PA1726	bglX	periplasmic beta-glucosidase	2.4	1.76E-01	Glucose	7.1	83003	7	Periplasmic	COG1472	Carbohydrate transport and metabolism
15596930	PA1733		conserved hypothetical protein	13.3	1.52E-03	Citronellsäure	5.3	26467	4	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones
15596933	PA1736		probable acyl-CoA thiolase	32.9	5.47E-06	Citronellsäure	5.3	42102	24	Cytoplasmic	COG0183	Lipid metabolism
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	40.6	5.71E-06	Citronellsäure	6.7	76666	41	Cytoplasmic	COG1250	Lipid metabolism
15596939	PA1742	pauD2	Glutamine amidotransferase class I	1.5	5.05E-02	Citronellsäure	5.0	27361	7	Cytoplasmic	COG0518	Nucleotide transport and metabolism
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	5.2	5.08E-03	Citronellsäure	7.8	24412	14	Cytoplasmic	COG1024	Lipid metabolism
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.0	9.21E-01	Citronellsäure	6.5	39132	13	Cytoplasmic	COG0722	Amino acid transport and metabolism
15596949	PA1752		hypothetical protein	1.1	2.85E-01	Glucose	6.7	34141	7	Cytoplasmic	COG1893	Coenzyme metabolism
15596950	PA1753		conserved hypothetical protein	9.7	3.82E-03	Citronellsäure	4.7	18372	4	Cytoplasmic	COG0589	Signal transduction mechanisms
15596951	PA1754	cysB	transcriptional regulator CysB	2.7	7.40E-02	Citronellsäure	7.0	36110	6	Periplasmic	COG0583	Transcription
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	1.2	1.51E-01	Glucose	6.4	30215	8	Cytoplasmic	COG0175	Amino acid transport and metabolism
15596954	PA1757	thrH	homoserine kinase	1.3	3.32E-01	Glucose	5.0	23501	10	Cytoplasmic	COG0560	Amino acid transport and metabolism
15596956	PA1759		probable transcriptional regulator	5.1	8.46E-03	Citronellsäure	6.3	101111	13	Unknown	COG2909	Transcription
15596957	PA1760		probable transcriptional regulator	16.9	6.69E-03	Citronellsäure	6.8	101628	9	Cytoplasmic	COG2909	Transcription
15596965	PA1768		hypothetical protein	6.4	3.97E-05	Citronellsäure	9.6	19720	7	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones
15596966	PA1769		conserved hypothetical protein	1.2	2.28E-01	Citronellsäure	6.1	31074	12	Cytoplasmic	COG1806	Function unknown
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.5	1.40E-01	Glucose	4.8	85798	73	Cytoplasmic	COG0574	Carbohydrate transport and metabolism
15596969	PA1772		probable methyltransferase	4.0	1.18E-04	Citronellsäure	4.6	17404	7	Cytoplasmic	COG0684	Coenzyme metabolism
15596972	PA1775	cmpX	conserved cytoplasmic membrane protein, CmpX protein	11.2	7.88E-03	Glucose	8.8	29019	4	Outer Membrane Vesicle		
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precurs	2.4	2.75E-02	Glucose	4.8	37639	14	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane
15596984	PA1787	acnB	aconitate hydratase 2	1.9	4.92E-02	Citronellsäure	5.0	93595	82	Periplasmic	COG1049	Energy production and conversion
15596987	PA1790		hypothetical protein	2.2	5.26E-02	Glucose	6.7	23312	5	Cytoplasmic	COG4445	Nucleotide transport and metabolism
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	1.2	2.59E-01	Citronellsäure	6.2	18126	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.8	2.96E-02	Glucose	5.6	62912	35	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	1.0	8.72E-01	Glucose	5.4	51245	21	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrola	1.0	7.72E-01	Glucose	5.8	30549	9	Periplasmic	COG0190	Coenzyme metabolism
15596997	PA1800	tig	trigger factor	1.3	8.29E-03	Citronellsäure	4.5	48582	26	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones
15596998	PA1801	clpP	ClpP	2.0	2.84E-02	Glucose	6.4	23502	16	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones
15596999	PA1802	clpX	ClpX	1.9	1.05E-01	Glucose	4.8	46991	29	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones
15597000	PA1803	lon	Lon protease	2.9	2.17E-02	Glucose	6.0	88647	33	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones
15597001	PA1804	hupB	DNA-binding protein HU	5.0	8.34E-03	Glucose	10.8	9054	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	2.2	3.97E-02	Glucose	4.7	68741	3	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	2.0	1.95E-04	Citronellsäure	5.7	28006	10	Cytoplasmic Membrane	COG0623	acyl-carrier-protein
15597007	PA1810		probable binding protein component of ABC transporter	1.3	4.25E-02	Citronellsäure	6.5	70473	15	Periplasmic	COG4166	Amino acid transport and metabolism
15597010	PA1813		probable hydroxyacylglutathione hydrolase	1.0	8.62E-01	Citronellsäure	6.3	28865	2	Cytoplasmic	COG0491	General function prediction only
15597012	PA1815	rnhA	ribonuclease H	1.0	9.64E-01	Citronellsäure	8.7	16697	5	Unknown	COG0328	DNA replication, recombination, and repair
15597013	PA1816	dnaQ	DNA polymerase III, epsilon chain	2.7	1.39E-03	Glucose	5.0	26814	7	Cytoplasmic	COG0847	DNA replication, recombination, and repair
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, L	1.4	1.94E-01	Citronellsäure	6.1	82757	15	Cytoplasmic	COG1982	Amino acid transport and metabolism
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	6.4	9.35E-04	Citronellsäure	5.4	29957	6	Cytoplasmic	COG1024	Lipid metabolism
15597019	PA1822	fimL	hypothetical protein	1.9	8.48E-02	Glucose	4.9	60868	2	Cytoplasmic		
15597020	PA1823		conserved hypothetical protein	1.8	2.90E-01	Glucose	4.9	31356	4	Cytoplasmic	COG2816	DNA replication, recombination, and repair
15597025	PA1828		probable short-chain dehydrogenase	1.6	2.96E-02	Citronellsäure	7.4	26919	14	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15597026	PA1829		hypothetical protein	5.7	1.05E-03	Citronellsäure	5.9	40833	8	Cytoplasmic	COG3173	General function prediction only
15597028	PA1831		hypothetical protein	5.0	2.92E-05	Citronellsäure	6.3	26378	7	Cytoplasmic	COG0406	General function prediction only
15597030	PA1833		probable oxidoreductase	2.7	1.28E-03	Citronellsäure	5.2	34552	14	Cytoplasmic	COG0604	Energy production and conversion
15597034	PA1837		hypothetical protein	3.5	3.65E-02	Citronellsäure	4.7	18765	10	Cytoplasmic	COG3749	Function unknown
15597035	PA1838	cysI	sulfite reductase	1.1	3.65E-01	Citronellsäure	5.9	62132	27	Periplasmic	COG0155	Inorganic ion transport and metabolism
15597038	PA1841		hypothetical protein	1.6	9.75E-02	Glucose	5.1	18654	5	Cytoplasmic	COG3760	Function unknown
15597040	PA1843	metH	methionine synthase	2.5	7.02E-03	Citronellsäure	4.6	135062	55	Periplasmic	COG1410	Amino acid transport and metabolism
15597042	PA1845		hypothetical protein	1.0	7.43E-01	Glucose	4.6	18757	2	Unknown		
15597043	PA1846	cti	cis/trans isomerase	2.0	4.58E-03	Glucose	6.0	86517	9	Periplasmic		
15597044	PA1847	nfuA	NfuA	1.6	2.48E-01	Glucose	4.2	21136	11	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	3.2	1.32E-02	Citronellsäure	6.8	26377	6	Periplasmic	COG0725	Inorganic ion transport and metabolism
15597071	PA1874		hypothetical protein	38.3	2.94E-03	Citronellsäure	3.1	238414	3	Unknown		
15597077	PA1880		probable oxidoreductase	5.0	4.46E-04	Citronellsäure	7.4	77656	11	Cytoplasmic Membrane	COG1529	Energy production and conversion
15597084	PA1887		hypothetical protein	274.7	4.15E-02	Citronellsäure	8.0	24376	2	Unknown		
15597087	PA1890		probable glutathione S-transferase	1.4	8.88E-02	Glucose	7.0	23440	11	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15597089	PA1892		hypothetical protein	37.1	2.43E-03	Glucose	7.1	27699	2	Unknown		
15597091	PA1894		hypothetical protein	2.4	2.36E-02	Glucose	5.3	26179	11	Unknown		
15597110	PA1914		conserved hypothetical protein	142.6	1.50E-05	Citronellsäure	6.9	46125	7	Extracellular		
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyl	2.9	2.06E-02	Citronellsäure	5.7	86211	11	Cytoplasmic	COG0620	Amino acid transport and metabolism
15597126	PA1930		probable chemotaxis transducer	11.3	2.14E-02	Citronellsäure	6.5	47801	5	Cytoplasmic Membrane	COG0840	Cell motility and secretion
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	15.7	2.77E-04	Citronellsäure	8.4	33860	8	Periplasmic	COG1879	Carbohydrate transport and metabolism
15597145	PA1949	rbsR	ribose operon repressor RbsR	2.7	2.71E-03	Citronellsäure	7.2	36446	4	Cytoplasmic	COG1609	Transcription
15597146	PA1950	rbsK	ribokinase	2.1	1.50E-02	Citronellsäure	4.9	31846	4	Cytoplasmic	COG0524	Carbohydrate transport and metabolism
15597160	PA1964		probable ATP-binding component of ABC transporter	2.3	1.25E-01	Glucose	4.8	57917	12	Cytoplasmic	COG0488	General function prediction only
15597170	PA1974		hypothetical protein	175.1	1.18E-04	Citronellsäure	4.3	43218	3	Outer Membrane		
15597171	PA1975		hypothetical protein	71.8	2.91E-03	Citronellsäure	6.0	42043	2	Cytoplasmic	COG3287	Function unknown
15597177	PA1981		hypothetical protein	20.7	3.48E-04	Citronellsäure	5.8	22869	7	Extracellular	COG1357	Function unknown
15597178	PA1982	exaA	quinoprotein ethanol dehydrogenase	45.5	7.31E-06	Citronellsäure	7.1	68123	44	Periplasmic	COG4993	Carbohydrate transport and metabolism
15597180	PA1984	exaC	NAD+ dependent aldehyde dehydrogenase ExaC	26.2	2.64E-06	Citronellsäure	5.4	54892	31	Periplasmic	COG1012	Energy production and conversion

15597182	PA1986	pqqB	pyrroloquinoline quinone biosynthesis protein B	14.0	5.53E-03	Citronellsäure	5.5	33018	6	Cytoplasmic	COG1235 General function prediction only
15597183	PA1987	pqqC	pyrroloquinoline quinone biosynthesis protein C	22.2	2.91E-06	Citronellsäure	7.4	29449	8	Cytoplasmic	COG5424 Coenzyme metabolism
15597190	PA1994		hypothetical protein	1.4	3.76E-01	Glucose	4.7	21561	5	Cytoplasmic	COG3554 Function unknown
15597193	PA1997		probable AMP-binding enzyme	8.4	1.05E-04	Citronellsäure	6.5	71929	9	Cytoplasmic	COG0365 Lipid metabolism
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	31.5	1.01E-05	Citronellsäure	5.0	25244	5	Cytoplasmic	COG1788 Lipid metabolism
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	13.4	1.93E-03	Citronellsäure	4.6	23187	18	Cytoplasmic	COG2057 Lipid metabolism
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	21.6	4.15E-05	Citronellsäure	6.4	40405	28	Cytoplasmic	COG0183 Lipid metabolism
15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase	9.6	3.47E-04	Citronellsäure	5.6	26727	8	Cytoplasmic	COG1028 Secondary metabolites biosynthesis, transport, and catabolism
15597203	PA2007	maiA	maleylacetoacetate isomerase	85.9	4.36E-03	Citronellsäure	6.9	23685	5	Cytoplasmic	COG0625 Posttranslational modification, protein turnover, chaperones
15597204	PA2008	fahA	fumarylacetoacetase	8.4	6.58E-04	Citronellsäure	6.0	46341	4	Cytoplasmic	COG0179 Secondary metabolites biosynthesis, transport, and catabolism
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase	12.7	1.02E-05	Citronellsäure	6.0	31837	11	Cytoplasmic	COG0119 Amino acid transport and metabolism
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containi	44.8	1.78E-04	Citronellsäure	5.6	71282	26	Cytoplasmic	COG4770 Lipid metabolism
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase	34.5	2.34E-06	Citronellsäure	5.2	28947	13	Cytoplasmic	COG1024 Lipid metabolism
15597210	PA2014	liuB	methylcrotonyl-CoA carboxylase, beta-subunit	60.1	2.35E-06	Citronellsäure	6.7	57433	26	Cytoplasmic	COG4799 Lipid metabolism
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase	25.9	6.65E-07	Citronellsäure	5.5	42209	33	Cytoplasmic	COG1960 Lipid metabolism
15597216	PA2020		probable transcriptional regulator	1.4	2.37E-01	Citronellsäure	7.1	23695	3	Cytoplasmic	COG1309 Transcription
15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase	1.6	8.74E-02	Citronellsäure	5.1	31236	21	Periplasmic	COG1210 Cell envelope biogenesis, outer membrane
15597221	PA2025	gor	glutathione reductase	3.0	3.82E-03	Citronellsäure	6.3	49237	9	Cytoplasmic	COG1249 Energy production and conversion
15597230	PA2034		hypothetical protein	4.5	1.25E-01	Glucose	6.3	24525	4	Cytoplasmic	COG2242 Coenzyme metabolism
15597240	PA2044		hypothetical protein	2.3	9.14E-03	Glucose	6.1	70083	14	Periplasmic	COG1305 Amino acid transport and metabolism
15597267	PA2071	fusA2	elongation factor G	3.4	2.46E-04	Citronellsäure	4.9	77574	20	Cytoplasmic	COG0480 Translation, ribosomal structure and biogenesis
15597272	PA2076		probable transcriptional regulator	3.8	2.22E-02	Glucose	6.0	32458	3	Cytoplasmic	COG0583 Transcription
15597276	PA2080	kynU	kynureninase KynU	1.7	1.27E-03	Citronellsäure	5.3	46294	11	Cytoplasmic	COG3844 Amino acid transport and metabolism
15597277	PA2081	kynB	kynurenine formamidase, KynB	4.9	4.87E-02	Citronellsäure	5.2	23152	8	Cytoplasmic	COG1878 Amino acid transport and metabolism
15597315	PA2119		alcohol dehydrogenase (Zn-dependent)	29.2	3.22E-04	Citronellsäure	5.4	38561	3	Cytoplasmic	COG1063 Amino acid transport and metabolism
15597372	PA2176		hypothetical protein	45.7	1.36E-03	Citronellsäure	4.9	20943	3	Unknown	COG2910 General function prediction only
15597380	PA2184		conserved hypothetical protein	11.1	1.81E-01	Citronellsäure	4.7	18990	2	Cytoplasmic	COG3685 Function unknown
15597393	PA2197		conserved hypothetical protein	1.6	8.11E-03	Citronellsäure	6.3	37135	13	Cytoplasmic	COG2130 General function prediction only
15597394	PA2198		hypothetical protein	9.3	3.35E-02	Glucose	5.2	12944	3	Cytoplasmic	COG1359 Function unknown
15597395	PA2199		probable dehydrogenase	1.1	8.32E-01	Citronellsäure	5.4	30886	7	Cytoplasmic	COG2084 Lipid metabolism
15597400	PA2204		probable binding protein component of ABC transporter	1.1	2.38E-01	Citronellsäure	9.7	29309	19	Periplasmic	COG0834 Amino acid transport and metabolism
15597418	PA2222		hypothetical protein	7.0	1.23E-04	Citronellsäure	5.0	23441	4	Unknown	
15597425	PA2229		conserved hypothetical protein	2.0	2.56E-02	Glucose	6.5	26560	4	Cytoplasmic	COG2258 Function unknown
15597428	PA2232	pslB	PslB	1.1	3.91E-01	Citronellsäure	6.0	53515	15	Periplasmic	COG0836 Cell envelope biogenesis, outer membrane
15597449	PA2253	ansA	L-asparaginase I	2.1	5.70E-02	Glucose	5.3	34755	3	Cytoplasmic	COG0252 Amino acid transport and metabolism
15597455	PA2259	ptxS	transcriptional regulator PtxS	11.6	2.31E-02	Glucose	6.9	37359	4	Cytoplasmic	COG1609 Transcription
15597456	PA2260		hypothetical protein	16.7	2.37E-05	Glucose	6.0	28980	16	Cytoplasmic	
15597457	PA2261		probable 2-ketogluconate kinase	25.8	2.15E-04	Glucose	5.7	34041	10	Cytoplasmic	COG0524 Carbohydrate transport and metabolism
15597459	PA2263		probable 2-hydroxyacid dehydrogenase	28.1	9.72E-07	Glucose	8.7	35615	22	Cytoplasmic	COG1052 Energy production and conversion
15597460	PA2264		conserved hypothetical protein	19.3	5.84E-04	Glucose	5.4	26359	3	Outer Membrane Vesicle	
15597461	PA2265		gluconate dehydrogenase	27.1	7.14E-05	Glucose	7.3	64716	14	Periplasmic	COG2303 Amino acid transport and metabolism
15597467	PA2271		probable acetyltransferase	2.0	1.46E-01	Citronellsäure	6.2	19165	3	Cytoplasmic	
15597497	PA2301		hypothetical protein	1.8	6.57E-02	Citronellsäure	6.5	19330	7	Cytoplasmic	COG2606 Function unknown
15597498	PA2302	ambE	AmbE	2.6	8.59E-02	Citronellsäure	4.8	229041	93	Cytoplasmic	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
15597499	PA2303	ambD	AmbD	1.1	3.03E-01	Glucose	6.6	38657	4	Cytoplasmic	COG2175 Secondary metabolites biosynthesis, transport, and catabolism
15597501	PA2305	ambB	AmbB	1.5	1.95E-01	Citronellsäure	6.3	134446	30	Unknown	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
15597516	PA2320	gntR	transcriptional regulator GntR	8.0	8.57E-03	Glucose	8.2	37147	4	Cytoplasmic	COG1609 Transcription
15597517	PA2321		gluconokinase	92.1	7.10E-05	Glucose	7.1	18456	12	Unknown	COG3265 Carbohydrate transport and metabolism
15597519	PA2323		probable glyceraldehyde-3-phosphate dehydrogenase	13.8	4.07E-04	Glucose	6.4	59960	41	Cytoplasmic	COG1012 Energy production and conversion
15597527	PA2331		hypothetical protein	7.4	1.27E-03	Glucose	5.0	19904	4	Unknown	COG2128 Function unknown
15597561	PA2365		conserved hypothetical protein	11.9	1.06E-04	Citronellsäure	4.4	20177	6	Cytoplasmic	COG3516 Intracellular trafficking, secretion, and vesicular transport
15597562	PA2366		uricase PuuD	19.0	5.51E-05	Citronellsäure	5.7	55042	13	Cytoplasmic Membrane	COG3517 Intracellular trafficking, secretion, and vesicular transport
15597563	PA2367		hypothetical protein	29.4	5.34E-05	Citronellsäure	4.6	17636	12	Extracellular	COG3157 Intracellular trafficking, secretion, and vesicular transport
15597567	PA2371		probable ClpA/B-type protease	219.6	1.08E-04	Citronellsäure	5.1	92424	6	Cytoplasmic	COG0542 Posttranslational modification, protein turnover, chaperones
15597568	PA2372		hypothetical protein	202.7	3.65E-03	Citronellsäure	8.4	21241	3	Unknown	
15597574	PA2378		probable aldehyde dehydrogenase	1.1	3.50E-01	Glucose	8.4	83665	21	Cytoplasmic Membrane	COG1529 Energy production and conversion
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ	1.1	4.04E-01	Glucose	7.1	84039	25	Periplasmic	COG2366 General function prediction only
15597582	PA2386	pvdA	L-ornithine N5-oxygenase	11.8	5.80E-04	Glucose	6.5	49478	22	Cytoplasmic	COG3486 Secondary metabolites biosynthesis, transport, and catabolism
15597590	PA2394	pvdN	PvdN	1.0	5.60E-01	Glucose	7.3	47981	10	Unknown	COG0520 Posttranslational modification, protein turnover, chaperones
15597591	PA2395	pvdO	PvdO	1.1	5.45E-01	Citronellsäure	5.4	31070	10	Periplasmic	COG1262 Function unknown
15597592	PA2396	pvdF	pyoverdine synthetase F	1.0	7.11E-01	Glucose	5.0	31039	19	Cytoplasmic	COG0299 Nucleotide transport and metabolism
15597594	PA2398	fpvA	ferripyoverdine receptor	2.4	9.40E-02	Glucose	5.3	91167	27	Periplasmic	COG4773 Inorganic ion transport and metabolism
15597595	PA2399	pvdD	pyoverdine synthetase D	1.0	7.72E-01	Glucose	5.0	273645	62	Cytoplasmic	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
110645305	PA2400	pvdJ	PvdJ	1.1	9.50E-01	Glucose	5.1	240213	10	Unknown	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
15597598	PA2402		probable non-ribosomal peptide synthetase	1.9	4.74E-01	Glucose	5.1	569179	218	Unknown	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
15597603	PA2407		probable adhesion protein	1.2	1.65E-01	Citronellsäure	9.6	34309	5	Periplasmic	COG0803 Inorganic ion transport and metabolism
15597606	PA2410		hypothetical protein	1.4	3.11E-01	Glucose	5.0	31732	6	Unknown	COG0803 Inorganic ion transport and metabolism
15597607	PA2411		probable thioesterase	5.5	1.92E-04	Glucose	5.4	27846	17	Cytoplasmic	COG3208 Secondary metabolites biosynthesis, transport, and catabolism
15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, Pvc	8.5	1.82E-05	Glucose	6.5	50215	22	Cytoplasmic	COG0160 Amino acid transport and metabolism
15597620	PA2424	pvdL	PvdL	3.7	1.12E-01	Glucose	5.1	480292	216	Unknown	COG1020 Secondary metabolites biosynthesis, transport, and catabolism
15597638	PA2442	gcvT2	glycine cleavage system protein T2	1.6	3.40E-03	Citronellsäure	6.4	39882	17	Periplasmic	COG0404 Amino acid transport and metabolism
15597640	PA2444	glyA2	serine hydroxymethyltransferase	1.0	8.46E-01	Glucose	6.5	44974	7	Periplasmic	COG0112 Amino acid transport and metabolism
15597641	PA2445	gcvP2	glycine cleavage system protein P2	3.2	2.54E-03	Glucose	6.0	103918	48	Periplasmic	COG1003 Amino acid transport and metabolism
15597646	PA2450		hypothetical protein	16.3	6.03E-03	Citronellsäure	6.4	34331	2	Periplasmic	
15597651	PA2455		hypothetical protein	45.4	1.07E-01	Citronellsäure	5.6	20332	2	Cytoplasmic	COG3153 General function prediction only
15597655	PA2459		hypothetical protein	2.1	1.77E-02	Glucose	5.6	23801	4	Cytoplasmic	
15597658	PA2462		hypothetical protein	1.2	4.88E-01	Citronellsäure	5.1	573168	29	Outer Membrane Vesicle	COG3210 Intracellular trafficking and secretion
15597660	PA2464		hypothetical protein	4.1	4.31E-02	Glucose	4.6	17626	5	Periplasmic	
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG	1.2	4.23E-01	Glucose	7.1	28053	4	Periplasmic	COG1651 Posttranslational modification, protein turnover, chaperones
15597679	PA2483		conserved hypothetical protein	4.2	1.19E-03	Citronellsäure	6.2	36102	6	Cytoplasmic	COG2141 Energy production and conversion
15597687	PA2491		probable oxidoreductase	1.7	1.14E-01	Citronellsäure	5.3	36832	15	Cytoplasmic	COG0604 Energy production and conversion
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux mem	3.6	5.74E-05	Glucose	8.8	45031	7	Cytoplasmic Membrane	COG0845 Cell envelope biogenesis, outer membrane
15597690	PA2494	mexF	Resistance-Nodulation-Cell Division (RND) multidrug efflux trans	6.3	9.77E-03	Glucose	5.4	115509	7	Cytoplasmic Membrane	COG0841 Defense mechanisms

15597691	PA2495	oprN	Multidrug efflux outer membrane protein OprN precursor	5.7	3.94E-02	Glucose	5.1	51165	3	Outer Membrane	COG1538	Cell envelope biogenesis, outer membrane
15597692	PA2496		hypothetical protein	5.4	4.24E-04	Glucose	6.6	19483	2	Cytoplasmic	COG2318	Function unknown
15597699	PA2503		hypothetical protein	1.6	4.03E-02	Citronellsäure	4.6	45895	2	Cytoplasmic		
15597700	PA2504		hypothetical protein	13.8	1.03E-03	Citronellsäure	4.3	22822	3	Cytoplasmic	COG4859	Function unknown
15597703	PA2507	catA	catechol 1,2-dioxygenase	79.7	8.86E-05	Citronellsäure	5.1	34160	5	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism
15597725	PA2529		hypothetical protein	2.9	6.55E-02	Glucose	5.6	52681	6	Cytoplasmic	COG0312	General function prediction only
15597726	PA2530		hypothetical protein	1.7	3.94E-02	Citronellsäure	5.7	48959	2	Unknown	COG0312	General function prediction only
15597728	PA2532	tpx	thiol peroxidase	5.6	2.97E-03	Citronellsäure	4.9	17234	15	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones
15597741	PA2545	xthA	exodeoxyribonuclease III	2.2	1.22E-02	Glucose	6.4	31003	8	Cytoplasmic	COG0708	DNA replication, recombination, and repair
15597747	PA2551		probable transcriptional regulator	5.1	6.75E-03	Citronellsäure	9.9	35144	3	Cytoplasmic	COG0583	Transcription
15597748	PA2552		probable acyl-CoA dehydrogenase	13.7	1.11E-04	Citronellsäure	5.6	40908	4	Cytoplasmic	COG1960	Lipid metabolism
15597749	PA2553		probable acyl-CoA thiolase	11.0	1.13E-06	Citronellsäure	5.9	41400	12	Cytoplasmic	COG0183	Lipid metabolism
15597750	PA2554		probable short-chain dehydrogenase	15.4	1.51E-05	Citronellsäure	6.6	26394	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15597751	PA2555		probable AMP-binding enzyme	807.7	2.22E-02	Citronellsäure	6.1	60159	2	Cytoplasmic	COG0365	Lipid metabolism
15597753	PA2557		probable AMP-binding enzyme	61.7	9.90E-08	Citronellsäure	6.1	62629	25	Cytoplasmic	COG0318	Lipid metabolism
15597771	PA2575		hypothetical protein	1.5	2.15E-01	Glucose	6.4	22222	11	Unknown	COG3560	General function prediction only
15597775	PA2579	kynA	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing) KynA	14.7	3.61E-04	Glucose	6.5	32931	2	Cytoplasmic	COG3483	Amino acid transport and metabolism
15597778	PA2582		hypothetical protein	1.1	8.12E-01	Glucose	10.5	19446	6	Unknown	COG3109	Signal transduction mechanisms
15597782	PA2586	gacA	response regulator GacA	2.3	1.41E-02	Citronellsäure	6.1	23576	3	Cytoplasmic	COG2197	Signal transduction mechanisms
15597788	PA2592		probable periplasmic spermidine/putrescine-binding protein	1.7	4.00E-02	Citronellsäure	6.7	40725	6	Periplasmic	COG0687	Amino acid transport and metabolism
15597790	PA2594		conserved hypothetical protein	1.8	1.14E-01	Citronellsäure	9.2	34686	3	Periplasmic	COG0715	Inorganic ion transport and metabolism
15597799	PA2603		probable thiosulfate sulfurtransferase	1.2	3.33E-01	Glucose	5.0	57285	3	Cytoplasmic	COG2897	Inorganic ion transport and metabolism
15597807	PA2611	cysG	siroheme synthase	1.2	5.22E-01	Glucose	6.3	50370	9	Cytoplasmic	COG0007	Coenzyme metabolism
15597808	PA2612	serS	seryl-tRNA synthetase	1.2	7.59E-02	Glucose	5.3	47231	16	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis
15597809	PA2613		conserved hypothetical protein	2.7	2.18E-01	Glucose	6.3	49047	3	Cytoplasmic	COG2256	DNA replication, recombination, and repair
15597810	PA2614	lolA	periplasmic chaperone LolA	1.8	1.04E-01	Citronellsäure	5.8	23072	11	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane
15597812	PA2616	trxB1	thioredoxin reductase 1	1.2	3.77E-01	Citronellsäure	5.2	33818	10	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones
15597815	PA2619	infA	initiation factor	12.1	4.67E-03	Glucose	9.6	8303	3	Cytoplasmic	COG0361	Translation, ribosomal structure and biogenesis
15597816	PA2620	clpA	ATP-binding protease component ClpA	1.2	5.22E-01	Glucose	5.9	84010	27	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
15597818	PA2622	cspD	cold-shock protein CspD	75.1	2.90E-06	Glucose	5.6	9600	4	Cytoplasmic	COG1278	Transcription
15597819	PA2623	icd	isocitrate dehydrogenase	1.4	1.34E-02	Citronellsäure	4.9	45577	44	Periplasmic	COG0538	Energy production and conversion
15597820	PA2624	idh	isocitrate dehydrogenase	2.9	6.70E-04	Glucose	6.1	81633	52	Periplasmic	COG2838	Energy production and conversion
15597821	PA2625		conserved hypothetical protein	1.2	7.14E-01	Citronellsäure	5.2	17525	7	Cytoplasmic	COG1051	Nucleotide transport and metabolism
15597822	PA2626	trmU	tRNA methyltransferase	1.3	1.03E-02	Glucose	5.9	41886	2	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis
15597823	PA2627		conserved hypothetical protein	1.0	7.04E-01	Glucose	10.9	23030	4	Unknown	COG2915	General function prediction only
15597825	PA2629	purB	adenylosuccinate lyase	1.2	1.35E-01	Citronellsäure	5.7	50500	16	Cytoplasmic	COG0015	Nucleotide transport and metabolism
15597826	PA2630		conserved hypothetical protein	1.1	4.70E-01	Glucose	4.1	44057	4	Cytoplasmic	COG2850	Function unknown
15597827	PA2631		probable acetyl transferase	2.3	1.15E-02	Citronellsäure	4.8	16040	5	Cytoplasmic	COG2153	General function prediction only
15597830	PA2634	aceA	isocitrate lyase AceA	9.5	2.00E-06	Citronellsäure	5.9	58886	46	Periplasmic	COG2224	Energy production and conversion
15597835	PA2639	nuoD	NADH dehydrogenase I chain C,D	8.8	4.14E-03	Glucose	6.7	68323	6	Cytoplasmic	COG0649	Energy production and conversion
15597836	PA2640	nuoE	NADH dehydrogenase I chain E	1.8	3.09E-02	Glucose	4.8	18088	3	Cytoplasmic	COG1905	Energy production and conversion
15597837	PA2641	nuoF	NADH dehydrogenase I chain F	2.9	1.15E-03	Glucose	7.0	48678	3	Cytoplasmic	COG1894	Energy production and conversion
15597838	PA2642	nuoG	NADH dehydrogenase I chain G	3.1	3.94E-04	Glucose	6.0	98999	15	Outer Membrane Vesicle	COG1034	Energy production and conversion
15597846	PA2650		conserved hypothetical protein	1.5	2.13E-02	Glucose	5.7	29513	4	Cytoplasmic	COG2226	Coenzyme metabolism
15597853	PA2657		probable two-component response regulator	2.1	2.55E-03	Citronellsäure	5.9	24729	3	Cytoplasmic	COG0745	Signal transduction mechanisms
15597875	PA2679		hypothetical protein	4.7	2.65E-03	Citronellsäure	5.2	27641	4	Cytoplasmic	COG2226	Coenzyme metabolism
15597879	PA2683		probable serine/threonine dehydratase, degradative	2.5	7.63E-02	Glucose	6.4	33957	2	Cytoplasmic	COG1171	Amino acid transport and metabolism
15597880	PA2684		conserved hypothetical protein	2.0	1.21E-01	Citronellsäure	6.6	145819	7	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane
15597888	PA2692		probable transcriptional regulator	2.0	1.66E-01	Glucose	6.5	19143	3	Cytoplasmic	COG1959	Transcription
15597898	PA2702	tse2	Tse2	2.5	6.34E-02	Glucose	6.8	17657	2	Extracellular		
15597903	PA2707		hypothetical protein	2.7	8.02E-03	Citronellsäure	6.1	32205	18	Cytoplasmic	COG0714	General function prediction only
15597905	PA2709	cysK	cysteine synthase A	1.3	1.48E-02	Citronellsäure	6.6	34309	15	Cytoplasmic	COG0031	Amino acid transport and metabolism
15597913	PA2717	cpo	chloroperoxidase precursor	12.1	1.07E-04	Citronellsäure	5.9	30435	7	Cytoplasmic	COG0596	General function prediction only
15597916	PA2720		hypothetical protein	1.1	4.05E-01	Citronellsäure	4.7	23816	8	Cytoplasmic		
15597921	PA2725		probable chaperone	1.6	2.74E-01	Glucose	6.2	68829	9	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
15597928	PA2732		hypothetical protein	2.8	3.63E-02	Citronellsäure	6.2	128671	29	Cytoplasmic	COG0610	Defense mechanisms
15597930	PA2734		hypothetical protein	1.6	1.75E-02	Glucose	6.1	48703	7	Cytoplasmic	COG0732	Defense mechanisms
15597931	PA2735		probable restriction-modification system protein	1.0	7.38E-01	Glucose	5.4	89570	27	Cytoplasmic	COG0286	Defense mechanisms
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit	1.0	9.43E-01	Citronellsäure	5.1	86799	40	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit	2.1	7.07E-02	Citronellsäure	5.8	38063	15	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis
15597937	PA2741	rplT	50S ribosomal protein L20	6.4	1.66E-03	Glucose	12.3	13365	5	Outer Membrane Vesicle	COG0292	Translation, ribosomal structure and biogenesis
15597939	PA2743	infC	translation initiation factor IF-3	4.4	1.85E-02	Glucose	10.3	20864	8	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis
15597940	PA2744	thrS	threonyl-tRNA synthetase	1.2	1.54E-01	Glucose	6.3	73080	39	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis
15597951	PA2755	eco	ecotin precursor	2.3	7.40E-02	Glucose	6.5	17228	6	Periplasmic	COG4574	General function prediction only
15597956	PA2760	oprQ	OprQ	1.3	3.57E-01	Citronellsäure	5.5	46850	12	Periplasmic		
15597960	PA2764		hypothetical protein	1.0	5.38E-01	Glucose	6.0	24519	5	Cytoplasmic		
15597961	PA2765		hypothetical protein	1.3	1.95E-01	Citronellsäure	4.5	32396	14	Unknown	COG2837	Inorganic ion transport and metabolism
15597966	PA2770		hypothetical protein	1.0	7.30E-01	Citronellsäure	4.7	28258	9	Cytoplasmic	COG0384	General function prediction only
15597988	PA2792		hypothetical protein	6.8	4.64E-02	Glucose	6.4	22070	4	Unknown		
15597992	PA2796	tal	transaldolase	1.1	2.17E-01	Glucose	4.9	33946	19	Cytoplasmic	COG0176	Carbohydrate transport and metabolism
15597993	PA2797		hypothetical protein	1.9	6.38E-02	Citronellsäure	4.6	17710	7	Cytoplasmic	COG1366	Signal transduction mechanisms
15597994	PA2798		probable two-component response regulator	1.1	1.89E-01	Citronellsäure	4.6	43485	10	Cytoplasmic	COG2208	Signal transduction mechanisms
15597996	PA2800		conserved hypothetical protein	7.0	2.30E-02	Glucose	5.3	26148	4	Periplasmic	COG2853	Cell envelope biogenesis, outer membrane
15598002	PA2806		conserved hypothetical protein	1.8	5.52E-02	Citronellsäure	5.4	30848	11	Cytoplasmic	COG2904	Function unknown
15598003	PA2807		hypothetical protein	47.0	6.89E-04	Citronellsäure	7.9	22458	4	Unknown	COG4454	Inorganic ion transport and metabolism
15598005	PA2809	copR	two-component response regulator, CopR	56.5	2.64E-03	Citronellsäure	4.6	25716	2	Cytoplasmic	COG0745	Signal transduction mechanisms
15598009	PA2813		probable glutathione S-transferase	1.9	1.88E-02	Glucose	4.8	23405	14	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15598010	PA2814		hypothetical protein	46.0	3.37E-06	Citronellsäure	6.9	25274	4	Cytoplasmic	COG1305	Amino acid transport and metabolism
15598017	PA2821		probable glutathione S-transferase	4.7	5.30E-04	Citronellsäure	6.1	24716	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15598018	PA2822		conserved hypothetical protein	1.8	3.03E-01	Glucose	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms
15598019	PA2823		conserved hypothetical protein	1.2	1.26E-01	Glucose	5.7	33760	9	Cytoplasmic	COG2607	General function prediction only
15598022	PA2826		probable glutathione peroxidase	3.2	1.15E-02	Citronellsäure	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones
15598024	PA2828		probable aminotransferase	1.1	5.09E-01	Citronellsäure	6.1	44799	10	Periplasmic	COG0436	Amino acid transport and metabolism

15598025	PA2829		hypothetical protein	18.4	6.07E-03	Glucose	5.2	16432	5	Unknown			
15598027	PA2831		conserved hypothetical protein	1.8	6.06E-04	Citronellsäure	5.3	42933	6	Cytoplasmic	COG2866	Amino acid transport and metabolism	
15598028	PA2832	tpm	thiopurine methyltransferase	2.5	9.49E-03	Glucose	4.7	24875	3	Cytoplasmic			
15598036	PA2840		probable ATP-dependent RNA helicase	4.7	7.16E-03	Glucose	9.0	62107	3	Outer Membrane Vesicle	COG0513	DNA replication, recombination, and repair	
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	2.4	1.81E-03	Citronellsäure	5.4	28612	7	Cytoplasmic	COG1024	Lipid metabolism	
15598039	PA2843		probable aldolase	1.7	1.70E-04	Glucose	6.1	49851	3	Cytoplasmic	COG3200	Amino acid transport and metabolism	
15598047	PA2851	efp	translation elongation factor P	1.1	5.94E-01	Glucose	4.5	20985	8	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis	
15598050	PA2854		conserved hypothetical protein	1.5	1.53E-02	Glucose	5.6	34799	11	Periplasmic	COG1376	Function unknown	
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	3.1	2.02E-02	Citronellsäure	5.9	21037	8	Periplasmic	COG2755	Amino acid transport and metabolism	
15598062	PA2866	mttC	secretion protein MttC	1.7	2.83E-01	Glucose	6.1	29544	2	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598065	PA2869		hypothetical protein	47.8	9.41E-02	Glucose	8.7	18206	3	Cytoplasmic Membrane	COG3915	Function unknown	
15598067	PA2871		hypothetical protein	1.1	4.80E-01	Glucose	5.4	28695	14	Unknown	COG1946	Lipid metabolism	
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	1.0	6.46E-01	Glucose	5.3	24394	12	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
15598081	PA2885	atuR	putative repressor of atu genes	5.6	1.56E-03	Citronellsäure	4.9	22057	7	Unknown	COG1309	Transcription	
15598082	PA2886	atuA	expressed protein with apparent function in citronellol catabolis	64.5	3.17E-07	Citronellsäure	5.1	64435	26	Cytoplasmic			
15598083	PA2887	atuB	putative dehydrogenase involved in catabolism of citronellol	88.2	4.28E-06	Citronellsäure	7.3	30751	16	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	
15598084	PA2888	atuC	geranyl-CoA carboxylase, beta-subunit	48.9	2.47E-05	Citronellsäure	6.5	57328	21	Cytoplasmic	COG4799	Lipid metabolism	
15598085	PA2889	atuD	citronellyl-CoA dehydrogenase, AtuD	36.4	1.56E-05	Citronellsäure	6.3	42714	31	Cytoplasmic	COG1960	Lipid metabolism	
15598086	PA2890	atuE	putative isohexenylglutaconyl-CoA hydratase	46.4	9.90E-05	Citronellsäure	5.2	27717	11	Cytoplasmic	COG1024	Lipid metabolism	
15598087	PA2891	atuF	geranyl-CoA carboxylase, alpha-subunit (biotin-containing)	31.0	3.80E-05	Citronellsäure	6.1	71747	29	Cytoplasmic	COG4770	Lipid metabolism	
15598088	PA2892	atuG	GCase, alpha-subunit (biotin-containing)	34.8	1.04E-05	Citronellsäure	7.2	29631	16	Cytoplasmic	COG4221	General function prediction only	
15598095	PA2899		probable transcriptional regulator	9.0	1.61E-02	Citronellsäure	7.6	23250	4	Cytoplasmic	COG2197	Signal transduction mechanisms	
15598099	PA2903	cobJ	precorrin-3 methylase CobJ	2.0	5.22E-02	Citronellsäure	5.9	58950	3	Cytoplasmic	COG1010	Coenzyme metabolism	
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	1.7	1.50E-01	Glucose	6.3	27275	4	Cytoplasmic	COG2243	Coenzyme metabolism	
15598101	PA2905	cobH	precorrin isomerase CobH	1.0	8.49E-01	Glucose	5.7	21650	8	Cytoplasmic	COG2082	Coenzyme metabolism	
15598114	PA2918		probable short-chain dehydrogenase	3.5	7.50E-04	Citronellsäure	7.2	26738	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	
15598135	PA2939		probable aminopeptidase	5.1	1.18E-01	Glucose	4.8	57511	4	Extracellular	COG2234	General function prediction only	
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	6.3	8.49E-03	Citronellsäure	5.2	138499	9	Cytoplasmic	COG1429	Coenzyme metabolism	
15598141	PA2945		conserved hypothetical protein	3.1	6.81E-03	Citronellsäure	4.9	41175	8	Cytoplasmic	COG0523	General function prediction only	
15598146	PA2950	pfmá	proton motive force protein, PMF	1.3	4.19E-03	Glucose	4.8	43528	25	Cytoplasmic	COG3007	Function unknown	
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	2.4	3.67E-04	Citronellsäure	4.8	31423	20	Periplasmic	COG2025	Energy production and conversion	
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	2.4	2.84E-03	Citronellsäure	9.6	26377	22	Outer Membrane Vesicle	COG2086	Energy production and conversion	
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	2.1	4.22E-03	Citronellsäure	5.6	59896	14	Outer Membrane Vesicle	COG0644	Energy production and conversion	
15598150	PA2954		hypothetical protein	1.0	8.69E-01	Citronellsäure	4.9	21240	7	Cytoplasmic	COG3816	Function unknown	
15598155	PA2959		conserved hypothetical protein	1.1	4.93E-02	Citronellsäure	5.3	28114	6	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598157	PA2961	holB	DNA polymerase III, delta prime subunit	1.1	7.02E-01	Citronellsäure	6.6	35746	6	Cytoplasmic	COG0470	DNA replication, recombination, and repair	
15598158	PA2962	tmk	thymidylate kinase	1.2	5.27E-01	Glucose	4.9	23077	7	Cytoplasmic	COG0125	Nucleotide transport and metabolism	
15598160	PA2964	pabC	4-amino-4-deoxychorismate lyase	1.4	1.10E-02	Glucose	5.7	29886	4	Cytoplasmic	COG0115	Amino acid transport and metabolism	
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.6	2.95E-04	Citronellsäure	5.8	43465	10	Periplasmic	COG0304	Lipid metabolism	
15598162	PA2966	acpP	acyl carrier protein	2.6	1.83E-02	Citronellsäure	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	3.2	2.86E-03	Glucose	6.6	25585	15	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	2.4	1.59E-03	Glucose	4.8	32444	15	Periplasmic	COG0331	Lipid metabolism	
15598168	PA2972		conserved hypothetical protein	2.1	6.77E-02	Citronellsäure	6.0	21054	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15598170	PA2974		probable hydrolase	5.8	1.37E-02	Glucose	5.4	25322	3	Cytoplasmic	COG0546	General function prediction only	
15598172	PA2976	rne	ribonuclease E	1.0	8.29E-01	Glucose	4.6	117463	37	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis	
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	2.8	3.15E-02	Citronellsäure	6.7	37595	4	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
15598174	PA2978	ptpA	phosphotyrosine protein phosphatase	31.8	1.94E-05	Glucose	6.1	17152	7	Cytoplasmic	COG0394	Signal transduction mechanisms	
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.1	5.75E-01	Glucose	5.4	27646	11	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
15598179	PA2983		probable tolQ-type transport protein	12.2	4.14E-03	Glucose	6.8	22858	2	Outer Membrane Vesicle	COG0811	Intracellular trafficking and secretion	
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	2.5	3.43E-02	Glucose	6.7	51161	14	Cytoplasmic	COG1249	Energy production and conversion	
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	2.6	3.77E-02	Citronellsäure	5.7	128763	40	Periplasmic	COG1197	DNA replication, recombination, and repair	
15598199	PA3003		hypothetical protein	1.4	8.34E-02	Glucose	4.5	22474	9	Periplasmic			
15598200	PA3004		5'-methylthioinosine phosphorylase	1.2	4.05E-01	Glucose	6.6	26266	7	Cytoplasmic	COG0005	Nucleotide transport and metabolism	
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.5	1.85E-02	Glucose	6.2	36101	10	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
15598202	PA3006	psrA	transcriptional regulator PsrA	12.1	1.97E-02	Citronellsäure	9.9	25784	3	Cytoplasmic	COG1309	Transcription	
15598206	PA3010		hypothetical protein	2.3	2.53E-01	Citronellsäure	4.6	19071	2	Unknown			
15598207	PA3011	topA	DNA topoisomerase I	1.3	4.99E-01	Glucose	8.7	97282	58	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	7.3	1.01E-05	Citronellsäure	6.8	41643	26	Cytoplasmic	COG0183	Lipid metabolism	
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	4.6	9.07E-04	Citronellsäure	5.6	76954	53	Periplasmic	COG1250	Lipid metabolism	
15598211	PA3015		hypothetical protein	32.7	1.28E-03	Citronellsäure	5.9	30469	6	Unknown			
15598215	PA3019		probable ATP-binding component of ABC transporter	1.4	1.79E-01	Glucose	5.0	71155	16	Cytoplasmic	COG0488	General function prediction only	
15598217	PA3021		hypothetical protein	18.4	4.53E-03	Glucose	7.8	14206	4	Unknown	COG3755	Function unknown	
15598218	PA3022		hypothetical protein	1.7	5.69E-02	Citronellsäure	5.9	29579	13	Cytoplasmic	COG3217	General function prediction only	
15598219	PA3023		conserved hypothetical protein	15.1	1.38E-03	Citronellsäure	4.7	31504	8	Cytoplasmic	COG1597	Lipid metabolism	
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.6	5.14E-03	Citronellsäure	5.0	43359	6	Cytoplasmic	COG0303	Coenzyme metabolism	
15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	2.1	1.31E-02	Citronellsäure	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism	
15598226	PA3030	mobA	molybdopterin-guanine dinucleotide biosynthesis protein MobA	6.3	6.38E-03	Glucose	7.6	21870	3	Cytoplasmic	COG0746	Coenzyme metabolism	
15598227	PA3031		hypothetical protein	47.7	7.53E-01	Glucose	4.7	8012	2	Outer Membrane Vesicle			
15598234	PA3038		probable porin	39.7	3.30E-03	Citronellsäure	7.1	46712	4	Periplasmic			
15598239	PA3043		conserved hypothetical protein	3.5	1.75E-01	Glucose	6.5	50083	3	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15598244	PA3048		conserved hypothetical protein	1.2	5.87E-01	Citronellsäure	8.0	81155	10	Cytoplasmic	COG0116	DNA replication, recombination, and repair	
15598249	PA3053		probable hydrolytic enzyme	1.1	5.52E-01	Glucose	8.0	37485	2	Periplasmic	COG0596	General function prediction only	
15598250	PA3054		hypothetical protein	1.3	2.00E-01	Citronellsäure	6.6	71165	2	Periplasmic	COG2866	Amino acid transport and metabolism	
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	37.6	2.54E-04	Citronellsäure	6.1	182637	14	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism	
15598276	PA3080		hypothetical protein	24.3	2.39E-03	Citronellsäure	4.8	38479	3	Unknown	COG4447	General function prediction only	
15598277	PA3081		conserved hypothetical protein	23.2	5.08E-04	Citronellsäure	9.2	50680	5	Periplasmic			
15598278	PA3082	gbt	glycine betaine transmethylase	5.0	1.21E-02	Citronellsäure	4.5	71403	3	Periplasmic			
15598279	PA3083	pepN	aminopeptidase N	1.3	2.56E-01	Citronellsäure	4.9	100046	51	Periplasmic	COG0308	Amino acid transport and metabolism	
15598280	PA3084		hypothetical protein	2.0	6.42E-02	Glucose	7.6	29990	2	Cytoplasmic			
15598284	PA3088		conserved hypothetical protein	1.3	6.02E-01	Citronellsäure	7.3	32140	4	Cytoplasmic	COG0061	Coenzyme metabolism	
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	30.7	3.18E-05	Citronellsäure	7.2	72969	28	Cytoplasmic	COG1902	Energy production and conversion	
15598302	PA3106		probable short-chain dehydrogenase	2.3	1.42E-03	Glucose	4.6	26997	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	
15598303	PA3107	metZ	o-succinylhomoserine sulfhydrylase	1.0	8.31E-01	Citronellsäure	6.3	43185	13	Periplasmic	COG0626	Amino acid transport and metabolism	

15598304	PA3108	purF	amidophosphoribosyltransferase	1.2	6.52E-02	Glucose	6.8	55370	16	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism
15598307	PA3111	folC	folylpolyglutamate synthetase	1.6	2.10E-01	Citronellsäure	5.0	46505	3	Cytoplasmic	COG0285	Coenzyme metabolism
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	1.4	1.80E-01	Citronellsäure	7.1	31843	12	Periplasmic	COG0777	Lipid metabolism
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	1.0	9.34E-01	Citronellsäure	6.8	22280	6	Cytoplasmic	COG0135	Amino acid transport and metabolism
15598312	PA3116		probable aspartate-semialdehyde dehydrogenase	1.1	9.95E-01	Citronellsäure	4.5	35349	3	Cytoplasmic	COG0136	Amino acid transport and metabolism
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	1.9	7.23E-03	Citronellsäure	5.5	40494	24	Periplasmic	COG0136	Amino acid transport and metabolism
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.4	6.44E-03	Citronellsäure	4.8	39120	9	Cytoplasmic	COG0473	Amino acid transport and metabolism
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	1.5	8.02E-02	Citronellsäure	4.7	24011	17	Cytoplasmic	COG0066	Amino acid transport and metabolism
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	1.3	1.16E-01	Glucose	6.3	51042	16	Cytoplasmic	COG0065	Amino acid transport and metabolism
15598318	PA3122		probable transcriptional regulator	1.1	9.06E-01	Citronellsäure	6.4	32835	4	Cytoplasmic	COG0583	Transcription
15598319	PA3123		conserved hypothetical protein	1112.8	1.51E-04	Glucose	4.6	13516	5	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis
15598322	PA3126	ibpA	heat-shock protein IbpA	31.2	2.32E-03	Glucose	6.1	16583	3	Cytoplasmic	COG0071	Posttranslational modification, protein turnover, chaperones
15598323	PA3127		hypothetical protein	1.0	9.40E-01	Citronellsäure	5.0	29403	5	Unknown		
15598324	PA3128		probable short-chain dehydrogenase	2.5	9.08E-06	Citronellsäure	6.8	26219	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15598326	PA3130		hypothetical protein	78.1	1.74E-04	Glucose	5.2	16555	5	Unknown	COG0824	General function prediction only
15598327	PA3131		probable aldolase	1.8	2.42E-02	Glucose	5.3	22852	10	Cytoplasmic	COG0800	Carbohydrate transport and metabolism
15598330	PA3134	gltX	glutamyl-tRNA synthetase	1.4	3.08E-02	Glucose	6.7	56749	25	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis
15598334	PA3138	uvrB	excinuclease ABC subunit B	2.7	1.03E-01	Glucose	5.1	76067	18	Cytoplasmic	COG0556	DNA replication, recombination, and repair
15598335	PA3139		probable amino acid aminotransferase	1.5	3.35E-03	Citronellsäure	6.6	43319	26	Periplasmic	COG1448	Amino acid transport and metabolism
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	1.0	8.00E-01	Glucose	5.8	38907	19	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane
15598346	PA3150	wbpG	LPS biosynthesis protein WbpG	2.9	3.35E-02	Glucose	8.3	43471	2	Outer Membrane Vesicle	COG0037	Cell cycle control, cell division, chromosome partitioning
15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	1.3	3.08E-01	Glucose	5.7	27448	9	Cytoplasmic	COG0107	Amino acid transport and metabolism
15598348	PA3152	hisH2	glutamine amidotransferase	1.6	4.29E-02	Glucose	7.1	22663	10	Cytoplasmic	COG0118	Amino acid transport and metabolism
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transam	1.7	5.64E-03	Citronellsäure	6.0	38924	16	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-ace	1.1	7.15E-01	Citronellsäure	7.8	20562	5	Cytoplasmic	COG1045	Amino acid transport and metabolism
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase,	1.3	4.90E-01	Glucose	6.6	35717	20	Cytoplasmic	COG0673	General function prediction only
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.1	1.67E-02	Citronellsäure	5.2	48155	32	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane
15598358	PA3162	rpsA	30S ribosomal protein S1	1.0	8.67E-01	Glucose	4.6	61869	32	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis
15598359	PA3163	cmk	cytidylate kinase	1.4	2.79E-02	Glucose	4.8	24637	11	Cytoplasmic	COG0283	Nucleotide transport and metabolism
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	4.9	2.46E-04	Glucose	4.8	39483	13	Cytoplasmic	COG0079	Amino acid transport and metabolism
15598362	PA3166	pheA	chorismate mutase	1.1	2.83E-01	Citronellsäure	6.3	40632	12	Cytoplasmic	COG0077	Amino acid transport and metabolism
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.1	5.56E-01	Citronellsäure	4.7	39917	14	Periplasmic	COG1932	Coenzyme metabolism
15598364	PA3168	gyrA	DNA gyrase subunit A	1.5	6.12E-02	Citronellsäure	4.6	101134	55	Cytoplasmic	COG0188	DNA replication, recombination, and repair
15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.0	8.14E-01	Citronellsäure	5.1	39425	9	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis
15598366	PA3170		conserved hypothetical protein	1.8	2.72E-01	Glucose	5.5	48493	3	Cytoplasmic	COG0402	Nucleotide transport and metabolism
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	2.9	1.94E-03	Glucose	6.3	25860	6	Cytoplasmic	COG2227	Coenzyme metabolism
15598368	PA3172		probable hydrolase	1.0	9.03E-01	Glucose	5.0	24944	11	Cytoplasmic	COG0546	General function prediction only
15598369	PA3173		probable short-chain dehydrogenase	1.0	9.26E-01	Citronellsäure	4.9	26332	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15598376	PA3180		hypothetical protein	25.9	4.58E-03	Glucose	4.7	16863	2	Unknown	COG1051	Nucleotide transport and metabolism
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	27.6	8.04E-08	Glucose	7.6	23953	14	Cytoplasmic	COG0800	Carbohydrate transport and metabolism
15598378	PA3182	pgl	6-phosphogluconolactonase	17.6	3.25E-05	Glucose	6.5	25571	13	Unknown	COG0363	Carbohydrate transport and metabolism
15598379	PA3183	zwf	glucose-6-phosphate 1-dehydrogenase	15.3	6.75E-05	Glucose	5.7	55620	26	Cytoplasmic	COG0364	Carbohydrate transport and metabolism
15598382	PA3186	oprB	Glucose/carbohydrate outer membrane porin OprB precursor	11.7	8.01E-03	Glucose	5.5	50753	8	Outer Membrane	COG3659	Cell envelope biogenesis, outer membrane
15598383	PA3187		probable ATP-binding component of ABC transporter	15.0	4.50E-03	Glucose	7.5	42240	5	Outer Membrane Vesicle	COG3839	Carbohydrate transport and metabolism
15598386	PA3190		probable binding protein component of ABC sugar transporter	7.0	1.78E-05	Glucose	5.8	45131	32	Periplasmic	COG1653	Carbohydrate transport and metabolism
15598388	PA3192	gltR	two-component response regulator GltR	7.9	1.46E-03	Glucose	5.7	27381	7	Cytoplasmic	COG0745	Signal transduction mechanisms
15598389	PA3193	glk	glucokinase	3.7	3.02E-04	Glucose	5.0	34606	9	Cytoplasmic	COG0837	Carbohydrate transport and metabolism
15598390	PA3194	edd	phosphogluconate dehydratase	16.4	1.98E-05	Glucose	6.7	65182	27	Cytoplasmic	COG0129	Amino acid transport and metabolism
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	16.1	7.05E-06	Glucose	6.6	36170	24	Cytoplasmic	COG0057	Carbohydrate transport and metabolism
15598392	PA3196		hypothetical protein	1.1	7.90E-01	Citronellsäure	3.9	19293	2	Unknown		
15598395	PA3199		conserved hypothetical protein	1.5	2.96E-01	Glucose	6.7	23144	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis
15598404	PA3208		conserved hypothetical protein	1.6	1.02E-01	Glucose	6.5	19948	13	Cytoplasmic Membrane	COG0778	Energy production and conversion
15598421	PA3225		probable transcriptional regulator	1.3	4.11E-01	Glucose	7.4	34098	2	Cytoplasmic	COG0583	Transcription
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.5	3.70E-02	Citronellsäure	8.5	20104	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones
15598439	PA3243	minC	cell division inhibitor MinC	2.1	3.95E-02	Glucose	6.5	28124	7	Cytoplasmic	COG0850	Cell division and chromosome partitioning
15598440	PA3244	minD	cell division inhibitor MinD	1.1	5.29E-01	Citronellsäure	5.5	29617	18	Periplasmic	COG2894	Cell division and chromosome partitioning
15598442	PA3246	rluA	pseudouridine synthase RluA	34.5	2.70E-03	Glucose	7.0	24339	3	Cytoplasmic	COG0564	Translation, ribosomal structure and biogenesis
15598443	PA3247		hypothetical protein	1.1	6.46E-01	Glucose	6.0	46658	5	Cytoplasmic	COG1362	Amino acid transport and metabolism
15598444	PA3248		hypothetical protein	12.3	3.87E-03	Citronellsäure	8.0	20759	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis
15598446	PA3250		hypothetical protein	12.7	1.80E-04	Citronellsäure	6.2	38285	10	Periplasmic	COG1840	Inorganic ion transport and metabolism
15598451	PA3255		hypothetical protein	1.0	6.26E-01	Glucose	4.4	21635	9	Cytoplasmic	COG0560	Amino acid transport and metabolism
15598452	PA3256		probable oxidoreductase	1.2	2.97E-01	Glucose	5.2	33387	10	Cytoplasmic Membrane	COG0604	Energy production and conversion
15598453	PA3257	prc	periplasmic tail-specific protease	1.2	4.07E-01	Glucose	6.6	78182	30	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.3	2.12E-01	Glucose	4.8	26845	13	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones
15598459	PA3263		conserved hypothetical protein	1.3	2.30E-02	Glucose	4.7	34015	18	Cytoplasmic	COG2974	DNA replication, recombination, and repair
15598466	PA3270		hypothetical protein	2.3	1.33E-01	Citronellsäure	9.9	21901	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis
15598473	PA3277		probable short-chain dehydrogenase	2.2	5.72E-02	Citronellsäure	6.5	29251	3	Cytoplasmic	COG0300	General function prediction only
15598482	PA3286		hypothetical protein	12.0	1.21E-03	Glucose	6.4	38139	14	Periplasmic	COG0332	acyl-carrier-protein
15598483	PA3287		conserved hypothetical protein	1.1	6.43E-01	Citronellsäure	5.5	18194	2	Periplasmic	COG0666	General function prediction only
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	6.0	2.70E-05	Citronellsäure	7.5	61654	17	Outer Membrane Vesicle	COG0318	Lipid metabolism
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	1.1	7.23E-01	Glucose	7.2	61736	4	Cytoplasmic	COG0318	Lipid metabolism
15598498	PA3302		conserved hypothetical protein	1.5	2.59E-01	Citronellsäure	5.0	16901	7	Unknown	COG2030	Lipid metabolism
15598504	PA3308	hepA	RNA helicase HepA	1.3	2.54E-01	Citronellsäure	4.8	106839	29	Periplasmic	COG0553	Transcription
15598505	PA3309		conserved hypothetical protein	3.4	1.35E-01	Citronellsäure	5.4	16496	9	Periplasmic	COG0589	Signal transduction mechanisms
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.7	1.08E-03	Glucose	5.5	30908	10	Cytoplasmic	COG2084	Lipid metabolism
15598509	PA3313		hypothetical protein	1.7	2.20E-02	Citronellsäure	10.2	36539	19	Periplasmic	COG3221	Inorganic ion transport and metabolism
15598522	PA3326	clpP2	ClpP2	3.1	2.11E-02	Citronellsäure	5.4	22142	11	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones
15598523	PA3327		probable non-ribosomal peptide synthetase	3.6	5.15E-02	Citronellsäure	5.5	259403	38	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism
15598525	PA3329		hypothetical protein	4.5	2.45E-01	Citronellsäure	6.2	49134	2	Cytoplasmic		
15598528	PA3332		conserved hypothetical protein	4.1	1.21E-01	Glucose	5.5	15920	5	Cytoplasmic	COG3631	General function prediction only
15598540	PA3344	recQ	ATP-dependent DNA helicase RecQ	3.4	3.44E-02	Glucose	5.8	79449	6	Cytoplasmic	COG0514	DNA replication, recombination, and repair
15598544	PA3348		probable chemotaxis protein methyltransferase	2.4	1.70E-02	Glucose	9.6	30615	5	Cytoplasmic	COG1352	Cell motility and secretion
15598545	PA3349		probable chemotaxis protein	1.5	3.62E-03	Citronellsäure	6.1	34402	12	Cytoplasmic	COG0835	Cell motility and secretion

15598550	PA3354		hypothetical protein	3.9	2.66E-02	Citronellsäure	5.6	22398	3	Cytoplasmic	COG3222	Function unknown
15598552	PA3356	pauA5	Glutamylpolyamine synthetase	2.2	7.39E-03	Citronellsäure	5.6	45161	2	Cytoplasmic	COG0174	Amino acid transport and metabolism
15598553	PA3357	dsdA	D-serine dehydratase	1.1	4.32E-01	Glucose	6.0	48200	6	Cytoplasmic	COG3048	Amino acid transport and metabolism
15598593	PA3397	fpr	NADP+-dependent ferredoxin reductase	1.0	6.67E-01	Glucose	5.9	29518	22	Periplasmic	COG1018	Energy production and conversion
15598611	PA3415		probable dihydrolipoamide acetyltransferase	117.9	4.88E-02	Citronellsäure	5.5	39521	2	Cytoplasmic	COG0508	Energy production and conversion
15598614	PA3418	ldh	leucine dehydrogenase	41.4	1.10E-02	Citronellsäure	5.9	35633	3	Cytoplasmic	COG0334	Amino acid transport and metabolism
15598623	PA3427		probable short-chain dehydrogenases	3.5	4.48E-03	Citronellsäure	5.8	32323	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15598626	PA3430		probable aldolase	19.4	2.41E-03	Citronellsäure	6.6	27993	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism
15598633	PA3437	folM	dihydromonapterin reductase, FolM	2534.2	7.70E-03	Citronellsäure	7.0	25403	2	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	1.3	5.28E-02	Glucose	7.6	20833	6	Cytoplasmic	COG0302	Coenzyme metabolism
15598646	PA3450		probable antioxidant protein	1.2	1.66E-01	Glucose	5.2	24164	8	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
15598649	PA3453		conserved hypothetical protein	1.4	1.68E-01	Glucose	5.4	24160	9	Unknown	COG3132	Function unknown
15598654	PA3458		probable transcriptional regulator	5.1	2.50E-01	Glucose	5.6	17599	3	Unknown	COG1846	Transcription
15598657	PA3461		conserved hypothetical protein	12.3	6.84E-05	Citronellsäure	5.1	43294	3	Cytoplasmic	COG1363	Carbohydrate transport and metabolism
15598666	PA3470		hypothetical protein	119.6	6.65E-02	Glucose	5.2	16673	2	Unknown	COG0494	DNA replication, recombination, and repair
15598667	PA3471		probable malic enzyme	4.1	8.09E-05	Glucose	5.2	62420	24	Periplasmic	COG0281	Energy production and conversion
15598673	PA3477	rhlR	transcriptional regulator RhlR	1.2	7.33E-01	Glucose	7.2	27577	5	Cytoplasmic	COG2771	Transcription
15598676	PA3480		probable deoxycytidine triphosphate deaminase	1.4	8.88E-02	Glucose	6.3	21154	8	Cytoplasmic	COG0717	Nucleotide transport and metabolism
15598677	PA3481		conserved hypothetical protein	2.5	2.97E-03	Citronellsäure	5.1	38889	9	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning
15598678	PA3482	metG	methionyl-tRNA synthetase	1.1	5.42E-01	Glucose	5.4	74903	29	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis
15598711	PA3515		hypothetical protein	68.2	7.40E-06	Citronellsäure	4.9	39764	32	Cytoplasmic	COG2227	Coenzyme metabolism
15598712	PA3516		probable lyase	109.0	6.28E-05	Citronellsäure	6.3	52927	22	Cytoplasmic	COG0015	Nucleotide transport and metabolism
15598713	PA3517		probable lyase	80.0	2.39E-07	Citronellsäure	6.4	52228	18	Cytoplasmic	COG0015	Nucleotide transport and metabolism
15598715	PA3519		hypothetical protein	98.2	3.73E-05	Citronellsäure	5.9	39369	9	Cytoplasmic		
15598721	PA3525	argG	argininosuccinate synthase	1.2	7.02E-02	Citronellsäure	5.3	45297	24	Periplasmic	COG0137	Amino acid transport and metabolism
15598723	PA3527	pyrC	dihydroorotase	2.8	3.16E-03	Citronellsäure	6.6	38406	14	Cytoplasmic	COG0418	Nucleotide transport and metabolism
15598724	PA3528	rnt	ribonuclease T	1.1	6.19E-01	Glucose	4.8	24723	9	Cytoplasmic	COG0847	DNA replication, recombination, and repair
15598725	PA3529		alkylhydroperoxide reductase C	2.1	1.36E-02	Glucose	5.3	21822	16	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones
15598727	PA3531	bfrB	bacterioferritin	2.4	9.46E-01	Glucose	4.8	18553	2	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.3	2.36E-01	Glucose	5.7	33924	15	Cytoplasmic	COG0078	Amino acid transport and metabolism
15598735	PA3539		conserved hypothetical protein	1.0	9.57E-01	Citronellsäure	6.7	29560	13	Cytoplasmic	COG3022	Function unknown
15598750	PA3554	arnA	ArnA	2.7	3.81E-02	Citronellsäure	6.7	74360	4	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis
15598758	PA3562	fruI	phosphotransferase system transporter enzyme I, FruI	1.1	5.75E-01	Glucose	4.8	101572	5	Cytoplasmic	COG1080	Carbohydrate transport and metabolism
15598759	PA3563	fruR	fructose transport system repressor FruR	1.9	6.34E-02	Citronellsäure	6.4	36369	3	Cytoplasmic	COG1609	Transcription
15598763	PA3567		probable oxidoreductase	1.1	7.47E-01	Citronellsäure	6.6	36678	4	Cytoplasmic	COG0604	Energy production and conversion
15598764	PA3568		probable acetyl-coa synthetase	561.0	3.51E-04	Citronellsäure	6.7	68990	4	Cytoplasmic	COG0365	Lipid metabolism
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	11.4	3.41E-02	Citronellsäure	6.4	53663	2	Cytoplasmic	COG1012	Energy production and conversion
15598774	PA3578		conserved hypothetical protein	1.3	3.61E-01	Citronellsäure	4.9	28906	5	Cytoplasmic Membrane	COG0384	General function prediction only
15598778	PA3582	glpK	glycerol kinase	6.9	6.35E-05	Citronellsäure	5.9	55966	22	Cytoplasmic	COG0554	Energy production and conversion
15598783	PA3587	metR	transcriptional regulator MetR	3.3	2.65E-03	Citronellsäure	5.6	34216	4	Cytoplasmic	COG0583	Transcription
15598800	PA3604	erdR	response regulator ErdR	1.2	2.20E-01	Citronellsäure	4.8	23531	11	Cytoplasmic	COG2197	Signal transduction mechanisms
15598806	PA3610	potD	polyamine transport protein PotD	1.1	5.88E-01	Glucose	5.5	39260	7	Periplasmic	COG0687	Amino acid transport and metabolism
15598809	PA3613		hypothetical protein	4.2	2.46E-01	Citronellsäure	6.4	88379	10	Periplasmic	COG3957	Carbohydrate transport and metabolism
15598810	PA3614		hypothetical protein	2.1	2.03E-01	Citronellsäure	7.0	51921	5	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis
15598811	PA3615		hypothetical protein	2.0	2.96E-03	Citronellsäure	6.0	40465	5	Cytoplasmic	COG1611	General function prediction only
15598813	PA3617	recA	RecA protein	1.1	8.02E-01	Citronellsäure	5.2	36879	10	Cytoplasmic	COG0468	DNA replication, recombination, and repair
15598814	PA3618		conserved hypothetical protein	103.6	5.94E-02	Glucose	5.0	17715	3	Unknown	COG1546	General function prediction only
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.7	1.01E-01	Glucose	6.1	94977	29	Cytoplasmic	COG0249	DNA replication, recombination, and repair
15598817	PA3621	fdxA	ferredoxin I	2.7	2.03E-02	Glucose	3.7	12159	3	Cytoplasmic	COG1146	Energy production and conversion
15598818	PA3622	rpoS	sigma factor RpoS	5.3	7.44E-03	Citronellsäure	5.1	38235	2	Cytoplasmic	COG0568	Transcription
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	2.4	2.19E-03	Citronellsäure	6.1	23407	6	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones
15598821	PA3625	surE	survival protein SurE	1.5	9.66E-02	Glucose	5.2	26368	6	Unknown	COG0496	General function prediction only
15598822	PA3626		conserved hypothetical protein	4.6	3.77E-02	Citronellsäure	6.8	38782	2	Cytoplasmic	COG0585	Function unknown
15598823	PA3627	ygbB	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	35.9	9.94E-02	Glucose	7.1	16662	3	Cytoplasmic	COG0245	Lipid metabolism
15598824	PA3628		probable esterase	1.4	2.47E-01	Citronellsäure	6.3	31243	3	Unknown	COG0627	General function prediction only
15598825	PA3629	adhC	alcohol dehydrogenase class III	2.0	9.24E-03	Citronellsäure	5.4	39208	4	Cytoplasmic	COG1062	Energy production and conversion
15598829	PA3633	ygbP	4-diphosphocytidyl-2-C-methylerythritol synthase	1.3	1.52E-01	Glucose	5.2	25613	2	Cytoplasmic	COG1211	Lipid metabolism
15598831	PA3635	eno	enolase	1.1	4.92E-01	Citronellsäure	4.8	45195	19	Cytoplasmic	COG0148	Carbohydrate transport and metabolism
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	1.2	1.19E-01	Citronellsäure	6.5	31143	21	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane
15598833	PA3637	pyrG	CTP synthase	1.5	4.37E-03	Glucose	5.4	59617	36	Periplasmic	COG0504	Nucleotide transport and metabolism
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subu	1.3	5.32E-02	Citronellsäure	5.2	34947	24	Outer Membrane Vesicle	COG0825	Lipid metabolism
15598836	PA3640	dnaE	DNA polymerase III, alpha chain	2.1	2.08E-02	Citronellsäure	5.1	130904	63	Cytoplasmic	COG0587	DNA replication, recombination, and repair
15598838	PA3642	rnhB	ribonuclease HII	3.3	1.85E-03	Glucose	6.5	21771	4	Cytoplasmic	COG0164	DNA replication, recombination, and repair
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase	1.0	9.97E-01	Glucose	7.1	28010	7	Cytoplasmic	COG1043	acyl carrier protein
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	13.6	1.71E-04	Citronellsäure	7.6	16774	8	Cytoplasmic	COG0764	Lipid metabolism
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase	1.8	2.04E-01	Glucose	6.2	36191	2	Cytoplasmic	COG1044	3-hydroxymyristoyl
15598843	PA3647		probable outer membrane protein precursor	22.3	1.77E-02	Glucose	10.0	19058	5	Unknown	COG2825	Cell envelope biogenesis, outer membrane
15598844	PA3648	opr86	outer membrane protein Opr86	2.5	8.37E-02	Glucose	4.8	88286	6	Periplasmic	COG4775	Cell envelope biogenesis, outer membrane
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase	1.0	8.40E-01	Citronellsäure	5.7	42508	5	Unknown	COG0743	Lipid metabolism
15598849	PA3653	frr	ribosome recycling factor	1.5	2.32E-01	Citronellsäure	5.9	20485	18	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis
15598850	PA3654	pyrH	uridylate kinase	1.5	7.64E-03	Glucose	5.4	26272	12	Periplasmic	COG0528	Nucleotide transport and metabolism
15598851	PA3655	tsf	elongation factor Ts	1.3	2.06E-02	Citronellsäure	5.0	30653	30	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis
15598852	PA3656	rpsB	30S ribosomal protein S2	1.6	3.69E-01	Glucose	9.0	27336	13	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis
15598853	PA3657	map	methionine aminopeptidase	1.1	5.50E-01	Glucose	6.3	29086	6	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis
15598854	PA3658	glnD	protein-PII uridylyltransferase	4.3	2.67E-01	Glucose	5.5	103403	2	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones
15598855	PA3659		probable aminotransferase	1.2	3.24E-01	Citronellsäure	5.5	44544	10	Cytoplasmic	COG0436	Amino acid transport and metabolism
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase	2.1	7.73E-03	Citronellsäure	6.0	35973	12	Periplasmic	COG2171	Amino acid transport and metabolism
15598871	PA3675		hypothetical protein	4.3	2.28E-03	Glucose	9.4	23645	5	Unknown		
15598874	PA3678		probable transcriptional regulator	2.7	2.05E-02	Glucose	6.3	23150	7	Cytoplasmic	COG1309	Transcription
15598878	PA3682		hypothetical protein	1.6	7.26E-03	Citronellsäure	5.0	29150	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
15598881	PA3685		conserved hypothetical protein	1.2	3.96E-01	Citronellsäure	4.8	24180	7	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones
15598882	PA3686	adk	adenylate kinase	1.8	9.65E-03	Citronellsäure	6.4	23107	16	Cytoplasmic	COG0563	Nucleotide transport and metabolism
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase	2.5	7.02E-02	Citronellsäure	6.2	97839	21	Cytoplasmic	COG2352	Energy production and conversion

15598888	PA3692	lptF	Lipotoxon F, LptF	3.1	4.29E-02	Citronellsäure	9.9	28514	4	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
15598889	PA3693		conserved hypothetical protein	1.6	9.87E-02	Citronellsäure	7.0	18219	2	Unknown	COG2110	General function prediction only
15598892	PA3696		conserved hypothetical protein	1.5	2.06E-01	Glucose	5.4	26551	3	Unknown	COG2013	Function unknown
15598894	PA3698		hypothetical protein	3.6	6.05E-02	Citronellsäure	4.5	20351	4	Unknown		
15598896	PA3700	lysS	lysyl-tRNA synthetase	1.6	1.72E-02	Glucose	5.0	57329	36	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis
15598897	PA3702	wspR	WspR	17.5	1.56E-01	Citronellsäure	5.6	37887	2	Cytoplasmic	COG3706	Signal transduction mechanisms
15598911	PA3716		hypothetical protein	5.7	4.22E-02	Glucose	4.1	60503	2	Outer Membrane Vesicle		
15598916	PA3721	nalC	NalC	1.5	3.17E-01	Citronellsäure	5.7	23533	2	Cytoplasmic	COG1309	Transcription
15598918	PA3723		probable FMN oxidoreductase	14.2	3.43E-04	Citronellsäure	6.3	40319	16	Cytoplasmic	COG1902	Energy production and conversion
15598921	PA3726		conserved hypothetical protein	1.2	6.68E-01	Citronellsäure	4.8	20596	6	Cytoplasmic	COG4681	Function unknown
15598922	PA3727		hypothetical protein	2.1	3.37E-02	Glucose	4.9	26461	2	Cytoplasmic	COG1502	Lipid metabolism
15598923	PA3728		hypothetical protein	3.9	3.48E-02	Citronellsäure	4.9	197133	61	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning
15598924	PA3729		conserved hypothetical protein	1.1	5.97E-01	Citronellsäure	4.9	75882	2	Outer Membrane Vesicle	COG2268	Function unknown
15598926	PA3731		conserved hypothetical protein	1.2	1.49E-01	Glucose	7.5	24893	7	Cytoplasmic	COG1842	Transcription
15598927	PA3732		conserved hypothetical protein	2.1	2.00E-02	Citronellsäure	4.0	15959	2	Unknown	COG3789	Function unknown
15598928	PA3733		hypothetical protein	1540.2	4.90E-03	Citronellsäure	5.9	44766	2	Cytoplasmic	COG1804	Energy production and conversion
15598930	PA3735	thrC	threonine synthase	1.1	2.25E-01	Citronellsäure	6.6	51795	20	Periplasmic	COG0498	Amino acid transport and metabolism
15598931	PA3736	hom	homoserine dehydrogenase	1.2	7.63E-02	Glucose	5.1	46192	16	Cytoplasmic	COG0460	Amino acid transport and metabolism
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC	3.5	3.21E-04	Glucose	8.8	26095	9	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones
15598935	PA3740		hypothetical protein	5.8	1.86E-02	Citronellsäure	10.0	24754	5	Unknown		
15598937	PA3742	rplS	50S ribosomal protein L19	6.2	6.82E-02	Glucose	11.1	13032	3	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis
15598938	PA3743	trmD	tRNA (guanine-N1)-methyltransferase	104.0	2.28E-03	Glucose	4.9	28359	2	Cytoplasmic	COG0336	Translation, ribosomal structure and biogenesis
15598941	PA3746	ffh	signal recognition particle protein Ffh	1.4	4.30E-02	Glucose	10.3	49359	4	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2	1.7	1.06E-03	Citronellsäure	6.1	42342	17	Periplasmic	COG0027	Nucleotide transport and metabolism
15598948	PA3753		conserved hypothetical protein	1.6	1.09E-01	Citronellsäure	7.0	18509	5	Cytoplasmic	COG0663	General function prediction only
15598949	PA3754		hypothetical protein	2.6	1.45E-02	Citronellsäure	4.5	22855	3	Cytoplasmic		
15598950	PA3755		conserved hypothetical protein	36.3	1.09E-01	Glucose	4.6	20829	2	Cytoplasmic	COG1051	Nucleotide transport and metabolism
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase	2.2	1.33E-02	Citronellsäure	4.8	140646	66	Periplasmic	COG0046	Nucleotide transport and metabolism
15598960	PA3765		hypothetical protein	1.3	4.72E-02	Glucose	6.3	20903	2	Unknown	COG3644	Function unknown
15598962	PA3767		conserved hypothetical protein	1.1	6.69E-01	Glucose	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism
15598964	PA3769	guaA	GMP synthase	1.3	9.23E-02	Glucose	5.6	57959	35	Periplasmic	COG0519	Nucleotide transport and metabolism
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase	1.1	1.72E-01	Glucose	6.7	51707	35	Periplasmic	COG0516	Nucleotide transport and metabolism
15598974	PA3779		hypothetical protein	12.1	1.09E-02	Citronellsäure	5.3	37696	3	Periplasmic	COG1638	Carbohydrate transport and metabolism
15598978	PA3783		hypothetical protein	1.7	1.14E-03	Glucose	6.4	23091	9	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15598980	PA3785		conserved hypothetical protein	2.3	4.50E-02	Glucose	6.8	17000	6	Periplasmic	COG2847	Inorganic ion transport and metabolism
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precurs	36.2	5.87E-03	Glucose	6.4	79303	5	Periplasmic	COG1629	Inorganic ion transport and metabolism
15598990	PA3795		probable oxidoreductase	1.8	5.68E-03	Citronellsäure	5.3	34803	5	Cytoplasmic	COG0667	Energy production and conversion
15598992	PA3797		conserved hypothetical protein	1.0	6.44E-01	Citronellsäure	5.8	29996	6	Cytoplasmic	COG0388	General function prediction only
15598993	PA3798		probable aminotransferase	1.2	2.65E-01	Citronellsäure	6.2	42594	7	Cytoplasmic	COG0436	Amino acid transport and metabolism
15598996	PA3801		conserved hypothetical protein	3.0	8.99E-02	Glucose	4.8	23108	3	Outer Membrane Vesicle	COG2976	Function unknown
15598997	PA3802	hisS	histidyl-tRNA synthetase	1.3	1.25E-02	Citronellsäure	5.0	47480	15	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE	1.1	3.56E-01	Glucose	6.4	40056	14	Cytoplasmic	COG0821	Lipid metabolism
15599000	PA3805	pilF	type 4 fimbrial biogenesis protein PilF	4.0	9.51E-02	Glucose	7.3	28537	2	Periplasmic	COG3063	Cell motility and secretion
15599002	PA3807	ndk	nucleoside diphosphate kinase	98.9	1.66E-04	Glucose	5.3	15592	12	Cytoplasmic	COG0105	Nucleotide transport and metabolism
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]	1.7	1.98E-01	Glucose	4.0	12241	5	Cytoplasmic	COG0633	Energy production and conversion
15599005	PA3810	hscA	heat shock protein HscA	1.0	8.54E-01	Glucose	4.6	66446	18	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones
15599006	PA3811	hscB	heat shock protein HscB	1.9	1.17E-01	Glucose	4.6	20203	3	Cytoplasmic	COG1076	Posttranslational modification, protein turnover, chaperones
15599008	PA3813	iscU	probable iron-binding protein IscU	18.3	2.41E-03	Glucose	5.8	13753	4	Cytoplasmic	COG0822	Energy production and conversion
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)	1.3	4.67E-02	Citronellsäure	5.9	44666	28	Cytoplasmic	COG1104	Amino acid transport and metabolism
15599010	PA3815	iscR	IscR	1.9	7.88E-02	Glucose	6.9	17853	7	Unknown	COG1959	Transcription
15599012	PA3817		probable methyltransferase	1.1	2.31E-01	Glucose	6.2	28493	6	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis
15599013	PA3818		extragenic suppressor protein SuhB	1.6	8.58E-03	Glucose	6.6	29521	10	Periplasmic	COG0483	Carbohydrate transport and metabolism
15599014	PA3819		conserved hypothetical protein	3.1	2.10E-01	Citronellsäure	9.4	18941	3	Outer Membrane	COG3134	Function unknown
15599017	PA3822		conserved hypothetical protein	Infinity	1.63E-08	Glucose	9.6	11862	2	Outer Membrane Vesicle	COG1862	Intracellular trafficking and secretion
15599018	PA3823	tgt	queuine tRNA-ribosyltransferase	1.1	6.06E-01	Citronellsäure	6.9	41205	4	Cytoplasmic	COG0343	Translation, ribosomal structure and biogenesis
15599029	PA3834	valS	valyl-tRNA synthetase	1.0	7.75E-01	Citronellsäure	5.2	107707	51	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis
15599031	PA3836		hypothetical protein	4.7	1.36E-04	Citronellsäure	8.7	34220	22	Periplasmic	COG2984	General function prediction only
15599039	PA3844		hypothetical protein	2.4	2.71E-02	Glucose	4.8	22795	3	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones
15599041	PA3846		hypothetical protein	11.0	2.10E-03	Citronellsäure	5.1	19892	7	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15599044	PA3849		conserved hypothetical protein	7.8	7.19E-02	Citronellsäure	5.1	37930	4	Cytoplasmic	COG3081	General function prediction only
15599045	PA3850		hypothetical protein	2.8	3.45E-02	Citronellsäure	4.4	33613	2	Unknown		
15599047	PA3852		hypothetical protein	2.9	8.79E-04	Citronellsäure	5.4	33979	7	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15599053	PA3858		probable amino acid-binding protein	14.5	4.19E-05	Citronellsäure	7.9	37043	6	Periplasmic	COG0834	Amino acid transport and metabolism
15599054	PA3859		carboxylesterase	2.0	4.49E-02	Citronellsäure	4.9	23420	5	Unknown	COG0400	General function prediction only
15599055	PA3860		probable AMP-binding enzyme	34.2	2.55E-06	Citronellsäure	6.2	68986	28	Cytoplasmic	COG0318	Lipid metabolism
15599060	PA3865		probable amino acid binding protein	4.7	1.62E-04	Citronellsäure	6.1	28433	5	Periplasmic	COG0834	Amino acid transport and metabolism
15599061	PA3866		pyocin protein	1.2	7.20E-01	Citronellsäure	8.8	80731	5	Extracellular		
15599074	PA3879	narL	two-component response regulator NarL	14.6	1.39E-02	Citronellsäure	4.8	24255	3	Cytoplasmic	COG2197	Signal transduction mechanisms
15599081	PA3886		hypothetical protein	1.2	2.48E-01	Glucose	4.9	32290	4	Cytoplasmic	COG0647	Carbohydrate transport and metabolism
15599091	PA3896		probable 2-hydroxyacid dehydrogenase	1.2	1.68E-01	Glucose	8.2	35632	8	Cytoplasmic	COG1052	Energy production and conversion
15599098	PA3903	prfC	peptide chain release factor 3	1.3	5.33E-01	Citronellsäure	5.7	59865	8	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis
15599100	PA3905		hypothetical protein	1.8	6.35E-02	Glucose	7.7	20024	4	Unknown		
15599103	PA3908		hypothetical protein	1.2	1.57E-01	Citronellsäure	5.0	27294	9	Cytoplasmic		
15599113	PA3918	moaC	molybdopterin biosynthetic protein C	3.7	1.56E-01	Glucose	7.0	17306	11	Cytoplasmic	COG0315	Coenzyme metabolism
15599114	PA3919		conserved hypothetical protein	12.1	1.59E-05	Citronellsäure	6.3	51700	12	Cytoplasmic	COG1875	General function prediction only
15599115	PA3920		probable metal transporting P-type ATPase	353.2	3.31E-02	Citronellsäure	6.9	83437	2	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism
15599117	PA3922		conserved hypothetical protein	10.1	1.80E-04	Citronellsäure	9.0	51229	28	Periplasmic		
15599118	PA3923		hypothetical protein	11.5	1.19E-03	Citronellsäure	4.7	69590	11	Outer Membrane		
15599119	PA3924		probable medium-chain acyl-CoA ligase	1.9	1.34E-03	Citronellsäure	6.0	62315	21	Cytoplasmic	COG0318	Lipid metabolism
15599120	PA3925		probable acyl-CoA thiolase	11.2	7.29E-06	Citronellsäure	6.4	40553	33	Cytoplasmic	COG0183	Lipid metabolism
15599126	PA3931		conserved hypothetical protein	1.0	8.51E-01	Glucose	8.6	28101	11	Periplasmic	COG1464	Inorganic ion transport and metabolism
15599136	PA3941		hypothetical protein	1.1	8.32E-01	Citronellsäure	5.8	22025	4	Cytoplasmic	COG0546	General function prediction only
15599137	PA3942	tesB	acyl-CoA thioesterase II	1.9	4.24E-02	Glucose	5.8	32934	7	Cytoplasmic	COG1946	Lipid metabolism

15599139	PA3944		conserved hypothetical protein	1.5	2.68E-02	Glucose	5.3	21857	4	Unknown	COG1670	Translation, ribosomal structure and biogenesis
15599140	PA3945		conserved hypothetical protein	4.5	1.42E-03	Citronellsäure	5.7	22403	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis
15599143	PA3948	rocA1	Two-component response regulator RocA1	3.4	1.29E-02	Glucose	6.8	22996	6	Cytoplasmic	COG2197	Signal transduction mechanisms
15599146	PA3951		conserved hypothetical protein	2.7	8.45E-02	Citronellsäure	7.5	18088	2	Unknown	COG1432	Function unknown
15599151	PA3956		hypothetical protein	2.1	5.39E-01	Citronellsäure	5.1	15453	3	Unknown	COG0346	Amino acid transport and metabolism
15599156	PA3961		probable ATP-dependent helicase	1.3	3.69E-01	Glucose	7.5	91833	2	Cytoplasmic	COG1643	DNA replication, recombination, and repair
15599160	PA3965		probable transcriptional regulator	1.3	3.24E-01	Citronellsäure	5.7	19289	6	Cytoplasmic	COG1522	Transcription
15599165	PA3970	amn	AMP nucleosidase	1.2	3.53E-01	Glucose	6.8	56225	9	Cytoplasmic	COG0775	Nucleotide transport and metabolism
15599167	PA3972		probable acyl-CoA dehydrogenase	14.3	5.70E-06	Citronellsäure	6.4	60338	21	Cytoplasmic	COG1960	Lipid metabolism
15599170	PA3975	thiD	phosphomethylpyrimidine kinase	1.1	6.36E-01	Glucose	6.2	27979	5	Periplasmic	COG0351	Coenzyme metabolism
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase	2.6	2.69E-04	Citronellsäure	7.1	22146	5	Unknown	COG0352	Coenzyme metabolism
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase	1.3	2.12E-02	Citronellsäure	5.6	45398	21	Cytoplasmic	COG0001	Coenzyme metabolism
15599173	PA3978		hypothetical protein	14.3	1.91E-03	Glucose	4.3	19636	2	Unknown	COG0790	General function prediction only
15599175	PA3980		conserved hypothetical protein	4.0	1.82E-02	Glucose	5.8	49978	4	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis
15599177	PA3982		conserved hypothetical protein	6.6	2.11E-03	Citronellsäure	4.1	17981	2	Cytoplasmic	COG0319	General function prediction only
15599178	PA3983		conserved hypothetical protein	2.3	1.10E-01	Glucose	4.6	31549	6	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism
15599182	PA3987	leuS	leucyl-tRNA synthetase	1.0	8.70E-01	Glucose	5.5	97647	44	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis
15599183	PA3988		hypothetical protein	5.0	8.52E-03	Glucose	5.0	22884	8	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane
15599184	PA3989	holA	DNA polymerase III, delta subunit	1.0	7.77E-01	Glucose	6.9	37378	5	Unknown	COG1466	DNA replication, recombination, and repair
15599191	PA3996	lis	lipoate synthase	5.1	2.06E-04	Glucose	6.9	36733	7	Cytoplasmic	COG0320	Coenzyme metabolism
15599192	PA3997	lipB	lipoate-protein ligase B	2.8	6.45E-02	Citronellsäure	6.0	23856	5	Cytoplasmic	COG0321	Coenzyme metabolism
15599199	PA4004		conserved hypothetical protein	1.7	3.03E-01	Glucose	9.2	17791	2	Cytoplasmic	COG1576	Function unknown
15599201	PA4006	nadD	nicotinic acid mononucleotide adenylyltransferase	1.2	6.65E-01	Citronellsäure	6.4	23801	4	Cytoplasmic	COG1057	Coenzyme metabolism
15599202	PA4007	proA	gamma-glutamyl phosphate reductase	1.3	5.27E-02	Citronellsäure	5.2	45044	10	Periplasmic	COG0014	Amino acid transport and metabolism
15599205	PA4010		hypothetical protein	1.7	5.54E-03	Glucose	8.8	26949	3	Cytoplasmic	COG2094	DNA replication, recombination, and repair
15599207	PA4012		hypothetical protein	3.5	5.45E-05	Citronellsäure	4.3	21808	4	Cytoplasmic	COG2802	General function prediction only
15599210	PA4015		conserved hypothetical protein	12.1	1.65E-04	Glucose	5.6	16700	11	Cytoplasmic	COG2030	Lipid metabolism
15599212	PA4017		conserved hypothetical protein	2.1	5.73E-02	Citronellsäure	7.1	23164	4	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane
15599214	PA4019		probable aromatic acid decarboxylase	1.0	8.26E-01	Glucose	4.8	22367	2	Cytoplasmic	COG0163	Coenzyme metabolism
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diar	1.1	6.19E-01	Citronellsäure	6.4	48469	5	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane
15599220	PA4025		probable ethanolamine ammonia-lyase light chain	4.8	3.65E-02	Citronellsäure	6.6	30144	2	Cytoplasmic	COG4302	Amino acid transport and metabolism
15599221	PA4026		probable acetyltransferase	2.2	7.66E-01	Citronellsäure	7.0	18049	9	Cytoplasmic	COG0456	General function prediction only
15599226	PA4031	ppa	inorganic pyrophosphatase	1.8	6.67E-02	Glucose	4.9	19396	14	Cytoplasmic	COG0221	Energy production and conversion
15599230	PA4035		hypothetical protein	2.4	1.33E-01	Citronellsäure	6.3	35895	6	Periplasmic	COG4254	Function unknown
15599238	PA4043	ispA	geranyltranstransferase	1.3	1.45E-02	Glucose	5.1	31464	6	Cytoplasmic	COG0142	Coenzyme metabolism
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase	2.8	2.64E-02	Glucose	5.5	68049	8	Cytoplasmic	COG1154	Coenzyme metabolism
15599242	PA4047	ribA	GTP cyclohydrolase II	1.0	7.31E-01	Citronellsäure	6.6	22067	2	Cytoplasmic	COG0807	Coenzyme metabolism
15599243	PA4048		hypothetical protein	1.1	6.81E-01	Citronellsäure	9.4	23085	2	Unknown	COG3577	General function prediction only
15599247	PA4052	nusB	NusB protein	1.6	2.09E-01	Citronellsäure	8.5	17675	4	Unknown	COG0781	Transcription
15599248	PA4053	ribE	6,7-dimethyl-8-ribityllumazine synthase	47.5	4.10E-02	Glucose	5.8	16413	5	Cytoplasmic	COG0054	Coenzyme metabolism
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate	2.5	1.72E-03	Citronellsäure	5.1	39438	14	Cytoplasmic	COG0108	Coenzyme metabolism
15599250	PA4055	ribC	riboflavin synthase alpha chain	2.1	2.62E-02	Citronellsäure	6.4	23469	5	Cytoplasmic	COG0307	Coenzyme metabolism
15599251	PA4056	ribD	riboflavin-specific deaminase/reductase	2.7	1.79E-01	Citronellsäure	7.3	39764	3	Cytoplasmic	COG0117	Coenzyme metabolism
15599252	PA4057	nrdR	NrdR	18.3	4.01E-03	Glucose	8.0	17925	7	Cytoplasmic	COG1327	Transcription
15599256	PA4061		probable thioredoxin	1.8	2.96E-02	Citronellsäure	4.4	31878	13	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones
15599258	PA4063		hypothetical protein	1.7	1.97E-01	Citronellsäure	6.4	21235	3	Periplasmic		
15599262	PA4067	oprG	Outer membrane protein OprG precursor	2.2	6.98E-01	Glucose	4.7	25193	2	Periplasmic	COG3047	Cell envelope biogenesis, outer membrane
15599263	PA4068		probable epimerase	1.2	2.99E-01	Citronellsäure	5.7	33310	11	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane
15599264	PA4069		hypothetical protein	1.3	3.79E-01	Glucose	6.3	32939	5	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane
15599274	PA4079		probable dehydrogenase	1.4	2.87E-02	Citronellsäure	5.1	24319	7	Extracellular	COG0300	General function prediction only
15599310	PA4115		conserved hypothetical protein	2.6	1.58E-03	Citronellsäure	7.1	51130	5	Cytoplasmic	COG1611	General function prediction only
15599311	PA4116	bphO	heme oxygenase, BphO	1.3	6.54E-01	Glucose	4.9	21464	2	Cytoplasmic	COG3230	Inorganic ion transport and metabolism
15599312	PA4117	bphP	bacterial phytochrome, BphP	5.2	2.18E-01	Glucose	5.7	80930	2	Cytoplasmic Membrane	COG4251	Signal transduction mechanisms
15599357	PA4162		probable short-chain dehydrogenase	2.7	8.56E-02	Glucose	8.0	24857	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15599358	PA4163		hypothetical protein	1.5	6.29E-02	Glucose	4.7	60494	19	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis
15599375	PA4180		probable acetolactate synthase large subunit	1.3	3.56E-01	Glucose	6.3	59806	5	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase
15599390	PA4195		probable binding protein component of ABC transporter	2.0	1.34E-03	Citronellsäure	7.9	29539	8	Periplasmic	COG0834	Amino acid transport and metabolism
15599394	PA4199		probable acyl-CoA dehydrogenase	2.2	1.26E-02	Citronellsäure	5.0	63926	10	Cytoplasmic	COG1960	Lipid metabolism
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	1.1	7.63E-01	Citronellsäure	4.9	36533	5	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane
15599397	PA4202		hypothetical protein	2.1	1.54E-01	Glucose	8.1	36782	7	Cytoplasmic	COG2070	General function prediction only
15599399	PA4204	ppgL	periplasmic gluconolactonase, PpgL	2.2	3.63E-02	Citronellsäure	7.4	41616	4	Periplasmic	COG2706	Carbohydrate transport and metabolism
15599423	PA4227	pchR	transcriptional regulator PchR	100.7	6.10E-04	Glucose	7.4	32339	2	Cytoplasmic	COG2207	Transcription
15599428	PA4232	ssb	single-stranded DNA-binding protein	1.1	5.25E-01	Glucose	5.3	18557	9	Cytoplasmic	COG0629	DNA replication, recombination, and repair
15599430	PA4234	uvrA	excinuclease ABC subunit A	2.1	7.78E-02	Citronellsäure	6.6	104456	36	Cytoplasmic	COG0178	DNA replication, recombination, and repair
15599431	PA4235	bfrA	bacterioferritin	3.8	1.95E-03	Glucose	4.8	17940	9	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism
15599432	PA4236	katA	catalase	3.7	9.93E-05	Citronellsäure	6.7	55589	21	Periplasmic	COG0753	Inorganic ion transport and metabolism
15599433	PA4237	rplQ	50S ribosomal protein L17	26.3	3.62E-03	Glucose	11.1	14504	3	Outer Membrane Vesicle	COG0203	Translation, ribosomal structure and biogenesis
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.0	9.53E-01	Glucose	4.6	36649	16	Outer Membrane Vesicle	COG0202	Transcription
15599435	PA4239	rpsD	30S ribosomal protein S4	4.8	4.93E-03	Glucose	10.5	23277	12	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis
15599436	PA4240	rpsK	30S ribosomal protein S11	220.4	1.27E-04	Glucose	11.5	13630	6	Outer Membrane Vesicle	COG0100	Translation, ribosomal structure and biogenesis
15599437	PA4241	rpsM	30S ribosomal protein S13	73.5	7.05E-04	Glucose	11.5	13265	9	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis
15599440	PA4244	rplO	50S ribosomal protein L15	187.8	1.58E-04	Glucose	11.6	15174	5	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis
15599442	PA4246	rpsE	30S ribosomal protein S5	2.6	1.04E-01	Glucose	10.6	17625	12	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis
15599443	PA4247	rplR	50S ribosomal protein L18	24.3	1.15E-01	Glucose	10.9	12662	2	Cytoplasmic	COG0256	Translation, ribosomal structure and biogenesis
15599444	PA4248	rplF	50S ribosomal protein L6	3.3	1.20E-01	Glucose	10.5	19099	9	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis
15599445	PA4249	rpsH	30S ribosomal protein S8	189.0	7.89E-04	Glucose	10.2	14171	7	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis
15599446	PA4250	rpsN	30S ribosomal protein S14	161.5	5.50E-04	Glucose	11.9	11565	4	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis
15599447	PA4251	rplE	50S ribosomal protein L5	2.4	2.51E-02	Citronellsäure	10.3	20392	18	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis
15599448	PA4252	rplX	50S ribosomal protein L24	151.9	2.54E-03	Glucose	11.0	11470	5	Cytoplasmic	COG0198	Translation, ribosomal structure and biogenesis
15599449	PA4253	rplN	50S ribosomal protein L14	20.8	2.42E-02	Glucose	11.4	13412	4	Outer Membrane Vesicle	COG0093	Translation, ribosomal structure and biogenesis
15599452	PA4256	rplP	50S ribosomal protein L16	18.5	2.12E-02	Glucose	11.8	15401	4	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis
15599453	PA4257	rpsC	30S ribosomal protein S3	3.3	1.33E-02	Glucose	10.8	25838	15	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis
15599454	PA4258	rplV	50S ribosomal protein L22	12.1	3.99E-02	Glucose	10.9	11911	3	Cytoplasmic	COG0091	Translation, ribosomal structure and biogenesis

15599456	PA4260	rplB	50S ribosomal protein L2	48.9	5.89E-04	Glucose	11.8	29579	3	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis
15599457	PA4261	rplW	50S ribosomal protein L23	303.4	5.07E-04	Glucose	10.8	10950	3	Cytoplasmic	COG0089	Translation, ribosomal structure and biogenesis
15599458	PA4262	rplD	50S ribosomal protein L4	21.6	1.03E-02	Glucose	10.6	21640	3	Outer Membrane Vesicle	COG0088	Translation, ribosomal structure and biogenesis
15599459	PA4263	rplC	50S ribosomal protein L3	3.9	9.38E-02	Glucose	10.6	22592	4	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis
15599461	PA4265	tufA	elongation factor Tu	1.8	8.29E-03	Citronellsäure	5.0	43337	58	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis
15599462	PA4266	fusA1	elongation factor G	1.1	5.99E-01	Glucose	4.8	77752	80	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis
15599463	PA4267	rpsG	30S ribosomal protein S7	5.6	4.24E-02	Glucose	10.9	17504	16	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis
15599464	PA4268	rpsL	30S ribosomal protein S12	110.7	3.35E-03	Glucose	11.6	13799	5	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	3.8	3.92E-03	Citronellsäure	7.1	154364	108	Outer Membrane Vesicle	COG0086	Transcription
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	2.7	9.27E-03	Citronellsäure	5.6	150837	118	Periplasmic	COG0085	Transcription
15599468	PA4272	rplJ	50S ribosomal protein L10	26.3	1.03E-04	Glucose	9.5	17602	7	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis
15599469	PA4273	rplA	50S ribosomal protein L1	3.0	1.22E-03	Citronellsäure	10.3	24234	13	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis
15599470	PA4274	rplK	50S ribosomal protein L11	322.2	1.17E-05	Glucose	10.4	14907	5	Outer Membrane Vesicle	COG0080	Translation, ribosomal structure and biogenesis
15599471	PA4275	nusG	transcription antitermination protein NusG	1.1	7.44E-01	Citronellsäure	5.8	20130	13	Cytoplasmic	COG0250	Transcription
15599474	PA4278		hypothetical protein	60.6	1.18E-03	Glucose	5.9	26077	2	Unknown		
15599475	PA4279		hypothetical protein	1.1	1.99E-01	Glucose	5.4	26758	6	Cytoplasmic	COG1521	Transcription
15599478	PA4282		probable exonuclease	2.4	3.36E-02	Citronellsäure	5.5	138959	16	Extracellular	COG0419	DNA replication, recombination, and repair
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	1.0	7.71E-01	Glucose	6.7	79084	3	Cytoplasmic	COG0507	DNA replication, recombination, and repair
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	2.8	6.66E-02	Citronellsäure	5.5	139379	18	Unknown	COG1074	DNA replication, recombination, and repair
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	2.3	4.50E-02	Citronellsäure	5.3	132646	11	Cytoplasmic	COG1330	DNA replication, recombination, and repair
15599482	PA4286		hypothetical protein	7.0	1.13E-02	Citronellsäure	5.2	24815	3	Unknown	COG0095	Coenzyme metabolism
15599492	PA4296	pprB	two-component response regulator, PprB	143.0	9.39E-02	Citronellsäure	6.7	30557	2	Cytoplasmic	COG2197	Signal transduction mechanisms
15599504	PA4308		conserved hypothetical protein	1.2	5.32E-01	Citronellsäure	6.5	53246	11	Unknown	COG0433	Replication, recombination, and repair
15599506	PA4310	pctB	chemotactic transducer PctB	1.3	4.39E-01	Glucose	4.8	68076	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	1.1	4.76E-01	Glucose	6.5	32410	9	Periplasmic	COG0788	Nucleotide transport and metabolism
15599511	PA4315	mvaT	transcriptional regulator MvaT, P16 subunit	84.1	7.89E-02	Glucose	10.1	14180	2	Cytoplasmic		
15599512	PA4316	sbcB	exodeoxyribonuclease I	2.9	1.82E-03	Glucose	5.4	55449	6	Cytoplasmic	COG2925	DNA replication, recombination, and repair
15599518	PA4322		conserved hypothetical protein	3.0	1.78E-02	Glucose	6.2	36661	5	Cytoplasmic	COG0714	General function prediction only
15599525	PA4329	pykA	pyruvate kinase II	2.1	4.69E-03	Glucose	6.7	52252	29	Periplasmic	COG0469	Carbohydrate transport and metabolism
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	49.9	1.71E-05	Citronellsäure	6.7	28152	13	Cytoplasmic	COG1024	Lipid metabolism
15599529	PA4333		probable fumarase	1.6	8.76E-02	Glucose	5.2	54763	25	Periplasmic	COG1951	Energy production and conversion
15599532	PA4336		conserved hypothetical protein	1.5	2.68E-02	Glucose	6.0	20993	6	Cytoplasmic	COG0693	General function prediction only
15599536	PA4340		hypothetical protein	1.5	1.98E-01	Glucose	6.1	20988	6	Periplasmic		
15599541	PA4345		hypothetical protein	1.1	7.56E-01	Citronellsäure	4.8	22161	2	Unknown	COG2353	Function unknown
15599545	PA4349		hypothetical protein	1.8	7.30E-03	Citronellsäure	6.2	31671	5	Unknown	COG1960	Lipid metabolism
15599548	PA4352		conserved hypothetical protein	17.6	3.68E-03	Citronellsäure	6.2	30972	8	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms
15599552	PA4356	xenB	xenobiotic reductase	1.8	1.49E-02	Citronellsäure	4.9	37796	18	Periplasmic	COG1902	Energy production and conversion
15599562	PA4366	sodB	superoxide dismutase	2.4	5.43E-02	Citronellsäure	5.2	21351	9	Periplasmic	COG0605	Inorganic ion transport and metabolism
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein pre	1.5	1.73E-01	Glucose	4.5	47230	22	Outer Membrane	COG3487	Inorganic ion transport and metabolism
15599568	PA4372		hypothetical protein	2.4	1.32E-03	Glucose	6.0	38323	9	Outer Membrane Vesicle	COG3489	General function prediction only
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	2.0	4.12E-03	Citronellsäure	6.7	45690	3	Cytoplasmic	COG1488	Coenzyme metabolism
15599577	PA4381		probable two-component response regulator	1.8	5.26E-02	Citronellsäure	5.9	25235	7	Cytoplasmic	COG0745	Signal transduction mechanisms
15599581	PA4385	groEL	GroEL protein	1.1	5.76E-01	Glucose	4.8	57086	57	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones
15599582	PA4386	groES	GroES protein	72.6	7.28E-06	Glucose	4.9	10267	7	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones
15599584	PA4388		hypothetical protein	1.1	5.07E-01	Glucose	6.4	26982	7	Cytoplasmic	COG0748	Inorganic ion transport and metabolism
15599585	PA4389		probable short-chain dehydrogenase	4.7	4.96E-04	Citronellsäure	7.3	26720	26	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15599591	PA4395		conserved hypothetical protein	2.2	5.98E-02	Citronellsäure	8.2	18044	13	Cytoplasmic	COG1666	Function unknown
15599595	PA4399		conserved hypothetical protein	5.7	4.53E-03	Citronellsäure	6.1	21065	4	Cytoplasmic	COG2096	Coenzyme transport and metabolism
15599596	PA4400		probable pyrophosphohydrolase	1.9	7.91E-03	Citronellsäure	5.1	34022	4	Cytoplasmic	COG0352	Coenzyme metabolism
15599597	PA4401		probable glutathione S-transferase	1.3	1.17E-01	Citronellsäure	5.4	23789	17	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones
15599598	PA4402	argJ	glutamate N-acetyltransferase	1.1	4.97E-01	Citronellsäure	5.3	41762	22	Cytoplasmic	COG1364	Amino acid transport and metabolism
15599599	PA4403	secA	secretion protein SecA	1.4	2.87E-02	Citronellsäure	5.4	103854	46	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.3	9.86E-02	Glucose	5.0	33435	14	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane
15599603	PA4407	ftsZ	cell division protein FtsZ	1.0	7.76E-01	Glucose	4.7	41218	13	Periplasmic	COG0206	Cell division and chromosome partitioning
15599604	PA4408	ftsA	cell division protein FtsA	1.1	5.00E-01	Glucose	5.0	44646	11	Cytoplasmic	COG0849	Cell division and chromosome partitioning
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.9	2.73E-02	Glucose	4.7	34363	11	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.8	4.13E-02	Glucose	6.1	51949	7	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.2	4.11E-01	Glucose	5.7	48080	14	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate	1.7	1.00E-03	Citronellsäure	6.5	47412	16	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimela	1.1	2.66E-01	Citronellsäure	5.1	51263	17	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane
15599616	PA4420		conserved hypothetical protein	1.4	1.93E-01	Glucose	7.7	34640	5	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane
15599619	PA4423		conserved hypothetical protein	43.6	1.89E-04	Glucose	7.2	65629	5	Periplasmic	COG3107	General function prediction only
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	2.2	7.79E-02	Citronellsäure	4.7	21413	9	Cytoplasmic	COG0279	Carbohydrate transport and metabolism
15599622	PA4426		conserved hypothetical protein	5.2	1.99E-02	Glucose	9.8	20619	4	Outer Membrane Vesicle	COG2823	General function prediction only
15599623	PA4427	sspB	stringent starvation protein B	123.2	6.33E-02	Glucose	4.3	14548	2	Unknown	COG2969	General function prediction only
15599624	PA4428	sspA	stringent starvation protein A	1.6	5.32E-03	Citronellsäure	6.1	23615	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15599625	PA4429		probable cytochrome c1 precursor	3.1	7.57E-03	Glucose	7.5	28993	4	Outer Membrane Vesicle	COG2857	Energy production and conversion
15599627	PA4431		probable iron-sulfur protein	5.5	9.37E-04	Glucose	6.5	20828	4	Outer Membrane Vesicle	COG0723	Energy production and conversion
15599628	PA4432	rpsI	30S ribosomal protein S9	135.0	8.78E-05	Glucose	11.8	14615	5	Outer Membrane Vesicle	COG0103	Translation, ribosomal structure and biogenesis
15599629	PA4433	rplM	50S ribosomal protein L13	3.0	6.59E-02	Glucose	10.4	16029	5	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis
15599630	PA4434		probable oxidoreductase	1.8	1.02E-02	Citronellsäure	5.7	38644	7	Periplasmic	COG0667	Energy production and conversion
15599631	PA4435		probable acyl-CoA dehydrogenase	30.5	7.73E-06	Citronellsäure	6.1	42128	18	Cytoplasmic	COG1960	Lipid metabolism
15599634	PA4438		conserved hypothetical protein	1.4	1.55E-01	Citronellsäure	6.2	41993	4	Cytoplasmic	COG1485	General function prediction only
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.0	3.05E-01	Glucose	5.8	48961	17	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis
15599636	PA4440		hypothetical protein	1.1	4.78E-01	Citronellsäure	6.2	22315	5	Unknown	COG2945	General function prediction only
15599637	PA4441		hypothetical protein	48.0	8.05E-03	Glucose	6.3	16386	3	Outer Membrane Vesicle	COG3105	Function unknown
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	1.1	4.47E-01	Glucose	5.6	69268	30	Periplasmic	COG2895	Inorganic ion transport and metabolism
15599639	PA4443	cysD	ATP sulfurylase small subunit	1.1	2.46E-01	Glucose	7.1	35478	15	Cytoplasmic	COG0175	Amino acid transport and metabolism
15599641	PA4445		conserved hypothetical protein	1.0	7.50E-01	Glucose	5.3	27360	7	Cytoplasmic	COG0327	Function unknown
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	1.7	1.33E-02	Glucose	6.0	38655	11	Periplasmic	COG0079	Amino acid transport and metabolism
15599644	PA4448	hisD	histidinol dehydrogenase	2.0	3.47E-02	Glucose	4.9	47179	20	Periplasmic	COG0141	Amino acid transport and metabolism
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	1.1	8.33E-01	Glucose	9.3	22844	18	Cytoplasmic	COG0040	Amino acid transport and metabolism
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.1	3.85E-01	Citronellsäure	5.5	44645	22	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane

15599649	PA4453		conserved hypothetical protein	1.2	1.91E-01	Glucose	9.7	23760	12	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism
15599650	PA4454		conserved hypothetical protein	22.7	8.06E-02	Glucose	4.7	16557	3	Outer Membrane Vesicle	COG1463	Secondary metabolites biosynthesis, transport, and catabolism
15599653	PA4457		arabinose-5-phosphate isomerase KdsD	1.5	1.23E-01	Glucose	5.6	34179	12	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane
15599654	PA4458		conserved hypothetical protein	1.3	2.12E-01	Citronellsäure	5.6	19334	10	Cytoplasmic	COG1778	General function prediction only
15599656	PA4460		conserved hypothetical protein	1.1	6.49E-01	Citronellsäure	9.6	19126	10	Periplasmic	COG1934	Function unknown
15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.3	3.87E-02	Glucose	4.4	56054	9	Cytoplasmic	COG1508	Transcription
15599660	PA4464	ptsN	nitrogen regulatory IIA protein	35.1	1.38E-01	Glucose	4.7	16730	2	Cytoplasmic	COG1762	Carbohydrate transport and metabolism
15599661	PA4465		conserved hypothetical protein	2.1	1.67E-03	Citronellsäure	5.7	32218	6	Cytoplasmic	COG1660	General function prediction only
15599664	PA4468	sodM	superoxide dismutase	1.2	5.51E-01	Glucose	6.2	22506	7	Periplasmic	COG0605	Inorganic ion transport and metabolism
15599665	PA4469		hypothetical protein	62.9	3.99E-04	Glucose	6.9	17141	2	Cytoplasmic		
15599666	PA4470	fumC1	fumarate hydratase	1.7	7.23E-02	Citronellsäure	5.9	48695	14	Cytoplasmic	COG0114	Energy production and conversion
15599668	PA4472	pmbA	PmbA protein	1.7	2.56E-03	Citronellsäure	5.5	47908	10	Cytoplasmic	COG0312	General function prediction only
15599670	PA4474		conserved hypothetical protein	1.1	9.76E-01	Citronellsäure	5.0	50266	6	Cytoplasmic	COG0312	General function prediction only
15599671	PA4475		conserved hypothetical protein	2.4	1.62E-03	Citronellsäure	6.8	30724	8	Cytoplasmic	COG0388	General function prediction only
15599673	PA4477	cafA	cytoplasmic axial filament protein	2.8	4.91E-03	Citronellsäure	5.0	54665	7	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis
15599674	PA4478		conserved hypothetical protein	1.3	2.86E-01	Glucose	4.7	20974	10	Cytoplasmic	COG0424	Cell division and chromosome partitioning
15599677	PA4481	mreB	rod shape-determining protein MreB	1.0	9.49E-01	Glucose	5.1	36976	17	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.2	2.62E-01	Glucose	5.5	51862	25	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.0	7.90E-01	Citronellsäure	5.1	53081	28	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis
15599685	PA4489		conserved hypothetical protein	1.2	2.35E-01	Glucose	5.3	167428	11	Outer Membrane Vesicle	COG2373	General function prediction only
15599689	PA4493	roxR	RoxR	1.4	1.12E-01	Citronellsäure	5.3	20616	9	Cytoplasmic	COG4567	Signal transduction mechanisms
15599691	PA4495		hypothetical protein	2.6	2.04E-03	Citronellsäure	5.9	24879	9	Periplasmic	COG3471	Function unknown
15599692	PA4496		probable binding protein component of ABC transporter	4.9	3.49E-05	Citronellsäure	7.6	60077	16	Periplasmic	COG0747	Amino acid transport and metabolism
15599695	PA4499		probable transcriptional regulator	1.2	3.48E-01	Citronellsäure	6.2	20435	3	Cytoplasmic	COG1396	Transcription
15599698	PA4502		probable binding protein component of ABC transporter	7.7	3.92E-03	Citronellsäure	6.6	58611	3	Periplasmic	COG0747	Amino acid transport and metabolism
15599711	PA4515		conserved hypothetical protein	14.4	6.34E-03	Glucose	6.6	25616	2	Cytoplasmic	COG3128	Function unknown
15599715	PA4519	speC	ornithine decarboxylase	1.0	8.03E-01	Citronellsäure	4.7	43559	17	Cytoplasmic	COG0019	Amino acid transport and metabolism
15599718	PA4522	ampD	beta-lactamase expression regulator AmpD	3.0	2.71E-02	Glucose	5.5	21028	4	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	1.1	2.53E-01	Citronellsäure	5.1	30552	13	Cytoplasmic	COG0157	Coenzyme metabolism
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	4.7	2.14E-02	Glucose	6.6	15512	6	Outer Membrane Vesicle	COG4969	Cell motility and secretion
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	1.1	4.25E-01	Glucose	5.7	62328	8	Cytoplasmic	COG2804	Cell motility and secretion
15599725	PA4529	coaE	dephosphocoenzyme A kinase	1.1	4.86E-01	Glucose	6.8	22843	10	Cytoplasmic	COG0237	Coenzyme metabolism
15599729	PA4533		hypothetical protein	12.9	1.81E-02	Glucose	9.5	17613	3	Periplasmic		
15599738	PA4542	clpB	ClpB protein	1.0	7.55E-01	Citronellsäure	5.1	95005	44	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
15599739	PA4543		conserved hypothetical protein	8.5	1.28E-03	Glucose	7.5	26047	5	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism
15599743	PA4547	pilR	two-component response regulator PilR	1.3	2.60E-01	Glucose	5.9	49737	4	Cytoplasmic	COG2204	Signal transduction mechanisms
15599744	PA4548		probable D-amino acid oxidase	1.9	3.92E-02	Citronellsäure	6.5	39413	3	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	1.6	2.61E-01	Citronellsäure	6.4	126583	6	Periplasmic	COG3419	Cell motility and secretion
15599753	PA4557	lytB	LytB protein	1.7	1.95E-02	Glucose	5.2	34762	5	Cytoplasmic	COG0761	Lipid metabolism
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	7.2	4.23E-02	Glucose	4.3	15984	9	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	1.6	2.30E-02	Citronellsäure	6.1	105464	44	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	1.7	6.21E-04	Glucose	9.1	34340	8	Cytoplasmic	COG0196	Coenzyme metabolism
15599760	PA4564		conserved hypothetical protein	29.1	1.39E-03	Glucose	9.2	16724	5	Periplasmic	COG3045	Function unknown
15599761	PA4565	proB	glutamate 5-kinase	1.0	8.36E-01	Glucose	7.3	39845	7	Cytoplasmic	COG0263	Amino acid transport and metabolism
15599762	PA4566	obg	GTP-binding protein Obg	2.2	6.88E-03	Citronellsäure	4.5	44338	6	Cytoplasmic	COG0536	General function prediction only
15599764	PA4568	rplU	50S ribosomal protein L21	68.1	8.56E-02	Glucose	10.6	11654	2	Outer Membrane Vesicle	COG0261	Translation, ribosomal structure and biogenesis
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.1	6.22E-02	Glucose	4.6	34851	15	Cytoplasmic	COG0142	Coenzyme metabolism
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	1.6	1.45E-02	Glucose	4.5	21795	10	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones
15599772	PA4576		probable ATP-dependent protease	1.5	6.63E-02	Glucose	4.7	90222	42	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones
15599783	PA4587	ccpR	cytochrome c551 peroxidase precursor	139.2	5.67E-03	Citronellsäure	6.7	37403	2	Periplasmic	COG1858	Inorganic ion transport and metabolism
15599784	PA4588	gdhA	glutamate dehydrogenase	1.3	4.60E-02	Glucose	6.0	48856	23	Unknown	COG0334	Amino acid transport and metabolism
15599791	PA4595		probable ATP-binding component of ABC transporter	1.1	2.20E-01	Glucose	5.4	61302	30	Periplasmic	COG0488	General function prediction only
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.2	1.82E-01	Citronellsäure	6.0	45157	19	Periplasmic	COG0112	Amino acid transport and metabolism
15599800	PA4604		conserved hypothetical protein	2.6	2.91E-02	Citronellsäure	4.5	37256	3	Cytoplasmic	COG0523	General function prediction only
15599810	PA4614	mscL	conductance mechanosensitive channel	2.6	1.07E-01	Glucose	4.6	14432	2	Outer Membrane Vesicle	COG1970	Cell envelope biogenesis, outer membrane
15599811	PA4615		probable oxidoreductase	1.2	1.92E-01	Citronellsäure	5.2	29377	10	Cytoplasmic	COG1018	Energy production and conversion
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	1.8	1.89E-02	Glucose	4.7	219755	2	Extracellular		
15599822	PA4626	hprA	glycerate dehydrogenase	1.4	4.32E-02	Glucose	6.7	34285	8	Cytoplasmic	COG1052	Energy production and conversion
15599823	PA4627		conserved hypothetical protein	2.3	3.64E-03	Glucose	8.1	35937	2	Cytoplasmic	COG2813	Translation, ribosomal structure and biogenesis
15599828	PA4632		hypothetical protein	2.1	5.86E-02	Citronellsäure	7.6	29159	5	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones
15599829	PA4633		probable chemotaxis transducer	21.1	1.01E-01	Glucose	4.5	76623	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion
15599830	PA4634		hypothetical protein	1.1	6.05E-01	Citronellsäure	8.7	22996	2	Unknown	COG2135	Function unknown
15599835	PA4639		hypothetical protein	1.1	6.10E-01	Glucose	9.8	20736	8	Outer Membrane Vesicle		
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.3	1.99E-01	Glucose	7.0	55498	6	Cytoplasmic	COG0579	General function prediction only
15599839	PA4644		hypothetical protein	4.9	1.68E-01	Glucose	5.9	17109	2	Unknown		
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	1.5	7.35E-02	Glucose	5.6	20639	15	Cytoplasmic	COG0634	Nucleotide transport and metabolism
15599841	PA4646	upp	uracil phosphoribosyltransferase	1.0	8.44E-01	Glucose	7.0	22938	19	Cytoplasmic	COG0035	Nucleotide transport and metabolism
15599852	PA4657		hypothetical protein	1.4	2.20E-02	Citronellsäure	6.8	35913	7	Unknown	COG3380	General function prediction only
15599857	PA4662	murI	glutamate racemase	2.2	2.60E-02	Glucose	5.2	28274	3	Cytoplasmic	COG0796	Cell envelope biogenesis, outer membrane
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	1.1	5.06E-01	Citronellsäure	5.6	26686	5	Cytoplasmic	COG0476	Coenzyme metabolism
15599860	PA4665	prfA	peptide chain release factor 1	1.5	2.95E-01	Citronellsäure	4.8	40040	5	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis
15599864	PA4669	ipk	isopentenyl monophosphate kinase	1.1	5.12E-01	Glucose	6.6	30843	6	Unknown	COG1947	Lipid metabolism
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.7	3.84E-02	Glucose	6.5	34008	19	Periplasmic	COG0462	Nucleotide transport and metabolism
15599866	PA4671		probable ribosomal protein L25	2.1	5.82E-03	Citronellsäure	6.2	21962	11	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis
15599867	PA4672		peptidyl-tRNA hydrolase	2.4	1.58E-03	Glucose	9.8	20772	5	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis
15599868	PA4673		conserved hypothetical protein	1.4	7.15E-02	Citronellsäure	4.8	40078	13	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis
15599870	PA4675		probable TonB-dependent receptor	1.0	9.52E-01	Citronellsäure	5.2	80952	10	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599871	PA4676		probable carbonic anhydrase	1.8	2.02E-02	Glucose	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism
15599873	PA4678	rimI	peptide n-acetyltransferase RimI	5.9	1.73E-02	Glucose	6.2	17095	3	Cytoplasmic	COG0456	General function prediction only
15599874	PA4679		hypothetical protein	15.5	1.59E-03	Glucose	5.0	24841	2	Unknown		
15599881	PA4686		hypothetical protein	21.7	2.37E-04	Glucose	5.3	106827	22	Periplasmic	COG1196	Cell division and chromosome partitioning
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	1.1	4.40E-01	Citronellsäure	5.5	36149	19	Periplasmic	COG1840	Inorganic ion transport and metabolism
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.1	3.96E-01	Glucose	5.7	36424	32	Periplasmic	COG0059	Amino acid transport and metabolism

15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	1.9	2.77E-01	Glucose	6.3	17784	10	Cytoplasmic	COG0440	Amino acid transport and metabolism
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.3	7.81E-02	Glucose	6.8	62986	34	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase
15599895	PA4701		conserved hypothetical protein	1.0	7.18E-01	Citronellsäure	6.0	58344	25	Periplasmic	COG2187	Function unknown
15599902	PA4708	phuT	Heme-transport protein, PhuT	1.1	2.23E-01	Glucose	7.8	31037	15	Periplasmic	COG4558	Inorganic ion transport and metabolism
15599903	PA4709		probable hemin degrading factor	1.7	9.42E-04	Glucose	5.6	39057	4	Cytoplasmic	COG3720	Inorganic ion transport and metabolism
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR pre	2.4	1.38E-01	Glucose	5.9	84724	3	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599909	PA4715		probable aminotransferase	1.3	3.01E-01	Glucose	8.1	46064	3	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599910	PA4716		hypothetical protein	1.6	1.12E-02	Citronellsäure	5.0	30850	2	Cytoplasmic	COG0384	General function prediction only
15599914	PA4720	trmA	tRNA (uracil-5-)-methyltransferase	1.3	3.07E-01	Glucose	7.0	41206	2	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis
15599916	PA4722		probable aminotransferase	1.2	4.44E-01	Glucose	5.7	42567	6	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599917	PA4723	dksA	suppressor protein DksA	2.2	4.12E-03	Citronellsäure	4.8	17344	11	Periplasmic	COG1734	Signal transduction mechanisms
15599920	PA4726	cbrB	two-component response regulator CbrB	1.1	4.84E-01	Glucose	5.5	52286	17	Cytoplasmic	COG2204	Signal transduction mechanisms
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophos	1.6	4.30E-01	Citronellsäure	4.6	18014	4	Cytoplasmic	COG0801	Coenzyme metabolism
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.0	7.46E-01	Glucose	5.8	27874	9	Periplasmic	COG0413	Coenzyme metabolism
15599924	PA4730	panC	pantoate--beta-alanine ligase	1.1	5.65E-01	Citronellsäure	6.5	30836	10	Cytoplasmic	COG0414	Coenzyme metabolism
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.3	3.84E-02	Glucose	6.6	61944	18	Periplasmic	COG0166	Carbohydrate transport and metabolism
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	4.3	7.17E-05	Citronellsäure	6.2	71624	18	Cytoplasmic	COG0365	Lipid metabolism
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.5	1.40E-02	Glucose	4.8	75421	57	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	1.6	1.21E-03	Glucose	6.9	33378	10	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis
15599938	PA4744	infB	translation initiation factor IF-2	1.6	1.31E-01	Glucose	6.0	90912	46	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis
15599939	PA4745	nusA	N utilization substance protein A	1.4	2.62E-01	Glucose	4.3	54658	22	Periplasmic	COG0195	Transcription
15599940	PA4746		conserved hypothetical protein	8.6	2.47E-02	Citronellsäure	4.3	17139	4	Cytoplasmic	COG0779	Function unknown
15599941	PA4747	secG	secretion protein SecG	80.1	1.30E-03	Glucose	5.1	13207	2	Outer Membrane Vesicle	COG1314	Intracellular trafficking and secretion
15599942	PA4748	tpiA	triosephosphate isomerase	1.4	1.02E-01	Citronellsäure	5.3	25621	9	Cytoplasmic	COG0149	Carbohydrate transport and metabolism
15599943	PA4749	glmM	phosphoglucosamine mutase	1.4	2.88E-02	Glucose	6.0	47796	8	Cytoplasmic	COG1109	Carbohydrate transport and metabolism
15599944	PA4750	folP	dihydropteroate synthase	1.1	6.37E-01	Glucose	5.4	30490	5	Cytoplasmic	COG0294	Coenzyme metabolism
15599945	PA4751	ftsH	cell division protein FtsH	2.4	2.22E-02	Glucose	5.6	69955	3	Outer Membrane Vesicle	COG0465	Posttranslational modification, protein turnover, chaperones
15599949	PA4755	greA	transcription elongation factor GreA	1.3	1.42E-01	Citronellsäure	4.7	17158	11	Periplasmic	COG0782	Function unknown
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	2.6	2.99E-02	Citronellsäure	4.8	117330	83	Periplasmic	COG0458	Amino acid transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.3	1.08E-02	Citronellsäure	5.2	40810	6	Cytoplasmic	COG0505	Amino acid transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.1	5.87E-01	Citronellsäure	6.0	28324	15	Periplasmic	COG0289	Amino acid transport and metabolism
15599954	PA4760	dnaJ	DnaJ protein	1.3	1.29E-01	Citronellsäure	7.4	40260	5	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones
15599955	PA4761	dnaK	DnaK protein	1.1	1.83E-01	Citronellsäure	4.5	68403	55	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones
15599956	PA4762	grpE	heat shock protein GrpE	1.8	1.07E-01	Citronellsäure	4.2	20702	12	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones
15599958	PA4764	fur	ferric uptake regulation protein	1.5	3.80E-01	Glucose	5.9	15234	9	Cytoplasmic	COG0735	Inorganic ion transport and metabolism
15599962	PA4768	smpB	SmpB protein	1.1	5.80E-01	Citronellsäure	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones
15600003	PA4809	fdhE	FdhE protein	82.0	3.56E-02	Glucose	5.8	33830	2	Cytoplasmic	COG3058	Posttranslational modification, protein turnover, chaperones
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.8	8.14E-02	Glucose	5.2	70667	17	Periplasmic	COG1166	Amino acid transport and metabolism
15600034	PA4841		conserved hypothetical protein	1.3	5.45E-01	Glucose	4.4	19733	3	Unknown	COG1443	Lipid metabolism
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	1.9	1.42E-01	Glucose	4.7	16455	10	Unknown	COG0511	Lipid metabolism
15600041	PA4848	accC	biotin carboxylase	1.7	7.05E-02	Glucose	6.3	48888	21	Periplasmic	COG0439	Lipid metabolism
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	1.7	1.65E-02	Glucose	4.2	32000	3	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	1.4	5.06E-02	Glucose	6.5	57665	30	Periplasmic	COG0138	Nucleotide transport and metabolism
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	1.0	1.11E-01	Glucose	4.7	45212	17	Periplasmic	COG0151	Nucleotide transport and metabolism
15600059	PA4866		conserved hypothetical protein	2.6	2.41E-01	Glucose	6.3	18743	3	Unknown	COG1247	Cell envelope biogenesis, outer membrane
15600061	PA4868	ureC	urease alpha subunit	1.5	4.79E-02	Glucose	6.2	60611	5	Cytoplasmic	COG0804	Amino acid transport and metabolism
15600065	PA4872		hypothetical protein	1.3	1.34E-01	Glucose	5.4	31320	10	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
15600071	PA4878		probable transcriptional regulator	21.7	9.47E-03	Citronellsäure	6.9	31168	4	Cytoplasmic	COG3708	Function unknown
15600073	PA4880		probable bacterioferritin	17.7	3.03E-04	Citronellsäure	4.4	20217	11	Cytoplasmic	COG2193	Inorganic ion transport and metabolism
15600086	PA4893	ureG	urease accessory protein UreG	1.2	6.59E-03	Glucose	4.6	21991	3	Cytoplasmic	COG0378	Posttranslational modification, protein turnover, chaperones
15600092	PA4899		probable aldehyde dehydrogenase	10.0	1.08E-03	Citronellsäure	5.8	52697	2	Cytoplasmic	COG1012	Energy production and conversion
15600100	PA4907		probable short-chain dehydrogenase	1.6	6.62E-03	Glucose	5.1	27384	12	Cytoplasmic	COG4221	General function prediction only
15600106	PA4913		probable binding protein component of ABC transporter	52.0	1.79E-05	Citronellsäure	6.6	39798	16	Periplasmic	COG0683	Amino acid transport and metabolism
15600109	PA4916		hypothetical protein	443.6	1.82E-03	Glucose	6.5	25457	2	Unknown	COG1051	Nucleotide transport and metabolism
15600111	PA4918		hypothetical protein	1.1	2.60E-01	Glucose	4.7	23821	10	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	1.9	3.61E-04	Glucose	6.3	46095	15	Cytoplasmic	COG1488	Coenzyme metabolism
15600113	PA4920	nadE	NH3-dependent NAD synthetase	1.9	1.01E-02	Glucose	5.4	29696	18	Periplasmic	COG0171	Coenzyme metabolism
15600115	PA4922	azu	azurin precursor	77.7	1.34E-03	Glucose	6.9	16008	12	Periplasmic	COG3241	Energy production and conversion
15600116	PA4923		conserved hypothetical protein	1.8	3.20E-01	Glucose	5.2	20725	4	Unknown	COG1611	General function prediction only
15600123	PA4930	alr	biosynthetic alanine racemase	2.2	1.66E-01	Citronellsäure	6.1	38310	2	Cytoplasmic	COG0787	Cell envelope biogenesis, outer membrane
15600124	PA4931	dnaB	replicative DNA helicase	1.7	1.24E-03	Glucose	4.7	51589	6	Cytoplasmic	COG0305	DNA replication, recombination, and repair
15600125	PA4932	rplI	50S ribosomal protein L9	28.0	3.44E-03	Glucose	5.3	15532	6	Periplasmic	COG0359	Translation, ribosomal structure and biogenesis
15600128	PA4935	rpsF	30S ribosomal protein S6	25.3	3.42E-03	Glucose	4.6	16165	13	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis
15600131	PA4938	purA	adenylosuccinate synthetase	1.1	5.77E-01	Glucose	6.0	46814	22	Periplasmic	COG0104	Nucleotide transport and metabolism
15600132	PA4939		conserved hypothetical protein	1.1	1.34E-01	Glucose	4.8	42546	9	Cytoplasmic	COG3705	Amino acid transport and metabolism
15600141	PA4948		conserved hypothetical protein	2.2	1.85E-01	Glucose	4.7	16463	3	Cytoplasmic	COG0802	General function prediction only
15600142	PA4949		conserved hypothetical protein	1.4	1.65E-01	Glucose	7.6	51550	7	Unknown	COG0063	Carbohydrate transport and metabolism
15600144	PA4951	orn	oligoribonuclease	1.0	7.76E-01	Citronellsäure	5.6	20826	3	Cytoplasmic	COG1949	RNA processing and modification
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	1.2	1.87E-01	Citronellsäure	5.3	29391	11	Cytoplasmic	COG2897	Inorganic ion transport and metabolism
15600150	PA4957	psd	phosphatidylserine decarboxylase	4.7	5.91E-03	Glucose	7.9	32001	2	Outer Membrane Vesicle	COG0688	Lipid metabolism
15600152	PA4959	fimX	FimX	1.0	9.02E-01	Citronellsäure	4.9	75992	15	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms
15600153	PA4960		probable phosphoserine phosphatase	1.3	2.35E-01	Citronellsäure	4.9	46438	6	Cytoplasmic	COG0560	Amino acid transport and metabolism
15600157	PA4964	parC	topoisomerase IV subunit A	2.5	9.29E-03	Glucose	5.9	83364	14	Cytoplasmic	COG0188	DNA replication, recombination, and repair
15600160	PA4967	parE	topoisomerase IV subunit B	1.5	8.58E-02	Glucose	5.9	69178	3	Cytoplasmic	COG0187	DNA replication, recombination, and repair
15600161	PA4968		conserved hypothetical protein	3.1	4.06E-02	Glucose	6.8	22645	3	Unknown	COG3150	General function prediction only
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	101.7	2.61E-05	Citronellsäure	4.8	30498	2	Cytoplasmic	COG1409	General function prediction only
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.1	2.25E-01	Citronellsäure	4.7	23133	6	Cytoplasmic		
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	2.8	1.73E-03	Glucose	5.8	69784	21	Cytoplasmic	COG0422	Coenzyme metabolism
15600167	PA4974		probable outer membrane protein precursor	3.6	7.54E-02	Glucose	5.9	53405	9	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane
15600168	PA4975		NAD(P)H quinone oxidoreductase	2.3	2.21E-01	Citronellsäure	6.0	26315	2	Cytoplasmic	COG2249	General function prediction only
15600185	PA4992		hypothetical protein	1.1	9.35E-01	Citronellsäure	6.4	29030	6	Cytoplasmic	COG0667	Energy production and conversion
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.3	1.70E-02	Glucose	6.2	50348	19	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane
15600194	PA5001		hypothetical protein	11.8	1.00E-02	Glucose	8.7	36625	5	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane

15600198	PA5005		probable carbamoyl transferase	2.6	2.39E-03	Glucose	6.9	66047	6	Outer Membrane Vesicle	COG2192	Posttranslational modification, protein turnover, chaperones
15600205	PA5012	waaF	heptosyltransferase II	1.7	1.06E-01	Glucose	8.0	38409	6	Cytoplasmic	COG0859	Cell envelope biogenesis, outer membrane
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.0	9.26E-01	Glucose	6.2	34084	23	Periplasmic	COG0115	Amino acid transport and metabolism
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	4.3	2.22E-03	Citronellsäure	5.2	110102	33	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones
15600208	PA5015	aceE	pyruvate dehydrogenase	3.5	7.57E-02	Glucose	5.6	99563	58	Periplasmic	COG2609	Energy production and conversion
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	5.4	2.86E-02	Glucose	5.0	56676	26	Periplasmic	COG0508	Energy production and conversion
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	1.0	7.99E-01	Citronellsäure	5.0	23517	6	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones
15600212	PA5019		conserved hypothetical protein	3.9	5.73E-02	Citronellsäure	6.0	31882	7	Cytoplasmic	COG2961	General function prediction only
15600218	PA5025	metY	homocysteine synthase	1.9	1.06E-04	Citronellsäure	6.5	45177	8	Cytoplasmic	COG2873	Amino acid transport and metabolism
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	1.8	7.67E-02	Citronellsäure	6.3	38792	9	Cytoplasmic	COG0407	Coenzyme metabolism
15600228	PA5035	gltD	glutamate synthase small chain	1.3	9.77E-02	Glucose	6.4	52625	22	Cytoplasmic	COG0493	Amino acid transport and metabolism
15600229	PA5036	gltB	glutamate synthase large chain precursor	2.4	3.46E-03	Citronellsäure	6.0	161607	78	Cytoplasmic	COG0069	Amino acid transport and metabolism
15600231	PA5038	aroB	3-dehydroquinate synthase	2.5	2.78E-02	Citronellsäure	5.6	40109	10	Cytoplasmic	COG0337	Amino acid transport and metabolism
15600232	PA5039	aroK	shikimate kinase	1.0	7.83E-01	Citronellsäure	8.8	19205	2	Cytoplasmic	COG0703	Amino acid transport and metabolism
15600233	PA5040	pilQ	Type 4 fimbrial biogenesis outer membrane protein PilQ precur	1.8	3.72E-02	Citronellsäure	5.2	77378	2	Periplasmic	COG4796	Intracellular trafficking and secretion
15600239	PA5046		malic enzyme	1.3	9.42E-03	Glucose	4.8	45428	33	Periplasmic	COG0281	Energy production and conversion
15600243	PA5050	priA	primosomal protein N'	1.1	5.85E-01	Glucose	8.8	82120	2	Unknown	COG1198	DNA replication, recombination, and repair
15600244	PA5051	argS	arginyl-tRNA synthetase	1.0	9.60E-01	Citronellsäure	5.2	65199	20	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis
15600246	PA5053	hslV	heat shock protein HslV	1.6	2.25E-01	Citronellsäure	6.7	18767	10	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones
15600247	PA5054	hslU	heat shock protein HslU	1.3	2.05E-01	Glucose	5.4	50082	19	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	2.4	1.63E-04	Glucose	9.5	28254	10	Cytoplasmic	COG2226	Coenzyme metabolism
15600257	PA5064		hypothetical protein	1.8	1.12E-01	Glucose	6.0	22767	4	Cytoplasmic	COG3165	Function unknown
15600259	PA5066	hisI	phosphoribosyl-AMP cyclohydrolase	41.5	5.67E-05	Glucose	6.0	15375	6	Cytoplasmic	COG0139	Amino acid transport and metabolism
15600264	PA5071		conserved hypothetical protein	3.8	2.03E-03	Citronellsäure	9.1	26065	4	Cytoplasmic	COG1385	Function unknown
15600269	PA5076		probable binding protein component of ABC transporter	1.7	1.09E-03	Citronellsäure	7.6	29736	20	Periplasmic	COG0834	Amino acid transport and metabolism
15600270	PA5077	mdoH	periplasmic glucans biosynthesis protein MdoH	12.1	7.19E-03	Glucose	8.9	96994	2	Outer Membrane Vesicle	COG2943	Cell envelope biogenesis, outer membrane
15600271	PA5078		conserved hypothetical protein	1.2	2.40E-01	Citronellsäure	7.0	59444	15	Periplasmic	COG3131	Inorganic ion transport and metabolism
15600272	PA5079		conserved hypothetical protein	92.7	4.25E-02	Glucose	6.3	15530	3	Unknown	COG1490	Translation, ribosomal structure and biogenesis
15600273	PA5080		prolyl aminopeptidase	1.3	1.09E-01	Glucose	6.2	36515	13	Cytoplasmic	COG0596	General function prediction only
15600275	PA5082		probable binding protein component of ABC transporter	9.4	7.57E-02	Citronellsäure	8.2	32866	3	Periplasmic	COG0834	Amino acid transport and metabolism
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	211.8	1.52E-04	Citronellsäure	5.9	29791	2	Cytoplasmic	COG3741	Amino acid transport and metabolism
15600291	PA5098	hutH	histidine ammonia-lyase	7.5	1.32E-03	Citronellsäure	5.8	53779	2	Cytoplasmic	COG2986	Amino acid transport and metabolism
15600293	PA5100	hutU	urocanase	3.7	1.62E-02	Citronellsäure	6.3	61161	2	Cytoplasmic	COG2987	Amino acid transport and metabolism
15600297	PA5104		conserved hypothetical protein	5.6	2.03E-02	Citronellsäure	5.6	21415	5	Unknown	COG3758	Function unknown
15600302	PA5109		hypothetical protein	1.1	6.46E-01	Glucose	5.1	22697	7	Cytoplasmic	COG3803	Function unknown
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	1.3	1.32E-01	Glucose	5.9	37216	12	Periplasmic	COG0158	Carbohydrate transport and metabolism
15600304	PA5111	gloA3	lactoylglutathione lyase	1.5	2.99E-01	Citronellsäure	4.8	20215	5	Cytoplasmic	COG0346	Amino acid transport and metabolism
15600305	PA5112	estA	esterase EstA	3.8	5.06E-02	Citronellsäure	4.5	69608	3	Periplasmic	COG3240	Lipid metabolism
15600310	PA5117	typA	regulatory protein TypA	1.2	1.91E-01	Glucose	5.0	66903	20	Periplasmic	COG1217	Signal transduction mechanisms
15600311	PA5118	thiI	thiazole biosynthesis protein ThiI	1.8	3.11E-01	Glucose	6.7	54849	2	Cytoplasmic	COG0301	Coenzyme metabolism
15600312	PA5119	glnA	glutamine synthetase	1.7	1.28E-02	Glucose	5.0	51944	24	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism
15600318	PA5125	ntrC	two-component response regulator NtrC	1.5	7.24E-02	Citronellsäure	5.8	52753	7	Cytoplasmic	COG2204	Signal transduction mechanisms
15600321	PA5128	secB	secretion protein SecB	3.1	2.65E-02	Citronellsäure	4.2	18146	10	Periplasmic	COG1952	Intracellular trafficking and secretion
15600324	PA5131	pgm	phosphoglycerate mutase	1.4	1.23E-01	Glucose	4.9	55601	27	Periplasmic	COG0696	Carbohydrate transport and metabolism
15600327	PA5134		probable carboxyl-terminal protease	3.6	7.37E-02	Glucose	5.4	46018	5	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane
15600330	PA5137		hypothetical protein	8.8	2.11E-05	Citronellsäure	7.5	27991	8	Unknown	COG0834	Amino acid transport and metabolism
15600331	PA5138		hypothetical protein	2.3	1.17E-03	Citronellsäure	4.9	27915	10	Periplasmic	COG0834	Amino acid transport and metabolism
15600332	PA5139		hypothetical protein	2.0	1.73E-01	Citronellsäure	5.8	27565	9	Periplasmic	COG0834	Amino acid transport and metabolism
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	1.0	6.97E-01	Glucose	4.7	25938	3	Cytoplasmic	COG0106	Amino acid transport and metabolism
15600335	PA5142	hisH1	glutamine amidotransferase	1.5	8.25E-03	Glucose	6.3	23666	15	Cytoplasmic	COG0118	Amino acid transport and metabolism
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	1.2	7.07E-01	Glucose	6.5	21937	6	Cytoplasmic	COG0131	Amino acid transport and metabolism
15600339	PA5146		hypothetical protein	6.0	1.52E-03	Glucose	8.3	80849	5	Outer Membrane Vesicle	COG2982	Cell envelope biogenesis, outer membrane
15600343	PA5150		probable short-chain dehydrogenase	1.5	8.20E-03	Citronellsäure	6.2	26191	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC tr	11.1	1.03E-06	Citronellsäure	4.9	27561	24	Periplasmic	COG0834	Amino acid transport and metabolism
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	1.6	4.03E-02	Citronellsäure	5.9	39542	14	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	1.2	1.41E-01	Citronellsäure	6.1	33106	7	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	1.7	7.13E-02	Citronellsäure	5.0	32457	14	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.3	4.42E-01	Citronellsäure	6.0	20766	10	Unknown	COG1898	Cell envelope biogenesis, outer membrane
15600359	PA5166	dctD	DctD	1.5	2.66E-02	Glucose	5.5	50864	5	Cytoplasmic	COG2204	Signal transduction mechanisms
15600360	PA5167	dctP	DctP	17.7	1.42E-05	Citronellsäure	8.8	37051	18	Periplasmic	COG1638	Carbohydrate transport and metabolism
15600364	PA5171	arcA	arginine deiminase	10.1	1.76E-03	Citronellsäure	5.5	46436	22	Cytoplasmic	COG2235	Amino acid transport and metabolism
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	26.6	3.87E-04	Citronellsäure	6.6	38108	14	Cytoplasmic	COG0078	Amino acid transport and metabolism
15600366	PA5173	arcC	carbamate kinase	12.4	8.74E-04	Citronellsäure	5.0	33080	7	Cytoplasmic	COG0549	Amino acid transport and metabolism
15600367	PA5174		probable beta-ketoacyl synthase	9.0	1.56E-04	Glucose	6.0	68763	29	Periplasmic	COG0304	Lipid metabolism
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	2.0	7.56E-02	Citronellsäure	4.8	29779	7	Cytoplasmic	COG1218	Inorganic ion transport and metabolism
15600369	PA5176		conserved hypothetical protein	2.4	7.25E-03	Citronellsäure	4.5	20983	9	Cytoplasmic	COG1051	Nucleotide transport and metabolism
15600370	PA5177		probable hydrolase	1.6	2.00E-02	Glucose	5.9	25629	5	Cytoplasmic	COG1011	General function prediction only
15600377	PA5184		hypothetical protein	1.3	4.35E-01	Glucose	8.8	20417	9	Periplasmic	COG1605	Amino acid transport and metabolism
15600379	PA5186		probable iron-containing alcohol dehydrogenase	145.5	6.48E-02	Citronellsäure	5.4	40354	3	Cytoplasmic	COG1454	Energy production and conversion
15600380	PA5187		probable acyl-CoA dehydrogenase	8.2	1.25E-02	Citronellsäure	5.3	64558	5	Cytoplasmic	COG1960	Lipid metabolism
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	7.7	2.14E-04	Citronellsäure	5.2	44810	6	Cytoplasmic	COG1250	Lipid metabolism
15600383	PA5190		probable nitroreductase	1.6	1.53E-02	Glucose	6.0	22450	11	Cytoplasmic	COG0778	Energy production and conversion
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.4	9.93E-02	Citronellsäure	5.1	55732	31	Periplasmic	COG1866	Energy production and conversion
15600386	PA5193	yrfI	heat shock protein HSP33	1.3	1.50E-01	Glucose	4.5	32834	9	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones
15600393	PA5200	amgR	AmgR	1.2	2.63E-01	Citronellsäure	6.6	27924	9	Cytoplasmic	COG0745	Signal transduction mechanisms
15600394	PA5201		conserved hypothetical protein	2.9	2.17E-02	Glucose	6.3	84963	38	Periplasmic	COG2183	Transcription
15600396	PA5203	gshA	glutamate--cysteine ligase	1.5	4.07E-02	Citronellsäure	4.9	59205	16	Cytoplasmic	COG2918	Coenzyme metabolism
15600397	PA5204	argA	N-acetylglutamate synthase	1.2	1.65E-01	Citronellsäure	6.5	47858	9	Cytoplasmic	COG0548	Amino acid transport and metabolism
15600403	PA5210		probable secretion pathway ATPase	3.2	1.10E-01	Glucose	6.5	65981	4	Cytoplasmic	COG2804	Cell motility and secretion
15600406	PA5213	gcvP1	glycine cleavage system protein P1	13.9	1.56E-03	Citronellsäure	6.5	104710	12	Cytoplasmic	COG1003	Amino acid transport and metabolism
15600407	PA5214	gcvH1	glycine cleavage system protein H1	9.8	1.05E-01	Glucose	3.9	13642	3	Unknown	COG0509	Amino acid transport and metabolism
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	1.3	2.48E-01	Citronellsäure	5.4	38907	7	Periplasmic	COG0404	Amino acid transport and metabolism
15600417	PA5224	pepP	aminopeptidase P	1.1	5.44E-01	Glucose	5.1	49710	12	Cytoplasmic	COG0006	Amino acid transport and metabolism

15600418	PA5225		hypothetical protein	1.4	1.34E-01	Glucose	4.0	19358	6	Unknown	COG3079 Function unknown
15600422	PA5229		conserved hypothetical protein	3.8	9.34E-03	Citronellsäure	7.5	16871	7	Unknown	COG2947 Function unknown
15600427	PA5234		probable oxidoreductase	1.4	2.06E-01	Citronellsäure	7.0	34011	12	Cytoplasmic	COG0604 Energy production and conversion
15600430	PA5237		conserved hypothetical protein	1.4	4.31E-01	Citronellsäure	6.5	54621	2	Cytoplasmic	COG0043 Coenzyme metabolism
15600432	PA5239	rho	transcription termination factor Rho	1.1	6.17E-01	Glucose	6.8	47069	18	Periplasmic	COG1158 Transcription
15600433	PA5240	trxA	thioredoxin	28.3	5.17E-06	Glucose	4.5	11870	7	Cytoplasmic	COG3118 Posttranslational modification, protein turnover, chaperones
15600434	PA5241	ppx	exopolyphosphatase	1.5	1.99E-01	Glucose	6.7	56419	9	Cytoplasmic	COG0248 Nucleotide transport and metabolism
15600435	PA5242	ppk	polyphosphate kinase	1.6	7.01E-02	Citronellsäure	7.7	83151	18	Cytoplasmic Membrane	COG0855 Inorganic ion transport and metabolism
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	2.3	1.46E-02	Citronellsäure	4.8	37005	6	Cytoplasmic	COG0113 Coenzyme metabolism
15600438	PA5245		conserved hypothetical protein	1.5	2.47E-01	Citronellsäure	4.7	23426	14	Cytoplasmic	COG3155 Secondary metabolites biosynthesis, transport, and catabolism
15600445	PA5252		probable ATP-binding component of ABC transporter	2.6	3.20E-04	Glucose	5.9	70871	13	Cytoplasmic	COG0488 General function prediction only
15600448	PA5255	algQ	Alginate regulatory protein AlgQ	108.3	2.86E-03	Glucose	4.6	18011	2	Cytoplasmic	COG3160 Transcription
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	2.2	6.53E-03	Glucose	4.8	27247	4	Unknown	COG1587 Coenzyme metabolism
15600453	PA5260	hemC	porphobilinogen deaminase	2.4	7.49E-03	Citronellsäure	5.3	33641	7	Cytoplasmic	COG0181 Coenzyme metabolism
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	4.7	1.31E-03	Citronellsäure	7.3	27608	8	Cytoplasmic	COG3279 Transcription
15600456	PA5263	argH	argininosuccinate lyase	1.3	1.04E-02	Citronellsäure	5.5	51640	19	Periplasmic	COG0165 Amino acid transport and metabolism
15600467	PA5274	rnk	nucleoside diphosphate kinase regulator	33.3	8.55E-02	Glucose	4.2	14405	2	Cytoplasmic	COG0782 Function unknown
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.4	1.28E-02	Citronellsäure	5.4	45490	17	Periplasmic	COG0019 Amino acid transport and metabolism
15600471	PA5278	dapF	diaminopimelate epimerase	2.2	1.33E-03	Citronellsäure	7.7	30320	7	Cytoplasmic	COG0253 Amino acid transport and metabolism
15600472	PA5279		conserved hypothetical protein	1.0	9.69E-01	Glucose	5.3	25767	4	Cytoplasmic	COG3159 Function unknown
15600474	PA5281		probable hydrolase	1.0	7.21E-01	Glucose	5.9	25852	4	Cytoplasmic	COG1011 General function prediction only
15600489	PA5296	rep	ATP-dependent DNA helicase Rep	1.9	1.09E-01	Glucose	6.0	77041	2	Cytoplasmic	COG0210 DNA replication, recombination, and repair
15600491	PA5298		xanthine phosphoribosyltransferase	1.5	1.06E-01	Glucose	6.6	20575	8	Cytoplasmic	COG0503 Nucleotide transport and metabolism
15600494	PA5301	pauR	probable transcriptional regulator	1.3	5.08E-01	Glucose	5.3	19944	4	Cytoplasmic	COG1396 Transcription
15600505	PA5312	pauC	Aldehyde dehydrogenase	2.4	2.46E-04	Citronellsäure	5.3	53143	25	Periplasmic	COG1012 Energy production and conversion
15600506	PA5313	gabT2	Transaminase	14.5	1.41E-04	Citronellsäure	6.7	48347	4	Cytoplasmic	COG0161 Coenzyme metabolism
15600510	PA5317		probable binding protein component of ABC dipeptide transpor	1.2	2.79E-01	Citronellsäure	7.0	57880	6	Periplasmic	COG0747 Amino acid transport and metabolism
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pant	1.0	7.38E-01	Glucose	6.3	43133	12	Cytoplasmic	COG0452 Coenzyme metabolism
15600515	PA5322	algC	phosphomannomutase AlgC	1.0	4.31E-01	Glucose	5.0	50295	24	Cytoplasmic	COG1109 Carbohydrate transport and metabolism
15600516	PA5323	argB	acetylglutamate kinase	1.1	3.14E-01	Citronellsäure	6.8	31849	19	Cytoplasmic	COG0548 Amino acid transport and metabolism
15600522	PA5329		conserved hypothetical protein	47.9	1.13E-02	Glucose	5.0	17712	4	Cytoplasmic	COG0824 General function prediction only
15600523	PA5330		hypothetical protein	1.3	2.75E-01	Citronellsäure	9.4	22434	7	Unknown	
15600524	PA5331	pyrE	orotate phosphoribosyltransferase	1.8	5.88E-03	Glucose	5.1	23320	12	Cytoplasmic	COG0461 Nucleotide transport and metabolism
15600525	PA5332	crc	catabolite repression control protein	1.1	5.65E-01	Glucose	5.2	29844	8	Cytoplasmic	COG0708 DNA replication, recombination, and repair
15600527	PA5334	rph	ribonuclease PH	1.5	1.95E-01	Glucose	5.9	25654	6	Cytoplasmic	COG0689 Translation, ribosomal structure and biogenesis
15600528	PA5335		conserved hypothetical protein	1.1	5.89E-01	Citronellsäure	5.8	31708	13	Cytoplasmic	COG1561 Function unknown
15600529	PA5336	gmk	guanylate kinase	2.0	6.52E-02	Glucose	5.3	23102	11	Cytoplasmic	COG0194 Nucleotide transport and metabolism
15600530	PA5337	rpoZ	RNA polymerase omega subunit	24.4	1.35E-01	Glucose	4.0	9775	3	Unknown	COG1758 Transcription
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.1	8.85E-01	Citronellsäure	9.4	78861	13	Cytoplasmic	COG0317 Signal transduction mechanisms
15600532	PA5339		conserved hypothetical protein	21.0	1.48E-02	Glucose	4.8	13610	6	Cytoplasmic	COG0251 Translation, ribosomal structure and biogenesis
15600536	PA5343		hypothetical protein	1.0	8.59E-01	Citronellsäure	6.2	30778	5	Unknown	COG0451 Cell envelope biogenesis, outer membrane
15600537	PA5344	oxyR	OxyR	1.5	1.15E-01	Glucose	6.7	34295	7	Cytoplasmic	COG0583 Transcription
15600539	PA5346	sadB	SadB	1.8	1.94E-02	Glucose	6.0	51427	3	Cytoplasmic	COG1639 Signal transduction mechanisms
15600540	PA5347		hypothetical protein	1.1	8.63E-01	Citronellsäure	11.1	14726	4	Unknown	
15600542	PA5349		probable rubredoxin reductase	1.2	1.76E-02	Citronellsäure	5.5	40617	10	Cytoplasmic	COG1251 Energy production and conversion
15600550	PA5357		hypothetical protein	1.6	1.35E-01	Citronellsäure	4.7	19512	7	Cytoplasmic	COG3161 Coenzyme metabolism
15600557	PA5364		probable two-component response regulator	4.5	2.42E-02	Glucose	9.4	32401	2	Cytoplasmic	COG2204 Signal transduction mechanisms
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU	2.5	4.45E-04	Citronellsäure	5.0	27487	4	Cytoplasmic	COG0704 Inorganic ion transport and metabolism
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding pro	1.8	1.23E-02	Glucose	9.5	34473	8	Periplasmic	COG0226 Inorganic ion transport and metabolism
15600564	PA5371		conserved hypothetical protein	841.1	2.85E-04	Glucose	4.5	14555	3	Unknown	COG1607 Lipid metabolism
15600566	PA5373	betB	betaine aldehyde dehydrogenase	1.4	1.07E-01	Citronellsäure	5.0	53332	5	Cytoplasmic	COG1012 Energy production and conversion
15600567	PA5374	betI	transcriptional regulator BetI	2.4	7.23E-02	Glucose	9.0	21861	5	Unknown	COG1309 Transcription
15600571	PA5378		hypothetical protein	2.3	6.06E-04	Citronellsäure	7.3	34427	8	Periplasmic	COG2113 Amino acid transport and metabolism
15600606	PA5413	ltaA	low specificity l-threonine aldolase	1.1	6.49E-01	Citronellsäure	5.0	38213	8	Cytoplasmic	COG2008 Amino acid transport and metabolism
15600615	PA5422		hypothetical protein	6.2	6.70E-03	Glucose	5.1	36107	6	Cytoplasmic	COG0676 Carbohydrate transport and metabolism
15600616	PA5423		hypothetical protein	3.6	3.89E-03	Citronellsäure	5.7	20002	3	Periplasmic	COG3495 Function unknown
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase	1.4	2.07E-01	Citronellsäure	5.4	38496	9	Cytoplasmic Membrane	COG0026 Nucleotide transport and metabolism
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	56.9	3.70E-04	Glucose	6.2	16889	10	Unknown	COG0041 Nucleotide transport and metabolism
15600622	PA5429	aspA	aspartate ammonia-lyase	5.7	1.69E-04	Citronellsäure	5.6	51069	9	Periplasmic	COG1027 Amino acid transport and metabolism
15600628	PA5435		probable transcarboxylase subunit	4.1	8.35E-05	Glucose	5.7	66095	52	Cytoplasmic	COG5016 Energy production and conversion
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase	4.2	1.75E-05	Glucose	6.6	51816	23	Cytoplasmic	COG0439 Lipid metabolism
15600632	PA5439		probable glucose-6-phosphate dehydrogenase	3.6	4.50E-03	Citronellsäure	7.2	54573	2	Cytoplasmic	COG0364 Carbohydrate transport and metabolism
15600634	PA5441		hypothetical protein	1.0	7.37E-01	Citronellsäure	4.6	80036	38	Periplasmic	
15600636	PA5443	uvrD	DNA helicase II	2.0	9.24E-03	Glucose	5.7	81494	15	Cytoplasmic	COG0210 DNA replication, recombination, and repair
15600645	PA5452	wbpW	phosphomannose isomerase/GDP-mannose WbpW	4.4	1.50E-03	Citronellsäure	6.4	52574	2	Cytoplasmic	COG0836 Cell envelope biogenesis, outer membrane
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase	4.3	9.86E-06	Citronellsäure	6.5	36399	13	Cytoplasmic	COG1089 Cell envelope biogenesis, outer membrane
15600647	PA5454	rmd	oxidoreductase Rmd	4.4	3.57E-05	Citronellsäure	6.7	33910	5	Cytoplasmic	COG0451 Cell envelope biogenesis, outer membrane
15600650	PA5457		hypothetical protein	3.8	3.10E-03	Citronellsäure	6.2	31744	4	Cytoplasmic	COG2227 Coenzyme metabolism
15600652	PA5459		hypothetical protein	5.7	4.42E-04	Citronellsäure	4.7	30701	8	Cytoplasmic	COG2226 Coenzyme metabolism
15600668	PA5475		hypothetical protein	10.4	4.50E-02	Citronellsäure	4.8	21000	3	Cytoplasmic	
15600676	PA5483	algB	two-component response regulator AlgB	1.2	5.01E-01	Glucose	5.2	49323	7	Cytoplasmic	COG2204 Signal transduction mechanisms
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA	1.8	1.10E-01	Glucose	6.4	23375	12	Periplasmic	COG1651 Posttranslational modification, protein turnover, chaperones
15600683	PA5490	cc4	cytochrome c4 precursor	1.6	2.84E-01	Citronellsäure	7.6	20735	4	Outer Membrane Vesicle	COG2863 Energy production and conversion
15600685	PA5492		conserved hypothetical protein	2.8	4.89E-02	Glucose	7.1	23786	5	Unknown	COG0218 General function prediction only
15600686	PA5493	polA	DNA polymerase I	1.5	5.93E-02	Citronellsäure	4.8	99792	52	Periplasmic	COG0749 DNA replication, recombination, and repair
15600691	PA5498		probable adhesin	3.0	1.75E-02	Citronellsäure	6.1	33576	2	Periplasmic	COG4531 Inorganic ion transport and metabolism
15600692	PA5499	np20	transcriptional regulator np20	1.3	2.29E-01	Citronellsäure	6.9	18216	2	Cytoplasmic	COG0735 Inorganic ion transport and metabolism
15600698	PA5505		probable TonB-dependent receptor	1.2	9.10E-02	Citronellsäure	8.7	28065	17	Periplasmic	COG1464 Inorganic ion transport and metabolism
15600700	PA5507		hypothetical protein	1.0	6.26E-01	Glucose	6.4	24262	6	Cytoplasmic	COG1335 Secondary metabolites biosynthesis, transport, and catabolism
15600709	PA5516	pdxY	pyridoxamine kinase	5.8	5.96E-02	Glucose	6.0	31285	4	Cytoplasmic	COG2240 Coenzyme metabolism
15600712	PA5519		conserved hypothetical protein	10.2	9.55E-02	Glucose	7.5	21215	2	Unknown	COG1607 Lipid metabolism
15600713	PA5520		hypothetical protein	20.0	4.32E-03	Glucose	5.1	26250	2	Unknown	
15600714	PA5521		probable short-chain dehydrogenase	1.2	2.95E-01	Glucose	5.8	26894	10	Cytoplasmic	COG1028 Secondary metabolites biosynthesis, transport, and catabolism

15600716	PA5523		probable aminotransferase	5.1	1.16E-02	Citronellsäure	6.7	48908	3	Cytoplasmic	COG0001	Coenzyme metabolism
15600717	PA5524		probable short-chain dehydrogenase	1.1	4.49E-01	Citronellsäure	5.0	27158	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15600735	PA5542		hypothetical protein	4.2	3.33E-04	Citronellsäure	6.3	45872	6	Unknown	COG1680	Defense mechanisms
15600738	PA5545		conserved hypothetical protein	13.4	6.62E-07	Citronellsäure	7.8	33627	13	Periplasmic	COG2358	General function prediction only
15600739	PA5546		conserved hypothetical protein	12.7	8.37E-06	Citronellsäure	5.7	44096	10	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.2	3.47E-02	Citronellsäure	5.9	66294	27	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamii	1.8	6.11E-03	Citronellsäure	6.2	48851	10	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane
15600747	PA5554	atpD	ATP synthase beta chain	1.3	6.21E-02	Glucose	4.7	49499	37	Periplasmic	COG0055	Energy production and conversion
15600748	PA5555	atpG	ATP synthase gamma chain	1.0	7.33E-01	Citronellsäure	8.1	31553	14	Outer Membrane Vesicle	COG0224	Energy production and conversion
15600749	PA5556	atpA	ATP synthase alpha chain	1.1	8.31E-01	Citronellsäure	5.1	55393	27	Periplasmic	COG0056	Energy production and conversion
15600750	PA5557	atpH	ATP synthase delta chain	1.0	8.09E-01	Glucose	5.9	19260	11	Outer Membrane Vesicle	COG0712	Energy production and conversion
15600751	PA5558	atpF	ATP synthase B chain	20.7	5.04E-03	Glucose	5.8	16924	10	Outer Membrane Vesicle	COG0711	Energy production and conversion
15600753	PA5560	atpB	ATP synthase A chain	33.8	6.50E-03	Glucose	6.5	31921	2	Outer Membrane Vesicle	COG0356	Energy production and conversion
15600755	PA5562	spoOJ	chromosome partitioning protein SpoOJ	4.2	3.78E-02	Glucose	10.0	31969	2	Cytoplasmic	COG1475	Transcription
15600756	PA5563	soj	chromosome partitioning protein Soj	1.0	8.48E-01	Glucose	6.1	28609	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning
15600757	PA5564	gidB	glucose inhibited division protein B	1.5	1.83E-02	Glucose	6.3	23735	5	Unknown	COG0357	Cell envelope biogenesis, outer membrane
15600758	PA5565	gidA	glucose-inhibited division protein A	2.4	1.07E-02	Glucose	6.5	69605	7	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning
15600761	PA5568		conserved hypothetical protein	7.2	4.31E-03	Glucose	8.0	64074	2	Outer Membrane Vesicle	COG0706	Intracellular trafficking and secretion
15600762	PA5569	rnpA	ribonuclease P protein component	1.7	1.27E-01	Glucose	11.5	15282	3	Unknown	COG0594	Translation, ribosomal structure and biogenesis
375041995				1.1	8.76E-01	Glucose			85			
313108864				114.2	3.19E-06	Citronellsäure			39			
22001796				1.7	2.86E-01	Glucose			29			
296388504				1.0	5.21E-01	Glucose			32			
313110180				1.2	8.80E-02	Glucose			29			
107100513				1.5	6.90E-03	Glucose			17			
308154506				4.5	7.85E-02	Citronellsäure			14			
296388215				6.1	2.02E-02	Citronellsäure			13			
239949861				1.2	1.42E-03	Citronellsäure			12			
375044686				1.1	7.06E-01	Glucose			12			
239949862				3.3	5.07E-03	Citronellsäure			13			
347307435				1.3	8.44E-01	Citronellsäure			11			
107099134				1.3	4.80E-02	Citronellsäure			12			
107102694				1.2	2.22E-01	Citronellsäure			11			
355640527				1.1	1.04E-01	Glucose			9			
308198348				1.2	7.65E-02	Citronellsäure			10			
254236126				2.7	1.98E-01	Glucose			9			
346058454				7.1	4.36E-02	Citronellsäure			9			
282403589				1.2	3.41E-01	Glucose			8			
99032099				63.1	1.99E-04	Glucose			9			
375041918				1.7	1.18E-01	Glucose			8			
107101116				1.4	1.89E-01	Glucose			8			
296389665				4.1	8.32E-03	Glucose			7			
116054234				27.1	1.22E-03	Citronellsäure			6			
107100575				2.4	7.02E-02	Citronellsäure			5			
254236426				1.4	1.17E-01	Glucose			6			
107099288				3.3	5.67E-03	Citronellsäure			4			
107099096				1.7	5.89E-02	Glucose			4			
359783701				1.3	1.22E-01	Citronellsäure			5			
359782167				32.1	6.20E-04	Glucose			3			
107103573				1.1	3.81E-01	Glucose			3			
330505213				2.0	9.47E-02	Citronellsäure			2			
104781332				17.3	1.85E-02	Glucose			3			
107103974				2.0	8.59E-02	Citronellsäure			2			
146282899				2.6	1.56E-02	Citronellsäure			3			
107104298				2.5	1.83E-02	Citronellsäure			2			
374702598				35.5	5.49E-02	Glucose			1			
107102668				19.7	7.58E-03	Citronellsäure			2			
107104524				24.2	7.79E-04	Citronellsäure			2			
244539066				1.1	6.73E-01	Citronellsäure			2			
226944916				14.5	3.31E-03	Citronellsäure			3			
116052531				17.6	4.78E-05	Citronellsäure			2			
229592164				8.8	2.10E-04	Citronellsäure			2			
356463779				1.1	6.61E-01	Glucose			1			
70732985				3.6	4.05E-02	Citronellsäure			2			
359394219				1.8	2.53E-01	Citronellsäure			2			
41019482				1.2	4.22E-01	Glucose			1			
146308929				3.0	3.08E-01	Citronellsäure			1			
331007094				1.8	2.66E-01	Glucose			1			
374704241				13.9	9.32E-03	Citronellsäure			2			
295698607				8.2	3.06E-01	Citronellsäure			2			
258591310				13.1	6.08E-02	Citronellsäure			2			
347305107				3.3	1.37E-01	Citronellsäure			2			
312386137				Infinity	1.56E-01	Glucose			2			

5.4.1.3 GeLCMSMS_P_aeruginosa_PAO1_Oktansäure_Citronellsäure_Tabelle

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfaktor	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595199	PA0001	dnaA	chromosomal replication initiator protein DnaA	3.1	1.05E-02	Oktansäure	8.9	57722	10	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.4	1.70E-02	Citronellsäure	4.9	40694	21	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	1.7	1.39E-02	Citronellsäure	5.7	90188	43	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	3.5	3.08E-02	Citronellsäure	4.5	19115	4	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	3.6	1.00E-03	Citronellsäure	7.9	61755	12	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.1	2.53E-01	Citronellsäure	4.8	73973	36	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	1.5	1.03E-01	Citronellsäure	4.7	36109	12	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	1.3	2.78E-02	Citronellsäure	7.0	33028	10	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	2.4	6.15E-03	Oktansäure	4.7	19365	7	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	1.5	2.52E-01	Oktansäure	9.4	37586	7	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	4.1	2.59E-03	Oktansäure	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	1.4	1.58E-01	Citronellsäure	6.3	35095	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	1.2	3.50E-01	Oktansäure	5.8	34774	9	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	2.7	6.58E-02	Oktansäure	5.5	29484	5	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	2.0	1.69E-02	Citronellsäure	5.0	28488	10	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	1.9	1.38E-02	Citronellsäure	6.3	43680	15	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	1.1	6.19E-01	Oktansäure	7.1	7863	3	Unknown	COG3360	Function unknown	
15595243	PA0045		hypothetical protein	1.4	8.04E-01	Citronellsäure	9.6	24395	2	Periplasmic	COG1462	Cell envelope biogenesis, outer membrane	
15595252	PA0054		conserved hypothetical protein	78.0	6.57E-03	Oktansäure	9.6	20024	3	Unknown	COG1859	Translation, ribosomal structure and biogenesis	
15595253	PA0055		hypothetical protein	1.3	2.75E-01	Citronellsäure	5.7	18433	11	Cytoplasmic	COG3812	Function unknown	
15595263	PA0065		hypothetical protein	4.1	2.71E-02	Citronellsäure	6.1	24951	4	Cytoplasmic	COG0546	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.2	1.17E-01	Oktansäure	4.9	76011	30	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	5.7	3.20E-03	Oktansäure	8.9	31716	6	Periplasmic			
15595273	PA0075	pppA	PppA	1.2	4.39E-01	Oktansäure	6.2	25904	9	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	2.8	5.49E-02	Citronellsäure	4.4	23856	4	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	1.2	4.77E-01	Oktansäure	6.1	48275	10	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595280	PA0082	tssA1	TssA1	1.6	9.42E-02	Oktansäure	4.1	36647	4	Cytoplasmic	COG3515	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	2.0	9.63E-02	Citronellsäure	4.9	18785	19	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.0	8.73E-01	Citronellsäure	5.0	55771	33	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	6.6	7.84E-02	Oktansäure	6.8	17415	12	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	4.0	3.22E-02	Citronellsäure	4.4	30361	4	Cytoplasmic	COG4455	General function prediction only	
15595286	PA0088	tssF1	TssF1	2.7	5.68E-02	Oktansäure	7.4	69483	6	Cytoplasmic	COG3519	Intracellular trafficking, secretion, and vesicular transport	
15595288	PA0090	clpV1	ClpV1	1.0	9.90E-01	Citronellsäure	5.3	98737	41	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	3.7	5.85E-02	Citronellsäure	6.4	72012	17	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	4.3	5.77E-02	Citronellsäure	8.9	44738	5	Cytoplasmic Membrane	COG4104	Function unknown	
15595292	PA0094		hypothetical protein	7.7	4.65E-02	Oktansäure	6.8	16456	3	Unknown	COG5435	Function unknown	
15595298	PA0100		hypothetical protein	1.2	5.83E-01	Oktansäure	4.1	33723	6	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.1	5.73E-01	Oktansäure	6.7	26622	9	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595313	PA0115		conserved hypothetical protein	27.7	3.32E-03	Oktansäure	6.3	17085	5	Cytoplasmic	COG2153	General function prediction only	
15595316	PA0118		hypothetical protein	2.0	1.58E-01	Citronellsäure	6.8	21473	5	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595320	PA0122	rahU	rahU	198.1	2.99E-04	Oktansäure	4.4	14579	7	Extracellular			
15595324	PA0126		hypothetical protein	4.8	1.78E-02	Oktansäure	8.0	22367	2	Outer Membrane Vesicle			
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.4	1.98E-02	Citronellsäure	6.0	53323	5	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	1.6	1.95E-02	Oktansäure	6.3	20541	12	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	2.1	3.38E-02	Citronellsäure	5.0	55835	7	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
119167454	PA0143	nuh	purine nucleosidase Nuh	1.5	2.10E-01	Citronellsäure	7.7	37542	13	Periplasmic	COG1957	Nucleotide transport and metabolism	
15595342	PA0144		hypothetical protein	2.3	4.83E-02	Oktansäure	8.4	22431	8	Unknown	COG3613	Nucleotide transport and metabolism	
15595343	PA0145		hypothetical protein	6.5	6.84E-03	Citronellsäure	4.4	18448	2	Cytoplasmic	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.6	4.06E-02	Citronellsäure	4.9	36163	6	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595357	PA0159		probable transcriptional regulator	1.3	4.16E-01	Oktansäure	6.0	34683	2	Cytoplasmic	COG0583	Transcription	
15595362	PA0164		probable gamma-glutamyltranspeptidase	1.6	1.51E-01	Oktansäure	6.5	58453	3	Periplasmic	COG0405	Amino acid transport and metabolism	
15595368	PA0170		hypothetical protein	91.2	7.87E-06	Oktansäure	4.3	14553	3	Cytoplasmic			
15595369	PA0171		hypothetical protein	1.5	1.70E-01	Citronellsäure	7.1	19800	12	Cytoplasmic			
15595372	PA0174		conserved hypothetical protein	2.3	3.54E-02	Citronellsäure	8.5	22206	2	Cytoplasmic	COG1871	Cell motility and secretion	Signal transduction mechanisms
15595374	PA0176	aer2	aerotaxis transducer Aer2	3.0	6.25E-02	Citronellsäure	4.8	72591	29	Cytoplasmic	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595375	PA0177		probable purine-binding chemotaxis protein	3.8	1.95E-01	Citronellsäure	4.3	17487	4	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595376	PA0178		probable two-component sensor	3.5	6.97E-02	Citronellsäure	4.5	68931	9	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595380	PA0182		probable short-chain dehydrogenase	1.6	2.25E-01	Oktansäure	4.7	25230	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	1.8	2.62E-02	Citronellsäure	5.9	38650	24	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595393	PA0196	pntB	pyridine nucleotide transhydrogenase, beta subunit	59.6	4.41E-02	Oktansäure	7.3	49947	2	Cytoplasmic Membrane	COG1282	Energy production and conversion	
15595405	PA0208	mdcA	malonate decarboxylase alpha subunit	12.9	9.73E-03	Citronellsäure	6.4	61424	4	Cytoplasmic	COG4670	Lipid metabolism	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	6.1	1.03E-02	Citronellsäure	4.5	30343	9	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	6.2	2.33E-02	Citronellsäure	7.1	28496	7	Cytoplasmic			
15595422	PA0225		probable transcriptional regulator	1746.3	1.16E-02	Oktansäure	6.9	19993	2	Cytoplasmic	COG1476	Transcription	
15595423	PA0226		probable CoA transferase, subunit A	8.7	1.95E-02	Citronellsäure	6.2	30920	2	Cytoplasmic	COG1788	Lipid metabolism	
15595424	PA0227		probable CoA transferase, subunit B	7.6	3.12E-02	Citronellsäure	5.4	27314	3	Cytoplasmic	COG2057	Lipid metabolism	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	1.8	1.39E-01	Oktansäure	6.2	49121	5	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	3.0	6.61E-02	Citronellsäure	5.1	27985	4	Unknown	COG0596	General function prediction only	
15595429	PA0232	pcaC	gamma-carboxymuconolactone decarboxylase	129.7	2.40E-02	Oktansäure	7.1	15084	2	Unknown	COG0599	Function unknown	
15595444	PA0247	pobA	p-hydroxybenzoate hydroxylase	5.5	6.95E-02	Citronellsäure	6.8	44323	5	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15595456	PA0259		hypothetical protein	3.3	1.48E-02	Oktansäure	5.0	52444	7	Unknown			
15595457	PA0260		hypothetical protein	801.9	2.39E-03	Oktansäure	7.0	78202	2	Unknown			
15595460	PA0263	hcpC	secreted protein Hcp	40.3	7.89E-05	Oktansäure	5.8	19091	8	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.4	7.56E-02	Citronellsäure	5.4	51622	24	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	1.4	1.11E-02	Citronellsäure	6.4	45220	21	Periplasmic	COG0160	Amino acid transport and metabolism	
15595471	PA0274		hypothetical protein	122.2	6.35E-02	Citronellsäure	8.8	28498	2	Outer Membrane			
15595474	PA0277		conserved hypothetical protein	1.2	6.14E-01	Oktansäure	6.5	26626	8	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	1.4	6.74E-03	Oktansäure	9.0	36433	19	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	1.8	1.24E-01	Oktansäure	9.1	49667	6	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.1	4.08E-01	Citronellsäure	4.6	41191	6	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595491	PA0294	aguR	transcriptional regulator AguR	8.3	3.04E-03	Citronellsäure	6.4	24424	3	Cytoplasmic	COG1309	Transcription	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	2.9	1.97E-04	Citronellsäure	4.6	50907	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595494	PA0297	spuA	probable glutamine amidotransferase	172.7	1.36E-03	Citronellsäure	6.4	26477	3	Unknown	COG2071	General function prediction only	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	1.4	1.62E-02	Citronellsäure	5.0	50965	8	Cytoplasmic	COG0174	Amino acid transport and metabolism	

15595496	PA0299	spuC	Polyamine:pyruvate transaminase	2.0	5.94E-02	Citronellsäure	6.0	50453	18	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	3.9	3.98E-05	Citronellsäure	7.6	40629	16	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	3.9	1.24E-03	Citronellsäure	5.5	40069	15	Periplasmic	COG0687	Amino acid transport and metabolism	
15595506	PA0309		hypothetical protein	1.9	1.26E-02	Oktansäure	7.6	27021	6	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	2.8	2.10E-03	Citronellsäure	9.7	28005	14	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15595512	PA0315		hypothetical protein	2.0	5.84E-01	Citronellsäure	7.2	15463	8	Unknown			
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.1	6.84E-01	Citronellsäure	6.5	44216	17	Periplasmic	COG0111	Amino acid transport and metabolism	
15595514	PA0317		hypothetical protein	1.2	8.71E-02	Citronellsäure	4.9	51286	13	Periplasmic	COG0277	Energy production and conversion	
15595515	PA0318		conserved hypothetical protein	1.6	3.64E-01	Citronellsäure	5.3	23843	7	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15595520	PA0323		probable binding protein component of ABC transporter	1.4	5.68E-01	Citronellsäure	6.8	38901	2	Periplasmic	COG0687	Amino acid transport and metabolism	
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	1.7	6.25E-02	Citronellsäure	5.3	23721	11	Cytoplasmic	COG0120	Carbohydrate transport and metabolism	
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	1.9	5.06E-04	Citronellsäure	6.5	55351	8	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15595532	PA0335		hypothetical protein	1.3	3.30E-01	Oktansäure	4.5	24353	16	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.7	1.46E-01	Citronellsäure	9.5	18726	7	Cytoplasmic	COG0494	DNA replication, recombination, and repair	General function prediction only
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.3	8.43E-02	Oktansäure	5.6	83606	24	Cytoplasmic	COG3605	Signal transduction mechanisms	
15595536	PA0339		hypothetical protein	4.2	1.19E-03	Citronellsäure	6.7	26527	7	Unknown	COG3332	Function unknown	
15595539	PA0342	thyA	thymidylate synthase	1.3	2.90E-01	Oktansäure	6.5	30016	7	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
15595547	PA0350	folA	dihydrofolate reductase	4.3	1.29E-01	Citronellsäure	5.3	18203	7	Unknown	COG0262	Coenzyme metabolism	
15595548	PA0351		conserved hypothetical protein	1.4	3.92E-01	Oktansäure	6.7	17217	3	Cytoplasmic	COG0622	General function prediction only	
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.5	1.60E-01	Citronellsäure	6.0	65160	33	Periplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15595552	PA0355	pfpI	protease PfpI	1.3	3.21E-01	Citronellsäure	5.0	19246	9	Cytoplasmic	COG0693	General function prediction only	
15595553	PA0356		hypothetical protein	1.2	3.73E-01	Citronellsäure	5.3	30360	4	Unknown	COG1639	Signal transduction mechanisms	
15595554	PA0357	mutM	formamidopyrimidine-DNA glycosylase	39.6	5.95E-04	Oktansäure	9.6	30046	2	Cytoplasmic	COG0266	DNA replication, recombination, and repair	
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	3.7	9.76E-02	Oktansäure	9.0	17771	11	Cytoplasmic	COG0669	Coenzyme metabolism	
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	1.5	3.96E-01	Citronellsäure	4.5	48391	10	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.0	8.81E-01	Oktansäure	4.8	28234	11	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
15595579	PA0382	micA	DNA mismatch repair protein MicA	2.7	2.75E-03	Citronellsäure	8.3	25331	3	Cytoplasmic	COG0220	General function prediction only	
15595580	PA0383		conserved hypothetical protein	7.5	3.72E-04	Citronellsäure	8.3	50243	3	Unknown			
15595584	PA0387		conserved hypothetical protein	2.7	5.26E-02	Oktansäure	6.1	21242	9	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	2.0	5.19E-03	Citronellsäure	4.5	28094	9	Cytoplasmic	COG0345	Amino acid transport and metabolism	
15595591	PA0394		conserved hypothetical protein	1.7	7.31E-02	Citronellsäure	6.7	24505	6	Cytoplasmic	COG0325	General function prediction only	
15595592	PA0395	pilT	twitching motility protein PilT	1.5	5.48E-02	Oktansäure	6.9	38021	7	Cytoplasmic	COG2805	Cell motility and secretion	Intracellular trafficking and secretion
15595596	PA0399		cystathionine beta-synthase	1.1	2.04E-01	Citronellsäure	5.5	49170	20	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15595597	PA0400		probable cystathionine gamma-lyase	1.1	6.29E-01	Citronellsäure	6.6	42786	10	Cytoplasmic	COG0626	Amino acid transport and metabolism	
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.2	7.13E-01	Oktansäure	5.8	44150	8	Periplasmic	COG0044	Nucleotide transport and metabolism	
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.1	1.53E-01	Citronellsäure	6.8	36629	12	Periplasmic	COG0540	Nucleotide transport and metabolism	
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.5	2.62E-01	Citronellsäure	5.7	18676	9	Cytoplasmic	COG2065	Nucleotide transport and metabolism	
15595602	PA0405		conserved hypothetical protein	10.3	3.74E-03	Oktansäure	4.6	20212	2	Unknown	COG1678	Transcription	
15595604	PA0407	gshB	glutathione synthetase	1.0	8.70E-01	Citronellsäure	5.8	35705	19	Periplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
15595605	PA0408	pilG	twitching motility protein PilG	10.4	2.72E-02	Oktansäure	7.4	14718	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595607	PA0410	pilI	twitching motility protein PilI	1.6	4.51E-01	Citronellsäure	6.6	19934	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595610	PA0413	chpA	component of chemotactic signal transduction system	2.8	4.32E-02	Citronellsäure	4.2	268573	28	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595612	PA0415	chpC	probable chemotaxis protein	1.3	7.89E-01	Citronellsäure	4.7	17625	6	Unknown			
15595615	PA0418		hypothetical protein	1.2	4.77E-01	Oktansäure	5.6	52140	7	Cytoplasmic			
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1.5	2.37E-01	Citronellsäure	6.3	52478	8	Cytoplasmic	COG0161	Coenzyme metabolism	
15595620	PA0423	pasP	PasP	3.2	1.03E-02	Oktansäure	6.5	20776	21	Periplasmic	COG2353	Function unknown	
15595621	PA0424	mexR	multidrug resistance operon repressor MexR	7.8	2.20E-01	Oktansäure	5.9	16964	2	Cytoplasmic	COG1846	Transcription	
15595622	PA0425	mexA	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein M	2.1	5.55E-03	Oktansäure	9.2	40969	2	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15595623	PA0426	mexB	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB	2.7	1.40E-02	Oktansäure	5.4	112790	7	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15595624	PA0427	oprM	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM pre	3.8	1.97E-02	Oktansäure	5.3	52598	5	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15595625	PA0428		probable ATP-dependent RNA helicase	13.8	1.14E-01	Oktansäure	10.7	70112	2	Cytoplasmic	COG0513	DNA replication, recombination, and repair	Transcription
15595626	PA0429		hypothetical protein	1.1	5.94E-01	Citronellsäure	7.0	40872	4	Cytoplasmic			
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	1.5	1.33E-01	Citronellsäure	6.5	32196	17	Periplasmic	COG0685	Amino acid transport and metabolism	
15595628	PA0431		hypothetical protein	3.4	1.28E-01	Oktansäure	6.8	20639	3	Unknown	COG0317	Signal transduction mechanisms	Transcription
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	2.2	1.39E-04	Citronellsäure	6.0	51400	30	Periplasmic	COG0499	Coenzyme metabolism	
15595631	PA0434		hypothetical protein	62.3	2.69E-03	Oktansäure	5.8	81304	12	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15595634	PA0437	codA	cytosine deaminase	1.9	2.22E-03	Citronellsäure	6.0	47074	4	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15595643	PA0446		conserved hypothetical protein	2.1	2.29E-01	Citronellsäure	5.3	43847	4	Cytoplasmic	COG1804	Energy production and conversion	
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	1.3	4.21E-02	Citronellsäure	6.1	43311	5	Cytoplasmic	COG1960	Lipid metabolism	
15595646	PA0449		hypothetical protein	20.3	2.35E-03	Oktansäure	10.5	19808	8	Cytoplasmic	COG1607	Lipid metabolism	
15595656	PA0459		probable ClpA/B protease ATP binding subunit	4.1	1.24E-01	Citronellsäure	6.7	94143	10	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595659	PA0462		hypothetical protein	1.1	7.20E-01	Citronellsäure	10.6	26230	8	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15595664	PA0467		conserved hypothetical protein	1.5	1.30E-01	Oktansäure	7.5	23301	6	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15595665	PA0468		hypothetical protein	3.1	2.79E-02	Oktansäure	4.8	33594	4	Periplasmic	COG4257	Defense mechanisms	
15595666	PA0469		hypothetical protein	3.1	1.69E-02	Oktansäure	4.7	32137	8	Cytoplasmic			
15595670	PA0473		probable glutathione S-transferase	7.9	1.34E-05	Citronellsäure	5.8	28294	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15595675	PA0478		probable N-acetyltransferase	57.5	3.47E-03	Oktansäure	4.6	18109	2	Cytoplasmic	COG0456	General function prediction only	
15595679	PA0482	glcB	malate synthase G	1.7	2.11E-02	Oktansäure	5.5	78659	74	Periplasmic	COG2225	Energy production and conversion	
15595681	PA0484		conserved hypothetical protein	2.9	1.40E-01	Citronellsäure	4.5	18553	3	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15595684	PA0487		probable molybdenum transport regulator	36.2	3.33E-03	Oktansäure	9.2	26948	2	Cytoplasmic	COG2005	General function prediction only	
15595697	PA0500	bioB	biotin synthase	1.6	2.93E-01	Citronellsäure	6.0	39113	4	Cytoplasmic	COG0502	Coenzyme metabolism	
15595698	PA0501	bioF	8-amino-7-oxononanoate synthase	77.7	3.02E-04	Citronellsäure	5.9	42237	3	Cytoplasmic	COG0156	Coenzyme metabolism	
15595699	PA0502		probable biotin biosynthesis protein bioH	30.7	1.01E-02	Citronellsäure	4.3	26494	2	Cytoplasmic	COG0596	General function prediction only	
15595700	PA0503		probable biotin synthesis protein BioC	1.0	8.51E-01	Oktansäure	9.0	29712	2	Unknown	COG2226	Coenzyme metabolism	
15595701	PA0504	bioD	dethiobiotin synthase	2.1	1.25E-01	Oktansäure	5.3	23337	9	Cytoplasmic	COG0132	Coenzyme metabolism	
15595703	PA0506		probable acyl-CoA dehydrogenase	1.6	2.38E-01	Citronellsäure	5.8	65358	47	Periplasmic	COG1960	Lipid metabolism	
15595705	PA0508		probable acyl-CoA dehydrogenase	2.0	6.90E-05	Citronellsäure	5.1	63628	49	Cytoplasmic	COG1960	Lipid metabolism	
15595716	PA0519	nirS	nitrite reductase precursor	2.2	1.66E-01	Oktansäure	8.2	62653	3	Periplasmic	COG2010	Energy production and conversion	
15595724	PA0527	dnr	transcriptional regulator Dnr	8.5	2.11E-02	Oktansäure	6.7	25933	3	Cytoplasmic	COG0664	Signal transduction mechanisms	
15595732	PA0535		probable transcriptional regulator	8.6	5.81E-03	Oktansäure	4.9	20231	2	Cytoplasmic	COG1396	Transcription	
15595734	PA0537		conserved hypothetical protein	3.2	1.06E-02	Oktansäure	8.9	22180	8	Outer Membrane Vesicle	COG1704	Function unknown	
15595743	PA0546	metK	methionine adenosyltransferase	1.6	2.99E-03	Citronellsäure	5.2	42709	24	Cytoplasmic	COG0192	Coenzyme metabolism	
15595745	PA0548	tktA	transketolase	1.1	6.76E-01	Citronellsäure	5.0	72220	37	Periplasmic	COG0021	Carbohydrate transport and metabolism	
15595747	PA0550		conserved hypothetical protein	1.1	7.15E-01	Citronellsäure	5.4	29834	7	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	1.5	9.18E-02	Citronellsäure	5.8	38743	4	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	

15595749	PA0552	pgk	phosphoglycerate kinase	2.7	4.22E-03	Citronellsäure	5.1	40404	19	Periplasmic	COG0126	Carbohydrate transport and metabolism	
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	3.0	2.91E-03	Citronellsäure	5.3	38574	23	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
15595755	PA0558		conserved hypothetical protein	1.9	2.47E-03	Oktansäure	6.2	27987	11	Cytoplasmic	COG2226	Coenzyme metabolism	
15595759	PA0562		probable hydrolase	1.2	5.02E-01	Oktansäure	5.4	24232	9	Cytoplasmic	COG0637	General function prediction only	
15595765	PA0568		hypothetical protein	2.7	4.07E-02	Oktansäure	4.2	17683	3	Cytoplasmic			
15595768	PA0571		hypothetical protein	1.3	6.16E-01	Citronellsäure	5.0	22501	5	Unknown			
15595773	PA0576	rpoD	sigma factor RpoD	1.5	3.63E-01	Citronellsäure	4.6	69643	32	Outer Membrane Vesicle	COG0568	Transcription	
15595775	PA0578		conserved hypothetical protein	3.5	2.38E-03	Citronellsäure	6.0	16842	2	Cytoplasmic	COG1610	Function unknown	
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	1.3	4.63E-02	Oktansäure	6.2	36561	3	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
15595780	PA0583		hypothetical protein	1.1	9.66E-01	Citronellsäure	5.6	20091	4	Cytoplasmic	COG0801	Coenzyme metabolism	
15595783	PA0586		conserved hypothetical protein	3.1	1.99E-02	Citronellsäure	5.1	60814	15	Cytoplasmic	COG2719	Function unknown	
15595784	PA0587		conserved hypothetical protein	1.6	1.62E-01	Citronellsäure	7.8	48742	11	Cytoplasmic	COG2718	Function unknown	
15595785	PA0588		conserved hypothetical protein	1.8	1.45E-01	Citronellsäure	5.5	73722	49	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms	
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	1.8	4.55E-03	Citronellsäure	7.2	32019	5	Cytoplasmic			
15595789	PA0592	ksgA	rRNA (adenine-N6,N6)-dimethyltransferase	2.6	1.24E-02	Oktansäure	7.4	30058	3	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.1	7.10E-01	Citronellsäure	6.6	34891	8	Cytoplasmic	COG1995	Coenzyme metabolism	
15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.0	6.29E-01	Citronellsäure	5.6	48441	19	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15595792	PA0595	ostA	organic solvent tolerance protein OstA precursor	17.1	1.65E-02	Oktansäure	5.3	104271	2	Periplasmic	COG1452	Cell envelope biogenesis, outer membrane	
15595793	PA0596		hypothetical protein	2.0	1.19E-02	Citronellsäure	5.1	38185	6	Cytoplasmic	COG3178	General function prediction only	
15595794	PA0597		probable nucleotidyl transferase	1.4	1.38E-02	Citronellsäure	6.1	24149	3	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
15595801	PA0604		probable binding protein component of ABC transporter	3.3	5.22E-03	Citronellsäure	5.6	38167	9	Periplasmic	COG0687	Amino acid transport and metabolism	
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.5	9.90E-02	Oktansäure	5.1	24096	11	Cytoplasmic	COG0036	Carbohydrate transport and metabolism	
15595806	PA0609	trpE	anthranilate synthetase component I	1.7	2.43E-03	Citronellsäure	4.7	54555	13	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
15595830	PA0633		hypothetical protein	2.3	3.38E-01	Oktansäure	4.7	17539	2	Outer Membrane Vesicle			
15595846	PA0649	trpG	anthranilate synthase component II	2.2	6.00E-02	Citronellsäure	6.0	22046	5	Cytoplasmic	COG0512	Amino acid transport and metabolism	Coenzyme metabolism
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	2.4	2.45E-02	Citronellsäure	5.6	37384	6	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	1.9	9.95E-03	Citronellsäure	4.6	30315	10	Cytoplasmic	COG0134	Amino acid transport and metabolism	
15595850	PA0653		conserved hypothetical protein	1.5	9.28E-01	Citronellsäure	6.4	15237	6	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones	
15595851	PA0654	speD	S-adenosylmethionine decarboxylase proenzyme	4.8	1.70E-01	Citronellsäure	4.5	30446	2	Cytoplasmic	COG1586	Amino acid transport and metabolism	
15595852	PA0655		hypothetical protein	3.3	1.09E-03	Oktansäure	5.3	23644	6	Unknown	COG2941	Coenzyme metabolism	
15595857	PA0660		hypothetical protein	1.1	7.29E-01	Oktansäure	6.2	34814	17	Cytoplasmic	COG2070	General function prediction only	
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	2.7	1.24E-03	Citronellsäure	6.7	36684	19	Cytoplasmic	COG0002	Amino acid transport and metabolism	
15595861	PA0664		hypothetical protein	35.9	3.43E-03	Oktansäure	5.6	14790	2	Cytoplasmic	COG1664	Cell envelope biogenesis, outer membrane	
15595862	PA0665		conserved hypothetical protein	21.6	1.49E-03	Oktansäure	4.0	12484	2	Cytoplasmic	COG0316	Posttranslational modification, protein turnover, chaperones	
15595863	PA0666		conserved hypothetical protein	14.4	3.09E-02	Citronellsäure	5.2	39087	3	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.8	4.96E-03	Citronellsäure	5.6	44129	25	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis	
15595869	PA0672	hemO	heme oxygenase	2.7	8.94E-03	Oktansäure	4.8	21953	11	Unknown	COG3230	Inorganic ion transport and metabolism	
15595902	PA0705	migA	alpha-1,6-rhamnosyltransferase MigA	2.8	3.16E-01	Oktansäure	8.4	34358	2	Cytoplasmic Membrane	COG1215	Cell envelope biogenesis, outer membrane	
15595903	PA0706	cat	chloramphenicol acetyltransferase	1.3	4.07E-01	Oktansäure	6.1	23524	3	Unknown	COG0110	General function prediction only	
15595912	PA0715		hypothetical protein	1.1	7.10E-01	Citronellsäure	9.9	36589	4	Cytoplasmic	COG3344	DNA replication, recombination, and repair	
15595938	PA0741		conserved hypothetical protein	1.2	8.90E-01	Oktansäure	6.6	22687	6	Unknown	COG2910	General function prediction only	
15595940	PA0743		probable 3-hydroxyisobutyrate dehydrogenase	1.0	8.05E-01	Citronellsäure	5.3	30754	3	Cytoplasmic	COG2084	Lipid metabolism	
15595941	PA0744		probable enoyl-CoA hydratase/isomerase	3.4	8.17E-03	Citronellsäure	5.1	40589	5	Cytoplasmic	COG1024	Lipid metabolism	
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	1.5	2.15E-01	Citronellsäure	6.4	29904	14	Cytoplasmic	COG1024	Lipid metabolism	
15595947	PA0750	ung	uracil-DNA glycosylase	1.1	6.38E-01	Citronellsäure	8.2	26010	8	Cytoplasmic	COG0692	DNA replication, recombination, and repair	
15595951	PA0754		hypothetical protein	2.4	5.47E-02	Citronellsäure	5.5	34918	17	Unknown	COG3181	Function unknown	
15595953	PA0756		probable two-component response regulator	1.0	4.85E-01	Oktansäure	5.2	24431	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595955	PA0758		hypothetical protein	1.2	4.94E-01	Citronellsäure	4.7	30875	8	Cytoplasmic	COG1639	Signal transduction mechanisms	
15595956	PA0759		conserved hypothetical protein	1.7	8.18E-02	Oktansäure	5.2	33667	14	Unknown	COG0354	General function prediction only	
15595958	PA0761	nadB	L-aspartate oxidase	1.2	1.57E-02	Citronellsäure	6.3	60004	6	Cytoplasmic	COG0029	Coenzyme metabolism	
15595959	PA0762	algU	sigma factor AlgU	1.1	9.01E-01	Citronellsäure	5.4	22196	6	Cytoplasmic	COG1595	Transcription	
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	2.4	3.31E-02	Oktansäure	6.1	34572	5	Periplasmic	COG3026	Signal transduction mechanisms	
15595963	PA0766	mucD	serine protease MucD precursor	1.7	1.82E-01	Oktansäure	7.8	50321	8	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
15595964	PA0767	lepA	GTP-binding protein LepA	1.8	4.82E-02	Oktansäure	5.3	66263	8	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
15595967	PA0770	rnc	ribonuclease III	1.7	8.36E-02	Oktansäure	6.6	25474	4	Cytoplasmic	COG0571	Transcription	
15595968	PA0771	era	GTP-binding protein Era	1.5	2.26E-02	Oktansäure	6.6	34550	4	Cytoplasmic Membrane	COG1159	General function prediction only	
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.2	1.08E-02	Citronellsäure	5.6	27228	6	Cytoplasmic	COG0854	Coenzyme metabolism	
15595972	PA0775		conserved hypothetical protein	1.6	8.51E-02	Citronellsäure	5.3	27608	2	Cytoplasmic	COG4106	General function prediction only	
15595976	PA0779		probable ATP-dependent protease	1.3	9.07E-01	Citronellsäure	6.8	88574	10	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15595979	PA0782	putA	proline dehydrogenase PutA	1.8	2.44E-01	Citronellsäure	6.0	115630	26	Periplasmic	COG4230	Energy production and conversion	
15595989	PA0792	prpD	propionate catabolic protein PrpD	3.1	2.39E-02	Oktansäure	6.6	54881	7	Cytoplasmic	COG2079	General function prediction only	
15595991	PA0794		probable aconitate hydratase	6.7	3.84E-04	Citronellsäure	5.3	94890	21	Cytoplasmic	COG1048	Energy production and conversion	
15595992	PA0795	prpC	citrate synthase 2	4.7	1.79E-04	Citronellsäure	6.4	41689	19	Cytoplasmic	COG0372	Energy production and conversion	
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.1	7.30E-01	Citronellsäure	5.2	32137	14	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15596001	PA0804		probable oxidoreductase	23.1	8.31E-03	Oktansäure	4.8	30017	2	Cytoplasmic	COG0656	General function prediction only	
15596004	PA0807	ampDh3	AmpDh3	1.0	8.76E-01	Citronellsäure	6.3	28720	2	Outer Membrane Vesicle	COG3023	Cell envelope biogenesis, outer membrane	
15596029	PA0832		conserved hypothetical protein	1.1	8.28E-01	Citronellsäure	6.2	23483	2	Cytoplasmic	COG0491	General function prediction only	
15596030	PA0833		hypothetical protein	1.3	2.91E-01	Oktansäure	9.0	24713	8	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596032	PA0835	pta	phosphate acetyltransferase	1.4	1.17E-01	Oktansäure	5.0	75696	18	Periplasmic	COG0280	Energy production and conversion	
15596033	PA0836	ackA	acetate kinase	2.2	4.37E-03	Oktansäure	7.1	42421	7	Cytoplasmic	COG0282	Energy production and conversion	
15596034	PA0837	slyD	peptidyl-prolyl cis-trans isomerase SlyD	452.1	1.07E-04	Oktansäure	4.2	17010	3	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15596035	PA0838		probable glutathione peroxidase	2.1	1.68E-01	Citronellsäure	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596037	PA0840		probable oxidoreductase	1.1	6.26E-01	Citronellsäure	5.5	40334	12	Cytoplasmic	COG1902	Energy production and conversion	
15596048	PA0851		hypothetical protein	1.5	2.45E-01	Citronellsäure	6.8	34024	8	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15596049	PA0852	cbpD	chitin-binding protein CbpD precursor	24.9	2.43E-04	Oktansäure	6.9	41917	9	Extracellular	COG3397	Function unknown	
15596050	PA0853		probable oxidoreductase	1.5	6.87E-03	Oktansäure	8.3	23485	7	Cytoplasmic	COG2249	General function prediction only	
15596051	PA0854	fumC2	fumarate hydratase	1.6	8.01E-03	Citronellsäure	6.1	49122	19	Cytoplasmic	COG0114	Energy production and conversion	
15596053	PA0856		hypothetical protein	39.0	4.72E-04	Oktansäure	10.1	19998	7	Unknown	COG3184	Function unknown	
15596055	PA0858		conserved hypothetical protein	2.4	5.25E-02	Oktansäure	5.7	35420	5	Cytoplasmic	COG1054	General function prediction only	
15596056	PA0859		hypothetical protein	1.2	8.89E-01	Citronellsäure	4.6	21466	4	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
15596059	PA0862		hypothetical protein	1.3	4.56E-01	Oktansäure	6.5	29845	5	Cytoplasmic	COG5424	Coenzyme metabolism	
15596060	PA0863		probable oxidoreductase	7.0	1.67E-01	Oktansäure	4.9	33368	2	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15596062	PA0865	hpd	4-hydroxyphenylpyruvate dioxygenase	1.6	9.32E-01	Oktansäure	4.9	39913	7	Periplasmic	COG3185	Amino acid transport and metabolism	General function prediction only
15596064	PA0867	mliC	membrane-bound lysozyme inhibitor of c-type lysozyme MliC	5.6	1.54E-04	Oktansäure	4.8	13695	7	Outer Membrane Vesicle	COG3895	General function prediction only	
15596067	PA0870	phhC	aromatic amino acid aminotransferase	1.7	8.87E-02	Citronellsäure	6.2	43273	9	Cytoplasmic	COG1448	Amino acid transport and metabolism	

15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	2.8	2.37E-01	Oktansäure	6.4	13333	4	Cytoplasmic	COG2154	Coenzyme metabolism	
15596069	PA0872	phhA	phenylalanine-4-hydroxylase	3.1	3.35E-01	Oktansäure	5.6	30322	3	Cytoplasmic	COG3186	Amino acid transport and metabolism	
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	2.8	4.80E-03	Citronellsäure	6.3	71762	39	Cytoplasmic	COG0365	Lipid metabolism	
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.3	1.44E-01	Citronellsäure	6.8	28010	19	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596088	PA0891		hypothetical protein	1.6	1.43E-01	Citronellsäure	4.9	40214	3	Cytoplasmic	COG3608	General function prediction only	
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.3	5.24E-02	Citronellsäure	5.8	43747	27	Periplasmic	COG4992	Amino acid transport and metabolism	
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	1.0	8.88E-01	Citronellsäure	4.7	36930	5	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	2.0	4.37E-03	Citronellsäure	6.5	37245	9	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596095	PA0898	aruD	succinylglutamate 5-semialdehyde dehydrogenase	2.2	3.65E-03	Citronellsäure	6.2	51510	10	Periplasmic	COG1012	Energy production and conversion	
15596096	PA0899	aruB	succinylarginine dihydrolase	1.0	9.28E-01	Citronellsäure	6.2	48875	9	Periplasmic	COG3724	Amino acid transport and metabolism	
15596098	PA0901	aruE	succinylglutamate desuccinylase	1.3	2.69E-01	Citronellsäure	6.0	36909	10	Cytoplasmic	COG2988	Amino acid transport and metabolism	
15596099	PA0902		hypothetical protein	1.2	5.15E-01	Citronellsäure	6.4	35430	8	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15596100	PA0903	alaS	alanyl-tRNA synthetase	2.1	3.68E-02	Citronellsäure	5.2	94701	46	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.5	4.36E-02	Citronellsäure	5.0	44388	26	Cytoplasmic	COG0527	Amino acid transport and metabolism	
15596112	PA0915		conserved hypothetical protein	34.3	7.04E-04	Oktansäure	6.3	17514	3	Cytoplasmic	COG4807	Function unknown	
15596124	PA0927	ldhA	D-lactate dehydrogenase (fermentative)	5.2	6.21E-02	Citronellsäure	6.1	35756	2	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15596129	PA0932	cysM	cysteine synthase B	1.9	7.46E-02	Citronellsäure	5.5	32448	13	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596131	PA0934	relA	GTP pyrophosphokinase	1.7	6.42E-02	Oktansäure	7.6	83815	25	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15596132	PA0935		conserved hypothetical protein	1.1	4.95E-01	Oktansäure	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only	
15596134	PA0937		conserved hypothetical protein	19.9	9.22E-04	Oktansäure	9.7	20789	2	Cytoplasmic	COG3122	Function unknown	
15596140	PA0943		hypothetical protein	1.2	4.03E-01	Citronellsäure	8.7	27183	15	Periplasmic			
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	2.1	2.25E-02	Citronellsäure	4.5	37122	11	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
15596144	PA0947		conserved hypothetical protein	1.6	2.30E-02	Citronellsäure	6.0	26843	3	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	3.9	2.54E-02	Oktansäure	6.8	20744	8	Unknown	COG0655	General function prediction only	
15596153	PA0956	proS	prolyl-tRNA synthetase	1.4	1.12E-02	Citronellsäure	5.1	63103	30	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis	
15596154	PA0957		hypothetical protein	14.7	1.09E-04	Citronellsäure	6.3	14622	3	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	1.2	6.29E-01	Citronellsäure	4.8	48360	7	Periplasmic			
15596159	PA0962		probable dna-binding stress protein	2.2	2.34E-01	Oktansäure	4.7	17493	12	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.3	1.92E-01	Citronellsäure	5.2	66207	38	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis	
15596161	PA0964	pmpR	pqsR-mediated PQS regulator, PmpR	1.0	7.37E-01	Citronellsäure	4.4	26557	4	Cytoplasmic	COG0217	Function unknown	
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.2	6.27E-01	Oktansäure	6.1	21927	9	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
15596164	PA0967	ruvB	Holliday junction DNA helicase RuvB	26.5	1.06E-02	Oktansäure	5.2	38932	2	Cytoplasmic	COG2255	DNA replication, recombination, and repair	
15596165	PA0968		conserved hypothetical protein	5.6	4.12E-02	Citronellsäure	8.7	16672	2	Cytoplasmic	COG0824	General function prediction only	
15596166	PA0969	tolQ	TolQ protein	26.6	5.11E-04	Oktansäure	6.3	25250	4	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
15596169	PA0972	tolB	TolB protein	1.2	2.59E-01	Oktansäure	9.2	47720	17	Periplasmic	COG0823	Intracellular trafficking and secretion	
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	2.1	6.14E-02	Oktansäure	6.3	17925	5	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596171	PA0974		conserved hypothetical protein	1.5	3.00E-02	Citronellsäure	8.7	29097	7	Outer Membrane Vesicle	COG1729	Function unknown	
15596172	PA0975		probable radical activating enzyme	1479.7	9.60E-03	Citronellsäure	7.1	29556	2	Cytoplasmic	COG0602	Posttranslational modification, protein turnover, chaperones	
15596173	PA0976		conserved hypothetical protein	2.3	4.90E-03	Citronellsäure	4.7	23900	3	Unknown	COG0603	General function prediction only	
15596178	PA0981		hypothetical protein	2.1	1.17E-01	Oktansäure	6.4	21871	3	Unknown			
15596192	PA0995	ogt	methylated-DNA--protein-cysteine methyltransferase	1.1	6.25E-01	Oktansäure	7.6	19253	2	Cytoplasmic	COG0350	DNA replication, recombination, and repair	
15596194	PA0997	pqsB	PqsB	7.8	1.75E-03	Oktansäure	4.6	30501	11	Cytoplasmic	COG0332	acyl-carrier-protein	
15596195	PA0998	pqsC	PqsC	8.8	5.34E-03	Oktansäure	4.9	38238	10	Cytoplasmic	COG0332	acyl-carrier-protein	
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	8.6	7.83E-04	Oktansäure	5.3	36378	19	Cytoplasmic	COG0332	acyl-carrier-protein	
15596197	PA1000	pqsE	Quinolone signal response protein	53.3	1.52E-03	Oktansäure	5.3	34306	7	Cytoplasmic	COG0491	General function prediction only	
15596201	PA1004	nadA	quinolinate synthetase A	2.4	1.31E-02	Citronellsäure	5.4	38418	5	Cytoplasmic	COG0379	Coenzyme metabolism	
15596202	PA1005		conserved hypothetical protein	7.2	5.07E-03	Oktansäure	8.4	52994	3	Periplasmic	COG4783	General function prediction only	
15596205	PA1008	bcp	bacterioferritin comigratory protein	1.0	6.19E-01	Oktansäure	7.3	17352	10	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones	
15596206	PA1009		hypothetical protein	6.0	4.34E-03	Oktansäure	5.6	20585	4	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15596207	PA1010	dapA	dihydrodipicolinate synthase	1.3	2.12E-01	Citronellsäure	6.4	31449	25	Periplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
15596208	PA1011		hypothetical protein	1.9	8.91E-02	Oktansäure	4.7	43055	6	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane	
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.7	7.20E-03	Citronellsäure	5.1	26831	20	Periplasmic	COG0152	Nucleotide transport and metabolism	
15596220	PA1023		probable short-chain dehydrogenase	1.4	1.06E-01	Citronellsäure	6.7	32821	5	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596223	PA1026		hypothetical protein	1.5	2.47E-01	Citronellsäure	4.8	17184	2	Cytoplasmic			
15596230	PA1033		probable glutathione S-transferase	1.1	6.58E-01	Oktansäure	6.8	24527	3	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596233	PA1036		hypothetical protein	209.4	4.45E-02	Citronellsäure	4.6	19537	1	Unknown			
15596236	PA1039		conserved hypothetical protein	2.5	1.62E-02	Citronellsäure	6.7	17189	3	Unknown	COG3012	Function unknown	
15596237	PA1040		hypothetical protein	1.3	7.72E-02	Citronellsäure	6.0	18721	5	Unknown			
15596240	PA1043		hypothetical protein	3.3	5.42E-03	Oktansäure	8.2	27276	3	Periplasmic			
15596244	PA1047		probable esterase	2.2	9.09E-02	Oktansäure	6.1	42335	7	Periplasmic	COG1680	Defense mechanisms	
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	1.4	9.38E-02	Oktansäure	6.8	24860	8	Cytoplasmic	COG0259	Coenzyme metabolism	
15596250	PA1053		conserved hypothetical protein	28.4	3.66E-03	Oktansäure	10.1	15649	3	Outer Membrane Vesicle	COG3133	Cell envelope biogenesis, outer membrane	
15596258	PA1061		conserved hypothetical protein	2.3	1.05E-03	Citronellsäure	6.6	39952	15	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596259	PA1062		hypothetical protein	1.8	6.76E-02	Citronellsäure	6.5	19155	4	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane	
15596261	PA1064		hypothetical protein	6.0	1.40E-03	Oktansäure	5.1	24172	2	Periplasmic	COG3650	Function unknown	
15596263	PA1066		probable short-chain dehydrogenase	2.0	5.13E-02	Oktansäure	7.6	23376	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596265	PA1068		probable heat shock protein (hsp90 family)	1.4	1.15E-02	Oktansäure	5.7	70659	16	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596266	PA1069		hypothetical protein	1.5	2.47E-01	Citronellsäure	4.3	86114	29	Cytoplasmic			
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	3.9	4.35E-03	Citronellsäure	5.5	39769	29	Periplasmic	COG0683	Amino acid transport and metabolism	
15596285	PA1088		hypothetical protein	1.0	8.16E-01	Oktansäure	4.8	28800	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15596286	PA1089		conserved hypothetical protein	2.4	2.76E-01	Oktansäure	5.0	22471	3	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596287	PA1090		hypothetical protein	1.2	4.49E-01	Citronellsäure	5.3	24703	5	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane	
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	6.1	1.39E-02	Citronellsäure	5.2	187155	31	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane	
15596289	PA1092	fliC	flagellin type B	1.7	2.70E-02	Citronellsäure	5.2	49242	14	Periplasmic	COG1344	Cell motility and secretion	
15596291	PA1094	fliD	flagellar capping protein FliD	2.1	7.51E-01	Citronellsäure	7.1	49449	9	Periplasmic	COG1345	Cell motility and secretion	
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.4	4.15E-02	Citronellsäure	5.0	55277	9	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596321	PA1124	dgt	deoxyguanosinetriphosphate triphosphohydrolase	1.6	1.99E-01	Citronellsäure	6.5	56741	1	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15596324	PA1127		probable oxidoreductase	1.6	1.65E-01	Citronellsäure	5.2	36474	3	Cytoplasmic	COG0667	Energy production and conversion	
15596332	PA1135		conserved hypothetical protein	1.1	6.11E-01	Citronellsäure	6.4	31898	9	Cytoplasmic	COG0693	General function prediction only	
15596336	PA1139		hypothetical protein	2.5	3.95E-03	Citronellsäure	5.1	29336	3	Periplasmic	COG2340	Function unknown	
15596337	PA1140		conserved hypothetical protein	2.2	1.97E-02	Oktansäure	6.3	31614	6	Cytoplasmic	COG3257	General function prediction only	
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucleotide reductase	1.4	5.92E-01	Oktansäure	4.5	47386	9	Periplasmic	COG0208	Nucleotide transport and metabolism	
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	1.9	1.50E-02	Citronellsäure	5.7	107105	54	Periplasmic	COG0209	Nucleotide transport and metabolism	
15596354	PA1157		probable two-component response regulator	1.5	4.54E-03	Citronellsäure	4.7	26373	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596358	PA1161	rrmA	rRNA methyltransferase	3.7	3.16E-02	Oktansäure	7.9	29644	2	Cytoplasmic	COG2226	Coenzyme metabolism	

15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	1.2	5.90E-02	Citronellsäure	5.0	41077	12	Cytoplasmic	COG0624	Amino acid transport and metabolism	
15596362	PA1165	pcpS	PcpS	1.2	4.23E-01	Citronellsäure	7.0	26715	4	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism	
15596363	PA1166		hypothetical protein	2.9	2.78E-02	Citronellsäure	7.3	28156	8	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596366	PA1169		probable lipoxygenase	20.4	1.94E-01	Oktansäure	6.8	74803	3	Periplasmic			
15596368	PA1171		probable transglycolase	1.1	4.27E-01	Oktansäure	9.3	42682	11	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane	
15596370	PA1173	napB	cytochrome c-type protein NapB precursor	12.4	1.39E-02	Citronellsäure	8.3	17918	4	Periplasmic	COG3043	Energy production and conversion	
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	4.1	3.81E-02	Citronellsäure	8.6	92942	16	Periplasmic	COG0243	Energy production and conversion	
15596376	PA1179	phoP	two-component response regulator PhoP	1.8	2.29E-02	Citronellsäure	5.2	25650	11	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596384	PA1187		probable acyl-CoA dehydrogenase	34.0	1.01E-04	Citronellsäure	6.5	42350	15	Cytoplasmic	COG1960	Lipid metabolism	
15596389	PA1192		conserved hypothetical protein	1.0	8.69E-01	Oktansäure	6.5	31260	3	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
15596390	PA1193		hypothetical protein	2.3	2.64E-01	Oktansäure	9.1	25292	4	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15596397	PA1200		conserved hypothetical protein	1.2	5.42E-01	Citronellsäure	5.1	24597	5	Cytoplasmic	COG4122	General function prediction only	
15596399	PA1202		probable hydrolase	2.3	7.18E-02	Citronellsäure	4.8	22471	12	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596401	PA1204		conserved hypothetical protein	1.9	1.31E-01	Citronellsäure	6.5	20224	5	Cytoplasmic	COG0431	General function prediction only	
15596403	PA1206		hypothetical protein	1.6	1.29E-01	Citronellsäure	4.4	17690	7	Cytoplasmic			
15596413	PA1216		hypothetical protein	5.0	4.41E-02	Oktansäure	6.1	28573	10	Cytoplasmic	COG4976	General function prediction only	
15596422	PA1225		probable NAD(P)H dehydrogenase	3.1	2.20E-01	Oktansäure	7.0	22551	2	Cytoplasmic	COG2249	General function prediction only	
15596457	PA1260		amino acid ABC transporter periplasmic binding protein	6.0	4.58E-03	Citronellsäure	5.2	29142	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596469	PA1272	cobO	cob(I)alamin adenosyltransferase	12.3	1.23E-03	Oktansäure	8.0	22292	5	Cytoplasmic	COG2109	Coenzyme metabolism	
15596475	PA1278	cobP	cobinamide kinase	1.6	9.28E-01	Citronellsäure	5.4	18862	2	Cytoplasmic	COG2087	Coenzyme metabolism	
15596476	PA1279	cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.3	6.47E-01	Citronellsäure	6.6	36531	2	Cytoplasmic	COG2038	Coenzyme metabolism	
15596477	PA1280		hypothetical protein	58.2	2.77E-02	Oktansäure	6.7	21591	4	Cytoplasmic	COG0406	General function prediction only	
15596480	PA1283		probable transcriptional regulator	1.1	7.03E-01	Oktansäure	4.9	20307	1	Unknown	COG1309	Transcription	
15596484	PA1287		probable glutathione peroxidase	2.0	1.17E-02	Citronellsäure	8.3	20217	12	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596485	PA1288		probable outer membrane protein precursor	1.1	6.51E-01	Citronellsäure	6.0	45561	12	Periplasmic	COG2067	Lipid metabolism	
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	1.0	8.96E-01	Oktansäure	5.3	30597	12	Periplasmic	COG2897	Inorganic ion transport and metabolism	
15596491	PA1294	rnd	ribonuclease D	4.4	1.03E-02	Oktansäure	4.8	43066	7	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
15596493	PA1296		probable 2-hydroxyacid dehydrogenase	3.2	4.51E-02	Oktansäure	5.6	33730	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596501	PA1304		probable oligopeptidase	1.1	5.78E-01	Oktansäure	4.7	75881	22	Periplasmic	COG1770	Amino acid transport and metabolism	
15596504	PA1307		conserved hypothetical protein	1.3	3.69E-01	Oktansäure	5.7	28544	5	Cytoplasmic	COG0121	General function prediction only	
15596521	PA1324		hypothetical protein	1.2	7.06E-01	Citronellsäure	5.8	18303	3	Unknown			
15596534	PA1337	ansB	glutaminase-asparaginase	1.6	3.74E-02	Citronellsäure	7.3	38644	15	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	5.2	8.79E-04	Citronellsäure	6.2	59874	16	Periplasmic	COG0405	Amino acid transport and metabolism	
15596539	PA1342		probable binding protein component of ABC transporter	2.5	2.04E-02	Citronellsäure	8.6	33054	45	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596541	PA1344		probable short-chain dehydrogenase	1.2	4.39E-01	Oktansäure	4.9	27397	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596568	PA1371		hypothetical protein	2.8	7.50E-02	Citronellsäure	5.2	27419	2	Unknown	COG5619	Function unknown	
15596569	PA1372		hypothetical protein	1.1	4.48E-01	Oktansäure	5.5	79820	20	Cytoplasmic	COG3972	General function prediction only	
15596572	PA1375	pdxB	erythronate-4-phosphate dehydrogenase	1.1	5.08E-01	Oktansäure	5.5	41001	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	3.2	1.07E-02	Citronellsäure	5.0	66760	19	Cytoplasmic	COG4579	Signal transduction mechanisms	
15596574	PA1377		conserved hypothetical protein	6.4	6.84E-03	Oktansäure	7.9	20068	3	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596599	PA1402		hypothetical protein	2.2	2.69E-04	Citronellsäure	4.7	23753	7	Cytoplasmic	COG4122	General function prediction only	
15596627	PA1430	lasR	transcriptional regulator LasR	1.4	1.43E-01	Citronellsäure	6.5	26618	12	Cytoplasmic	COG2771	Transcription	
15596637	PA1440		hypothetical protein	1.4	1.24E-01	Oktansäure	3.9	22382	4	Cytoplasmic	COG3318	General function prediction only	
15596639	PA1442		conserved hypothetical protein	1.9	3.50E-01	Oktansäure	10.3	18760	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
15596640	PA1443	fliM	flagellar motor switch protein FliM	5.2	1.30E-03	Citronellsäure	5.0	36282	3	Cytoplasmic	COG1868	Cell motility and secretion	
15596641	PA1444	fliN	flagellar motor switch protein FliN	3.5	3.93E-02	Oktansäure	4.0	16620	4	Cytoplasmic Membrane	COG1886	Cell motility and secretion	Intracellular trafficking and secretion
15596652	PA1455	fliA	sigma factor FliA	1.2	1.55E-01	Citronellsäure	5.9	27522	4	Cytoplasmic	COG1191	Transcription	
15596654	PA1457	cheZ	chemotaxis protein CheZ	1.3	2.62E-01	Citronellsäure	4.6	29622	13	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
15596655	PA1458		probable two-component sensor	2.5	5.77E-03	Citronellsäure	4.3	79737	21	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15596656	PA1459		probable methyltransferase	1.1	2.49E-01	Oktansäure	8.6	39004	8	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
15596659	PA1462		probable plasmid partitioning protein	16.4	1.35E-02	Oktansäure	10.1	28407	2	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
15596661	PA1464		probable purine-binding chemotaxis protein	2.4	4.04E-02	Citronellsäure	4.1	17536	11	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15596667	PA1470		probable short-chain dehydrogenase	2.2	2.36E-02	Citronellsäure	4.9	25365	7	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	2.4	1.52E-03	Citronellsäure	8.6	36485	19	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15596692	PA1495		hypothetical protein	3.3	5.55E-02	Oktansäure	5.9	23443	2	Unknown	COG4339	Function unknown	
15596706	PA1509		hypothetical protein	3.8	3.46E-03	Oktansäure	6.8	42364	7	Cytoplasmic			
15596707	PA1510		hypothetical protein	15.6	1.18E-02	Oktansäure	5.1	63320	12	Unknown			
15596708	PA1511		conserved hypothetical protein	42.1	1.59E-04	Oktansäure	6.4	93635	8	Cytoplasmic	COG3501	Function unknown	
15596711	PA1514		ureidoglycolate hydrolaseYbbT	52.2	9.44E-04	Citronellsäure	5.6	18983	2	Unknown	COG3194	Nucleotide transport and metabolism	
15596713	PA1516		hypothetical protein	5.9	1.21E-03	Oktansäure	4.8	18896	7	Cytoplasmic	COG3195	Function unknown	
15596723	PA1526		probable transcriptional regulator	40.1	4.32E-03	Oktansäure	7.8	25070	3	Cytoplasmic	COG1802	Transcription	
15596724	PA1527		conserved hypothetical protein	3.3	9.53E-03	Citronellsäure	4.8	131580	12	Cytoplasmic	COG1196	Cell division and chromosome partitioning	
15596725	PA1528	zipA	cell division protein ZipA	2.0	1.49E-02	Oktansäure	5.7	32236	3	Outer Membrane Vesicle	COG3115	Cell division and chromosome partitioning	
15596726	PA1529	lig	DNA ligase	1.0	6.76E-01	Citronellsäure	5.1	86767	20	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	1.9	1.42E-02	Citronellsäure	4.4	73309	11	Cytoplasmic	COG2812	DNA replication, recombination, and repair	
15596731	PA1534	recR	recombination protein RecR	5.0	1.07E-01	Oktansäure	6.0	21173	7	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
15596732	PA1535		citronellyl-CoA dehydrogenase	39.9	2.13E-05	Citronellsäure	5.6	42041	15	Cytoplasmic	COG1960	Lipid metabolism	
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.0	8.67E-01	Citronellsäure	4.6	19804	7	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15596741	PA1544	anr	transcriptional regulator Anr	1.0	8.00E-01	Citronellsäure	5.2	27129	7	Cytoplasmic	COG0664	Signal transduction mechanisms	
15596747	PA1550		hypothetical protein	87.2	3.50E-03	Oktansäure	5.1	20338	2	Outer Membrane Vesicle	COG3198	Function unknown	
15596750	PA1553	ccoO1	Cytochrome c oxidase, cbb3-type, CcoO subunit	10.3	4.20E-03	Oktansäure	8.2	22758	5	Outer Membrane Vesicle	COG2993	Energy production and conversion	
15596759	PA1562	acnA	aconitate hydratase 1	6.8	1.28E-04	Citronellsäure	5.4	99147	43	Cytoplasmic	COG1048	Energy production and conversion	
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	2.3	1.72E-02	Oktansäure	5.2	30777	9	Cytoplasmic	COG2084	Lipid metabolism	
15596776	PA1579		hypothetical protein	2.1	4.58E-02	Oktansäure	8.2	22110	13	Periplasmic			
15596777	PA1580	gltA	citrate synthase	1.7	1.96E-03	Citronellsäure	7.0	47695	35	Periplasmic	COG0372	Energy production and conversion	
15596778	PA1581	sdhC	succinate dehydrogenase (C subunit)	15.4	1.62E-03	Oktansäure	10.4	13738	2	Outer Membrane Vesicle	COG2009	Energy production and conversion	
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	1.0	7.63E-01	Oktansäure	6.5	63532	28	Periplasmic	COG1053	Energy production and conversion	
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	1.8	1.31E-01	Oktansäure	6.9	26155	8	Outer Membrane Vesicle	COG0479	Energy production and conversion	
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	3.6	4.61E-03	Oktansäure	6.5	105877	39	Outer Membrane Vesicle	COG0567	Energy production and conversion	
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	4.5	3.60E-03	Oktansäure	5.2	42887	21	Periplasmic	COG0508	Energy production and conversion	
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.0	9.92E-01	Oktansäure	7.0	50165	22	Periplasmic	COG1249	Energy production and conversion	
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	2.7	3.39E-04	Citronellsäure	6.1	41542	28	Periplasmic	COG0045	Energy production and conversion	
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	1.3	4.52E-01	Citronellsäure	6.0	30266	28	Periplasmic	COG0074	Energy production and conversion	
15596793	PA1596	htpG	heat shock protein HtpG	1.6	3.94E-02	Citronellsäure	4.9	71667	52	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596794	PA1597		hypothetical protein	1.3	9.29E-02	Citronellsäure	5.9	25791	9	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	

15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.7	6.96E-02	Citronellsäure	5.3	42806	20	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	1.5	3.49E-01	Oktansäure	6.9	18747	11	Cytoplasmic	COG0764	Lipid metabolism	
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.1	6.02E-01	Oktansäure	6.2	36773	14	Cytoplasmic	COG0240	Energy production and conversion	
15596813	PA1616		conserved hypothetical protein	21.5	3.61E-02	Oktansäure	6.4	16715	4	Unknown	COG2062	Signal transduction mechanisms	
15596814	PA1617		probable AMP-binding enzyme	14.5	1.42E-04	Citronellsäure	7.2	61370	21	Cytoplasmic	COG1022	Lipid metabolism	
15596815	PA1618		conserved hypothetical protein	118.9	3.02E-03	Oktansäure	7.0	15595	7	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596819	PA1622		probable hydrolase	7.3	8.17E-04	Citronellsäure	7.1	31290	8	Cytoplasmic	COG0596	General function prediction only	
15596820	PA1623		conserved hypothetical protein	1.2	2.75E-01	Citronellsäure	6.1	24924	14	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596821	PA1624		hypothetical protein	1.2	3.86E-01	Oktansäure	6.4	29533	5	Periplasmic			
15596836	PA1639		hypothetical protein	1.8	2.11E-01	Oktansäure	5.4	22457	6	Periplasmic			
15596839	PA1642	selD	selenophosphate synthetase	1.2	4.42E-01	Citronellsäure	4.7	36354	11	Cytoplasmic	COG0709	Amino acid transport and metabolism	
15596841	PA1644		conserved hypothetical protein	1.5	3.07E-01	Oktansäure	5.5	21838	5	Unknown	COG1853	General function prediction only	
15596845	PA1648		probable oxidoreductase	1.7	1.96E-01	Oktansäure	6.1	36168	3	Cytoplasmic	COG2130	General function prediction only	
15596851	PA1654		probable aminotransferase	1.1	9.26E-01	Citronellsäure	5.3	43311	5	Cytoplasmic	COG1167	Transcription	Amino acid transport and metabolism
15596852	PA1655		probable glutathione S-transferase	2.9	3.48E-02	Oktansäure	5.3	22738	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596854	PA1657		conserved hypothetical protein	4.3	5.58E-03	Oktansäure	4.5	18165	8	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15596855	PA1658		conserved hypothetical protein	4.9	8.26E-05	Oktansäure	5.1	55560	13	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15596859	PA1662		probable ClpA/B-type protease	28.4	3.70E-04	Oktansäure	5.5	95774	31	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15596860	PA1663		probable transcriptional regulator	12.3	1.43E-02	Oktansäure	6.1	55290	2	Cytoplasmic	COG3604	Transcription	Signal transduction mechanisms
15596863	PA1666		hypothetical protein	234.1	2.60E-02	Oktansäure	7.4	18440	2	Unknown	COG3521	Intracellular trafficking, secretion, and vesicular transport	
15596864	PA1667		hypothetical protein	23.7	6.90E-04	Oktansäure	6.5	49689	6	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15596870	PA1673		hypothetical protein	20.5	9.92E-03	Oktansäure	6.2	17853	5	Cytoplasmic	COG2703	Inorganic ion transport and metabolism	
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.0	8.85E-01	Oktansäure	7.6	20236	12	Outer Membrane Vesicle	COG0302	Coenzyme metabolism	
15596874	PA1677		conserved hypothetical protein	2.7	4.93E-03	Oktansäure	6.5	21034	11	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596875	PA1678		probable DNA methylase	16.0	1.16E-01	Oktansäure	4.4	34229	3	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
15596878	PA1681	aroC	chorismate synthase	1.2	6.76E-01	Citronellsäure	6.6	38987	8	Cytoplasmic	COG0082	Amino acid transport and metabolism	
15596880	PA1683		probable sugar aldolase	2.5	1.36E-02	Citronellsäure	6.5	22868	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	2.8	3.02E-02	Oktansäure	5.0	20552	7	Cytoplasmic	COG1791	Function unknown	
15596884	PA1687	speE	spermidine synthase	1.1	6.81E-01	Oktansäure	4.9	32238	10	Periplasmic	COG0421	Amino acid transport and metabolism	
15596923	PA1726	bglX	periplasmic beta-glucosidase	1.5	3.04E-01	Oktansäure	7.1	83003	6	Periplasmic	COG1472	Carbohydrate transport and metabolism	
15596930	PA1733		conserved hypothetical protein	18.8	4.10E-03	Citronellsäure	5.3	26467	5	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones	
15596931	PA1734		hypothetical protein	17.7	1.72E-01	Oktansäure	8.2	30246	2	Unknown	COG2857	Energy production and conversion	
15596933	PA1736		probable acyl-CoA thiolase	11.9	7.19E-05	Citronellsäure	5.3	42102	19	Cytoplasmic	COG0183	Lipid metabolism	
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	7.6	8.93E-05	Citronellsäure	6.7	76666	44	Cytoplasmic	COG1250	Lipid metabolism	
15596939	PA1742	pauD2	Glutamine amidotransferase class I	1.2	4.77E-01	Citronellsäure	5.0	27361	8	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
15596943	PA1746		hypothetical protein	266.8	3.71E-03	Oktansäure	6.6	18189	5	Outer Membrane Vesicle	COG2110	General function prediction only	
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	1.7	1.26E-01	Citronellsäure	7.8	24412	15	Cytoplasmic	COG1024	Lipid metabolism	
15596946	PA1749		hypothetical protein	42.9	7.35E-04	Oktansäure	10.0	17672	2	Unknown	COG2388	General function prediction only	
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.2	9.66E-02	Citronellsäure	6.5	39132	11	Cytoplasmic	COG0722	Amino acid transport and metabolism	
15596949	PA1752		hypothetical protein	2.1	2.92E-02	Oktansäure	6.7	34141	11	Cytoplasmic	COG1893	Coenzyme metabolism	
15596950	PA1753		conserved hypothetical protein	2.6	1.22E-01	Citronellsäure	4.7	18372	6	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596951	PA1754	cysB	transcriptional regulator CysB	1.1	7.19E-01	Citronellsäure	7.0	36110	10	Periplasmic	COG0583	Transcription	
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	2.4	2.32E-03	Citronellsäure	6.4	30215	5	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15596954	PA1757	thrH	homoserine kinase	2.4	8.80E-04	Citronellsäure	5.0	23501	7	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596956	PA1759		probable transcriptional regulator	1.6	3.88E-01	Citronellsäure	6.3	101111	20	Unknown	COG2909	Transcription	
15596957	PA1760		probable transcriptional regulator	5.0	6.90E-02	Citronellsäure	6.8	101628	12	Cytoplasmic	COG2909	Transcription	
15596965	PA1768		hypothetical protein	2.7	2.31E-01	Citronellsäure	9.6	19720	6	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15596966	PA1769		conserved hypothetical protein	1.5	1.20E-01	Citronellsäure	6.1	31074	13	Cytoplasmic	COG1806	Function unknown	
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.1	8.62E-01	Citronellsäure	4.8	85798	66	Cytoplasmic	COG0574	Carbohydrate transport and metabolism	
15596969	PA1772		probable methyltransferase	1.2	1.86E-01	Oktansäure	4.6	17404	9	Cytoplasmic	COG0684	Coenzyme metabolism	
15596972	PA1775	cmpX	conserved cytoplasmic membrane protein, CmpX protein	19.4	7.33E-02	Oktansäure	8.8	29019	2	Outer Membrane Vesicle			
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precursor	2.0	4.89E-02	Oktansäure	4.8	37639	15	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596984	PA1787	acnB	aconitate hydratase 2	3.1	4.60E-03	Citronellsäure	5.0	93595	73	Periplasmic	COG1049	Energy production and conversion	
15596986	PA1789		hypothetical protein	7.4	8.84E-03	Oktansäure	5.3	31273	12	Cytoplasmic	COG0589	Signal transduction mechanisms	
15596987	PA1790		hypothetical protein	4.8	1.34E-03	Oktansäure	6.7	23312	5	Cytoplasmic	COG4445	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	1.1	1.59E-01	Citronellsäure	6.2	18126	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.2	4.09E-01	Oktansäure	5.6	62912	32	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	2.1	1.80E-03	Citronellsäure	5.4	51245	20	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis	
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase	1.4	6.83E-02	Citronellsäure	5.8	30549	11	Periplasmic	COG0190	Coenzyme metabolism	
15596997	PA1800	tig	trigger factor	1.9	3.09E-03	Citronellsäure	4.5	48582	24	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones	
15596998	PA1801	clpP	ClpP	3.8	1.93E-03	Oktansäure	6.4	23502	19	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15596999	PA1802	clpX	ClpX	1.1	9.65E-01	Citronellsäure	4.8	46991	25	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones	
15597000	PA1803	lon	Lon protease	2.2	3.01E-02	Oktansäure	6.0	88647	31	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	1.6	1.33E-01	Oktansäure	4.7	68741	5	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	2.4	1.46E-03	Citronellsäure	5.7	28006	10	Cytoplasmic Membrane	COG0623	acyl-carrier-protein	
15597007	PA1810		probable binding protein component of ABC transporter	1.1	2.53E-01	Citronellsäure	6.5	70473	16	Periplasmic	COG4166	Amino acid transport and metabolism	
15597010	PA1813		probable hydroxyacylglutathione hydrolase	1.2	1.77E-01	Oktansäure	6.3	28865	5	Cytoplasmic	COG0491	General function prediction only	
15597012	PA1815	rnhA	ribonuclease H	1.5	1.27E-01	Citronellsäure	8.7	16697	4	Unknown	COG0328	DNA replication, recombination, and repair	
15597013	PA1816	dnaQ	DNA polymerase III, epsilon chain	2.3	3.65E-02	Oktansäure	5.0	26814	6	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	1.1	6.35E-01	Oktansäure	6.1	82757	21	Cytoplasmic	COG1982	Amino acid transport and metabolism	
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	4.6	1.49E-02	Citronellsäure	5.4	29957	7	Cytoplasmic	COG1024	Lipid metabolism	
15597019	PA1822	fimL	hypothetical protein	1.5	1.50E-01	Citronellsäure	4.9	60868	1	Cytoplasmic			
15597020	PA1823		conserved hypothetical protein	1.4	1.98E-01	Citronellsäure	4.9	31356	5	Cytoplasmic	COG2816	DNA replication, recombination, and repair	
15597025	PA1828		probable short-chain dehydrogenase	1.2	3.26E-01	Oktansäure	7.4	26919	15	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597026	PA1829		hypothetical protein	2.3	8.91E-03	Citronellsäure	5.9	40833	8	Cytoplasmic	COG3173	General function prediction only	
15597028	PA1831		hypothetical protein	2.0	9.86E-02	Citronellsäure	6.3	26378	8	Cytoplasmic	COG0406	General function prediction only	
15597030	PA1833		probable oxidoreductase	1.9	4.47E-03	Citronellsäure	5.2	34552	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597034	PA1837		hypothetical protein	7.8	6.66E-03	Citronellsäure	4.7	18765	7	Cytoplasmic	COG3749	Function unknown	
15597035	PA1838	cysI	sulfite reductase	2.6	2.51E-04	Citronellsäure	5.9	62132	17	Periplasmic	COG0155	Inorganic ion transport and metabolism	
15597040	PA1843	metH	methionine synthase	5.9	1.46E-04	Citronellsäure	4.6	135062	47	Periplasmic	COG1410	Amino acid transport and metabolism	
15597041	PA1844	tse1	Tse1	8.5	1.24E-02	Oktansäure	8.8	16443	2	Extracellular			
15597042	PA1845		hypothetical protein	1.6	6.40E-02	Oktansäure	4.6	18757	3	Unknown			
15597043	PA1846	cti	cis/trans isomerase	2.3	4.22E-02	Oktansäure	6.0	86517	9	Periplasmic			
15597044	PA1847	nfuA	NfuA	1.3	6.91E-01	Oktansäure	4.2	21136	9	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones	
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	34.6	1.23E-01	Citronellsäure	6.8	26377	2	Periplasmic	COG0725	Inorganic ion transport and metabolism	

15597071	PA1874		hypothetical protein	10.8	8.51E-03	Citronellsäure	3.1	238414	4	Unknown			
15597077	PA1880		probable oxidoreductase	2.4	1.23E-02	Citronellsäure	7.4	77656	11	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597084	PA1887		hypothetical protein	1.7	7.96E-01	Oktansäure	8.0	24376	4	Unknown			
15597087	PA1890		probable glutathione S-transferase	1.1	5.83E-01	Oktansäure	7.0	23440	11	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597091	PA1894		hypothetical protein	3.3	4.48E-03	Oktansäure	5.3	26179	11	Unknown			
15597099	PA1902	phzD2	phenazine biosynthesis protein PhzD	1.9	8.26E-01	Oktansäure	5.6	23195	3	Unknown	COG1535	Secondary metabolites biosynthesis, transport, and catabolism	
15599411	PA1905	phzG2	probable pyridoxamine 5'-phosphate oxidase	116.3	7.04E-04	Oktansäure	6.4	24367	3	Cytoplasmic	COG0259	Coenzyme metabolism	
15597109	PA1913		hypothetical protein	27.4	1.36E-01	Oktansäure	8.4	25410	2	Unknown			
15597110	PA1914		conserved hypothetical protein	8.7	2.67E-03	Citronellsäure	6.9	46125	6	Extracellular			
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	1.7	1.29E-01	Oktansäure	5.7	86211	26	Cytoplasmic	COG0620	Amino acid transport and metabolism	
15597126	PA1930		probable chemotaxis transducer	2.4	1.08E-01	Citronellsäure	6.5	47801	4	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	3.5	1.41E-02	Citronellsäure	8.4	33860	12	Periplasmic	COG1879	Carbohydrate transport and metabolism	
15597145	PA1949	rbsR	ribose operon repressor RbsR	1.0	9.80E-01	Oktansäure	7.2	36446	6	Cytoplasmic	COG1609	Transcription	
15597146	PA1950	rbsK	ribokinase	2.8	1.79E-02	Citronellsäure	4.9	31846	5	Cytoplasmic	COG0524	Carbohydrate transport and metabolism	
15597160	PA1964		probable ATP-binding component of ABC transporter	1.2	5.15E-01	Oktansäure	4.8	57917	8	Cytoplasmic	COG0488	General function prediction only	
15597170	PA1974		hypothetical protein	36.5	2.38E-03	Citronellsäure	4.3	43218	3	Outer Membrane			
15597177	PA1981		hypothetical protein	213.6	4.28E-05	Citronellsäure	5.8	22869	6	Extracellular	COG1357	Function unknown	
15597178	PA1982	exaA	quinoprotein ethanol dehydrogenase	60.8	1.51E-02	Citronellsäure	7.1	68123	36	Periplasmic	COG4993	Carbohydrate transport and metabolism	
15597180	PA1984	exaC	NAD+ dependent aldehyde dehydrogenase ExaC	20.4	1.35E-03	Citronellsäure	5.4	54892	32	Periplasmic	COG1012	Energy production and conversion	
15597182	PA1986	pqqB	pyrroloquinoline quinone biosynthesis protein B	12.4	8.76E-03	Citronellsäure	5.5	33018	6	Cytoplasmic	COG1235	General function prediction only	
15597183	PA1987	pqqC	pyrroloquinoline quinone biosynthesis protein C	24.8	5.22E-05	Citronellsäure	7.4	29449	10	Cytoplasmic	COG5424	Coenzyme metabolism	
15597193	PA1997		probable AMP-binding enzyme	2.2	5.20E-02	Citronellsäure	6.5	71929	9	Cytoplasmic	COG0365	Lipid metabolism	
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	2.2	5.97E-03	Citronellsäure	5.0	25244	6	Cytoplasmic	COG1788	Lipid metabolism	
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	1.5	1.59E-01	Citronellsäure	4.6	23187	17	Cytoplasmic	COG2057	Lipid metabolism	
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	2.7	2.89E-03	Citronellsäure	6.4	40405	28	Cytoplasmic	COG0183	Lipid metabolism	
15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase	1.8	6.97E-02	Oktansäure	5.6	26727	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597203	PA2007	maiA	maleylacetoacetate isomerase	2.6	4.20E-02	Citronellsäure	6.9	23685	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15597204	PA2008	fahA	fumarylacetoacetase	2.8	5.83E-02	Citronellsäure	6.0	46341	7	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase	13.5	5.46E-04	Citronellsäure	6.0	31837	11	Cytoplasmic	COG0119	Amino acid transport and metabolism	
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containing)	17.2	2.22E-04	Citronellsäure	5.6	71282	27	Cytoplasmic	COG4770	Lipid metabolism	
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase	40.5	3.76E-06	Citronellsäure	5.2	28947	14	Cytoplasmic	COG1024	Lipid metabolism	
15597210	PA2014	liuB	methylcrotonyl-CoA carboxylase, beta-subunit	46.7	1.31E-06	Citronellsäure	6.7	57433	26	Cytoplasmic	COG4799	Lipid metabolism	
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase	24.2	2.68E-05	Citronellsäure	5.5	42209	32	Cytoplasmic	COG1960	Lipid metabolism	
15597216	PA2020		probable transcriptional regulator	1.5	9.93E-02	Citronellsäure	7.1	23695	3	Cytoplasmic	COG1309	Transcription	
15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase	1.4	2.94E-01	Citronellsäure	5.1	31236	24	Periplasmic	COG1210	Cell envelope biogenesis, outer membrane	
15597221	PA2025	gor	glutathione reductase	1.0	7.90E-01	Citronellsäure	6.3	49237	14	Cytoplasmic	COG1249	Energy production and conversion	
15597230	PA2034		hypothetical protein	15.2	9.53E-04	Oktansäure	6.3	24525	6	Cytoplasmic	COG2242	Coenzyme metabolism	
15597240	PA2044		hypothetical protein	2.1	4.94E-02	Oktansäure	6.1	70083	8	Periplasmic	COG1305	Amino acid transport and metabolism	
15597265	PA2069		probable carbamoyl transferase	12.1	8.06E-02	Oktansäure	6.2	63382	3	Cytoplasmic	COG2192	Posttranslational modification, protein turnover, chaperones	
15597267	PA2071	fusA2	elongation factor G	1.5	1.93E-01	Citronellsäure	4.9	77574	23	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15597272	PA2076		probable transcriptional regulator	1.6	3.51E-01	Oktansäure	6.0	32458	2	Cytoplasmic	COG0583	Transcription	
15597276	PA2080	kynU	kynureninase KynU	1.1	6.51E-01	Citronellsäure	5.3	46294	11	Cytoplasmic	COG3844	Amino acid transport and metabolism	
15597277	PA2081	kynB	kynurenine formamidase, KynB	2.4	2.54E-02	Citronellsäure	5.2	23152	8	Cytoplasmic	COG1878	Amino acid transport and metabolism	
15597278	PA2082	kynR	KynR	37.5	5.30E-02	Oktansäure	6.5	17846	3	Cytoplasmic	COG1522	Transcription	
15597315	PA2119		alcohol dehydrogenase (Zn-dependent)	2.9	1.05E-01	Oktansäure	5.4	38561	4	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
15597348	PA2152		probable trehalose synthase	20.5	5.19E-03	Citronellsäure	5.7	124521	2	Cytoplasmic	COG3281	Carbohydrate transport and metabolism	
15597372	PA2176		hypothetical protein	1.8	2.33E-01	Citronellsäure	4.9	20943	3	Unknown	COG2910	General function prediction only	
15597380	PA2184		conserved hypothetical protein	1.2	6.52E-01	Citronellsäure	4.7	18990	5	Cytoplasmic	COG3685	Function unknown	
15597393	PA2197		conserved hypothetical protein	1.2	1.42E-01	Oktansäure	6.3	37135	16	Cytoplasmic	COG2130	General function prediction only	
15597394	PA2198		hypothetical protein	117.9	2.23E-03	Oktansäure	5.2	12944	4	Cytoplasmic	COG1359	Function unknown	
15597395	PA2199		probable dehydrogenase	1.8	2.70E-02	Oktansäure	5.4	30886	10	Cytoplasmic	COG2084	Lipid metabolism	
15597400	PA2204		probable binding protein component of ABC transporter	1.7	1.26E-02	Oktansäure	9.7	29309	21	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15597418	PA2222		hypothetical protein	1.6	1.49E-01	Citronellsäure	5.0	23441	6	Unknown			
15597425	PA2229		conserved hypothetical protein	1.1	7.90E-01	Oktansäure	6.5	26560	6	Cytoplasmic	COG2258	Function unknown	
15597428	PA2232	pslB	PslB	1.2	1.99E-02	Citronellsäure	6.0	53515	15	Periplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15597449	PA2253	ansA	L-asparaginase I	3.6	1.77E-03	Oktansäure	5.3	34755	2	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15597467	PA2271		probable acetyltransferase	1.4	1.93E-01	Citronellsäure	6.2	19165	3	Cytoplasmic			
15597496	PA2300	chiC	chitinase	7.2	4.53E-03	Oktansäure	5.1	53042	7	Extracellular	COG3469	Carbohydrate transport and metabolism	
15597497	PA2301		hypothetical protein	1.0	7.25E-01	Oktansäure	6.5	19330	10	Cytoplasmic	COG2606	Function unknown	
15597498	PA2302	ambE	AmbE	1.7	8.60E-02	Citronellsäure	4.8	229041	96	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597499	PA2303	ambD	AmbD	1.9	2.57E-03	Oktansäure	6.6	38657	6	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597500	PA2304	ambC	AmbC	2.3	7.94E-03	Oktansäure	6.8	40696	6	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597501	PA2305	ambB	AmbB	1.6	1.06E-01	Citronellsäure	6.3	134446	29	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597519	PA2323		probable glyceraldehyde-3-phosphate dehydrogenase	1.2	4.50E-01	Citronellsäure	6.4	59960	2	Cytoplasmic	COG1012	Energy production and conversion	
15597526	PA2330		hypothetical protein	4.3	1.42E-02	Oktansäure	6.6	37680	4	Unknown	COG1960	Lipid metabolism	
15597527	PA2331		hypothetical protein	41.6	1.30E-03	Oktansäure	5.0	19904	7	Unknown	COG2128	Function unknown	
15597549	PA2353		conserved hypothetical protein	8.5	2.40E-03	Oktansäure	6.2	43286	2	Cytoplasmic	COG1485	General function prediction only	
15597561	PA2365		conserved hypothetical protein	1.6	1.60E-01	Oktansäure	4.4	20177	8	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15597562	PA2366		uricase PuuD	6.6	2.39E-03	Citronellsäure	5.7	55042	15	Cytoplasmic Membrane	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15597563	PA2367		hypothetical protein	5.3	9.12E-04	Citronellsäure	4.6	17636	13	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15597567	PA2371		probable ClpA/B-type protease	3.3	5.63E-02	Citronellsäure	5.1	92424	7	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597568	PA2372		hypothetical protein	65.5	9.11E-04	Citronellsäure	8.4	21241	3	Unknown			
15597574	PA2378		probable aldehyde dehydrogenase	4.3	1.70E-03	Citronellsäure	8.4	83665	14	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ	1.2	5.93E-01	Oktansäure	7.1	84039	25	Periplasmic	COG2366	General function prediction only	
15597582	PA2386	pvdA	L-ornithine N5-oxygenase	13.9	2.10E-03	Oktansäure	6.5	49478	21	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
15597590	PA2394	pvdN	PvdN	2.1	2.69E-02	Oktansäure	7.3	47981	11	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
15597591	PA2395	pvdO	PvdO	1.8	4.73E-02	Oktansäure	5.4	31070	12	Periplasmic	COG1262	Function unknown	
15597592	PA2396	pvdF	pyoverdine synthetase F	1.9	3.26E-02	Oktansäure	5.0	31039	23	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15597594	PA2398	fpvA	ferripyoverdine receptor	2.7	2.68E-02	Oktansäure	5.3	91167	26	Periplasmic	COG4773	Inorganic ion transport and metabolism	
15597595	PA2399	pvdD	pyoverdine synthetase D	1.1	6.77E-01	Oktansäure	5.0	273645	59	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
110645305	PA2400	pvdJ	PvdJ	1.1	9.69E-01	Citronellsäure	5.1	240213	9	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597598	PA2402		probable non-ribosomal peptide synthetase	1.7	6.07E-02	Oktansäure	5.1	569179	197	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597603	PA2407		probable adhesion protein	1.3	2.56E-01	Oktansäure	9.6	34309	8	Periplasmic	COG0803	Inorganic ion transport and metabolism	
15597606	PA2410		hypothetical protein	1.8	1.36E-01	Oktansäure	5.0	31732	11	Unknown	COG0803	Inorganic ion transport and metabolism	
15597607	PA2411		probable thioesterase	4.5	7.73E-03	Oktansäure	5.4	27846	11	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	

15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, PvdH		4.8	1.13E-02	Oktansäure	6.5	50215	18	Cytoplasmic	COG0160	Amino acid transport and metabolism	
15597620	PA2424	pvdL	PvdL		2.8	3.89E-04	Oktansäure	5.1	480292	176	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597638	PA2442	gcvT2	glycine cleavage system protein T2		1.3	2.55E-01	Citronellsäure	6.4	39882	20	Periplasmic	COG0404	Amino acid transport and metabolism	
15597640	PA2444	glyA2	serine hydroxymethyltransferase		1.7	2.32E-01	Oktansäure	6.5	44974	6	Periplasmic	COG0112	Amino acid transport and metabolism	
15597641	PA2445	gcvP2	glycine cleavage system protein P2		1.2	2.84E-01	Oktansäure	6.0	103918	41	Periplasmic	COG1003	Amino acid transport and metabolism	
15597646	PA2450		hypothetical protein		6.7	3.13E-03	Oktansäure	6.4	34331	5	Periplasmic			
15597651	PA2455		hypothetical protein		1121.3	1.66E-02	Oktansäure	5.6	20332	3	Cytoplasmic	COG3153	General function prediction only	
15597655	PA2459		hypothetical protein	Infinity		1.16E-01	Citronellsäure	5.6	23801	2	Cytoplasmic			
15597658	PA2462		hypothetical protein		1.3	3.82E-01	Citronellsäure	5.1	573168	34	Outer Membrane Vesicle	COG3210	Intracellular trafficking and secretion	
15597660	PA2464		hypothetical protein		3.2	1.08E-01	Oktansäure	4.6	17626	5	Periplasmic			
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG		1.2	3.27E-01	Oktansäure	7.1	28053	6	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15597678	PA2482		probable cytochrome c		6.0	1.61E-02	Oktansäure	6.8	22526	2	Periplasmic	COG2863	Energy production and conversion	
15597679	PA2483		conserved hypothetical protein		2.6	3.53E-02	Citronellsäure	6.2	36102	6	Cytoplasmic	COG2141	Energy production and conversion	
15597687	PA2491		probable oxidoreductase		1.5	1.57E-01	Citronellsäure	5.3	36832	14	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein M		4.9	7.06E-03	Oktansäure	8.8	45031	5	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15597692	PA2496		hypothetical protein		13.1	2.29E-02	Oktansäure	6.6	19483	2	Cytoplasmic	COG2318	Function unknown	
15597699	PA2503		hypothetical protein		1.6	2.59E-01	Oktansäure	4.6	45895	4	Cytoplasmic			
15597700	PA2504		hypothetical protein		6.4	2.92E-02	Citronellsäure	4.3	22822	3	Cytoplasmic	COG4859	Function unknown	
15597703	PA2507	catA	catechol 1,2-dioxygenase		28.0	3.30E-04	Citronellsäure	5.1	34160	6	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
15597725	PA2529		hypothetical protein		2.3	1.90E-01	Oktansäure	5.6	52681	2	Cytoplasmic	COG0312	General function prediction only	
15597726	PA2530		hypothetical protein		1.1	5.34E-01	Citronellsäure	5.7	48959	4	Unknown	COG0312	General function prediction only	
15597727	PA2531		probable aminotransferase		19.5	8.00E-03	Oktansäure	9.4	40715	6	Unknown	COG0079	Amino acid transport and metabolism	
15597728	PA2532	tpx	thiol peroxidase		5.1	8.19E-03	Citronellsäure	4.9	17234	15	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
15597741	PA2545	xthA	exodeoxyribonuclease III		2.7	1.16E-01	Oktansäure	6.4	31003	8	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15597746	PA2550		probable acyl-CoA dehydrogenase		1.4	4.21E-01	Oktansäure	6.6	45482	3	Cytoplasmic	COG1960	Lipid metabolism	
15597747	PA2551		probable transcriptional regulator		1.6	6.75E-03	Citronellsäure	9.9	35144	6	Cytoplasmic	COG0583	Transcription	
15597748	PA2552		probable acyl-CoA dehydrogenase		14.7	1.35E-02	Citronellsäure	5.6	40908	3	Cytoplasmic	COG1960	Lipid metabolism	
15597749	PA2553		probable acyl-CoA thiolase		4.3	1.18E-04	Citronellsäure	5.9	41400	12	Cytoplasmic	COG0183	Lipid metabolism	
15597750	PA2554		probable short-chain dehydrogenase		5.8	5.24E-04	Citronellsäure	6.6	26394	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597751	PA2555		probable AMP-binding enzyme		11.3	7.26E-03	Citronellsäure	6.1	60159	2	Cytoplasmic	COG0365	Lipid metabolism	
15597753	PA2557		probable AMP-binding enzyme		11.7	5.13E-03	Citronellsäure	6.1	62629	26	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15597758	PA2562		hypothetical protein		69.6	1.32E-05	Oktansäure	10.0	17384	2	Unknown			
15597763	PA2567		hypothetical protein		11.0	2.13E-01	Oktansäure	4.8	65617	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15597771	PA2575		hypothetical protein		6.5	7.34E-04	Oktansäure	6.4	22222	13	Unknown	COG3560	General function prediction only	
15597778	PA2582		hypothetical protein		5.0	5.06E-03	Oktansäure	10.5	19446	7	Unknown	COG3109	Signal transduction mechanisms	
15597782	PA2586	gacA	response regulator GacA		1.4	8.82E-02	Citronellsäure	6.1	23576	5	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15597788	PA2592		probable periplasmic spermidine/putrescine-binding protein		1.2	7.83E-02	Oktansäure	6.7	40725	7	Periplasmic	COG0687	Amino acid transport and metabolism	
15597790	PA2594		conserved hypothetical protein		1.6	5.56E-02	Oktansäure	9.2	34686	4	Periplasmic	COG0715	Inorganic ion transport and metabolism	
15597797	PA2601		probable transcriptional regulator		1.1	6.11E-01	Oktansäure	5.5	32375	2	Cytoplasmic	COG0583	Transcription	
15597805	PA2609		hypothetical protein		1.9	6.72E-01	Citronellsäure	6.7	36625	3	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15597807	PA2611	cysG	siroheme synthase		1.7	5.95E-02	Citronellsäure	6.3	50370	6	Cytoplasmic	COG0007	Coenzyme metabolism	
15597808	PA2612	serS	seryl-tRNA synthetase		1.3	1.99E-01	Citronellsäure	5.3	47231	20	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis	
15597809	PA2613		conserved hypothetical protein		2.0	2.51E-01	Oktansäure	6.3	49047	2	Cytoplasmic	COG2256	DNA replication, recombination, and repair	
15597810	PA2614	lolA	periplasmic chaperone LolA		1.5	1.76E-01	Oktansäure	5.8	23072	15	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane	
15597812	PA2616	trxB1	thioredoxin reductase 1		1.0	8.18E-01	Oktansäure	5.2	33818	11	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones	
15597816	PA2620	clpA	ATP-binding protease component ClpA		2.6	8.91E-03	Oktansäure	5.9	84010	33	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597818	PA2622	cspD	cold-shock protein CspD		26.7	2.72E-03	Oktansäure	5.6	9600	4	Cytoplasmic	COG1278	Transcription	
15597819	PA2623	icd	isocitrate dehydrogenase		1.5	1.00E-02	Citronellsäure	4.9	45577	41	Periplasmic	COG0538	Energy production and conversion	
15597820	PA2624	idh	isocitrate dehydrogenase		1.4	2.19E-01	Oktansäure	6.1	81633	39	Periplasmic	COG2838	Energy production and conversion	
15597821	PA2625		conserved hypothetical protein		1.3	1.70E-01	Citronellsäure	5.2	17525	5	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15597822	PA2626	trmU	tRNA methyltransferase		34.3	7.94E-03	Citronellsäure	5.9	41886	2	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
15597823	PA2627		conserved hypothetical protein		2.6	2.60E-01	Oktansäure	10.9	23030	4	Unknown	COG2915	General function prediction only	
15597825	PA2629	purB	adenylosuccinate lyase		1.6	6.86E-03	Citronellsäure	5.7	50500	15	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15597826	PA2630		conserved hypothetical protein		6.7	5.75E-02	Oktansäure	4.1	44057	3	Cytoplasmic	COG2850	Function unknown	
15597827	PA2631		probable acetyl transferase		3.0	2.21E-02	Citronellsäure	4.8	16040	4	Cytoplasmic	COG2153	General function prediction only	
15597828	PA2632		hypothetical protein		25.1	3.47E-03	Oktansäure	8.0	23249	2	Unknown			
15597830	PA2634	aceA	isocitrate lyase AceA		1.1	3.04E-01	Oktansäure	5.9	58886	57	Periplasmic	COG2224	Energy production and conversion	
15597835	PA2639	nuoD	NADH dehydrogenase I chain C,D		7.1	1.19E-03	Oktansäure	6.7	68323	8	Cytoplasmic	COG0649	Energy production and conversion	
15597837	PA2641	nuoF	NADH dehydrogenase I chain F		1.1	8.92E-01	Oktansäure	7.0	48678	2	Cytoplasmic	COG1894	Energy production and conversion	
15597838	PA2642	nuoG	NADH dehydrogenase I chain G		1.1	6.34E-01	Citronellsäure	6.0	98999	7	Outer Membrane Vesicle	COG1034	Energy production and conversion	
15597846	PA2650		conserved hypothetical protein		1.5	2.79E-01	Citronellsäure	5.7	29513	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15597853	PA2657		probable two-component response regulator		1.7	4.75E-03	Citronellsäure	5.9	24729	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15597875	PA2679		hypothetical protein		1.7	6.88E-02	Citronellsäure	5.2	27641	5	Cytoplasmic	COG2226	Coenzyme metabolism	
15597879	PA2683		probable serine/threonine dehydratase, degradative		1.8	1.13E-01	Oktansäure	6.4	33957	3	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15597880	PA2684		conserved hypothetical protein		1.6	2.65E-01	Citronellsäure	6.6	145819	8	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane	
15597881	PA2685	vgrG4	VgrG4		5.2	2.03E-03	Oktansäure	6.3	81620	4	Cytoplasmic	COG3501	Function unknown	
15597888	PA2692		probable transcriptional regulator		3.0	6.83E-02	Oktansäure	6.5	19143	3	Cytoplasmic	COG1959	Transcription	
15597898	PA2702	tse2	Tse2		5.0	1.56E-02	Oktansäure	6.8	17657	2	Extracellular			
15597902	PA2706		hypothetical protein		1.1	6.87E-01	Oktansäure	6.6	14228	2	Unknown	COG3791	Function unknown	
15597903	PA2707		hypothetical protein		1.7	1.79E-01	Oktansäure	6.1	32205	21	Cytoplasmic	COG0714	General function prediction only	
15597905	PA2709	cysK	cysteine synthase A		1.0	9.68E-01	Citronellsäure	6.6	34309	18	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15597913	PA2717	cpo	chloroperoxidase precursor		2.9	5.82E-03	Citronellsäure	5.9	30435	9	Cytoplasmic	COG0596	General function prediction only	
15597916	PA2720		hypothetical protein		1.3	1.45E-01	Citronellsäure	4.7	23816	6	Cytoplasmic			
15597917	PA2721		hypothetical protein		4.6	7.38E-02	Oktansäure	4.6	17356	2	Cytoplasmic	COG3865	Function unknown	
15597925	PA2729		hypothetical protein		27.7	9.38E-04	Oktansäure	6.1	49885	2	Cytoplasmic			
15597928	PA2732		hypothetical protein		3.8	8.55E-03	Citronellsäure	6.2	128671	26	Cytoplasmic	COG0610	Defense mechanisms	
15597930	PA2734		hypothetical protein		1.1	5.60E-01	Oktansäure	6.1	48703	6	Cytoplasmic	COG0732	Defense mechanisms	
15597931	PA2735		probable restriction-modification system protein		1.1	9.70E-01	Citronellsäure	5.4	89570	31	Cytoplasmic	COG0286	Defense mechanisms	
15597933	PA2737		conserved hypothetical protein		5.8	1.91E-02	Oktansäure	10.2	10254	2	Unknown	COG0789	Transcription	
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit		1.5	1.89E-01	Citronellsäure	5.1	86799	37	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis	
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit		5.4	2.96E-03	Citronellsäure	5.8	38063	14	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis	
15597937	PA2741	rplT	50S ribosomal protein L20		7.3	5.47E-03	Oktansäure	12.3	13365	7	Outer Membrane Vesicle	COG0292	Translation, ribosomal structure and biogenesis	
15597939	PA2743	infC	translation initiation factor IF-3		15.2	1.77E-03	Oktansäure	10.3	20864	8	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
15597940	PA2744	thrS	threonyl-tRNA synthetase		1.2	1.38E-01	Citronellsäure	6.3	73080	39	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis	
15597951	PA2755	eco	ecotin precursor		2.2	8.83E-02	Oktansäure	6.5	17228	8	Periplasmic	COG4574	General function prediction only	

15597956	PA2760	oprQ	OprQ	1.4	3.40E-01	Citronellsäure	5.5	46850	16	Periplasmic			
15597960	PA2764		hypothetical protein	1.4	1.20E-01	Oktansäure	6.0	24519	10	Cytoplasmic			
15597961	PA2765		hypothetical protein	1.2	5.22E-01	Citronellsäure	4.5	32396	13	Unknown	COG2837	Inorganic ion transport and metabolism	
15597966	PA2770		hypothetical protein	1.4	5.45E-02	Citronellsäure	4.7	28258	7	Cytoplasmic	COG0384	General function prediction only	
15597988	PA2792		hypothetical protein	2.3	1.05E-01	Oktansäure	6.4	22070	3	Unknown			
15597992	PA2796	tal	transaldolase	1.3	1.05E-01	Oktansäure	4.9	33946	21	Cytoplasmic	COG0176	Carbohydrate transport and metabolism	
15597993	PA2797		hypothetical protein	2.1	3.06E-02	Citronellsäure	4.6	17710	7	Cytoplasmic	COG1366	Signal transduction mechanisms	
15597994	PA2798		probable two-component response regulator	1.4	3.23E-02	Citronellsäure	4.6	43485	7	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription
15597996	PA2800		conserved hypothetical protein	27.3	1.34E-04	Oktansäure	5.3	26148	2	Periplasmic	COG2853	Cell envelope biogenesis, outer membrane	
15598002	PA2806		conserved hypothetical protein	2.4	8.00E-04	Citronellsäure	5.4	30848	6	Cytoplasmic	COG2904	Function unknown	
15598003	PA2807		hypothetical protein	24.0	8.41E-04	Citronellsäure	7.9	22458	5	Unknown	COG4454	Inorganic ion transport and metabolism	
15598005	PA2809	copR	two-component response regulator, CopR	2.9	3.27E-02	Citronellsäure	4.6	25716	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15598009	PA2813		probable glutathione S-transferase	5.8	1.24E-03	Oktansäure	4.8	23405	14	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598010	PA2814		hypothetical protein	35.9	1.94E-03	Citronellsäure	6.9	25274	3	Cytoplasmic	COG1305	Amino acid transport and metabolism	
15598011	PA2815		probable acyl-CoA dehydrogenase	3.9	7.42E-02	Oktansäure	5.9	88762	3	Outer Membrane Vesicle	COG1960	Lipid metabolism	
15598017	PA2821		probable glutathione S-transferase	3.0	2.72E-03	Citronellsäure	6.1	24716	9	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598018	PA2822		conserved hypothetical protein	1.1	4.90E-01	Oktansäure	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms	
15598019	PA2823		conserved hypothetical protein	1.3	1.09E-01	Citronellsäure	5.7	33760	7	Cytoplasmic	COG2607	General function prediction only	
15598022	PA2826		probable glutathione peroxidase	3.4	8.38E-03	Citronellsäure	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15598024	PA2828		probable aminotransferase	1.8	4.00E-02	Citronellsäure	6.1	44799	9	Periplasmic	COG0436	Amino acid transport and metabolism	
15598025	PA2829		hypothetical protein	49.3	1.02E-02	Oktansäure	5.2	16432	2	Unknown			
15598027	PA2831		conserved hypothetical protein	1.4	1.90E-01	Citronellsäure	5.3	42933	6	Cytoplasmic	COG2866	Amino acid transport and metabolism	
15598028	PA2832	tpm	thiopurine methyltransferase	3.4	6.30E-03	Oktansäure	4.7	24875	5	Cytoplasmic			
15598036	PA2840		probable ATP-dependent RNA helicase	4.8	1.29E-01	Oktansäure	9.0	62107	2	Outer Membrane Vesicle	COG0513	DNA replication, recombination, and repair	Transcription
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	2.5	1.81E-02	Citronellsäure	5.4	28612	6	Cytoplasmic	COG1024	Lipid metabolism	
15598039	PA2843		probable aldolase	1.2	4.75E-01	Citronellsäure	6.1	49851	4	Cytoplasmic	COG3200	Amino acid transport and metabolism	
15598047	PA2851	efp	translation elongation factor P	1.1	5.65E-01	Citronellsäure	4.5	20985	9	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis	
15598049	PA2853	oprI	Outer membrane lipoprotein OprI precursor	4.5	4.96E-02	Oktansäure	8.5	8835	2	Outer Membrane			
15598050	PA2854		conserved hypothetical protein	1.1	6.76E-01	Oktansäure	5.6	34799	10	Periplasmic	COG1376	Function unknown	
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	3.6	2.26E-02	Citronellsäure	5.9	21037	9	Periplasmic	COG2755	Amino acid transport and metabolism	
15598062	PA2866	mttC	secretion protein MttC	2.4	1.55E-01	Oktansäure	6.1	29544	2	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598065	PA2869		hypothetical protein	71.6	1.74E-03	Oktansäure	8.7	18206	4	Cytoplasmic Membrane	COG3915	Function unknown	
15598067	PA2871		hypothetical protein	1.3	2.08E-01	Citronellsäure	5.4	28695	14	Unknown	COG1946	Lipid metabolism	
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	1.3	2.61E-01	Citronellsäure	5.3	24394	11	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
15598081	PA2885	atuR	putative repressor of atu genes	2.3	5.03E-02	Citronellsäure	4.9	22057	6	Unknown	COG1309	Transcription	
15598082	PA2886	atuA	expressed protein with apparent function in citronellol catabolism	92.8	2.40E-07	Citronellsäure	5.1	64435	33	Cytoplasmic			
15598083	PA2887	atuB	putative dehydrogenase involved in catabolism of citronellol	115.6	5.71E-05	Citronellsäure	7.3	30751	16	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598084	PA2888	atuC	geranyl-CoA carboxylase, beta-subunit	50.3	1.40E-06	Citronellsäure	6.5	57328	22	Cytoplasmic	COG4799	Lipid metabolism	
15598085	PA2889	atuD	citronellyl-CoA dehydrogenase, AtuD	25.2	8.54E-05	Citronellsäure	6.3	42714	32	Cytoplasmic	COG1960	Lipid metabolism	
15598086	PA2890	atuE	putative isohexenylglutaconyl-CoA hydratase	23.1	8.33E-05	Citronellsäure	5.2	27717	12	Cytoplasmic	COG1024	Lipid metabolism	
15598087	PA2891	atuF	geranyl-CoA carboxylase, alpha-subunit (biotin-containing)	38.2	2.99E-05	Citronellsäure	6.1	71747	34	Cytoplasmic	COG4770	Lipid metabolism	
15598088	PA2892	atuG	GCase, alpha-subunit (biotin-containing)	43.5	1.27E-06	Citronellsäure	7.2	29631	17	Cytoplasmic	COG4221	General function prediction only	
15598095	PA2899		probable transcriptional regulator	2.7	3.24E-02	Oktansäure	7.6	23250	9	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598098	PA2902		hypothetical protein	13.5	1.23E-03	Oktansäure	4.8	30448	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	1848.1	1.08E-02	Citronellsäure	6.3	27275	2	Cytoplasmic	COG2243	Coenzyme metabolism	
15598101	PA2905	cobH	precorrin isomerase CobH	2.3	5.96E-02	Citronellsäure	5.7	21650	6	Cytoplasmic	COG2082	Coenzyme metabolism	
15598114	PA2918		probable short-chain dehydrogenase	2.2	1.13E-02	Citronellsäure	7.2	26738	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598135	PA2939		probable aminopeptidase	4.0	7.33E-03	Oktansäure	4.8	57511	6	Extracellular	COG2234	General function prediction only	
15598136	PA2940		probable acyl-CoA thiolase	41.6	1.18E-02	Citronellsäure	5.5	39211	2	Cytoplasmic	COG0183	Lipid metabolism	
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	13.0	2.60E-04	Citronellsäure	5.2	138499	7	Cytoplasmic	COG1429	Coenzyme metabolism	
15598141	PA2945		conserved hypothetical protein	4.7	1.56E-02	Citronellsäure	4.9	41175	5	Cytoplasmic	COG0523	General function prediction only	
15598146	PA2950	pfmá	proton motive force protein, PMF	2.2	1.39E-03	Citronellsäure	4.8	43528	17	Cytoplasmic	COG3007	Function unknown	
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	1.2	2.89E-01	Citronellsäure	4.8	31423	23	Periplasmic	COG2025	Energy production and conversion	
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	1.3	1.28E-01	Citronellsäure	9.6	26377	26	Outer Membrane Vesicle	COG2086	Energy production and conversion	
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	2.0	5.60E-03	Citronellsäure	5.6	59896	11	Outer Membrane Vesicle	COG0644	Energy production and conversion	
15598150	PA2954		hypothetical protein	2.5	5.53E-03	Oktansäure	4.9	21240	8	Cytoplasmic	COG3816	Function unknown	
15598155	PA2959		conserved hypothetical protein	1.5	4.80E-02	Citronellsäure	5.3	28114	5	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598158	PA2962	tmk	thymidylate kinase	1.3	1.09E-01	Citronellsäure	4.9	23077	6	Cytoplasmic	COG0125	Nucleotide transport and metabolism	
15598160	PA2964	pabC	4-amino-4-deoxychorismate lyase	1.3	2.35E-01	Oktansäure	5.7	29886	2	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.3	3.16E-02	Citronellsäure	5.8	43465	12	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598162	PA2966	acpP	acyl carrier protein	2.1	3.52E-02	Citronellsäure	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	1.1	9.65E-01	Oktansäure	6.6	25585	13	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	1.7	4.99E-02	Citronellsäure	4.8	32444	10	Periplasmic	COG0331	Lipid metabolism	
15598168	PA2972		conserved hypothetical protein	1.2	3.65E-01	Oktansäure	6.0	21054	9	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15598172	PA2976	rne	ribonuclease E	1.2	7.30E-01	Citronellsäure	4.6	117463	36	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis	
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	1.9	1.20E-01	Citronellsäure	6.7	37595	5	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
15598174	PA2978	ptpA	phosphotyrosine protein phosphatase	39.5	1.43E-03	Oktansäure	6.1	17152	5	Cytoplasmic	COG0394	Signal transduction mechanisms	
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.3	2.10E-01	Citronellsäure	5.4	27646	10	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	1.1	5.14E-01	Oktansäure	6.7	51161	9	Cytoplasmic	COG1249	Energy production and conversion	
15598197	PA3001		probable glyceraldehyde-3-phosphate dehydrogenase	13.2	5.28E-02	Citronellsäure	8.0	50111	17	Periplasmic	COG0057	Carbohydrate transport and metabolism	
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	3.2	2.01E-02	Citronellsäure	5.7	128763	39	Periplasmic	COG1197	DNA replication, recombination, and repair	Transcription
15598199	PA3003		hypothetical protein	2.3	8.93E-03	Oktansäure	4.5	22474	7	Periplasmic			
15598200	PA3004		5'-methylthioinosine phosphorylase	1.2	4.28E-01	Citronellsäure	6.6	26266	4	Cytoplasmic	COG0005	Nucleotide transport and metabolism	
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.0	9.89E-01	Citronellsäure	6.2	36101	10	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
15598202	PA3006	psrA	transcriptional regulator PsrA	1.3	3.51E-01	Oktansäure	9.9	25784	5	Cytoplasmic	COG1309	Transcription	
15598206	PA3010		hypothetical protein	12.1	7.83E-02	Citronellsäure	4.6	19071	2	Unknown			
15598207	PA3011	topA	DNA topoisomerase I	1.6	2.64E-01	Citronellsäure	8.7	97282	49	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	1.3	2.92E-01	Citronellsäure	6.8	41643	32	Cytoplasmic	COG0183	Lipid metabolism	
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	1.2	1.97E-01	Oktansäure	5.6	76954	55	Periplasmic	COG1250	Lipid metabolism	
15598211	PA3015		hypothetical protein	18.7	2.20E-02	Citronellsäure	5.9	30469	6	Unknown			
15598215	PA3019		probable ATP-binding component of ABC transporter	1.1	5.92E-01	Oktansäure	5.0	71155	16	Cytoplasmic	COG0488	General function prediction only	
15598217	PA3021		hypothetical protein	38.8	9.94E-04	Oktansäure	7.8	14206	7	Unknown	COG3755	Function unknown	
15598218	PA3022		hypothetical protein	1.2	2.64E-01	Citronellsäure	5.9	29579	12	Cytoplasmic	COG3217	General function prediction only	
15598219	PA3023		conserved hypothetical protein	3.7	2.55E-03	Citronellsäure	4.7	31504	10	Cytoplasmic	COG1597	Lipid metabolism	General function prediction only
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.7	1.05E-01	Citronellsäure	5.0	43359	4	Cytoplasmic	COG0303	Coenzyme metabolism	

15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	1.6	9.11E-02	Citronellsäure	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism	
15598226	PA3030	mobA	molybdopterin-guanine dinucleotide biosynthesis protein MobA	9.0	6.80E-04	Oktansäure	7.6	21870	8	Cytoplasmic	COG0746	Coenzyme metabolism	
15598230	PA3034		probable transcriptional regulator	101.5	1.49E-04	Oktansäure	8.5	20988	2	Cytoplasmic			
15598234	PA3038		probable porin	5.5	1.69E-02	Citronellsäure	7.1	46712	5	Periplasmic			
15598239	PA3043		conserved hypothetical protein	3.4	2.63E-01	Oktansäure	6.5	50083	2	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15598244	PA3048		conserved hypothetical protein	1.0	7.22E-01	Citronellsäure	8.0	81155	11	Cytoplasmic	COG0116	DNA replication, recombination, and repair	
15598249	PA3053		probable hydrolytic enzyme	1.2	4.37E-01	Oktansäure	8.0	37485	2	Periplasmic	COG0596	General function prediction only	
15598250	PA3054		hypothetical protein	4.2	7.37E-05	Oktansäure	6.6	71165	7	Periplasmic	COG2866	Amino acid transport and metabolism	
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	6.1	2.29E-02	Citronellsäure	6.1	182637	22	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism	
15598276	PA3080		hypothetical protein	58.4	2.62E-04	Citronellsäure	4.8	38479	4	Unknown	COG4447	General function prediction only	
15598277	PA3081		conserved hypothetical protein	2.8	1.93E-03	Citronellsäure	9.2	50680	7	Periplasmic			
15598278	PA3082	gbt	glycine betaine transmethylase	1.0	9.65E-01	Citronellsäure	4.5	71403	7	Periplasmic			
15598279	PA3083	pepN	aminopeptidase N	1.9	6.74E-02	Citronellsäure	4.9	100046	50	Periplasmic	COG0308	Amino acid transport and metabolism	
15598283	PA3087		hypothetical protein	1.3	3.46E-01	Citronellsäure	6.3	37211	2	Cytoplasmic			
15598284	PA3088		conserved hypothetical protein	1.1	5.44E-01	Citronellsäure	7.3	32140	7	Cytoplasmic	COG0061	Coenzyme metabolism	
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	17.9	1.90E-04	Citronellsäure	7.2	72969	26	Cytoplasmic	COG1902	Energy production and conversion	
15598297	PA3101	xcpT	general secretion pathway protein G	32.0	1.26E-01	Oktansäure	8.8	16112	2	Cytoplasmic Membrane	COG2165	Cell motility and secretion	Intracellular trafficking and secretion
15598302	PA3106		probable short-chain dehydrogenase	1.0	7.10E-01	Oktansäure	4.6	26997	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598303	PA3107	metZ	o-succinylhomoserine sulfhydrylase	1.6	6.72E-03	Citronellsäure	6.3	43185	11	Periplasmic	COG0626	Amino acid transport and metabolism	
15598304	PA3108	purF	amidophosphoribosyltransferase	2.3	3.66E-03	Citronellsäure	6.8	55370	12	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism	
15598307	PA3111	folC	folylpolyglutamate synthetase	3.2	6.91E-02	Citronellsäure	5.0	46505	2	Cytoplasmic	COG0285	Coenzyme metabolism	
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	1.5	7.55E-02	Citronellsäure	7.1	31843	11	Periplasmic	COG0777	Lipid metabolism	
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	1.5	1.27E-01	Oktansäure	6.8	22280	4	Cytoplasmic	COG0135	Amino acid transport and metabolism	
15598311	PA3115	fimV	Motility protein FimV	2.2	2.54E-01	Citronellsäure	4.0	96928	4	Outer Membrane Vesicle	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	2.3	1.90E-03	Citronellsäure	5.5	40494	26	Periplasmic	COG0136	Amino acid transport and metabolism	
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.3	1.39E-01	Citronellsäure	4.8	39120	16	Cytoplasmic	COG0473	Amino acid transport and metabolism	
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	2.3	5.27E-03	Citronellsäure	4.7	24011	17	Cytoplasmic	COG0066	Amino acid transport and metabolism	
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	2.2	2.10E-03	Citronellsäure	6.3	51042	11	Cytoplasmic	COG0065	Amino acid transport and metabolism	
15598318	PA3122		probable transcriptional regulator	1.4	2.00E-01	Oktansäure	6.4	32835	7	Cytoplasmic	COG0583	Transcription	
15598319	PA3123		conserved hypothetical protein	154.9	9.17E-04	Oktansäure	4.6	13516	5	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
15598322	PA3126	ibpA	heat-shock protein IbpA	206.6	5.23E-02	Oktansäure	6.1	16583	3	Cytoplasmic	COG0071	Posttranslational modification, protein turnover, chaperones	
15598323	PA3127		hypothetical protein	1.6	6.94E-02	Oktansäure	5.0	29403	9	Unknown			
15598324	PA3128		probable short-chain dehydrogenase	1.6	1.90E-02	Citronellsäure	6.8	26219	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598326	PA3130		hypothetical protein	4.9	6.60E-02	Oktansäure	5.2	16555	6	Unknown	COG0824	General function prediction only	
15598327	PA3131		probable aldolase	1.6	7.62E-02	Oktansäure	5.3	22852	6	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598330	PA3134	gltX	glutamyl-tRNA synthetase	2.0	6.02E-04	Citronellsäure	6.7	56749	15	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15598334	PA3138	uvrB	excinuclease ABC subunit B	1.8	2.12E-01	Oktansäure	5.1	76067	12	Cytoplasmic	COG0556	DNA replication, recombination, and repair	
15598335	PA3139		probable amino acid aminotransferase	3.0	1.10E-03	Citronellsäure	6.6	43319	23	Periplasmic	COG1448	Amino acid transport and metabolism	
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	1.8	1.35E-02	Citronellsäure	5.8	38907	19	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane	
15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	1.2	5.71E-01	Citronellsäure	5.7	27448	7	Cytoplasmic	COG0107	Amino acid transport and metabolism	
15598348	PA3152	hisH2	glutamine amidotransferase	1.5	4.74E-02	Oktansäure	7.1	22663	9	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase, wbpE	1.7	1.66E-02	Citronellsäure	6.0	38924	19	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-acetyltransferase, WbpD	1.1	7.32E-01	Citronellsäure	7.8	20562	5	Cytoplasmic	COG1045	Amino acid transport and metabolism	
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	1.6	1.05E-01	Citronellsäure	6.6	35717	19	Cytoplasmic	COG0673	General function prediction only	
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.6	1.87E-03	Citronellsäure	5.2	48155	30	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane	
15598358	PA3162	rpsA	30S ribosomal protein S1	1.1	4.32E-01	Oktansäure	4.6	61869	31	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis	
15598359	PA3163	cmk	cytidylate kinase	1.1	8.12E-01	Oktansäure	4.8	24637	9	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	2.7	9.44E-04	Oktansäure	4.8	39483	7	Cytoplasmic	COG0079	Amino acid transport and metabolism	
15598362	PA3166	pheA	chorismate mutase	1.1	5.64E-01	Citronellsäure	6.3	40632	9	Cytoplasmic	COG0077	Amino acid transport and metabolism	
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.3	8.50E-02	Citronellsäure	4.7	39917	12	Periplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
15598364	PA3168	gyrA	DNA gyrase subunit A	3.1	7.91E-04	Citronellsäure	4.6	101134	50	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.4	2.14E-03	Citronellsäure	5.1	39425	8	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis	
15598366	PA3170		conserved hypothetical protein	1.2	4.38E-01	Oktansäure	5.5	48493	2	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	3.3	7.99E-03	Oktansäure	6.3	25860	8	Cytoplasmic	COG2227	Coenzyme metabolism	
15598368	PA3172		probable hydrolase	1.3	3.77E-02	Oktansäure	5.0	24944	12	Cytoplasmic	COG0546	General function prediction only	
15598369	PA3173		probable short-chain dehydrogenase	1.1	9.69E-01	Citronellsäure	4.9	26332	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	6.7	2.78E-03	Citronellsäure	7.6	23953	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598378	PA3182	pgl	6-phosphogluconolactonase	4.6	2.15E-03	Citronellsäure	6.5	25571	3	Unknown	COG0363	Carbohydrate transport and metabolism	
15598386	PA3190		probable binding protein component of ABC sugar transporter	11.0	9.13E-04	Citronellsäure	5.8	45131	10	Periplasmic	COG1653	Carbohydrate transport and metabolism	
15598390	PA3194	edd	phosphogluconate dehydratase	1.5	2.82E-01	Citronellsäure	6.7	65182	5	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	2.9	1.02E-02	Citronellsäure	6.6	36170	8	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15598392	PA3196		hypothetical protein	1.4	1.17E-01	Citronellsäure	3.9	19293	2	Unknown			
15598395	PA3199		conserved hypothetical protein	1.5	2.70E-01	Oktansäure	6.7	23144	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15598404	PA3208		conserved hypothetical protein	4.9	9.06E-04	Oktansäure	6.5	19948	12	Cytoplasmic Membrane	COG0778	Energy production and conversion	
15598410	PA3214		hypothetical protein	1.2	7.34E-01	Citronellsäure	10.4	23214	3	Unknown	COG3218	General function prediction only	
15598421	PA3225		probable transcriptional regulator	3.7	1.17E-03	Oktansäure	7.4	34098	5	Cytoplasmic	COG0583	Transcription	
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.8	2.10E-03	Citronellsäure	8.5	20104	12	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15598439	PA3243	minC	cell division inhibitor MinC	2.7	5.75E-03	Oktansäure	6.5	28124	9	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
15598440	PA3244	minD	cell division inhibitor MinD	1.1	5.80E-01	Citronellsäure	5.5	29617	20	Periplasmic	COG2894	Cell division and chromosome partitioning	
15598443	PA3247		hypothetical protein	1.0	8.86E-01	Citronellsäure	6.0	46658	7	Cytoplasmic	COG1362	Amino acid transport and metabolism	
15598446	PA3250		hypothetical protein	4.0	1.09E-04	Citronellsäure	6.2	38285	12	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15598451	PA3255		hypothetical protein	1.5	4.92E-02	Citronellsäure	4.4	21635	7	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15598452	PA3256		probable oxidoreductase	1.1	5.42E-01	Oktansäure	5.2	33387	12	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15598453	PA3257	prc	periplasmic tail-specific protease	1.3	2.19E-01	Oktansäure	6.6	78182	36	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.3	5.80E-02	Citronellsäure	4.8	26845	12	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones	
15598459	PA3263		conserved hypothetical protein	1.1	4.18E-01	Oktansäure	4.7	34015	16	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
15598466	PA3270		hypothetical protein	1.6	3.95E-01	Citronellsäure	9.9	21901	5	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15598473	PA3277		probable short-chain dehydrogenase	1.5	2.74E-01	Citronellsäure	6.5	29251	4	Cytoplasmic	COG0300	General function prediction only	
15598482	PA3286		hypothetical protein	10.4	3.35E-03	Oktansäure	6.4	38139	9	Periplasmic	COG0332	acyl-carrier-protein	
15598483	PA3287		conserved hypothetical protein	1.2	3.39E-01	Oktansäure	5.5	18194	3	Periplasmic	COG0666	General function prediction only	
15598493	PA3297		probable ATP-dependent helicase	1.7	1.71E-01	Citronellsäure	8.5	149907	2	Cytoplasmic Membrane	COG1643	DNA replication, recombination, and repair	
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	2.2	1.26E-04	Citronellsäure	7.5	61654	13	Outer Membrane Vesicle	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	1.2	5.86E-01	Citronellsäure	7.2	61736	6	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598498	PA3302		conserved hypothetical protein	1.5	1.98E-01	Oktansäure	5.0	16901	7	Unknown	COG2030	Lipid metabolism	
15598504	PA3308	hepA	RNA helicase HepA	2.8	6.96E-03	Citronellsäure	4.8	106839	21	Periplasmic	COG0553	Transcription	DNA replication, recombination, and repair

15598505	PA3309		conserved hypothetical protein	10.2	1.06E-02	Oktansäure	5.4	16496	16	Periplasmic	COG0589	Signal transduction mechanisms	
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.3	2.13E-01	Citronellsäure	5.5	30908	8	Cytoplasmic	COG2084	Lipid metabolism	
15598509	PA3313		hypothetical protein	1.8	4.24E-02	Citronellsäure	10.2	36539	23	Periplasmic	COG3221	Inorganic ion transport and metabolism	
15598522	PA3326	clpP2	ClpP2	8.2	1.34E-03	Oktansäure	5.4	22142	16	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15598523	PA3327		probable non-ribosomal peptide synthetase	7.3	4.41E-04	Oktansäure	5.5	259403	102	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15598524	PA3328		probable FAD-dependent monooxygenase	27.7	1.09E-06	Oktansäure	8.3	42498	6	Unknown	COG0654	Coenzyme metabolism	Energy production and conversion
15598525	PA3329		hypothetical protein	24.5	9.09E-04	Oktansäure	6.2	49134	9	Cytoplasmic			
15598526	PA3330		probable short chain dehydrogenase	20.3	2.82E-04	Oktansäure	8.8	32031	9	Cytoplasmic	COG4221	General function prediction only	
15598527	PA3331		cytochrome P450	9.6	4.54E-04	Oktansäure	5.7	46345	8	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
15598528	PA3332		conserved hypothetical protein	111.8	9.03E-04	Oktansäure	5.5	15920	8	Cytoplasmic	COG3631	General function prediction only	
15598529	PA3333	fabH2	3-oxoacyl-[acyl-carrier-protein] synthase III	62.7	1.35E-03	Oktansäure	5.0	34003	10	Cytoplasmic	COG0332	acyl-carrier-protein	
15598531	PA3335		hypothetical protein	25.0	2.33E-03	Oktansäure	5.2	27632	6	Cytoplasmic			
15598533	PA3337	rfaD	ADP-L-glycero-D-mannoheptose 6-epimerase	20.1	1.88E-02	Oktansäure	6.5	37384	4	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15598537	PA3341		probable transcriptional regulator	Infinity	2.38E-06	Oktansäure	8.6	16071	2	Cytoplasmic	COG1846	Transcription	
15598540	PA3344	recQ	ATP-dependent DNA helicase RecQ	1.0	9.52E-01	Citronellsäure	5.8	79449	2	Cytoplasmic	COG0514	DNA replication, recombination, and repair	
15598544	PA3348		probable chemotaxis protein methyltransferase	1.9	8.19E-02	Oktansäure	9.6	30615	7	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
15598545	PA3349		probable chemotaxis protein	1.5	8.12E-02	Oktansäure	6.1	34402	17	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15598549	PA3353		hypothetical protein	1.3	2.51E-01	Citronellsäure	6.8	29852	8	Cytoplasmic	COG5581	Signal transduction mechanisms	
15598550	PA3354		hypothetical protein	1.1	6.98E-01	Citronellsäure	5.6	22398	3	Cytoplasmic	COG3222	Function unknown	
15598553	PA3357	dsdA	D-serine dehydratase	1.6	3.16E-02	Citronellsäure	6.0	48200	5	Cytoplasmic	COG3048	Amino acid transport and metabolism	
15598593	PA3397	fpr	NADP+-dependent ferredoxin reductase	1.4	2.12E-01	Oktansäure	5.9	29518	23	Periplasmic	COG1018	Energy production and conversion	
15598611	PA3415		probable dihydrolipoamide acetyltransferase	4.3	1.85E-01	Oktansäure	5.5	39521	5	Cytoplasmic	COG0508	Energy production and conversion	
15598612	PA3416		probable pyruvate dehydrogenase E1 component, beta chain	6.5	2.82E-01	Oktansäure	5.7	36143	3	Unknown	COG0022	Energy production and conversion	
15598613	PA3417		probable pyruvate dehydrogenase E1 component, alpha subunit	15.8	2.35E-02	Oktansäure	5.2	40414	4	Cytoplasmic	COG1071	Energy production and conversion	
15598614	PA3418	ldh	leucine dehydrogenase	3.3	2.88E-02	Citronellsäure	5.9	35633	6	Cytoplasmic	COG0334	Amino acid transport and metabolism	
15598623	PA3427		probable short-chain dehydrogenases	1.1	8.11E-01	Oktansäure	5.8	32323	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598626	PA3430		probable aldolase	1.2	7.81E-01	Citronellsäure	6.6	27993	3	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15598633	PA3437	folM	dihydromonapterin reductase, FolM	20.3	1.28E-02	Citronellsäure	7.0	25403	4	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	3.7	6.65E-04	Oktansäure	7.6	20833	7	Cytoplasmic	COG0302	Coenzyme metabolism	
15598640	PA3444		conserved hypothetical protein	5.8	1.67E-01	Oktansäure	6.1	41567	2	Cytoplasmic	COG2141	Energy production and conversion	
15598641	PA3445		conserved hypothetical protein	9.6	1.92E-03	Oktansäure	9.0	35184	4	Unknown	COG0715	Inorganic ion transport and metabolism	
15598646	PA3450		probable antioxidant protein	3.1	4.08E-03	Oktansäure	5.2	24164	14	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598649	PA3453		conserved hypothetical protein	1.0	9.76E-01	Oktansäure	5.4	24160	9	Unknown	COG3132	Function unknown	
15598652	PA3456		hypothetical protein	2.7	5.21E-03	Oktansäure	7.2	70517	7	Cytoplasmic	COG4121	Function unknown	
15598654	PA3458		probable transcriptional regulator	8.8	2.07E-01	Oktansäure	5.6	17599	4	Unknown	COG1846	Transcription	
15598657	PA3461		conserved hypothetical protein	6.1	3.48E-04	Citronellsäure	5.1	43294	3	Cytoplasmic	COG1363	Carbohydrate transport and metabolism	
15598667	PA3471		probable malic enzyme	1.6	1.77E-01	Oktansäure	5.2	62420	18	Periplasmic	COG0281	Energy production and conversion	
15598671	PA3475	pheC	cyclohexadienyl dehydratase precursor	1.1	6.77E-01	Citronellsäure	6.9	30448	6	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598672	PA3476	rhlI	autoinducer synthesis protein RhlI	5.4	3.01E-01	Oktansäure	5.3	22630	3	Unknown	COG3916	Signal transduction mechanisms	Secondary metabolites biosynthesis, transport, and catabolism
15598673	PA3477	rhlR	transcriptional regulator RhlR	1.0	7.19E-01	Citronellsäure	7.2	27577	4	Cytoplasmic	COG2771	Transcription	
15598676	PA3480		probable deoxycytidine triphosphate deaminase	2.6	1.40E-02	Oktansäure	6.3	21154	9	Cytoplasmic	COG0717	Nucleotide transport and metabolism	
15598677	PA3481		conserved hypothetical protein	1.7	5.41E-03	Citronellsäure	5.1	38889	11	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
15598678	PA3482	metG	methionyl-tRNA synthetase	1.3	6.68E-02	Citronellsäure	5.4	74903	30	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis	
15598682	PA3486		conserved hypothetical protein	13.3	9.71E-04	Oktansäure	6.3	90635	6	Cytoplasmic	COG3501	Function unknown	
15598683	PA3487	pldA	phospholipase D	5.4	6.02E-03	Oktansäure	6.7	122340	11	Periplasmic	COG1502	Lipid metabolism	
15598704	PA3508		probable transcriptional regulator	Infinity	1.93E-04	Oktansäure	5.8	30877	2	Cytoplasmic	COG1414	Transcription	
15598711	PA3515		hypothetical protein	57.6	3.70E-05	Citronellsäure	4.9	39764	33	Cytoplasmic	COG2227	Coenzyme metabolism	
15598712	PA3516		probable lyase	71.7	5.96E-04	Citronellsäure	6.3	52927	22	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15598713	PA3517		probable lyase	27.3	1.43E-04	Citronellsäure	6.4	52228	18	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15598714	PA3518		hypothetical protein	977.3	1.36E-03	Citronellsäure	6.3	37520	1	Cytoplasmic			
15598715	PA3519		hypothetical protein	92.2	5.49E-06	Citronellsäure	5.9	39369	10	Cytoplasmic			
15598721	PA3525	argG	argininosuccinate synthase	1.7	2.78E-03	Citronellsäure	5.3	45297	19	Periplasmic	COG0137	Amino acid transport and metabolism	
15598723	PA3527	pyrC	dihydroorotase	2.0	1.14E-02	Citronellsäure	6.6	38406	14	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
15598724	PA3528	rnt	ribonuclease T	1.4	8.31E-02	Citronellsäure	4.8	24723	8	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15598725	PA3529		alkylhydroperoxide reductase C	1.0	8.05E-01	Citronellsäure	5.3	21822	15	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598727	PA3531	bfrB	bacterioferritin	8.1	1.97E-02	Oktansäure	4.8	18553	3	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.5	1.98E-01	Citronellsäure	5.7	33924	14	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15598735	PA3539		conserved hypothetical protein	1.2	8.79E-02	Citronellsäure	6.7	29560	15	Cytoplasmic	COG3022	Function unknown	
15598748	PA3552	arnB	ArnB	4.6	3.90E-02	Citronellsäure	8.0	41867	2	Cytoplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598750	PA3554	arnA	ArnA	1.0	9.19E-01	Oktansäure	6.7	74360	10	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis	
15598758	PA3562	fruI	phosphotransferase system transporter enzyme I, FruI	2.7	5.43E-01	Citronellsäure	4.8	101572	2	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598759	PA3563	fruR	fructose transport system repressor FruR	1.6	3.93E-02	Citronellsäure	6.4	36369	3	Cytoplasmic	COG1609	Transcription	
15598763	PA3567		probable oxidoreductase	2.5	2.06E-01	Citronellsäure	6.6	36678	4	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15598764	PA3568		probable acetyl-coa synthetase	1.4	4.12E-01	Citronellsäure	6.7	68990	9	Cytoplasmic	COG0365	Lipid metabolism	
15598765	PA3569	mmsB	3-hydroxyisobutyrate dehydrogenase	1.3	4.85E-01	Citronellsäure	6.2	30486	3	Cytoplasmic	COG2084	Lipid metabolism	
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	1.1	8.95E-01	Oktansäure	6.4	53663	3	Cytoplasmic	COG1012	Energy production and conversion	
15598774	PA3578		conserved hypothetical protein	2.1	1.47E-01	Oktansäure	4.9	28906	6	Cytoplasmic Membrane	COG0384	General function prediction only	
15598776	PA3580		conserved hypothetical protein	5.5	9.19E-02	Oktansäure	10.1	16493	4	Cytoplasmic	COG2606	Function unknown	
15598778	PA3582	glpK	glycerol kinase	3.6	4.54E-03	Citronellsäure	5.9	55966	22	Cytoplasmic	COG0554	Energy production and conversion	
15598783	PA3587	metR	transcriptional regulator MetR	1.7	2.59E-02	Oktansäure	5.6	34216	5	Cytoplasmic	COG0583	Transcription	
15598800	PA3604	erdR	response regulator ErdR	1.3	1.57E-01	Citronellsäure	4.8	23531	11	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598806	PA3610	potD	polyamine transport protein PotD	2.5	2.20E-01	Citronellsäure	5.5	39260	5	Periplasmic	COG0687	Amino acid transport and metabolism	
15598809	PA3613		hypothetical protein	4.1	2.45E-02	Oktansäure	6.4	88379	24	Periplasmic	COG3957	Carbohydrate transport and metabolism	
15598810	PA3614		hypothetical protein	1.1	6.86E-01	Citronellsäure	7.0	51921	5	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
15598811	PA3615		hypothetical protein	1.4	7.32E-02	Citronellsäure	6.0	40465	5	Cytoplasmic	COG1611	General function prediction only	
15598813	PA3617	recA	RecA protein	1.2	6.58E-01	Oktansäure	5.2	36879	12	Cytoplasmic	COG0468	DNA replication, recombination, and repair	
15598814	PA3618		conserved hypothetical protein	17.7	5.52E-03	Oktansäure	5.0	17715	5	Unknown	COG1546	General function prediction only	
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.0	7.47E-01	Oktansäure	6.1	94977	23	Cytoplasmic	COG0249	DNA replication, recombination, and repair	
15598817	PA3621	fdxA	ferredoxin I	1.6	2.77E-01	Oktansäure	3.7	12159	3	Cytoplasmic	COG1146	Energy production and conversion	
15598818	PA3622	rpoS	sigma factor RpoS	1.3	6.24E-01	Oktansäure	5.1	38235	5	Cytoplasmic	COG0568	Transcription	
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	1.9	3.55E-02	Citronellsäure	6.1	23407	5	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones	
15598821	PA3625	surE	survival protein SurE	1.1	9.24E-01	Citronellsäure	5.2	26368	6	Unknown	COG0496	General function prediction only	
15598824	PA3628		probable esterase	2.4	2.15E-02	Oktansäure	6.3	31243	5	Unknown	COG0627	General function prediction only	
15598825	PA3629	adhC	alcohol dehydrogenase class III	2.0	2.14E-02	Citronellsäure	5.4	39208	5	Cytoplasmic	COG1062	Energy production and conversion	
15598829	PA3633	ygbP	4-diphosphocytidyl-2-C-methylerythritol synthase	4718.5	2.93E-01	Citronellsäure	5.2	25613	1	Cytoplasmic	COG1211	Lipid metabolism	

15598831	PA3635	eno	enolase	1.9	3.40E-03	Citronellsäure	4.8	45195	17	Cytoplasmic	COG0148	Carbohydrate transport and metabolism	
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	1.3	2.75E-01	Citronellsäure	6.5	31143	21	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane	
15598833	PA3637	pyrG	CTP synthase	1.4	1.57E-01	Citronellsäure	5.4	59617	33	Periplasmic	COG0504	Nucleotide transport and metabolism	
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)	1.5	8.50E-02	Citronellsäure	5.2	34947	24	Outer Membrane Vesicle	COG0825	Lipid metabolism	
15598836	PA3640	dnaE	DNA polymerase III, alpha chain	3.4	2.97E-03	Citronellsäure	5.1	130904	57	Cytoplasmic	COG0587	DNA replication, recombination, and repair	
15598838	PA3642	rnhB	ribonuclease HII	9.3	4.62E-02	Oktansäure	6.5	21771	2	Cytoplasmic	COG0164	DNA replication, recombination, and repair	
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase	1.3	1.45E-01	Citronellsäure	7.1	28010	8	Cytoplasmic	COG1043	acyl carrier protein	
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	10.4	1.25E-03	Citronellsäure	7.6	16774	8	Cytoplasmic	COG0764	Lipid metabolism	
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase	1.8	2.03E-01	Oktansäure	6.2	36191	2	Cytoplasmic	COG1044	3-hydroxymyristoyl	
15598843	PA3647		probable outer membrane protein precursor	42.3	5.11E-03	Oktansäure	10.0	19058	5	Unknown	COG2825	Cell envelope biogenesis, outer membrane	
15598844	PA3648	opr86	outer membrane protein Opr86	2.0	9.66E-02	Oktansäure	4.8	88286	2	Periplasmic	COG4775	Cell envelope biogenesis, outer membrane	
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase	1.3	1.03E-01	Citronellsäure	5.7	42508	3	Unknown	COG0743	Lipid metabolism	
15598849	PA3653	frr	ribosome recycling factor	1.6	1.53E-01	Oktansäure	5.9	20485	19	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis	
15598850	PA3654	pyrH	uridylate kinase	1.1	4.65E-01	Citronellsäure	5.4	26272	10	Periplasmic	COG0528	Nucleotide transport and metabolism	
15598851	PA3655	tsf	elongation factor Ts	1.5	3.81E-02	Citronellsäure	5.0	30653	29	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis	
15598852	PA3656	rpsB	30S ribosomal protein S2	3.2	1.52E-03	Oktansäure	9.0	27336	15	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis	
15598853	PA3657	map	methionine aminopeptidase	1.4	1.30E-01	Oktansäure	6.3	29086	10	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis	
15598854	PA3658	glnD	protein-PII uridylyltransferase	2.1	2.63E-01	Oktansäure	5.5	103403	3	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones	
15598855	PA3659		probable aminotransferase	1.4	2.71E-02	Citronellsäure	5.5	44544	11	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase	2.0	1.39E-02	Citronellsäure	6.0	35973	10	Periplasmic	COG2171	Amino acid transport and metabolism	
15598871	PA3675		hypothetical protein	2.3	9.90E-02	Oktansäure	9.4	23645	6	Unknown			
15598874	PA3678		probable transcriptional regulator	7.5	4.60E-03	Oktansäure	6.3	23150	8	Cytoplasmic	COG1309	Transcription	
15598878	PA3682		hypothetical protein	1.0	8.14E-01	Oktansäure	5.0	29150	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15598881	PA3685		conserved hypothetical protein	1.4	9.42E-02	Citronellsäure	4.8	24180	6	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones	
15598882	PA3686	adk	adenylate kinase	1.4	9.75E-02	Citronellsäure	6.4	23107	17	Cytoplasmic	COG0563	Nucleotide transport and metabolism	
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase	1.5	4.57E-01	Citronellsäure	6.2	97839	24	Cytoplasmic	COG2352	Energy production and conversion	
15598886	PA3690		probable metal-transporting P-type ATPase	10.4	9.84E-02	Citronellsäure	5.9	78728	2	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
15598887	PA3691		hypothetical protein	3.9	4.35E-02	Oktansäure	8.5	14468	3	Outer Membrane Vesicle			
15598888	PA3692	lptF	Lipotoxon F, LptF	1.2	1.82E-01	Oktansäure	9.9	28514	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
15598889	PA3693		conserved hypothetical protein	1.0	8.17E-01	Citronellsäure	7.0	18219	3	Unknown	COG2110	General function prediction only	
15598894	PA3698		hypothetical protein	3.0	2.59E-02	Citronellsäure	4.5	20351	5	Unknown			
15598896	PA3700	lysS	lysyl-tRNA synthetase	1.1	5.50E-01	Citronellsäure	5.0	57329	34	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis	
15598911	PA3716		hypothetical protein	1.8	6.16E-01	Oktansäure	4.1	60503	6	Outer Membrane Vesicle			
15598918	PA3723		probable FMN oxidoreductase	2.5	6.88E-02	Citronellsäure	6.3	40319	15	Cytoplasmic	COG1902	Energy production and conversion	
15598921	PA3726		conserved hypothetical protein	1.6	1.98E-01	Citronellsäure	4.8	20596	5	Cytoplasmic	COG4681	Function unknown	
15598922	PA3727		hypothetical protein	2.8	4.45E-02	Oktansäure	4.9	26461	6	Cytoplasmic	COG1502	Lipid metabolism	
15598923	PA3728		hypothetical protein	3.1	3.93E-02	Citronellsäure	4.9	197133	71	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning	
15598924	PA3729		conserved hypothetical protein	4.8	2.57E-01	Oktansäure	4.9	75882	3	Outer Membrane Vesicle	COG2268	Function unknown	
15598926	PA3731		conserved hypothetical protein	2.1	6.29E-03	Oktansäure	7.5	24893	10	Cytoplasmic	COG1842	Transcription	Signal transduction mechanisms
15598927	PA3732		conserved hypothetical protein	2.1	2.38E-02	Citronellsäure	4.0	15959	2	Unknown	COG3789	Function unknown	
15598928	PA3733		hypothetical protein	1.7	2.41E-01	Oktansäure	5.9	44766	3	Cytoplasmic	COG1804	Energy production and conversion	
15598930	PA3735	thrC	threonine synthase	1.4	3.10E-03	Citronellsäure	6.6	51795	23	Periplasmic	COG0498	Amino acid transport and metabolism	
15598931	PA3736	hom	homoserine dehydrogenase	1.7	6.35E-03	Citronellsäure	5.1	46192	14	Cytoplasmic	COG0460	Amino acid transport and metabolism	
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC	2.5	1.70E-01	Oktansäure	8.8	26095	6	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15598935	PA3740		hypothetical protein	5.6	3.06E-03	Citronellsäure	10.0	24754	4	Unknown			
15598941	PA3746	ffh	signal recognition particle protein Ffh	3.6	5.47E-02	Oktansäure	10.3	49359	5	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion	
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2	1.4	7.05E-03	Citronellsäure	6.1	42342	16	Periplasmic	COG0027	Nucleotide transport and metabolism	
15598948	PA3753		conserved hypothetical protein	2.3	7.63E-03	Citronellsäure	7.0	18509	6	Cytoplasmic	COG0663	General function prediction only	
15598949	PA3754		hypothetical protein	2.0	8.12E-02	Citronellsäure	4.5	22855	3	Cytoplasmic			
15598950	PA3755		conserved hypothetical protein	161.0	8.19E-02	Oktansäure	4.6	20829	2	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase	4.7	6.79E-04	Citronellsäure	4.8	140646	62	Periplasmic	COG0046	Nucleotide transport and metabolism	
15598960	PA3765		hypothetical protein	2.8	1.65E-03	Oktansäure	6.3	20903	2	Unknown	COG3644	Function unknown	
15598962	PA3767		conserved hypothetical protein	1.4	2.26E-01	Oktansäure	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism	Translation, ribosomal structure and biogenesis
15598964	PA3769	guaA	GMP synthase	1.9	3.32E-04	Citronellsäure	5.6	57959	25	Periplasmic	COG0519	Nucleotide transport and metabolism	
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase	1.7	5.67E-03	Citronellsäure	6.7	51707	28	Periplasmic	COG0516	Nucleotide transport and metabolism	
15598974	PA3779		hypothetical protein	244.6	9.04E-04	Citronellsäure	5.3	37696	2	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15598978	PA3783		hypothetical protein	1.1	3.15E-01	Citronellsäure	6.4	23091	6	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15598980	PA3785		conserved hypothetical protein	11.6	3.66E-05	Oktansäure	6.8	17000	11	Periplasmic	COG2847	Inorganic ion transport and metabolism	
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precursor	11.6	1.82E-03	Oktansäure	6.4	79303	15	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15598990	PA3795		probable oxidoreductase	1.2	2.08E-01	Citronellsäure	5.3	34803	7	Cytoplasmic	COG0667	Energy production and conversion	
15598992	PA3797		conserved hypothetical protein	1.1	9.05E-01	Citronellsäure	5.8	29996	6	Cytoplasmic	COG0388	General function prediction only	
15598993	PA3798		probable aminotransferase	1.1	3.17E-01	Citronellsäure	6.2	42594	6	Cytoplasmic	COG0436	Amino acid transport and metabolism	
15598996	PA3801		conserved hypothetical protein	20.0	1.53E-03	Oktansäure	4.8	23108	3	Outer Membrane Vesicle	COG2976	Function unknown	
15598997	PA3802	hisS	histidyl-tRNA synthetase	1.8	6.21E-03	Citronellsäure	5.0	47480	14	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis	
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE	1.9	4.96E-02	Citronellsäure	6.4	40056	10	Cytoplasmic	COG0821	Lipid metabolism	
15599002	PA3807	ndk	nucleoside diphosphate kinase	75.5	2.19E-04	Oktansäure	5.3	15592	10	Cytoplasmic	COG0105	Nucleotide transport and metabolism	
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]	1.5	3.31E-01	Oktansäure	4.0	12241	2	Cytoplasmic	COG0633	Energy production and conversion	
15599005	PA3810	hscA	heat shock protein HscA	1.4	7.84E-02	Citronellsäure	4.6	66446	18	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599006	PA3811	hscB	heat shock protein HscB	15.0	2.13E-03	Oktansäure	4.6	20203	2	Cytoplasmic	COG1076	Posttranslational modification, protein turnover, chaperones	
15599008	PA3813	iscU	probable iron-binding protein IscU	10.0	4.59E-03	Oktansäure	5.8	13753	3	Cytoplasmic	COG0822	Energy production and conversion	
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)	3.6	2.01E-04	Citronellsäure	5.9	44666	25	Cytoplasmic	COG1104	Amino acid transport and metabolism	
15599010	PA3815	iscR	IscR	1.3	2.39E-01	Oktansäure	6.9	17853	6	Unknown	COG1959	Transcription	
15599012	PA3817		probable methyltransferase	1.3	9.47E-02	Citronellsäure	6.2	28493	8	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis	
15599013	PA3818		extragenic suppressor protein SuhB	1.0	8.92E-01	Citronellsäure	6.6	29521	10	Periplasmic	COG0483	Carbohydrate transport and metabolism	
15599014	PA3819		conserved hypothetical protein	10.0	2.98E-02	Citronellsäure	9.4	18941	3	Outer Membrane	COG3134	Function unknown	
15599019	PA3824	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	8.5	9.05E-02	Citronellsäure	6.5	38160	2	Cytoplasmic	COG0809	Translation, ribosomal structure and biogenesis	
15599029	PA3834	valS	valyl-tRNA synthetase	2.0	4.94E-03	Citronellsäure	5.2	107707	48	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis	
15599031	PA3836		hypothetical protein	3.0	5.06E-03	Citronellsäure	8.7	34220	21	Periplasmic	COG2984	General function prediction only	
15599039	PA3844		hypothetical protein	4.5	7.93E-04	Oktansäure	4.8	22795	6	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599041	PA3846		hypothetical protein	1.1	7.57E-01	Oktansäure	5.1	19892	9	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15599044	PA3849		conserved hypothetical protein	4.7	9.31E-05	Citronellsäure	5.1	37930	6	Cytoplasmic	COG3081	General function prediction only	
15599045	PA3850		hypothetical protein	2.3	8.72E-02	Citronellsäure	4.4	33613	2	Unknown			
15599047	PA3852		hypothetical protein	1.4	6.00E-03	Citronellsäure	5.4	33979	4	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599050	PA3855		hypothetical protein	5.6	3.63E-02	Oktansäure	7.9	26286	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599053	PA3858		probable amino acid-binding protein	1.0	9.47E-01	Oktansäure	7.9	37043	8	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms

15599054	PA3859		carboxylesterase	3.1	1.10E-02	Oktansäure	4.9	23420	7	Unknown	COG0400	General function prediction only	
15599055	PA3860		probable AMP-binding enzyme	6.6	2.04E-05	Citronellsäure	6.2	68986	30	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599060	PA3865		probable amino acid binding protein	3.2	1.42E-04	Citronellsäure	6.1	28433	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599061	PA3866		pyocin protein	3.5	6.51E-02	Citronellsäure	8.8	80731	6	Extracellular			
15599074	PA3879	narL	two-component response regulator NarL	1.2	9.27E-01	Oktansäure	4.8	24255	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599081	PA3886		hypothetical protein	1.0	8.34E-01	Citronellsäure	4.9	32290	5	Cytoplasmic	COG0647	Carbohydrate transport and metabolism	
15599091	PA3896		probable 2-hydroxyacid dehydrogenase	1.3	3.06E-02	Oktansäure	8.2	35632	10	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599098	PA3903	prfC	peptide chain release factor 3	1.2	6.21E-01	Oktansäure	5.7	59865	14	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
15599100	PA3905		hypothetical protein	1.5	1.99E-01	Oktansäure	7.7	20024	4	Unknown			
15599103	PA3908		hypothetical protein	1.2	2.38E-01	Oktansäure	5.0	27294	10	Cytoplasmic			
15599113	PA3918	moaC	molybdopterin biosynthetic protein C	3.2	1.89E-01	Oktansäure	7.0	17306	10	Cytoplasmic	COG0315	Coenzyme metabolism	
15599114	PA3919		conserved hypothetical protein	2.6	2.12E-03	Citronellsäure	6.3	51700	23	Cytoplasmic	COG1875	General function prediction only	
15599115	PA3920		probable metal transporting P-type ATPase	45.8	5.85E-02	Citronellsäure	6.9	83437	2	Cytoplasmic Membrane	COG2217	Inorganic ion transport and metabolism	
15599117	PA3922		conserved hypothetical protein	6.7	5.37E-03	Citronellsäure	9.0	51229	28	Periplasmic			
15599118	PA3923		hypothetical protein	6.1	1.17E-03	Citronellsäure	4.7	69590	16	Outer Membrane			
15599119	PA3924		probable medium-chain acyl-CoA ligase	1.9	8.00E-02	Citronellsäure	6.0	62315	23	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599120	PA3925		probable acyl-CoA thiolase	2.0	1.01E-02	Citronellsäure	6.4	40553	37	Cytoplasmic	COG0183	Lipid metabolism	
15599126	PA3931		conserved hypothetical protein	1.6	1.50E-02	Oktansäure	8.6	28101	15	Periplasmic	COG1464	Inorganic ion transport and metabolism	
15599130	PA3935	tauD	taurine dioxygenase	1.3	5.71E-01	Oktansäure	6.4	31029	2	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15599133	PA3938		probable periplasmic taurine-binding protein precursor	5.3	3.75E-03	Oktansäure	7.9	35859	13	Unknown	COG4521	Inorganic ion transport and metabolism	
15599136	PA3941		hypothetical protein	6.8	2.53E-03	Oktansäure	5.8	22025	4	Cytoplasmic	COG0546	General function prediction only	
15599137	PA3942	tesB	acyl-CoA thioesterase II	1.8	2.73E-01	Oktansäure	5.8	32934	5	Cytoplasmic	COG1946	Lipid metabolism	
15599139	PA3944		conserved hypothetical protein	2.1	5.80E-02	Oktansäure	5.3	21857	4	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15599140	PA3945		conserved hypothetical protein	1.1	7.05E-01	Oktansäure	5.7	22403	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
15599143	PA3948	rocA1	Two-component response regulator RocA1	6.5	1.95E-03	Oktansäure	6.8	22996	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599151	PA3956		hypothetical protein	1.0	6.44E-01	Oktansäure	5.1	15453	4	Unknown	COG0346	Amino acid transport and metabolism	
15599156	PA3961		probable ATP-dependent helicase	2.1	1.08E-01	Oktansäure	7.5	91833	2	Cytoplasmic	COG1643	DNA replication, recombination, and repair	
15599160	PA3965		probable transcriptional regulator	1.1	7.09E-01	Oktansäure	5.7	19289	8	Cytoplasmic	COG1522	Transcription	
15599165	PA3970	amn	AMP nucleosidase	1.5	3.45E-02	Citronellsäure	6.8	56225	11	Cytoplasmic	COG0775	Nucleotide transport and metabolism	
15599167	PA3972		probable acyl-CoA dehydrogenase	4.9	3.21E-04	Citronellsäure	6.4	60338	23	Cytoplasmic	COG1960	Lipid metabolism	
15599170	PA3975	thiD	phosphomethylpyrimidine kinase	2.1	7.58E-02	Citronellsäure	6.2	27979	2	Periplasmic	COG0351	Coenzyme metabolism	
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase	1.9	3.97E-03	Citronellsäure	7.1	22146	7	Unknown	COG0352	Coenzyme metabolism	
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase	1.3	1.37E-01	Citronellsäure	5.6	45398	16	Cytoplasmic	COG0001	Coenzyme metabolism	
15599173	PA3978		hypothetical protein	108.4	6.42E-04	Oktansäure	4.3	19636	2	Unknown	COG0790	General function prediction only	
15599178	PA3983		conserved hypothetical protein	2.2	1.38E-01	Oktansäure	4.6	31549	7	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism	
15599182	PA3987	leuS	leucyl-tRNA synthetase	1.6	1.76E-01	Citronellsäure	5.5	97647	43	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis	
15599183	PA3988		hypothetical protein	3.9	4.09E-02	Oktansäure	5.0	22884	4	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane	
15599184	PA3989	holA	DNA polymerase III, delta subunit	1.0	6.87E-01	Citronellsäure	6.9	37378	3	Unknown	COG1466	DNA replication, recombination, and repair	
15599191	PA3996	lis	lipoate synthase	2.0	4.49E-01	Oktansäure	6.9	36733	2	Cytoplasmic	COG0320	Coenzyme metabolism	
15599192	PA3997	lipB	lipoate-protein ligase B	2.5	8.62E-02	Citronellsäure	6.0	23856	5	Cytoplasmic	COG0321	Coenzyme metabolism	
15599199	PA4004		conserved hypothetical protein	1.3	4.15E-01	Oktansäure	9.2	17791	2	Cytoplasmic	COG1576	Function unknown	
15599201	PA4006	nadD	nicotinic acid mononucleotide adenylyltransferase	15.6	8.46E-02	Citronellsäure	6.4	23801	2	Cytoplasmic	COG1057	Coenzyme metabolism	
15599202	PA4007	proA	gamma-glutamyl phosphate reductase	1.1	2.65E-01	Citronellsäure	5.2	45044	11	Periplasmic	COG0014	Amino acid transport and metabolism	
15599205	PA4010		hypothetical protein	1.4	7.98E-02	Oktansäure	8.8	26949	6	Cytoplasmic	COG2094	DNA replication, recombination, and repair	
15599207	PA4012		hypothetical protein	25.0	3.03E-05	Citronellsäure	4.3	21808	3	Cytoplasmic	COG2802	General function prediction only	
15599210	PA4015		conserved hypothetical protein	38.5	2.32E-03	Oktansäure	5.6	16700	11	Cytoplasmic	COG2030	Lipid metabolism	
15599212	PA4017		conserved hypothetical protein	1.6	8.62E-02	Oktansäure	7.1	23164	5	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599214	PA4019		probable aromatic acid decarboxylase	11.4	4.80E-03	Oktansäure	4.8	22367	3	Cytoplasmic	COG0163	Coenzyme metabolism	
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	1.3	1.54E-01	Citronellsäure	6.4	48469	8	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599220	PA4025		probable ethanolamine ammonia-lyase light chain	1.1	7.35E-01	Oktansäure	6.6	30144	2	Cytoplasmic	COG4302	Amino acid transport and metabolism	
15599221	PA4026		probable acetyltransferase	1.3	8.34E-01	Citronellsäure	7.0	18049	11	Cytoplasmic	COG0456	General function prediction only	
15599226	PA4031	ppa	inorganic pyrophosphatase	3.8	2.78E-03	Oktansäure	4.9	19396	15	Cytoplasmic	COG0221	Energy production and conversion	
15599227	PA4032		probable two-component response regulator	50.4	1.29E-03	Oktansäure	5.7	27422	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599230	PA4035		hypothetical protein	2.2	5.83E-02	Citronellsäure	6.3	35895	6	Periplasmic	COG4254	Function unknown	
15599238	PA4043	ispA	geranyltranstransferase	1.7	3.21E-01	Citronellsäure	5.1	31464	4	Cytoplasmic	COG0142	Coenzyme metabolism	
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase	3.6	3.66E-02	Oktansäure	5.5	68049	8	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism
15599242	PA4047	ribA	GTP cyclohydrolase II	12.1	1.09E-03	Citronellsäure	6.6	22067	3	Cytoplasmic	COG0807	Coenzyme metabolism	
15599243	PA4048		hypothetical protein	1323.2	1.76E-03	Oktansäure	9.4	23085	2	Unknown	COG3577	General function prediction only	
15599247	PA4052	nusB	NusB protein	2.0	6.29E-02	Citronellsäure	8.5	17675	3	Unknown	COG0781	Transcription	
15599248	PA4053	ribE	6,7-dimethyl-8-ribityllumazine synthase	16.9	1.11E-02	Oktansäure	5.8	16413	3	Cytoplasmic	COG0054	Coenzyme metabolism	
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	1.3	2.26E-01	Citronellsäure	5.1	39438	15	Cytoplasmic	COG0108	Coenzyme metabolism	
15599250	PA4055	ribC	riboflavin synthase alpha chain	1.7	3.53E-02	Citronellsäure	6.4	23469	5	Cytoplasmic	COG0307	Coenzyme metabolism	
15599251	PA4056	ribD	riboflavin-specific deaminase/reductase	5.5	7.53E-02	Citronellsäure	7.3	39764	3	Cytoplasmic	COG0117	Coenzyme metabolism	
15599252	PA4057	nrdR	NrdR	81.7	8.33E-04	Oktansäure	8.0	17925	6	Cytoplasmic	COG1327	Transcription	
15599256	PA4061		probable thioredoxin	1.5	5.28E-02	Citronellsäure	4.4	31878	13	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15599258	PA4063		hypothetical protein	18.2	6.69E-02	Citronellsäure	6.4	21235	2	Periplasmic			
15599262	PA4067	oprG	Outer membrane protein OprG precursor	26.7	1.78E-02	Oktansäure	4.7	25193	5	Periplasmic	COG3047	Cell envelope biogenesis, outer membrane	
15599263	PA4068		probable epimerase	1.3	1.97E-01	Citronellsäure	5.7	33310	11	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599264	PA4069		hypothetical protein	1.7	4.26E-02	Oktansäure	6.3	32939	4	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15599274	PA4079		probable dehydrogenase	1.3	8.39E-02	Citronellsäure	5.1	24319	9	Extracellular	COG0300	General function prediction only	
15599310	PA4115		conserved hypothetical protein	2.1	1.38E-02	Citronellsäure	7.1	51130	3	Cytoplasmic	COG1611	General function prediction only	
15599314	PA4119	aph	aminoglycoside 3'-phosphotransferase type IIb	1.5	4.06E-01	Citronellsäure	4.9	29812	2	Cytoplasmic	COG3231	Translation, ribosomal structure and biogenesis	
15599324	PA4129		hypothetical protein	73.4	2.11E-02	Oktansäure	5.3	18122	5	Unknown	COG3749	Function unknown	
15599357	PA4162		probable short-chain dehydrogenase	6.3	1.10E-02	Oktansäure	8.0	24857	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599358	PA4163		hypothetical protein	1.2	3.80E-01	Citronellsäure	4.7	60494	16	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599375	PA4180		probable acetolactate synthase large subunit	1.9	1.02E-02	Oktansäure	6.3	59806	6	Cytoplasmic	COG0028		
15599385	PA4190	pqsL	probable FAD-dependent monooxygenase	11.4	3.74E-02	Oktansäure	6.3	43975	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15599386	PA4191		probable iron/ascorbate oxidoreductase	1.5	7.01E-01	Oktansäure	5.8	37441	2	Cytoplasmic	COG3491	General function prediction only	
15599390	PA4195		probable binding protein component of ABC transporter	1.8	2.54E-02	Oktansäure	7.9	29539	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599394	PA4199		probable acyl-CoA dehydrogenase	2.1	2.42E-04	Citronellsäure	5.0	63926	8	Cytoplasmic	COG1960	Lipid metabolism	
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	1.3	5.83E-02	Citronellsäure	4.9	36533	5	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599397	PA4202		hypothetical protein	1.8	2.36E-01	Oktansäure	8.1	36782	8	Cytoplasmic	COG2070	General function prediction only	
15599399	PA4204	ppgL	periplasmic gluconolactonase, PpgL	2.2	1.93E-01	Citronellsäure	7.4	41616	7	Periplasmic	COG2706	Carbohydrate transport and metabolism	
15599406	PA4211	phzB1	probable phenazine biosynthesis protein	18.8	8.43E-04	Oktansäure	5.9	18888	5	Cytoplasmic			
15599413	PA4217	phzS	flavin-containing monooxygenase	9.4	6.35E-03	Oktansäure	5.9	43644	3	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion

15599428	PA4232	ssb	single-stranded DNA-binding protein	3.1	6.18E-03	Oktansäure	5.3	18557	9	Cytoplasmic	COG0629	DNA replication, recombination, and repair	
15599430	PA4234	uvrA	excinuclease ABC subunit A	3.2	1.75E-02	Citronellsäure	6.6	104456	34	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
15599431	PA4235	bfrA	bacterioferritin	5.8	4.42E-03	Oktansäure	4.8	17940	11	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15599432	PA4236	katA	catalase	1.4	2.55E-01	Citronellsäure	6.7	55589	25	Periplasmic	COG0753	Inorganic ion transport and metabolism	
15599433	PA4237	rplQ	50S ribosomal protein L17	86.8	9.20E-02	Oktansäure	11.1	14504	2	Outer Membrane Vesicle	COG0203	Translation, ribosomal structure and biogenesis	
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.0	7.93E-01	Oktansäure	4.6	36649	15	Outer Membrane Vesicle	COG0202	Transcription	
15599435	PA4239	rpsD	30S ribosomal protein S4	2.7	4.14E-02	Oktansäure	10.5	23277	11	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis	
15599436	PA4240	rpsK	30S ribosomal protein S11	168.2	1.72E-05	Oktansäure	11.5	13630	5	Outer Membrane Vesicle	COG0100	Translation, ribosomal structure and biogenesis	
15599437	PA4241	rpsM	30S ribosomal protein S13	51.8	3.17E-03	Oktansäure	11.5	13265	7	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
15599440	PA4244	rplO	50S ribosomal protein L15	197.6	2.28E-03	Oktansäure	11.6	15174	5	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
15599442	PA4246	rpsE	30S ribosomal protein S5	2.0	3.50E-02	Oktansäure	10.6	17625	13	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
15599444	PA4248	rplF	50S ribosomal protein L6	25.4	2.53E-03	Oktansäure	10.5	19099	8	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
15599445	PA4249	rpsH	30S ribosomal protein S8	227.4	3.75E-05	Oktansäure	10.2	14171	6	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
15599446	PA4250	rpsN	30S ribosomal protein S14	242.2	5.02E-04	Oktansäure	11.9	11565	3	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	
15599447	PA4251	rplE	50S ribosomal protein L5	1.9	4.01E-02	Citronellsäure	10.3	20392	18	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis	
15599449	PA4253	rplN	50S ribosomal protein L14	126.4	1.38E-02	Oktansäure	11.4	13412	6	Outer Membrane Vesicle	COG0093	Translation, ribosomal structure and biogenesis	
15599452	PA4256	rplP	50S ribosomal protein L16	25.3	5.83E-03	Oktansäure	11.8	15401	5	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
15599453	PA4257	rpsC	30S ribosomal protein S3	2.5	1.06E-02	Oktansäure	10.8	25838	16	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis	
15599456	PA4260	rplB	50S ribosomal protein L2	34.4	1.07E-03	Oktansäure	11.8	29579	5	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
15599458	PA4262	rplD	50S ribosomal protein L4	60.9	2.02E-03	Oktansäure	10.6	21640	4	Outer Membrane Vesicle	COG0088	Translation, ribosomal structure and biogenesis	
15599459	PA4263	rplC	50S ribosomal protein L3	4.8	7.79E-02	Oktansäure	10.6	22592	5	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis	
15599461	PA4265	tufA	elongation factor Tu	2.0	8.85E-03	Citronellsäure	5.0	43337	51	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
15599462	PA4266	fusA1	elongation factor G	1.9	9.31E-02	Citronellsäure	4.8	77752	75	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15599463	PA4267	rpsG	30S ribosomal protein S7	4.3	5.56E-02	Oktansäure	10.9	17504	17	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis	
15599464	PA4268	rpsL	30S ribosomal protein S12	78.0	3.09E-05	Oktansäure	11.6	13799	6	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	3.4	3.29E-03	Citronellsäure	7.1	154364	111	Outer Membrane Vesicle	COG0086	Transcription	
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	4.3	2.55E-05	Citronellsäure	5.6	150837	113	Periplasmic	COG0085	Transcription	
15599468	PA4272	rplJ	50S ribosomal protein L10	24.6	1.76E-04	Oktansäure	9.5	17602	9	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
15599469	PA4273	rplA	50S ribosomal protein L1	1.9	9.21E-03	Citronellsäure	10.3	24234	15	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis	
15599470	PA4274	rplK	50S ribosomal protein L11	865.0	3.28E-05	Oktansäure	10.4	14907	4	Outer Membrane Vesicle	COG0080	Translation, ribosomal structure and biogenesis	
15599471	PA4275	nusG	transcription antitermination protein NusG	1.5	2.18E-01	Oktansäure	5.8	20130	11	Cytoplasmic	COG0250	Transcription	
15599474	PA4278		hypothetical protein	18.5	7.32E-03	Oktansäure	5.9	26077	3	Unknown			
15599475	PA4279		hypothetical protein	1.3	5.97E-02	Citronellsäure	5.4	26758	4	Cytoplasmic	COG1521	Transcription	
15599478	PA4282		probable exonuclease	3.2	1.22E-02	Citronellsäure	5.5	138959	17	Extracellular	COG0419	DNA replication, recombination, and repair	
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	1.2	5.00E-01	Oktansäure	6.7	79084	7	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	5.2	1.01E-03	Citronellsäure	5.5	139379	19	Unknown	COG1074	DNA replication, recombination, and repair	
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	3.9	7.76E-03	Citronellsäure	5.3	132646	11	Cytoplasmic	COG1330	DNA replication, recombination, and repair	
15599482	PA4286		hypothetical protein	5.7	3.74E-02	Oktansäure	5.2	24815	3	Unknown	COG0095	Coenzyme metabolism	
15599492	PA4296	pprB	two-component response regulator, PprB	2.7	2.23E-01	Oktansäure	6.7	30557	5	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599504	PA4308		conserved hypothetical protein	1.3	7.14E-02	Citronellsäure	6.5	53246	8	Unknown	COG0433	Replication, recombination, and repair	
15599506	PA4310	pctB	chemotactic transducer PctB	3.1	5.37E-02	Oktansäure	4.8	68076	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	2.0	2.15E-01	Citronellsäure	6.5	32410	7	Periplasmic	COG0788	Nucleotide transport and metabolism	
15599511	PA4315	mvaT	transcriptional regulator MvaT, P16 subunit	146.1	6.58E-02	Oktansäure	10.1	14180	3	Cytoplasmic			
15599518	PA4322		conserved hypothetical protein	2.2	7.37E-03	Oktansäure	6.2	36661	3	Cytoplasmic	COG0714	General function prediction only	
15599525	PA4329	pykA	pyruvate kinase II	1.5	5.79E-02	Citronellsäure	6.7	52252	26	Periplasmic	COG0469	Carbohydrate transport and metabolism	
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	21.2	2.49E-04	Citronellsäure	6.7	28152	13	Cytoplasmic	COG1024	Lipid metabolism	
15599529	PA4333		probable fumarase	5.3	1.49E-02	Citronellsäure	5.2	54763	14	Periplasmic	COG1951	Energy production and conversion	
15599532	PA4336		conserved hypothetical protein	2.3	2.63E-02	Oktansäure	6.0	20993	7	Cytoplasmic	COG0693	General function prediction only	
15599536	PA4340		hypothetical protein	4.5	3.41E-03	Oktansäure	6.1	20988	7	Periplasmic			
15599541	PA4345		hypothetical protein	2.6	7.73E-01	Oktansäure	4.8	22161	2	Unknown	COG2353	Function unknown	
15599545	PA4349		hypothetical protein	1.1	2.97E-01	Oktansäure	6.2	31671	9	Unknown	COG1960	Lipid metabolism	
15599548	PA4352		conserved hypothetical protein	3.2	4.80E-02	Oktansäure	6.2	30972	15	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms	
15599549	PA4353		conserved hypothetical protein	4.2	7.55E-02	Oktansäure	8.5	22029	2	Cytoplasmic	COG3124	Function unknown	
15599552	PA4356	xenB	xenobiotic reductase	1.0	9.39E-01	Oktansäure	4.9	37796	20	Periplasmic	COG1902	Energy production and conversion	
15599562	PA4366	sodB	superoxide dismutase	2.6	5.39E-02	Citronellsäure	5.2	21351	7	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein precursor	1.2	4.98E-01	Oktansäure	4.5	47230	16	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
15599568	PA4372		hypothetical protein	1.0	7.41E-01	Citronellsäure	6.0	38323	6	Outer Membrane Vesicle	COG3489	General function prediction only	
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	1.3	3.37E-01	Oktansäure	6.7	45690	5	Cytoplasmic	COG1488	Coenzyme metabolism	
15599577	PA4381		probable two-component response regulator	1.8	7.57E-03	Citronellsäure	5.9	25235	6	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599581	PA4385	groEL	GroEL protein	1.2	3.25E-01	Citronellsäure	4.8	57086	57	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
15599582	PA4386	groES	GroES protein	74.3	6.97E-06	Oktansäure	4.9	10267	7	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
15599584	PA4388		hypothetical protein	1.1	3.75E-01	Oktansäure	6.4	26982	7	Cytoplasmic	COG0748	Inorganic ion transport and metabolism	
15599585	PA4389		probable short-chain dehydrogenase	1.2	4.25E-01	Citronellsäure	7.3	26720	27	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599591	PA4395		conserved hypothetical protein	1.1	7.84E-01	Citronellsäure	8.2	18044	15	Cytoplasmic	COG1666	Function unknown	
15599595	PA4399		conserved hypothetical protein	1.3	1.39E-01	Citronellsäure	6.1	21065	4	Cytoplasmic	COG2096	Coenzyme transport and metabolism	
15599596	PA4400		probable pyrophosphohydrolase	2.1	6.81E-02	Citronellsäure	5.1	34022	5	Cytoplasmic	COG0352	Coenzyme metabolism	
15599597	PA4401		probable glutathione S-transferase	3.4	6.65E-04	Citronellsäure	5.4	23789	16	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599598	PA4402	argJ	glutamate N-acetyltransferase	1.9	1.23E-02	Citronellsäure	5.3	41762	22	Cytoplasmic	COG1364	Amino acid transport and metabolism	
15599599	PA4403	secA	secretion protein SecA	1.8	2.03E-02	Citronellsäure	5.4	103854	44	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion	
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.5	2.27E-02	Citronellsäure	5.0	33435	13	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane	
15599603	PA4407	ftsZ	cell division protein FtsZ	1.7	8.43E-02	Citronellsäure	4.7	41218	13	Periplasmic	COG0206	Cell division and chromosome partitioning	
15599604	PA4408	ftsA	cell division protein FtsA	1.2	3.05E-01	Citronellsäure	5.0	44646	10	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.5	1.98E-01	Oktansäure	4.7	34363	11	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.0	9.54E-01	Citronellsäure	6.1	51949	7	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599608	PA4412	murG	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecap	24.8	7.17E-03	Oktansäure	10.0	37799	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.2	7.79E-01	Citronellsäure	5.7	48080	9	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane	
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl liga	1.6	2.88E-02	Citronellsäure	6.5	47412	14	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1.6	9.09E-03	Citronellsäure	5.1	51263	14	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
15599616	PA4420		conserved hypothetical protein	2.1	7.07E-02	Oktansäure	7.7	34640	7	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane	
15599617	PA4421		conserved hypothetical protein	4.1	2.51E-01	Oktansäure	4.9	17079	1	Cytoplasmic	COG2001	Function unknown	
15599619	PA4423		conserved hypothetical protein	56.1	1.59E-01	Oktansäure	7.2	65629	2	Periplasmic	COG3107	General function prediction only	
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	1.6	3.29E-01	Citronellsäure	4.7	21413	9	Cytoplasmic	COG0279	Carbohydrate transport and metabolism	
15599622	PA4426		conserved hypothetical protein	8.8	9.84E-02	Oktansäure	9.8	20619	2	Outer Membrane Vesicle	COG2823	General function prediction only	
15599624	PA4428	sspA	stringent starvation protein A	2.2	1.38E-02	Citronellsäure	6.1	23615	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599625	PA4429		probable cytochrome c1 precursor	7.7	3.90E-04	Oktansäure	7.5	28993	2	Outer Membrane Vesicle	COG2857	Energy production and conversion	

15599627	PA4431		probable iron-sulfur protein	7.2	5.82E-03	Oktansäure	6.5	20828	4	Outer Membrane Vesicle	COG0723	Energy production and conversion	
15599628	PA4432	rpsI	30S ribosomal protein S9	508.5	8.87E-04	Oktansäure	11.8	14615	3	Outer Membrane Vesicle	COG0103	Translation, ribosomal structure and biogenesis	
15599629	PA4433	rplM	50S ribosomal protein L13	3.9	6.82E-02	Oktansäure	10.4	16029	4	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis	
15599630	PA4434		probable oxidoreductase	1.1	5.69E-01	Oktansäure	5.7	38644	11	Periplasmic	COG0667	Energy production and conversion	
15599631	PA4435		probable acyl-CoA dehydrogenase	13.4	3.17E-04	Citronellsäure	6.1	42128	18	Cytoplasmic	COG1960	Lipid metabolism	
15599634	PA4438		conserved hypothetical protein	1.4	7.47E-02	Citronellsäure	6.2	41993	4	Cytoplasmic	COG1485	General function prediction only	
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.1	5.20E-01	Citronellsäure	5.8	48961	16	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis	
15599636	PA4440		hypothetical protein	1.1	7.56E-01	Oktansäure	6.2	22315	6	Unknown	COG2945	General function prediction only	
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	1.1	7.36E-01	Citronellsäure	5.6	69268	31	Periplasmic	COG2895	Inorganic ion transport and metabolism	
15599639	PA4443	cysD	ATP sulfurylase small subunit	1.1	4.49E-01	Citronellsäure	7.1	35478	14	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15599641	PA4445		conserved hypothetical protein	2.1	2.30E-02	Citronellsäure	5.3	27360	4	Cytoplasmic	COG0327	Function unknown	
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	1.1	6.41E-01	Oktansäure	6.0	38655	9	Periplasmic	COG0079	Amino acid transport and metabolism	
15599644	PA4448	hisD	histidinol dehydrogenase	1.2	6.35E-01	Citronellsäure	4.9	47179	12	Periplasmic	COG0141	Amino acid transport and metabolism	
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	1.2	2.58E-01	Citronellsäure	9.3	22844	16	Cytoplasmic	COG0040	Amino acid transport and metabolism	
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.1	2.91E-01	Citronellsäure	5.5	44645	19	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane	
15599649	PA4453		conserved hypothetical protein	1.4	1.22E-01	Citronellsäure	9.7	23760	13	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
15599653	PA4457		arabinose-5-phosphate isomerase KdsD	48.9	6.88E-05	Oktansäure	5.6	34179	7	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
15599654	PA4458		conserved hypothetical protein	2.1	1.39E-02	Citronellsäure	5.6	19334	10	Cytoplasmic	COG1778	General function prediction only	
15599656	PA4460		conserved hypothetical protein	1.1	6.78E-01	Citronellsäure	9.6	19126	10	Periplasmic	COG1934	Function unknown	
15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.1	5.97E-01	Citronellsäure	4.4	56054	8	Cytoplasmic	COG1508	Transcription	
15599661	PA4465		conserved hypothetical protein	1.6	5.41E-03	Citronellsäure	5.7	32218	6	Cytoplasmic	COG1660	General function prediction only	
15599664	PA4468	sodM	superoxide dismutase	3.5	2.24E-02	Oktansäure	6.2	22506	7	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599666	PA4470	fumC1	fumarate hydratase	2.5	4.19E-02	Oktansäure	5.9	48695	23	Cytoplasmic	COG0114	Energy production and conversion	
15599668	PA4472	pmbA	PmbA protein	1.3	1.13E-01	Citronellsäure	5.5	47908	9	Cytoplasmic	COG0312	General function prediction only	
15599670	PA4474		conserved hypothetical protein	1.0	8.06E-01	Citronellsäure	5.0	50266	4	Cytoplasmic	COG0312	General function prediction only	
15599671	PA4475		conserved hypothetical protein	2.3	1.48E-02	Citronellsäure	6.8	30724	12	Cytoplasmic	COG0388	General function prediction only	
15599673	PA4477	cafA	cytoplasmic axial filament protein	2.0	3.28E-02	Citronellsäure	5.0	54665	7	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis	
15599674	PA4478		conserved hypothetical protein	2.6	1.34E-02	Oktansäure	4.7	20974	9	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15599677	PA4481	mreB	rod shape-determining protein MreB	1.2	4.80E-01	Citronellsäure	5.1	36976	14	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning	
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.7	3.17E-02	Citronellsäure	5.5	51862	18	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.6	4.78E-02	Citronellsäure	5.1	53081	21	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis	
15599685	PA4489		conserved hypothetical protein	2.7	8.84E-03	Oktansäure	5.3	167428	25	Outer Membrane Vesicle	COG2373	General function prediction only	
15599686	PA4490		conserved hypothetical protein	47.0	3.10E-05	Oktansäure	10.3	23969	5	Cytoplasmic Membrane	COG3234	Function unknown	
15599689	PA4493	roxR	RoxR	3.2	8.62E-03	Oktansäure	5.3	20616	9	Cytoplasmic	COG4567	Signal transduction mechanisms	Transcription
15599691	PA4495		hypothetical protein	1.2	1.93E-01	Oktansäure	5.9	24879	12	Periplasmic	COG3471	Function unknown	
15599692	PA4496		probable binding protein component of ABC transporter	3.7	3.62E-03	Citronellsäure	7.6	60077	18	Periplasmic	COG0747	Amino acid transport and metabolism	
15599695	PA4499		probable transcriptional regulator	6.0	4.33E-02	Oktansäure	6.2	20435	4	Cytoplasmic	COG1396	Transcription	
15599698	PA4502		probable binding protein component of ABC transporter	4.7	2.75E-03	Citronellsäure	6.6	58611	3	Periplasmic	COG0747	Amino acid transport and metabolism	
15599704	PA4508		probable transcriptional regulator	2.1	6.96E-04	Citronellsäure	6.7	17334	2	Cytoplasmic	COG1522	Transcription	
15599711	PA4515		conserved hypothetical protein	5.5	3.30E-02	Oktansäure	6.6	25616	3	Cytoplasmic	COG3128	Function unknown	
15599715	PA4519	speC	ornithine decarboxylase	1.6	8.02E-03	Citronellsäure	4.7	43559	16	Cytoplasmic	COG0019	Amino acid transport and metabolism	
15599718	PA4522	ampD	beta-lactamase expression regulator AmpD	2.5	5.77E-03	Oktansäure	5.5	21028	2	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane	
15599719	PA4523		hypothetical protein	7.1	1.17E-01	Oktansäure	5.5	83588	2	Cytoplasmic			
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	1.2	2.66E-01	Citronellsäure	5.1	30552	14	Cytoplasmic	COG0157	Coenzyme metabolism	
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	9.5	7.14E-03	Oktansäure	6.6	15512	6	Outer Membrane Vesicle	COG4969	Cell motility and secretion	Intracellular trafficking and secretion
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	1.6	3.22E-02	Oktansäure	5.7	62328	7	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15599725	PA4529	coaE	dephosphocoenzyme A kinase	1.4	2.15E-01	Citronellsäure	6.8	22843	9	Cytoplasmic	COG0237	Coenzyme metabolism	
15599729	PA4533		hypothetical protein	25.9	1.81E-03	Oktansäure	9.5	17613	3	Periplasmic			
15599738	PA4542	clpB	ClpB protein	1.1	6.50E-01	Oktansäure	5.1	95005	48	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15599739	PA4543		conserved hypothetical protein	1.5	1.67E-01	Oktansäure	7.5	26047	4	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism	
15599743	PA4547	pilR	two-component response regulator PilR	1.6	7.62E-02	Citronellsäure	5.9	49737	2	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599744	PA4548		probable D-amino acid oxidase	1.8	1.08E-01	Oktansäure	6.5	39413	4	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism	
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	2.2	3.17E-02	Citronellsäure	6.4	126583	5	Periplasmic	COG3419	Cell motility and secretion	Intracellular trafficking and secretion
15599753	PA4557	lytB	LytB protein	1.1	7.88E-01	Citronellsäure	5.2	34762	4	Cytoplasmic	COG0761	Lipid metabolism	
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	5.3	1.03E-01	Oktansäure	4.3	15984	6	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	3.6	6.45E-04	Citronellsäure	6.1	105464	42	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis	
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	2.1	1.45E-03	Oktansäure	9.1	34340	7	Cytoplasmic	COG0196	Coenzyme metabolism	
15599760	PA4564		conserved hypothetical protein	45.0	6.43E-03	Oktansäure	9.2	16724	2	Periplasmic	COG3045	Function unknown	
15599761	PA4565	proB	glutamate 5-kinase	1.4	3.00E-01	Oktansäure	7.3	39845	5	Cytoplasmic	COG0263	Amino acid transport and metabolism	
15599762	PA4566	obg	GTP-binding protein Obg	1.9	5.37E-02	Citronellsäure	4.5	44338	4	Cytoplasmic	COG0536	General function prediction only	
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.2	3.19E-01	Oktansäure	4.6	34851	17	Cytoplasmic	COG0142	Coenzyme metabolism	
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	1.1	5.82E-01	Citronellsäure	4.5	21795	7	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15599772	PA4576		probable ATP-dependent protease	1.1	3.71E-01	Oktansäure	4.7	90222	43	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones	
15599776	PA4580		conserved hypothetical protein	1.0	7.09E-01	Oktansäure	8.2	20498	3	Cytoplasmic	COG3236	Function unknown	
15599783	PA4587	ccpR	cytochrome c551 peroxidase precursor	2.0	3.72E-01	Oktansäure	6.7	37403	6	Periplasmic	COG1858	Inorganic ion transport and metabolism	
15599784	PA4588	gdhA	glutamate dehydrogenase	1.0	7.83E-01	Citronellsäure	6.0	48856	20	Unknown	COG0334	Amino acid transport and metabolism	
15599791	PA4595		probable ATP-binding component of ABC transporter	1.0	7.34E-01	Oktansäure	5.4	61302	32	Periplasmic	COG0488	General function prediction only	
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.8	3.18E-04	Citronellsäure	6.0	45157	14	Periplasmic	COG0112	Amino acid transport and metabolism	
15599800	PA4604		conserved hypothetical protein	6.7	9.70E-03	Citronellsäure	4.5	37256	3	Cytoplasmic	COG0523	General function prediction only	
15599805	PA4609	radA	DNA repair protein RadA	10.0	4.10E-02	Oktansäure	6.9	48411	2	Unknown	COG1066	Posttranslational modification, protein turnover, chaperones	
15599810	PA4614	mscL	conductance mechanosensitive channel	5.5	1.24E-01	Oktansäure	4.6	14432	3	Outer Membrane Vesicle	COG1970	Cell envelope biogenesis, outer membrane	
15599811	PA4615		probable oxidoreductase	1.2	3.10E-01	Citronellsäure	5.2	29377	9	Cytoplasmic	COG1018	Energy production and conversion	
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	1.6	6.03E-02	Oktansäure	4.7	219755	2	Extracellular			
15599822	PA4626	hprA	glycerate dehydrogenase	1.1	2.41E-01	Oktansäure	6.7	34285	7	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599827	PA4631		hypothetical protein	3.0	6.01E-02	Oktansäure	7.7	37231	2	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599828	PA4632		hypothetical protein	2.1	4.58E-02	Citronellsäure	7.6	29159	4	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15599830	PA4634		hypothetical protein	2.2	3.36E-01	Oktansäure	8.7	22996	2	Unknown	COG2135	Function unknown	
15599835	PA4639		hypothetical protein	1.6	4.36E-03	Oktansäure	9.8	20736	7	Outer Membrane Vesicle			
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.0	9.09E-01	Citronellsäure	7.0	55498	5	Cytoplasmic	COG0579	General function prediction only	
15599839	PA4644		hypothetical protein	6.3	2.43E-01	Oktansäure	5.9	17109	2	Unknown			
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	3.2	1.47E-02	Oktansäure	5.6	20639	13	Cytoplasmic	COG0634	Nucleotide transport and metabolism	
15599841	PA4646	upp	uracil phosphoribosyltransferase	1.6	5.01E-02	Citronellsäure	7.0	22938	16	Cytoplasmic	COG0035	Nucleotide transport and metabolism	
15599846	PA4651	cupE4	Pilin assembly chaperone CupE4	57.7	1.82E-03	Citronellsäure	9.7	28981	2	Unknown	COG3121	Cell motility and secretion	Intracellular trafficking and secretion
15599851	PA4656		conserved hypothetical protein	7.0	3.35E-02	Oktansäure	8.3	33852	5	Cytoplasmic	COG1090	General function prediction only	
15599852	PA4657		hypothetical protein	1.8	1.04E-01	Oktansäure	6.8	35913	8	Unknown	COG3380	General function prediction only	

15599854	PA4659		probable transcriptional regulator	5.1	1.69E-03	Oktansäure	8.0	33959	2	Cytoplasmic	COG0789	Transcription
15599857	PA4662	murI	glutamate racemase	2.1	1.83E-02	Oktansäure	5.2	28274	4	Cytoplasmic	COG0796	Cell envelope biogenesis, outer membrane
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	1.1	6.26E-01	Citronellsäure	5.6	26686	5	Cytoplasmic	COG0476	Coenzyme metabolism
15599860	PA4665	prfA	peptide chain release factor 1	1.1	5.75E-01	Oktansäure	4.8	40040	4	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis
15599864	PA4669	ipk	isopentenyl monophosphate kinase	1.4	1.14E-01	Citronellsäure	6.6	30843	4	Unknown	COG1947	Lipid metabolism
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.1	5.37E-01	Oktansäure	6.5	34008	22	Periplasmic	COG0462	Nucleotide transport and metabolism Amino acid transport and metabolism
15599866	PA4671		probable ribosomal protein L25	1.7	6.78E-02	Citronellsäure	6.2	21962	11	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis
15599867	PA4672		peptidyl-tRNA hydrolase	4.8	9.62E-04	Oktansäure	9.8	20772	3	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis
15599868	PA4673		conserved hypothetical protein	2.9	1.30E-03	Citronellsäure	4.8	40078	13	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis
15599870	PA4675		probable TonB-dependent receptor	1.2	7.68E-01	Citronellsäure	5.2	80952	10	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599871	PA4676		probable carbonic anhydrase	1.2	1.99E-01	Oktansäure	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism
15599873	PA4678	rimI	peptide n-acetyltransferase RimI	3.4	2.99E-01	Oktansäure	6.2	17095	2	Cytoplasmic	COG0456	General function prediction only
15599874	PA4679		hypothetical protein	16.5	1.28E-02	Oktansäure	5.0	24841	2	Unknown		
15599881	PA4686		hypothetical protein	3.8	1.66E-01	Oktansäure	5.3	106827	5	Periplasmic	COG1196	Cell division and chromosome partitioning
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	1.3	3.53E-01	Citronellsäure	5.5	36149	21	Periplasmic	COG1840	Inorganic ion transport and metabolism
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.1	1.51E-01	Citronellsäure	5.7	36424	32	Periplasmic	COG0059	Amino acid transport and metabolism Coenzyme metabolism
15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	2.4	2.38E-01	Oktansäure	6.3	17784	9	Cytoplasmic	COG0440	Amino acid transport and metabolism
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.1	4.85E-01	Citronellsäure	6.8	62986	31	Cytoplasmic	COG0028	
15599895	PA4701		conserved hypothetical protein	1.8	5.18E-04	Citronellsäure	6.0	58344	24	Periplasmic	COG2187	Function unknown
15599902	PA4708	phuT	Heme-transport protein, PhuT	1.4	2.18E-02	Oktansäure	7.8	31037	16	Periplasmic	COG4558	Inorganic ion transport and metabolism
15599903	PA4709		probable hemin degrading factor	2.1	3.30E-02	Oktansäure	5.6	39057	10	Cytoplasmic	COG3720	Inorganic ion transport and metabolism
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR precursor	5.1	3.92E-02	Oktansäure	5.9	84724	10	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599909	PA4715		probable aminotransferase	1.7	1.48E-02	Oktansäure	8.1	46064	7	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599910	PA4716		hypothetical protein	1.8	1.49E-01	Citronellsäure	5.0	30850	2	Cytoplasmic	COG0384	General function prediction only
15599911	PA4717		conserved hypothetical protein	11.6	2.03E-03	Oktansäure	6.1	31861	2	Unknown	COG2321	General function prediction only
15599914	PA4720	trmA	tRNA (uracil-5-)-methyltransferase	1.0	8.89E-01	Oktansäure	7.0	41206	2	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis
15599916	PA4722		probable aminotransferase	1.2	3.99E-01	Oktansäure	5.7	42567	5	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599917	PA4723	dksA	suppressor protein DksA	1.6	4.93E-02	Citronellsäure	4.8	17344	13	Periplasmic	COG1734	Signal transduction mechanisms
15599920	PA4726	cbrB	two-component response regulator CbrB	1.2	2.12E-01	Oktansäure	5.5	52286	19	Cytoplasmic	COG2204	Signal transduction mechanisms
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	1.7	5.22E-01	Citronellsäure	4.6	18014	4	Cytoplasmic	COG0801	Coenzyme metabolism
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.4	1.92E-01	Citronellsäure	5.8	27874	9	Periplasmic	COG0413	Coenzyme metabolism
15599924	PA4730	panC	pantoate--beta-alanine ligase	1.4	1.96E-01	Citronellsäure	6.5	30836	10	Cytoplasmic	COG0414	Coenzyme metabolism
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.2	3.03E-02	Citronellsäure	6.6	61944	13	Periplasmic	COG0166	Carbohydrate transport and metabolism
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	2.2	6.67E-02	Citronellsäure	6.2	71624	18	Cytoplasmic	COG0365	Lipid metabolism
15599929	PA4735		hypothetical protein	1.0	9.24E-01	Oktansäure	5.1	118589	2	Outer Membrane Vesicle		
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.2	4.26E-01	Oktansäure	4.8	75421	52	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	1.4	1.00E-01	Citronellsäure	6.9	33378	6	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis
15599938	PA4744	infB	translation initiation factor IF-2	1.0	9.77E-01	Citronellsäure	6.0	90912	37	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis
15599939	PA4745	nusA	N utilization substance protein A	1.7	3.79E-02	Oktansäure	4.3	54658	26	Periplasmic	COG0195	Transcription
15599940	PA4746		conserved hypothetical protein	1.2	7.59E-01	Oktansäure	4.3	17139	4	Cytoplasmic	COG0779	Function unknown
15599941	PA4747	secG	secretion protein SecG	295.7	5.99E-02	Oktansäure	5.1	13207	2	Outer Membrane Vesicle	COG1314	Intracellular trafficking and secretion
15599942	PA4748	tpiA	triosephosphate isomerase	1.2	1.24E-01	Citronellsäure	5.3	25621	8	Cytoplasmic	COG0149	Carbohydrate transport and metabolism
15599943	PA4749	glmM	phosphoglucosamine mutase	1.7	4.21E-02	Citronellsäure	6.0	47796	5	Cytoplasmic	COG1109	Carbohydrate transport and metabolism
15599944	PA4750	folP	dihydropteroate synthase	2.3	5.58E-03	Citronellsäure	5.4	30490	6	Cytoplasmic	COG0294	Coenzyme metabolism
15599945	PA4751	ftsH	cell division protein FtsH	1.6	5.73E-02	Oktansäure	5.6	69955	2	Outer Membrane Vesicle	COG0465	Posttranslational modification, protein turnover, chaperones
15599949	PA4755	greA	transcription elongation factor GreA	2.5	6.36E-03	Oktansäure	4.7	17158	12	Periplasmic	COG0782	Function unknown
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	5.3	2.44E-03	Citronellsäure	4.8	117330	74	Periplasmic	COG0458	Amino acid transport and metabolism Nucleotide transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.6	7.72E-04	Citronellsäure	5.2	40810	9	Cytoplasmic	COG0505	Amino acid transport and metabolism Nucleotide transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.6	1.91E-02	Citronellsäure	6.0	28324	14	Periplasmic	COG0289	Amino acid transport and metabolism
15599954	PA4760	dnaJ	DnaJ protein	1.1	5.39E-01	Citronellsäure	7.4	40260	6	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones
15599955	PA4761	dnaK	DnaK protein	1.0	9.72E-01	Oktansäure	4.5	68403	57	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones
15599956	PA4762	grpE	heat shock protein GrpE	1.6	1.36E-01	Citronellsäure	4.2	20702	13	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones
15599958	PA4764	fur	ferric uptake regulation protein	1.7	2.81E-01	Oktansäure	5.9	15234	9	Cytoplasmic	COG0735	Inorganic ion transport and metabolism
15599962	PA4768	smpB	SmpB protein	1.0	9.85E-01	Citronellsäure	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones
15599970	PA4776	pmrA	PmrA: two-component regulator system response regulator PmrA	1.6	2.05E-01	Citronellsäure	5.6	24394	2	Cytoplasmic	COG0745	Signal transduction mechanisms Transcription
15599975	PA4781		cyclic di-GMP phosphodiesterase	1.4	3.03E-01	Citronellsäure	5.0	43628	2	Cytoplasmic	COG3437	Transcription Signal transduction mechanisms
15599990	PA4796		hypothetical protein	24.6	1.59E-01	Oktansäure	4.8	17129	3	Unknown	COG0509	Amino acid transport and metabolism
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.4	2.13E-01	Oktansäure	5.2	70667	13	Periplasmic	COG1166	Amino acid transport and metabolism
15600034	PA4841		conserved hypothetical protein	3.8	4.31E-03	Oktansäure	4.4	19733	4	Unknown	COG1443	Lipid metabolism
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	3.0	3.11E-03	Oktansäure	4.7	16455	7	Unknown	COG0511	Lipid metabolism
15600041	PA4848	accC	biotin carboxylase	1.5	1.10E-01	Citronellsäure	6.3	48888	15	Periplasmic	COG0439	Lipid metabolism
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	3.3	3.56E-03	Citronellsäure	4.2	32000	4	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	2.1	8.97E-04	Citronellsäure	6.5	57665	25	Periplasmic	COG0138	Nucleotide transport and metabolism
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	1.9	1.51E-03	Citronellsäure	4.7	45212	15	Periplasmic	COG0151	Nucleotide transport and metabolism
15600059	PA4866		conserved hypothetical protein	3.0	2.05E-01	Oktansäure	6.3	18743	2	Unknown	COG1247	Cell envelope biogenesis, outer membrane
15600061	PA4868	ureC	urease alpha subunit	2.4	2.41E-02	Oktansäure	6.2	60611	14	Cytoplasmic	COG0804	Amino acid transport and metabolism
15600065	PA4872		hypothetical protein	1.5	9.59E-02	Citronellsäure	5.4	31320	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
15600071	PA4878		probable transcriptional regulator	14.5	1.12E-03	Citronellsäure	6.9	31168	5	Cytoplasmic	COG3708	Function unknown
15600073	PA4880		probable bacterioferritin	10.1	1.12E-03	Citronellsäure	4.4	20217	10	Cytoplasmic	COG2193	Inorganic ion transport and metabolism
15600077	PA4884		hypothetical protein	486.4	1.02E-02	Oktansäure	9.7	21561	3	Periplasmic		
15600083	PA4890	desT	DesT	21.7	7.48E-04	Oktansäure	9.1	22899	3	Cytoplasmic	COG1309	Transcription
15600086	PA4893	ureG	urease accessory protein UreG	5.7	6.83E-05	Oktansäure	4.6	21991	8	Cytoplasmic	COG0378	Posttranslational modification, protein turnover, chaperones Transcription
15600092	PA4899		probable aldehyde dehydrogenase	4.3	9.32E-03	Citronellsäure	5.8	52697	3	Cytoplasmic	COG1012	Energy production and conversion
15600100	PA4907		probable short-chain dehydrogenase	1.1	4.24E-01	Oktansäure	5.1	27384	11	Cytoplasmic	COG4221	General function prediction only
15600106	PA4913		probable binding protein component of ABC transporter	6.9	1.10E-03	Citronellsäure	6.6	39798	17	Periplasmic	COG0683	Amino acid transport and metabolism
15600109	PA4916		hypothetical protein	1858.2	7.17E-03	Oktansäure	6.5	25457	2	Unknown	COG1051	Nucleotide transport and metabolism
15600111	PA4918		hypothetical protein	2.5	6.42E-03	Citronellsäure	4.7	23821	9	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	7.5	2.51E-03	Citronellsäure	6.3	46095	8	Cytoplasmic	COG1488	Coenzyme metabolism
15600113	PA4920	nadE	NH3-dependent NAD synthetase	1.6	7.03E-02	Citronellsäure	5.4	29696	15	Periplasmic	COG0171	Coenzyme metabolism
15600115	PA4922	azu	azurin precursor	102.0	7.29E-05	Oktansäure	6.9	16008	18	Periplasmic	COG3241	Energy production and conversion
15600116	PA4923		conserved hypothetical protein	2.0	3.78E-01	Oktansäure	5.2	20725	4	Unknown	COG1611	General function prediction only
15600123	PA4930	alr	biosynthetic alanine racemase	4.1	8.33E-02	Citronellsäure	6.1	38310	2	Cytoplasmic	COG0787	Cell envelope biogenesis, outer membrane
15600124	PA4931	dnaB	replicative DNA helicase	1.3	1.61E-02	Citronellsäure	4.7	51589	2	Cytoplasmic	COG0305	DNA replication, recombination, and repair
15600125	PA4932	rplI	50S ribosomal protein L9	21.6	1.49E-03	Oktansäure	5.3	15532	7	Periplasmic	COG0359	Translation, ribosomal structure and biogenesis
15600128	PA4935	rpsF	30S ribosomal protein S6	26.1	1.00E-03	Oktansäure	4.6	16165	16	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis

15600129	PA4936		probable rRNA methylase	5.0	1.78E-02	Oktansäure	7.2	27081	2	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis	
15600131	PA4938	purA	adenylosuccinate synthetase	2.3	1.11E-03	Citronellsäure	6.0	46814	18	Periplasmic	COG0104	Nucleotide transport and metabolism	
15600132	PA4939		conserved hypothetical protein	1.4	5.24E-02	Citronellsäure	4.8	42546	9	Cytoplasmic	COG3705	Amino acid transport and metabolism	
15600139	PA4946	mutL	DNA mismatch repair protein MutL	1.1	6.20E-01	Oktansäure	6.5	69748	5	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
15600141	PA4948		conserved hypothetical protein	2.8	1.23E-01	Oktansäure	4.7	16463	3	Cytoplasmic	COG0802	General function prediction only	
15600142	PA4949		conserved hypothetical protein	1.2	5.96E-01	Citronellsäure	7.6	51550	2	Unknown	COG0063	Carbohydrate transport and metabolism	
15600144	PA4951	orn	oligoribonuclease	1.0	7.25E-01	Citronellsäure	5.6	20826	4	Cytoplasmic	COG1949	RNA processing and modification	
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	1.4	1.23E-01	Citronellsäure	5.3	29391	9	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15600152	PA4959	fimX	FimX	1.2	4.30E-01	Citronellsäure	4.9	75992	13	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15600153	PA4960		probable phosphoserine phosphatase	1.0	9.68E-01	Oktansäure	4.9	46438	9	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15600157	PA4964	parC	topoisomerase IV subunit A	3.0	1.73E-03	Oktansäure	5.9	83364	17	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15600160	PA4967	parE	topoisomerase IV subunit B	2.1	1.06E-02	Oktansäure	5.9	69178	8	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	6.2	1.06E-02	Oktansäure	4.8	30498	2	Cytoplasmic	COG1409	General function prediction only	
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.2	1.70E-01	Citronellsäure	4.7	23133	6	Cytoplasmic			
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	1.4	9.78E-02	Citronellsäure	5.8	69784	13	Cytoplasmic	COG0422	Coenzyme metabolism	
15600167	PA4974		probable outer membrane protein precursor	1.6	2.86E-01	Oktansäure	5.9	53405	6	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15600168	PA4975		NAD(P)H quinone oxidoreductase	13.2	4.42E-03	Citronellsäure	6.0	26315	2	Cytoplasmic	COG2249	General function prediction only	
15600180	PA4987		probable transcriptional regulator	4.5	4.52E-02	Oktansäure	5.6	22368	2	Cytoplasmic	COG1917	Function unknown	
15600185	PA4992		hypothetical protein	2.1	3.51E-02	Citronellsäure	6.4	29030	7	Cytoplasmic	COG0667	Energy production and conversion	
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.5	2.43E-01	Oktansäure	6.2	50348	15	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane	
15600194	PA5001		hypothetical protein	29.7	1.14E-01	Oktansäure	8.7	36625	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
15600198	PA5005		probable carbamoyl transferase	3.5	3.03E-02	Oktansäure	6.9	66047	9	Outer Membrane Vesicle	COG2192	Posttranslational modification, protein turnover, chaperones	
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.2	2.06E-01	Citronellsäure	6.2	34084	24	Periplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	4.0	1.77E-03	Citronellsäure	5.2	110102	33	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
15600208	PA5015	aceE	pyruvate dehydrogenase	1.2	5.30E-01	Oktansäure	5.6	99563	44	Periplasmic	COG2609	Energy production and conversion	
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	3.0	3.04E-02	Oktansäure	5.0	56676	23	Periplasmic	COG0508	Energy production and conversion	
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	2.0	3.04E-02	Oktansäure	5.0	23517	8	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
15600212	PA5019		conserved hypothetical protein	1.3	3.25E-01	Citronellsäure	6.0	31882	11	Cytoplasmic	COG2961	General function prediction only	
15600218	PA5025	metY	homocysteine synthase	1.2	2.09E-01	Oktansäure	6.5	45177	13	Cytoplasmic	COG2873	Amino acid transport and metabolism	
15600219	PA5026		hypothetical protein	3.7	1.27E-02	Oktansäure	6.3	16786	1	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	2.4	6.04E-03	Citronellsäure	6.3	38792	8	Cytoplasmic	COG0407	Coenzyme metabolism	
15600228	PA5035	gltD	glutamate synthase small chain	2.4	1.06E-02	Citronellsäure	6.4	52625	23	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
15600229	PA5036	gltB	glutamate synthase large chain precursor	5.9	5.98E-06	Citronellsäure	6.0	161607	72	Cytoplasmic	COG0069	Amino acid transport and metabolism	
15600231	PA5038	aroB	3-dehydroquinate synthase	2.0	7.72E-02	Citronellsäure	5.6	40109	11	Cytoplasmic	COG0337	Amino acid transport and metabolism	
15600232	PA5039	aroK	shikimate kinase	1.1	1.49E-01	Citronellsäure	8.8	19205	2	Cytoplasmic	COG0703	Amino acid transport and metabolism	
15600239	PA5046		malic enzyme	1.9	3.98E-03	Citronellsäure	4.8	45428	26	Periplasmic	COG0281	Energy production and conversion	
15600243	PA5050	priA	primosomal protein N'	1.3	6.62E-01	Oktansäure	8.8	82120	2	Unknown	COG1198	DNA replication, recombination, and repair	
15600244	PA5051	argS	arginyl-tRNA synthetase	2.2	5.14E-03	Citronellsäure	5.2	65199	16	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis	
15600246	PA5053	hslV	heat shock protein HslV	2.1	1.15E-01	Citronellsäure	6.7	18767	7	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones	
15600247	PA5054	hslU	heat shock protein HslU	1.1	6.06E-01	Oktansäure	5.4	50082	15	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
15600253	PA5060	phaF	polyhydroxyalkanoate synthesis protein PhaF	5.7	5.91E-01	Oktansäure	11.1	30577	3	Cytoplasmic	COG3937	Function unknown	
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	2.9	2.76E-03	Oktansäure	9.5	28254	11	Cytoplasmic	COG2226	Coenzyme metabolism	
15600257	PA5064		hypothetical protein	4.8	4.08E-02	Oktansäure	6.0	22767	6	Cytoplasmic	COG3165	Function unknown	
15600259	PA5066	hisI	phosphoribosyl-AMP cyclohydrolase	37.6	5.48E-04	Oktansäure	6.0	15375	4	Cytoplasmic	COG0139	Amino acid transport and metabolism	
15600264	PA5071		conserved hypothetical protein	169.3	4.47E-04	Citronellsäure	9.1	26065	4	Cytoplasmic	COG1385	Function unknown	
15600269	PA5076		probable binding protein component of ABC transporter	2.7	5.75E-04	Citronellsäure	7.6	29736	19	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600270	PA5077	mdoH	periplasmic glucans biosynthesis protein MdoH	6.9	9.72E-03	Oktansäure	8.9	96994	2	Outer Membrane Vesicle	COG2943	Cell envelope biogenesis, outer membrane	
15600271	PA5078		conserved hypothetical protein	1.5	2.60E-02	Citronellsäure	7.0	59444	12	Periplasmic	COG3131	Inorganic ion transport and metabolism	
15600272	PA5079		conserved hypothetical protein	65.5	1.57E-05	Oktansäure	6.3	15530	3	Unknown	COG1490	Translation, ribosomal structure and biogenesis	
15600273	PA5080		prolyl aminopeptidase	2.0	4.31E-02	Oktansäure	6.2	36515	18	Cytoplasmic	COG0596	General function prediction only	
15600274	PA5081		hypothetical protein	2.6	3.23E-01	Oktansäure	4.7	17918	3	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600275	PA5082		probable binding protein component of ABC transporter	56.6	3.82E-02	Citronellsäure	8.2	32866	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600283	PA5090		conserved hypothetical protein	48.5	2.96E-02	Oktansäure	5.8	87821	5	Cytoplasmic	COG3501	Function unknown	
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	1.5	2.70E-01	Oktansäure	5.9	29791	7	Cytoplasmic	COG3741	Amino acid transport and metabolism	
15600289	PA5096		probable binding protein component of ABC transporter	8.0	3.22E-02	Oktansäure	5.2	35496	3	Periplasmic	COG2113	Amino acid transport and metabolism	
15600291	PA5098	hutH	histidine ammonia-lyase	1.2	5.78E-01	Citronellsäure	5.8	53779	5	Cytoplasmic	COG2986	Amino acid transport and metabolism	
15600296	PA5103		hypothetical protein	3.2	2.56E-01	Citronellsäure	6.2	37890	2	Periplasmic	COG2113	Amino acid transport and metabolism	
15600297	PA5104		conserved hypothetical protein	1.4	6.12E-01	Oktansäure	5.6	21415	7	Unknown	COG3758	Function unknown	
15600298	PA5105	hutC	histidine utilization repressor HutC	1.1	9.77E-01	Oktansäure	7.4	27779	2	Cytoplasmic	COG2188	Transcription	
15600302	PA5109		hypothetical protein	2.4	1.58E-02	Oktansäure	5.1	22697	7	Cytoplasmic	COG3803	Function unknown	
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	1.4	1.80E-01	Citronellsäure	5.9	37216	12	Periplasmic	COG0158	Carbohydrate transport and metabolism	
15600304	PA5111	gloA3	lactoylglutathione lyase	1.1	5.69E-01	Oktansäure	4.8	20215	4	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15600305	PA5112	estA	esterase EstA	2.6	3.73E-02	Citronellsäure	4.5	69608	6	Periplasmic	COG3240	Lipid metabolism	General function prediction only
15600308	PA5115		conserved hypothetical protein	8.8	7.39E-04	Oktansäure	5.2	20998	4	Cytoplasmic			
15600310	PA5117	typA	regulatory protein TypA	1.3	1.07E-01	Citronellsäure	5.0	66903	17	Periplasmic	COG1217	Signal transduction mechanisms	
15600311	PA5118	thiI	thiazole biosynthesis protein ThiI	1.5	6.77E-01	Citronellsäure	6.7	54849	3	Cytoplasmic	COG0301	Coenzyme metabolism	
15600312	PA5119	glnA	glutamine synthetase	1.7	2.87E-01	Oktansäure	5.0	51944	25	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism	
15600318	PA5125	ntrC	two-component response regulator NtrC	2.2	1.20E-02	Citronellsäure	5.8	52753	5	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600321	PA5128	secB	secretion protein SecB	2.9	3.77E-02	Citronellsäure	4.2	18146	11	Periplasmic	COG1952	Intracellular trafficking and secretion	
15600324	PA5131	pgm	phosphoglycerate mutase	1.1	6.67E-01	Citronellsäure	4.9	55601	24	Periplasmic	COG0696	Carbohydrate transport and metabolism	
15600327	PA5134		probable carboxyl-terminal protease	3.8	4.21E-02	Oktansäure	5.4	46018	7	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15600330	PA5137		hypothetical protein	31.7	1.45E-04	Citronellsäure	7.5	27991	7	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600331	PA5138		hypothetical protein	3.1	4.08E-04	Citronellsäure	4.9	27915	11	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600332	PA5139		hypothetical protein	4.1	2.38E-03	Citronellsäure	5.8	27565	10	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	1.5	7.39E-02	Citronellsäure	4.7	25938	3	Cytoplasmic	COG0106	Amino acid transport and metabolism	
15600335	PA5142	hisH1	glutamine amidotransferase	1.9	6.41E-03	Citronellsäure	6.3	23666	12	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	1.1	5.96E-01	Citronellsäure	6.5	21937	8	Cytoplasmic	COG0131	Amino acid transport and metabolism	
15600339	PA5146		hypothetical protein	5.9	4.51E-04	Oktansäure	8.3	80849	5	Outer Membrane Vesicle	COG2982	Cell envelope biogenesis, outer membrane	
15600343	PA5150		probable short-chain dehydrogenase	1.9	2.39E-02	Oktansäure	6.2	26191	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic	7.0	8.55E-04	Citronellsäure	4.9	27561	27	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	1.7	1.46E-02	Citronellsäure	5.9	39542	15	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	1.0	9.96E-01	Citronellsäure	6.1	33106	11	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	1.1	4.77E-01	Oktansäure	5.0	32457	15	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.3	3.76E-01	Citronellsäure	6.0	20766	9	Unknown	COG1898	Cell envelope biogenesis, outer membrane	
15600359	PA5166	dctD	DctD	1.8	7.48E-03	Citronellsäure	5.5	50864	4	Cytoplasmic	COG2204	Signal transduction mechanisms	

15600360	PA5167	dctP	DctP	3.0	7.48E-03	Citronellsäure	8.8	37051	19	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15600364	PA5171	arcA	arginine deiminase	2.3	6.25E-02	Oktansäure	5.5	46436	28	Cytoplasmic	COG2235	Amino acid transport and metabolism	
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	2.4	1.34E-01	Oktansäure	6.6	38108	21	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15600366	PA5173	arcC	carbamate kinase	2.2	2.93E-02	Oktansäure	5.0	33080	19	Cytoplasmic	COG0549	Amino acid transport and metabolism	
15600367	PA5174		probable beta-ketoacyl synthase	1.6	1.07E-01	Oktansäure	6.0	68763	8	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	1.4	2.92E-01	Citronellsäure	4.8	29779	6	Cytoplasmic	COG1218	Inorganic ion transport and metabolism	
15600369	PA5176		conserved hypothetical protein	1.2	4.34E-01	Citronellsäure	4.5	20983	10	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600370	PA5177		probable hydrolase	1.3	2.25E-01	Citronellsäure	5.9	25629	4	Cytoplasmic	COG1011	General function prediction only	
15600372	PA5179		probable transcriptional regulator	34.5	1.59E-03	Oktansäure	6.4	32533	2	Cytoplasmic	COG0583	Transcription	
15600377	PA5184		hypothetical protein	1.9	2.89E-01	Oktansäure	8.8	20417	10	Periplasmic	COG1605	Amino acid transport and metabolism	
15600379	PA5186		probable iron-containing alcohol dehydrogenase	1.3	3.22E-01	Citronellsäure	5.4	40354	5	Cytoplasmic	COG1454	Energy production and conversion	
15600380	PA5187		probable acyl-CoA dehydrogenase	1.4	4.66E-01	Oktansäure	5.3	64558	6	Cytoplasmic	COG1960	Lipid metabolism	
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	1.6	6.55E-02	Oktansäure	5.2	44810	8	Cytoplasmic	COG1250	Lipid metabolism	
15600383	PA5190		probable nitroreductase	1.6	1.15E-01	Oktansäure	6.0	22450	8	Cytoplasmic	COG0778	Energy production and conversion	
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.8	1.08E-02	Citronellsäure	5.1	55732	30	Periplasmic	COG1866	Energy production and conversion	
15600386	PA5193	yrfI	heat shock protein HSP33	1.5	5.06E-02	Oktansäure	4.5	32834	6	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
15600393	PA5200	amgR	AmgR	1.0	9.47E-01	Citronellsäure	6.6	27924	12	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600394	PA5201		conserved hypothetical protein	1.9	1.38E-02	Oktansäure	6.3	84963	35	Periplasmic	COG2183	Transcription	
15600396	PA5203	gshA	glutamate--cysteine ligase	1.5	1.24E-01	Citronellsäure	4.9	59205	16	Cytoplasmic	COG2918	Coenzyme metabolism	
15600397	PA5204	argA	N-acetylglutamate synthase	1.0	9.59E-01	Oktansäure	6.5	47858	9	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600401	PA5208		conserved hypothetical protein	3.3	1.20E-02	Oktansäure	5.2	25644	3	Cytoplasmic	COG1392	Inorganic ion transport and metabolism	
15600403	PA5210		probable secretion pathway ATPase	1.8	1.57E-01	Oktansäure	6.5	65981	4	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15600406	PA5213	gcvP1	glycine cleavage system protein P1	3.0	1.18E-01	Citronellsäure	6.5	104710	15	Cytoplasmic	COG1003	Amino acid transport and metabolism	
15600407	PA5214	gcvH1	glycine cleavage system protein H1	20.6	2.50E-02	Oktansäure	3.9	13642	2	Unknown	COG0509	Amino acid transport and metabolism	
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	1.3	6.81E-02	Oktansäure	5.4	38907	6	Periplasmic	COG0404	Amino acid transport and metabolism	
15600410	PA5217		probable binding protein component of ABC iron transporter	1.9	1.47E-01	Oktansäure	6.4	36292	5	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15600413	PA5220		hypothetical protein	4.4	6.69E-01	Oktansäure	6.2	30542	3	Unknown			
15600417	PA5224	pepP	aminopeptidase P	1.1	7.20E-01	Oktansäure	5.1	49710	11	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15600418	PA5225		hypothetical protein	1.5	1.91E-01	Citronellsäure	4.0	19358	6	Unknown	COG3079	Function unknown	
15600422	PA5229		conserved hypothetical protein	2.3	6.25E-02	Citronellsäure	7.5	16871	6	Unknown	COG2947	Function unknown	
15600427	PA5234		probable oxidoreductase	1.5	2.39E-01	Citronellsäure	7.0	34011	10	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15600430	PA5237		conserved hypothetical protein	2.2	8.88E-02	Citronellsäure	6.5	54621	2	Cytoplasmic	COG0043	Coenzyme metabolism	
15600432	PA5239	rho	transcription termination factor Rho	1.4	2.77E-01	Oktansäure	6.8	47069	14	Periplasmic	COG1158	Transcription	
15600433	PA5240	trxA	thioredoxin	16.3	1.86E-04	Oktansäure	4.5	11870	9	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15600434	PA5241	ppx	exopolyphosphatase	1.3	4.34E-01	Oktansäure	6.7	56419	7	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
15600435	PA5242	ppk	polyphosphate kinase	1.2	1.86E-01	Oktansäure	7.7	83151	22	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	1.0	9.46E-01	Oktansäure	4.8	37005	7	Cytoplasmic	COG0113	Coenzyme metabolism	
15600438	PA5245		conserved hypothetical protein	1.2	6.50E-01	Citronellsäure	4.7	23426	14	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	
15600445	PA5252		probable ATP-binding component of ABC transporter	1.9	1.29E-03	Oktansäure	5.9	70871	10	Cytoplasmic	COG0488	General function prediction only	
15600447	PA5254		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	3.1	3.28E-03	Oktansäure	5.4	23047	2	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	2.2	3.37E-02	Oktansäure	4.8	27247	4	Unknown	COG1587	Coenzyme metabolism	
15600453	PA5260	hemC	porphobilinogen deaminase	2.1	2.89E-04	Citronellsäure	5.3	33641	8	Cytoplasmic	COG0181	Coenzyme metabolism	
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	1.3	3.24E-01	Citronellsäure	7.3	27608	13	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
15600456	PA5263	argH	argininosuccinate lyase	1.8	9.44E-04	Citronellsäure	5.5	51640	20	Periplasmic	COG0165	Amino acid transport and metabolism	
15600459	PA5266		conserved hypothetical protein	13.4	5.31E-03	Oktansäure	6.4	76707	10	Cytoplasmic	COG3501	Function unknown	
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.5	5.92E-03	Citronellsäure	5.4	45490	16	Periplasmic	COG0019	Amino acid transport and metabolism	
15600471	PA5278	dapF	diaminopimelate epimerase	1.3	8.67E-02	Citronellsäure	7.7	30320	8	Cytoplasmic	COG0253	Amino acid transport and metabolism	
15600472	PA5279		conserved hypothetical protein	1.2	3.61E-01	Citronellsäure	5.3	25767	4	Cytoplasmic	COG3159	Function unknown	
15600474	PA5281		probable hydrolase	1.6	1.59E-03	Oktansäure	5.9	25852	4	Cytoplasmic	COG1011	General function prediction only	
15600485	PA5292	pchP	phosphorylcholine phosphatase	1.1	6.52E-01	Oktansäure	5.8	39117	2	Periplasmic			
15600490	PA5297	poxB	pyruvate dehydrogenase (cytochrome)	6.6	1.90E-02	Oktansäure	6.0	62320	3	Cytoplasmic Membrane	COG0028		
15600491	PA5298		xanthine phosphoribosyltransferase	2.1	2.13E-02	Oktansäure	6.6	20575	7	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15600492	PA5299		hypothetical protein	1.0	7.34E-01	Oktansäure	5.7	68673	5	Cytoplasmic	COG0427	Energy production and conversion	
15600494	PA5301	pauR	probable transcriptional regulator	3.0	2.27E-02	Oktansäure	5.3	19944	5	Cytoplasmic	COG1396	Transcription	
15600505	PA5312	pauC	Aldehyde dehydrogenase	2.2	1.47E-03	Citronellsäure	5.3	53143	24	Periplasmic	COG1012	Energy production and conversion	
15600506	PA5313	gabT2	Transaminase	4.4	5.98E-03	Citronellsäure	6.7	48347	8	Cytoplasmic	COG0161	Coenzyme metabolism	
15600510	PA5317		probable binding protein component of ABC dipeptide transporter	1.3	8.55E-02	Citronellsäure	7.0	57880	6	Periplasmic	COG0747	Amino acid transport and metabolism	
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine decai	1.1	1.42E-01	Citronellsäure	6.3	43133	10	Cytoplasmic	COG0452	Coenzyme metabolism	
15600515	PA5322	algC	phosphomannomutase AlgC	1.6	9.80E-03	Citronellsäure	5.0	50295	25	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15600516	PA5323	argB	acetylglutamate kinase	1.5	1.23E-01	Citronellsäure	6.8	31849	19	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600522	PA5329		conserved hypothetical protein	12.5	7.23E-04	Oktansäure	5.0	17712	4	Cytoplasmic	COG0824	General function prediction only	
15600523	PA5330		hypothetical protein	1.7	3.89E-02	Citronellsäure	9.4	22434	8	Unknown			
15600524	PA5331	pyrE	orotate phosphoribosyltransferase	1.3	1.78E-01	Citronellsäure	5.1	23320	11	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
15600525	PA5332	crc	catabolite repression control protein	1.2	4.24E-01	Citronellsäure	5.2	29844	9	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15600527	PA5334	rph	ribonuclease PH	1.9	5.90E-02	Oktansäure	5.9	25654	8	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis	
15600528	PA5335		conserved hypothetical protein	1.2	2.25E-01	Citronellsäure	5.8	31708	10	Cytoplasmic	COG1561	Function unknown	
15600529	PA5336	gmk	guanylate kinase	1.1	8.61E-01	Oktansäure	5.3	23102	9	Cytoplasmic	COG0194	Nucleotide transport and metabolism	
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.1	4.53E-01	Oktansäure	9.4	78861	20	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15600532	PA5339		conserved hypothetical protein	38.5	3.93E-04	Oktansäure	4.8	13610	6	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
15600536	PA5343		hypothetical protein	1.8	2.03E-02	Oktansäure	6.2	30778	6	Unknown	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15600537	PA5344	oxyR	OxyR	2.8	9.57E-02	Oktansäure	6.7	34295	12	Cytoplasmic	COG0583	Transcription	
15600538	PA5345	recG	ATP-dependent DNA helicase RecG	5.1	4.42E-03	Oktansäure	7.3	76178	5	Cytoplasmic	COG1200	DNA replication, recombination, and repair	Transcription
15600539	PA5346	sadB	SadB	1.0	7.52E-01	Oktansäure	6.0	51427	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
15600540	PA5347		hypothetical protein	6.1	1.02E-02	Oktansäure	11.1	14726	6	Unknown			
15600542	PA5349		probable rubredoxin reductase	1.3	9.21E-02	Citronellsäure	5.5	40617	10	Cytoplasmic	COG1251	Energy production and conversion	
15600550	PA5357		hypothetical protein	1.3	5.11E-01	Citronellsäure	4.7	19512	9	Cytoplasmic	COG3161	Coenzyme metabolism	
15600552	PA5359		hypothetical protein	31.3	8.88E-02	Oktansäure	8.0	16472	2	Periplasmic	COG4315	Function unknown	
15600553	PA5360	phoB	two-component response regulator PhoB	1.3	4.83E-01	Citronellsäure	5.1	25711	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600557	PA5364		probable two-component response regulator	1.9	1.47E-01	Oktansäure	9.4	32401	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU	1.0	8.60E-01	Citronellsäure	5.0	27487	5	Cytoplasmic	COG0704	Inorganic ion transport and metabolism	
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding protein, PstS	1.2	2.40E-01	Oktansäure	9.5	34473	8	Periplasmic	COG0226	Inorganic ion transport and metabolism	
15600564	PA5371		conserved hypothetical protein	277.4	4.30E-02	Oktansäure	4.5	14555	2	Unknown	COG1607	Lipid metabolism	
15600566	PA5373	betB	betaine aldehyde dehydrogenase	2.1	3.07E-02	Citronellsäure	5.0	53332	6	Cytoplasmic	COG1012	Energy production and conversion	
15600567	PA5374	betI	transcriptional regulator BetI	128.3	1.30E-03	Oktansäure	9.0	21861	2	Unknown	COG1309	Transcription	
15600571	PA5378		hypothetical protein	3.0	6.86E-03	Citronellsäure	7.3	34427	8	Periplasmic	COG2113	Amino acid transport and metabolism	

15600588	PA5395		conserved hypothetical protein	4.7	2.67E-01	Oktansäure	7.8	18513	2	Unknown	COG3558	Function unknown	
15600606	PA5413	ltaA	low specificity l-threonine aldolase	1.3	2.63E-01	Citronellsäure	5.0	38213	8	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15600607	PA5414		hypothetical protein	13.1	1.07E-02	Oktansäure	5.8	22547	2	Outer Membrane Vesicle			
15600614	PA5421	fdhA	glutathione-independent formaldehyde dehydrogenase	5.4	1.20E-02	Citronellsäure	6.8	42008	2	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
15600616	PA5423		hypothetical protein	1.0	8.68E-01	Oktansäure	5.7	20002	3	Periplasmic	COG3495	Function unknown	
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase	2.0	1.90E-02	Citronellsäure	5.4	38496	5	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	45.4	9.97E-04	Oktansäure	6.2	16889	8	Unknown	COG0041	Nucleotide transport and metabolism	
15600620	PA5427	adhA	alcohol dehydrogenase	3.0	1.19E-01	Oktansäure	5.8	35911	12	Outer Membrane Vesicle	COG1064	General function prediction only	
15600622	PA5429	aspA	aspartate ammonia-lyase	3.0	1.82E-02	Citronellsäure	5.6	51069	10	Periplasmic	COG1027	Amino acid transport and metabolism	
15600626	PA5433		conserved hypothetical protein	219.3	3.87E-02	Citronellsäure	9.0	25584	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15600628	PA5435		probable transcarboxylase subunit	1.7	7.59E-02	Citronellsäure	5.7	66095	28	Cytoplasmic	COG5016	Energy production and conversion	
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase	1.6	5.58E-01	Citronellsäure	6.6	51816	9	Cytoplasmic	COG0439	Lipid metabolism	
15600631	PA5438		probable transcriptional regulator	40.4	2.77E-03	Oktansäure	7.2	31648	3	Cytoplasmic	COG1737	Transcription	
15600634	PA5441		hypothetical protein	1.1	5.67E-01	Oktansäure	4.6	80036	36	Periplasmic			
15600636	PA5443	uvrD	DNA helicase II	1.5	2.27E-01	Oktansäure	5.7	81494	15	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
15600645	PA5452	wbpW	phosphomannose isomerase/GDP-mannose WbpW	3.3	2.76E-03	Citronellsäure	6.4	52574	4	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase	2.7	1.69E-02	Citronellsäure	6.5	36399	12	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
15600647	PA5454	rmd	oxidoreductase Rmd	1.1	2.35E-01	Citronellsäure	6.7	33910	7	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15600650	PA5457		hypothetical protein	2.0	2.25E-03	Citronellsäure	6.2	31744	5	Cytoplasmic	COG2227	Coenzyme metabolism	
15600652	PA5459		hypothetical protein	1.5	1.05E-01	Citronellsäure	4.7	30701	8	Cytoplasmic	COG2226	Coenzyme metabolism	
15600668	PA5475		hypothetical protein	8.7	2.38E-02	Oktansäure	4.8	21000	7	Cytoplasmic			
15600674	PA5481		hypothetical protein	21.5	1.15E-03	Oktansäure	5.2	17366	4	Periplasmic			
15600676	PA5483	algB	two-component response regulator AlgB	1.1	6.60E-01	Oktansäure	5.2	49323	6	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA	3.6	9.45E-04	Oktansäure	6.4	23375	10	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15600683	PA5490	cc4	cytochrome c4 precursor	1.9	4.26E-02	Citronellsäure	7.6	20735	4	Outer Membrane Vesicle	COG2863	Energy production and conversion	
15600685	PA5492		conserved hypothetical protein	8.6	1.97E-03	Oktansäure	7.1	23786	6	Unknown	COG0218	General function prediction only	
15600686	PA5493	polA	DNA polymerase I	2.7	6.85E-04	Citronellsäure	4.8	99792	48	Periplasmic	COG0749	DNA replication, recombination, and repair	
15600689	PA5496	nrdJb	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, NrdJb	4.3	2.00E-02	Oktansäure	6.4	24886	4	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
15600690	PA5497	nrdJa	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, NrdJa	7.8	2.78E-02	Oktansäure	6.0	82741	8	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
15600692	PA5499	np20	transcriptional regulator np20	2.2	4.36E-02	Citronellsäure	6.9	18216	2	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15600698	PA5505		probable TonB-dependent receptor	1.7	1.06E-02	Citronellsäure	8.7	28065	16	Periplasmic	COG1464	Inorganic ion transport and metabolism	
15600700	PA5507		hypothetical protein	2.0	3.93E-03	Oktansäure	6.4	24262	7	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15600709	PA5516	pdxY	pyridoxamine kinase	5.5	1.86E-02	Oktansäure	6.0	31285	3	Cytoplasmic	COG2240	Coenzyme metabolism	
15600712	PA5519		conserved hypothetical protein	4.2	1.72E-01	Oktansäure	7.5	21215	3	Unknown	COG1607	Lipid metabolism	
15600714	PA5521		probable short-chain dehydrogenase	1.1	5.97E-01	Citronellsäure	5.8	26894	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600716	PA5523		probable aminotransferase	4.1	3.14E-02	Citronellsäure	6.7	48908	3	Cytoplasmic	COG0001	Coenzyme metabolism	
15600735	PA5542		hypothetical protein	3.0	2.02E-02	Citronellsäure	6.3	45872	7	Unknown	COG1680	Defense mechanisms	
15600738	PA5545		conserved hypothetical protein	5.6	7.15E-03	Citronellsäure	7.8	33627	16	Periplasmic	COG2358	General function prediction only	
15600739	PA5546		conserved hypothetical protein	2.7	2.54E-03	Citronellsäure	5.7	44096	11	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.2	5.04E-02	Citronellsäure	5.9	66294	26	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane	
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridylt	1.5	1.28E-01	Citronellsäure	6.2	48851	8	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane	
15600747	PA5554	atpD	ATP synthase beta chain	1.2	9.42E-02	Citronellsäure	4.7	49499	31	Periplasmic	COG0055	Energy production and conversion	
15600748	PA5555	atpG	ATP synthase gamma chain	1.3	9.75E-02	Citronellsäure	8.1	31553	14	Outer Membrane Vesicle	COG0224	Energy production and conversion	
15600749	PA5556	atpA	ATP synthase alpha chain	1.9	3.70E-02	Citronellsäure	5.1	55393	22	Periplasmic	COG0056	Energy production and conversion	
15600750	PA5557	atpH	ATP synthase delta chain	1.4	2.98E-01	Oktansäure	5.9	19260	10	Outer Membrane Vesicle	COG0712	Energy production and conversion	
15600751	PA5558	atpF	ATP synthase B chain	13.2	1.43E-02	Oktansäure	5.8	16924	9	Outer Membrane Vesicle	COG0711	Energy production and conversion	
15600755	PA5562	spoOJ	chromosome partitioning protein Spo0J	29.9	2.27E-04	Oktansäure	10.0	31969	6	Cytoplasmic	COG1475	Transcription	
15600756	PA5563	soj	chromosome partitioning protein Soj	6.5	5.55E-03	Oktansäure	6.1	28609	2	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
15600757	PA5564	gidB	glucose inhibited division protein B	1.1	4.93E-01	Oktansäure	6.3	23735	5	Unknown	COG0357	Cell envelope biogenesis, outer membrane	
15600758	PA5565	gidA	glucose-inhibited division protein A	1.1	8.24E-01	Citronellsäure	6.5	69605	7	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning	
15600760	PA5567		conserved hypothetical protein	4.9	7.83E-02	Oktansäure	4.9	48744	2	Cytoplasmic	COG0486	General function prediction only	
15600762	PA5569	rnpA	ribonuclease P protein component	1.2	2.57E-01	Oktansäure	11.5	15282	4	Unknown	COG0594	Translation, ribosomal structure and biogenesis	
375041995				1.0	7.79E-01	Oktansäure			72				
313108864				124.4	6.37E-06	Citronellsäure			38				
10120672				73.5	1.13E-03	Citronellsäure			31				
22001796				1.2	7.57E-01	Oktansäure			29				
313111914				2.4	1.85E-01	Oktansäure			23				
313110180				1.3	5.27E-02	Citronellsäure			27				
296388504				1.6	3.03E-01	Oktansäure			25				
346058454				2.7	2.13E-02	Citronellsäure			18				
239949861				1.5	1.87E-01	Citronellsäure			14				
239949862				2.4	2.74E-03	Citronellsäure			16				
375044686				3.6	2.47E-01	Oktansäure			15				
347307435				1.1	5.57E-01	Oktansäure			13				
355641798				1.6	5.14E-02	Oktansäure			11				
296388215				7.7	1.15E-02	Citronellsäure			11				
308198348				1.7	1.41E-02	Citronellsäure			11				
254241852				1.0	6.11E-01	Oktansäure			9				
282403589				1.6	1.43E-01	Oktansäure			9				
99032099				63.2	4.46E-04	Oktansäure			10				
107104524				1.9	1.66E-02	Oktansäure			10				
107102694				1.2	6.69E-02	Citronellsäure			11				
344189438				1.5	1.59E-01	Citronellsäure			8				
375041918				4.7	1.62E-03	Oktansäure			9				
107101116				1.4	5.13E-02	Citronellsäure			8				
107104196				1.0	6.68E-01	Oktansäure			7				
218889002				21.5	4.06E-04	Oktansäure			7				
107099288				1.0	9.54E-01	Oktansäure			7				
107100575				1.7	8.02E-02	Oktansäure			6				
107099078				10.1	1.10E-02	Oktansäure			6				
109158147				5.3	8.97E-04	Oktansäure			5				
107102668				1.1	5.77E-01	Oktansäure			5				
116053335				5.4	3.05E-01	Oktansäure			5				
107099958				31.7	1.59E-04	Citronellsäure			4				
359783701				1.4	2.65E-01	Citronellsäure			5				

296389665	5.1	3.13E-02	Oktansäure	4
146308929	3.9	1.61E-01	Citronellsäure	2
104780016	4.5	1.34E-01	Citronellsäure	1
359782167	18.8	5.32E-04	Oktansäure	3
107104298	1.7	3.63E-02	Citronellsäure	3
107102789	6.6	7.10E-02	Oktansäure	3
107099096	1.3	3.22E-01	Citronellsäure	3
107103573	1.0	9.25E-01	Citronellsäure	3
107101938	103.1	2.27E-04	Oktansäure	3
107102888	1.0	8.85E-01	Citronellsäure	4
182677049	7.6	4.68E-02	Oktansäure	3
374702386	1.4	5.79E-01	Oktansäure	2
107101092	14.5	6.31E-03	Oktansäure	3
70732985	1.7	1.14E-01	Oktansäure	3
41019482	2.1	4.36E-02	Citronellsäure	1
258591310	4.8	1.25E-01	Citronellsäure	2
104781332	6.7	1.64E-03	Oktansäure	3
146282899	2.7	1.59E-02	Citronellsäure	3
107103974	3.2	1.32E-02	Citronellsäure	2
355639818	17.8	2.65E-02	Oktansäure	2
218891628	5.7	3.13E-02	Oktansäure	2
93007153	1.2	7.78E-01	Citronellsäure	1
50083773	1.8	1.28E-01	Citronellsäure	3
226944916	1.8	1.10E-01	Citronellsäure	3
333902277	4.8	2.09E-04	Citronellsäure	2
116052531	4.4	7.02E-03	Citronellsäure	2
339494273	1.2	6.17E-01	Oktansäure	2
327479614	3.6	3.14E-02	Oktansäure	2
88798958	1.0	7.19E-01	Citronellsäure	2
56459460	1.6	2.81E-01	Citronellsäure	2
356463779	1.3	4.24E-01	Citronellsäure	1
379708778	1.9	8.80E-02	Oktansäure	3
302186668	1.2	5.58E-01	Oktansäure	2
359394219	1.1	9.26E-01	Oktansäure	2
77456641	1.2	2.45E-01	Citronellsäure	2
222478051	5.0	1.22E-01	Citronellsäure	3
212288600	5.4	1.36E-01	Citronellsäure	1
239907751	4.6	9.78E-02	Citronellsäure	1
347305107	1.1	6.12E-01	Citronellsäure	2
222477179	1.4	2.93E-01	Citronellsäure	1
254240896	1.4	3.75E-01	Oktansäure	2
222477799	806867.6	1.22E-01	Citronellsäure	1

gi Nummer	Locus-Tag	Gen	Protein-Name	Regulationsfa	p-Wert	Hochreguliert in	pI	MW (Da)	Zahl identifizierter Peptide	Lokalisation	COG ID	COG Funktion	COG Funktion 2
15595199	PA0001	dnaA	chromosomal replication initiator protein DnaA	2.7	1.01E-03	Oktansaeure	8.9	57722	10	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15595200	PA0002	dnaN	DNA polymerase III, beta chain	1.2	2.53E-01	Citronellol	4.9	40694	22	Cytoplasmic	COG0592	DNA replication, recombination, and repair	
15595202	PA0004	gyrB	DNA gyrase subunit B	1.1	5.08E-01	Oktansaeure	5.7	90188	33	Periplasmic	COG0187	DNA replication, recombination, and repair	
15595204	PA0006		conserved hypothetical protein	3.9	8.98E-02	Citronellol	4.5	19115	2	Cytoplasmic	COG0241	Amino acid transport and metabolism	
15595205	PA0007		hypothetical protein	4.0	5.18E-03	Citronellol	7.9	61755	21	Unknown			
15595206	PA0008	glyS	glycyl-tRNA synthetase beta chain	1.4	4.64E-02	Oktansaeure	4.8	73973	30	Periplasmic	COG0751	Translation, ribosomal structure and biogenesis	
15595207	PA0009	glyQ	glycyl-tRNA synthetase alpha chain	1.2	4.97E-01	Oktansaeure	4.7	36109	10	Periplasmic	COG0752	Translation, ribosomal structure and biogenesis	
15595216	PA0018	fmt	methionyl-tRNA formyltransferase	1.5	1.37E-02	Citronellol	7.0	33028	11	Cytoplasmic	COG0223	Translation, ribosomal structure and biogenesis	
15595217	PA0019	def	polypeptide deformylase	1.0	8.06E-01	Oktansaeure	4.7	19365	6	Cytoplasmic	COG0242	Translation, ribosomal structure and biogenesis	
15595218	PA0020		hypothetical protein	1.1	6.25E-01	Citronellol	9.4	37586	7	Periplasmic	COG1652	Function unknown	
15595220	PA0022		conserved hypothetical protein	1.2	2.03E-01	Oktansaeure	6.5	20371	2	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15595221	PA0023	qor	quinone oxidoreductase	1.6	6.23E-02	Citronellol	6.3	35095	14	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15595222	PA0024	hemF	coproporphyrinogen III oxidase, aerobic	1.3	1.58E-01	Citronellol	5.8	34774	10	Periplasmic	COG0408	Coenzyme metabolism	
15595223	PA0025	aroE	shikimate dehydrogenase	1.1	5.38E-01	Citronellol	5.5	29484	4	Cytoplasmic	COG0169	Amino acid transport and metabolism	
15595233	PA0035	trpA	tryptophan synthase alpha chain	1.3	1.78E-01	Oktansaeure	5.0	28488	7	Periplasmic	COG0159	Amino acid transport and metabolism	
15595234	PA0036	trpB	tryptophan synthase beta chain	1.1	5.81E-01	Citronellol	6.3	43680	12	Cytoplasmic	COG0133	Amino acid transport and metabolism	
15595236	PA0038		hypothetical protein	1.1	4.51E-01	Oktansaeure	7.1	7863	4	Unknown	COG3360	Function unknown	
15595239	PA0041		probable hemagglutinin	7.4	6.63E-05	Citronellol	5.1	361591	4	Extracellular			
15595243	PA0045		hypothetical protein	1.5	4.04E-01	Citronellol	9.6	24395	2	Periplasmic	COG1462	Cell envelope biogenesis, outer membrane	
15595252	PA0054		conserved hypothetical protein	2.3	1.12E-01	Oktansaeure	9.6	20024	3	Unknown	COG1859	Translation, ribosomal structure and biogenesis	
15595253	PA0055		hypothetical protein	1.8	8.20E-02	Citronellol	5.7	18433	11	Cytoplasmic	COG3812	Function unknown	
15595257	PA0059	osmC	osmotically inducible protein OsmC	35.3	9.65E-02	Citronellol	6.3	15610	2	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
15595264	PA0066		conserved hypothetical protein	13.4	2.12E-03	Citronellol	6.6	19198	4	Cytoplasmic	COG0663	General function prediction only	
15595265	PA0067	prlC	oligopeptidase A	1.3	8.89E-02	Oktansaeure	4.9	76011	28	Periplasmic	COG0339	Amino acid transport and metabolism	
15595268	PA0070	tagQ1	TagQ1	1.3	9.45E-01	Citronellol	8.9	31716	5	Periplasmic			
15595273	PA0075	pppA	PppA	1.1	8.38E-01	Citronellol	6.2	25904	8	Unknown	COG0631	Signal transduction mechanisms	
15595274	PA0076	tagF1	TagF1	1.4	7.55E-01	Citronellol	4.4	23856	3	Unknown	COG3913	Function unknown	
15595277	PA0079	tssK1	TssK1	1.4	1.42E-01	Oktansaeure	6.1	48275	11	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15595280	PA0082	tssA1	TssA1	2.6	3.75E-02	Oktansaeure	4.1	36647	2	Cytoplasmic	COG3515	Intracellular trafficking, secretion, and vesicular transport	
15595281	PA0083	tssB1	TssB1	1.0	9.03E-01	Oktansaeure	4.9	18785	18	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15595282	PA0084	tssC1	TssC1	1.8	7.80E-04	Oktansaeure	5.0	55771	38	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15595283	PA0085	hcp1	Hcp1	1.2	4.57E-01	Citronellol	6.8	17415	12	Periplasmic	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595284	PA0086	tagJ1	TagJ1	1.5	8.96E-01	Oktansaeure	4.4	30361	5	Cytoplasmic	COG4455	General function prediction only	
15595286	PA0088	tssF1	TssF1	8.7	5.14E-04	Oktansaeure	7.4	69483	6	Cytoplasmic	COG3519	Intracellular trafficking, secretion, and vesicular transport	
15595288	PA0090	clpV1	ClpV1	3.9	1.28E-02	Oktansaeure	5.3	98737	34	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595289	PA0091	vgrG1	VgrG1	3.3	4.58E-03	Citronellol	6.4	72012	18	Extracellular	COG3501	Function unknown	
15595291	PA0093		hypothetical protein	4.0	1.31E-02	Citronellol	8.9	44738	6	Cytoplasmic Membrane	COG4104	Function unknown	
15595292	PA0094		hypothetical protein	1.0	8.59E-01	Oktansaeure	6.8	16456	4	Unknown	COG5435	Function unknown	
15595298	PA0100		hypothetical protein	1.2	4.51E-01	Oktansaeure	4.1	33723	5	Unknown			
15595300	PA0102		probable carbonic anhydrase	1.1	7.07E-01	Oktansaeure	6.7	26622	10	Cytoplasmic	COG0288	Inorganic ion transport and metabolism	
15595313	PA0115		conserved hypothetical protein	2.1	1.74E-02	Citronellol	6.3	17085	5	Cytoplasmic	COG2153	General function prediction only	
15595316	PA0118		hypothetical protein	2.2	3.14E-02	Oktansaeure	6.8	21473	4	Unknown	COG3917	Secondary metabolites biosynthesis, transport, and catabolism	
15595320	PA0122	rahU	rahU	1.9	1.34E-01	Citronellol	4.4	14579	8	Extracellular			
15595324	PA0126		hypothetical protein	3.4	1.38E-01	Oktansaeure	8.0	22367	2	Outer Membrane Vesicle			
15595325	PA0127		hypothetical protein	2.1	7.06E-02	Citronellol	8.8	17611	2	Unknown	COG5608	Defense mechanisms	
15595328	PA0130	bauC	3-Oxopropanoate dehydrogenase	1.1	4.95E-01	Citronellol	6.0	53323	8	Cytoplasmic	COG1012	Energy production and conversion	
15595337	PA0139	ahpC	alkyl hydroperoxide reductase subunit C	1.1	7.30E-01	Citronellol	6.3	20541	13	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15595338	PA0140	ahpF	alkyl hydroperoxide reductase subunit F	2.9	1.23E-01	Oktansaeure	5.0	55835	3	Cytoplasmic	COG3634	Posttranslational modification, protein turnover, chaperones	
119167454	PA0143	nuh	purine nucleosidase Nuh	1.1	9.03E-01	Oktansaeure	7.7	37542	14	Periplasmic	COG1957	Nucleotide transport and metabolism	
15595342	PA0144		hypothetical protein	1.2	4.63E-01	Oktansaeure	8.4	22431	8	Unknown	COG3613	Nucleotide transport and metabolism	
15595343	PA0145		hypothetical protein	1.7	2.45E-02	Citronellol	4.4	18448	2	Cytoplasmic	COG3613	Nucleotide transport and metabolism	
15595346	PA0148		adenine deaminase	1.2	7.76E-01	Citronellol	4.9	36163	6	Cytoplasmic	COG1816	Nucleotide transport and metabolism	
15595353	PA0155	pcaR	transcriptional regulator PcaR	2.4	7.71E-03	Oktansaeure	7.6	30581	2	Cytoplasmic	COG1414	Transcription	
15595357	PA0159		probable transcriptional regulator	2.7	3.18E-01	Oktansaeure	6.0	34683	3	Cytoplasmic	COG0583	Transcription	
15595362	PA0164		probable gamma-glutamyltranspeptidase	1.3	4.81E-01	Citronellol	6.5	58453	3	Periplasmic	COG0405	Amino acid transport and metabolism	
15595368	PA0170		hypothetical protein	3.0	1.27E-03	Oktansaeure	4.3	14553	4	Cytoplasmic			
15595369	PA0171		hypothetical protein	1.0	7.78E-01	Oktansaeure	7.1	19800	13	Cytoplasmic			
15595372	PA0174		conserved hypothetical protein	3.8	8.89E-02	Citronellol	8.5	22206	3	Cytoplasmic	COG1871	Cell motility and secretion	Signal transduction mechanisms
15595374	PA0176	aer2	aerotaxis transducer Aer2	1.9	1.47E-01	Citronellol	4.8	72591	26	Cytoplasmic	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595375	PA0177		probable purine-binding chemotaxis protein	3.0	4.29E-02	Citronellol	4.3	17487	3	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595376	PA0178		probable two-component sensor	1.6	7.29E-01	Citronellol	4.5	68931	5	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595380	PA0182		probable short-chain dehydrogenase	2.0	2.36E-02	Citronellol	4.7	25230	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600764	PA0195	pntAA	putative NAD(P) transhydrogenase, subunit alpha part 1	1.1	7.59E-01	Citronellol	5.9	38650	24	Cytoplasmic Membrane	COG3288	Energy production and conversion	
15595393	PA0196	pntB	pyridine nucleotide transhydrogenase, beta subunit	1.3	4.15E-01	Citronellol	7.3	49947	3	Cytoplasmic Membrane	COG1282	Energy production and conversion	
15595400	PA0203		probable binding protein component of ABC transporter	1.1	6.71E-01	Citronellol	6.3	37860	3	Periplasmic	COG0687	Amino acid transport and metabolism	
15595408	PA0211	mdcD	malonate decarboxylase beta subunit	5.1	3.87E-03	Citronellol	4.5	30343	10	Cytoplasmic	COG0777	Lipid metabolism	
15595409	PA0212	mdcE	malonate decarboxylase gamma subunit	6.2	1.78E-02	Citronellol	7.1	28496	9	Cytoplasmic			
15595422	PA0225		probable transcriptional regulator	2.2	3.98E-01	Oktansaeure	6.9	19993	2	Cytoplasmic	COG1476	Transcription	
15595424	PA0227		probable CoA transferase, subunit B	3.7	6.23E-02	Citronellol	5.4	27314	4	Cytoplasmic	COG2057	Lipid metabolism	
15595427	PA0230	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	1.9	2.35E-01	Citronellol	6.2	49121	6	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15595428	PA0231	pcaD	beta-ketoadipate enol-lactone hydrolase	1.6	3.21E-01	Citronellol	5.1	27985	3	Unknown	COG0596	General function prediction only	
15595429	PA0232	pcaC	gamma-carboxymuconolactone decarboxylase	3.4	3.02E-03	Citronellol	7.1	15084	4	Unknown	COG0599	Function unknown	
15595444	PA0247	pobA	p-hydroxybenzoate hydroxylase	3.9	1.26E-01	Citronellol	6.8	44323	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15595456	PA0259		hypothetical protein	4.9	8.22E-05	Oktansaeure	5.0	52444	6	Unknown			
15595457	PA0260		hypothetical protein	161.8	2.40E-02	Oktansaeure	7.0	78202	2	Unknown			
15595460	PA0263	hcpC	secreted protein Hcp	23.4	4.72E-04	Oktansaeure	5.8	19091	9	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15595462	PA0265	gabD	succinate-semialdehyde dehydrogenase	1.1	7.50E-01	Oktansaeure	5.4	51622	28	Periplasmic	COG1012	Energy production and conversion	
15595463	PA0266	gabT	4-aminobutyrate aminotransferase	1.3	3.29E-03	Oktansaeure	6.4	45220	20	Periplasmic	COG0160	Amino acid transport and metabolism	
15595471	PA0274		hypothetical protein	12.1	3.88E-02	Citronellol	8.8	28498	3	Outer Membrane			
15595474	PA0277		conserved hypothetical protein	1.6	1.19E-01	Oktansaeure	6.5	26626	7	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones	
15595480	PA0283	sbp	sulfate-binding protein precursor	5.5	8.32E-03	Oktansaeure	9.0	36433	17	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15595488	PA0291	oprE	Anaerobically-induced outer membrane porin OprE precursor	2.8	4.97E-02	Oktansaeure	9.1	49667	5	Periplasmic			
15595489	PA0292	aguA	agmatine deiminase	1.2	4.77E-01	Citronellol	4.6	41191	6	Cytoplasmic	COG2957	Amino acid transport and metabolism	
15595493	PA0296	spuI	Glutamylpolyamine synthetase	1.2	3.87E-01	Citronellol	4.6	50907	11	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595494	PA0297	spuA	probable glutamine amidotransferase	2.3	1.93E-02	Citronellol	6.4	26477	3	Unknown	COG2071	General function prediction only	
15595495	PA0298	spuB	Glutamylpolyamine synthetase	3.2	7.59E-02	Oktansaeure	5.0	50965	7	Cytoplasmic	COG0174	Amino acid transport and metabolism	
15595496	PA0299	spuC	Polyamine:pyruvate transaminase	1.4	1.56E-01	Citronellol	6.0	50453	19	Cytoplasmic	COG0161	Coenzyme metabolism	
15595497	PA0300	spuD	polyamine transport protein	1.6	8.07E-02	Citronellol	7.6	40629	16	Periplasmic	COG0687	Amino acid transport and metabolism	
15595498	PA0301	spuE	polyamine transport protein	1.0	9.53E-01	Citronellol	5.5	40069	16	Periplasmic	COG0687	Amino acid transport and metabolism	
15595505	PA0308		hypothetical protein	1.2	4.08E-01	Oktansaeure	6.8	38245	2	Cytoplasmic	COG2267	Lipid metabolism	
15595506	PA0309		hypothetical protein	1.1	9.01E-01	Citronellol	7.6	27021	7	Unknown			
15595511	PA0314		L-cysteine transporter of ABC system FliY	2.4	1.07E-02	Citronellol	9.7	28005	10	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15595512	PA0315		hypothetical protein	5.2	2.33E-02	Citronellol	7.2	15463	8	Unknown			
15595513	PA0316	serA	D-3-phosphoglycerate dehydrogenase	1.1	6.90E-01	Citronellol	6.5	44216	20	Periplasmic	COG0111	Amino acid transport and metabolism	
15595514	PA0317		hypothetical protein	1.8	1.63E-02	Citronellol	4.9	51286	17	Periplasmic	COG0277	Energy production and conversion	
15595515	PA0318		conserved hypothetical protein	1.5	1.13E-01	Oktansaeure	5.3	23843	8	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism	

15595520	PA0323		probable binding protein component of ABC transporter	5.1	4.51E-04	Citronellol	6.8	38901	5	Periplasmic	COG0687	Amino acid transport and metabolism	
15595527	PA0330	rpiA	ribose 5-phosphate isomerase	1.4	4.61E-02	Citronellol	5.3	23721	11	Cytoplasmic	COG0120	Carbohydrate transport and metabolism	
15595528	PA0331	ilvA1	threonine dehydratase, biosynthetic	2.3	6.31E-02	Citronellol	6.5	55351	12	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15595532	PA0335		hypothetical protein	1.5	2.83E-02	Citronellol	4.5	24353	15	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15595533	PA0336	ygdP	Nudix hydrolase YgdP	1.2	2.33E-01	Oktansaeure	9.5	18726	5	Cytoplasmic	COG0494	DNA replication, recombination, and repair	General function prediction only
15595534	PA0337	ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	1.3	1.28E-02	Oktansaeure	5.6	83606	25	Cytoplasmic	COG3605	Signal transduction mechanisms	
15595536	PA0339		hypothetical protein	1.3	1.53E-01	Citronellol	6.7	26527	3	Unknown	COG3332	Function unknown	
15595539	PA0342	thyA	thymidylate synthase	1.5	8.14E-02	Citronellol	6.5	30016	7	Cytoplasmic	COG0207	Nucleotide transport and metabolism	
15595547	PA0350	folA	dihydrofolate reductase	1.4	2.50E-02	Oktansaeure	5.3	18203	4	Unknown	COG0262	Coenzyme metabolism	
15595548	PA0351		conserved hypothetical protein	2.6	1.16E-02	Citronellol	6.7	17217	2	Cytoplasmic	COG0622	General function prediction only	
15595550	PA0353	ilvD	dihydroxy-acid dehydratase	1.0	9.56E-01	Oktansaeure	6.0	65160	30	Periplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15595552	PA0355	pfpI	protease PfpI	2.7	1.50E-01	Citronellol	5.0	19246	9	Cytoplasmic	COG0693	General function prediction only	
15595553	PA0356		hypothetical protein	1.2	3.95E-01	Oktansaeure	5.3	30360	4	Unknown	COG1639	Signal transduction mechanisms	
15595560	PA0363	coaD	phosphopantetheine adenylyltransferase	1.3	1.68E-01	Citronellol	9.0	17771	10	Cytoplasmic	COG0669	Coenzyme metabolism	
15595561	PA0364		probable oxidoreductase	10.9	4.17E-04	Citronellol	7.0	57805	8	Unknown	COG2303	Amino acid transport and metabolism	
15595563	PA0366		probable aldehyde dehydrogenase	10.7	5.08E-05	Citronellol	9.2	52876	16	Cytoplasmic	COG1012	Energy production and conversion	
15595564	PA0367		probable transcriptional regulator	8.4	1.80E-04	Citronellol	5.9	24540	3	Cytoplasmic	COG1309	Transcription	
15595570	PA0373	ftsY	signal recognition particle receptor FtsY	3.5	7.45E-02	Oktansaeure	4.5	48391	7	Cytoplasmic	COG0552	Intracellular trafficking and secretion	
15595578	PA0381	thiG	thiamine biosynthesis protein, thiazole moiety	1.0	9.84E-01	Citronellol	4.8	28234	10	Cytoplasmic	COG2022	Nucleotide transport and metabolism	
15595579	PA0382	micA	DNA mismatch repair protein MicA	1.6	2.23E-02	Oktansaeure	8.3	25331	2	Cytoplasmic	COG0220	General function prediction only	
15595580	PA0383		conserved hypothetical protein	3.0	2.20E-04	Citronellol	8.3	50243	6	Unknown			
15595584	PA0387		conserved hypothetical protein	1.2	9.10E-01	Citronellol	6.1	21242	7	Cytoplasmic	COG0127	Nucleotide transport and metabolism	
15595585	PA0388		hypothetical protein	6.6	2.68E-01	Citronellol	7.4	15303	2	Periplasmic			
15595589	PA0392		conserved hypothetical protein	1.3	6.36E-01	Citronellol	10.1	21745	2	Cytoplasmic Membrane			
15595590	PA0393	proC	pyrroline-5-carboxylate reductase	1.0	8.91E-01	Oktansaeure	4.5	28094	10	Cytoplasmic	COG0345	Amino acid transport and metabolism	
15595591	PA0394		conserved hypothetical protein	1.7	3.69E-02	Citronellol	6.7	24505	5	Cytoplasmic	COG0325	General function prediction only	
15595592	PA0395	pilT	twitching motility protein PilT	1.2	1.14E-01	Citronellol	6.9	38021	7	Cytoplasmic	COG2805	Cell motility and secretion	Intracellular trafficking and secretion
15595596	PA0399		cystathionine beta-synthase	1.2	2.17E-01	Oktansaeure	5.5	49170	21	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15595597	PA0400		probable cystathionine gamma-lyase	1.2	4.05E-01	Oktansaeure	6.6	42786	9	Cytoplasmic	COG0626	Amino acid transport and metabolism	
15595598	PA0401		noncatalytic dihydroorotase-like protein	1.0	7.80E-01	Citronellol	5.8	44150	9	Periplasmic	COG0044	Nucleotide transport and metabolism	
15595599	PA0402	pyrB	aspartate carbamoyltransferase	1.2	5.00E-01	Oktansaeure	6.8	36629	17	Periplasmic	COG0540	Nucleotide transport and metabolism	
15595600	PA0403	pyrR	transcriptional regulator PyrR	1.2	9.26E-02	Citronellol	5.7	18676	6	Cytoplasmic	COG2065	Nucleotide transport and metabolism	
15595604	PA0407	gshB	glutathione synthetase	1.0	7.02E-01	Citronellol	5.8	35705	19	Periplasmic	COG0189	Coenzyme metabolism	Translation, ribosomal structure and biogenesis
15595605	PA0408	pilG	twitching motility protein PilG	18.8	1.18E-03	Oktansaeure	7.4	14718	4	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595607	PA0410	pilI	twitching motility protein PilI	1.9	1.66E-01	Oktansaeure	6.6	19934	2	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15595608	PA0411	pilJ	twitching motility protein PilJ	1.4	3.99E-01	Oktansaeure	4.4	72528	3	Outer Membrane Vesicle	COG0840	Cell motility and secretion	Signal transduction mechanisms
15595610	PA0413	chpA	component of chemotactic signal transduction system	1.4	3.58E-01	Oktansaeure	4.2	268573	24	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15595612	PA0415	chpC	probable chemotaxis protein	2.8	4.25E-02	Oktansaeure	4.7	17625	4	Unknown			
15595615	PA0418		hypothetical protein	1.8	1.88E-01	Oktansaeure	5.6	52140	5	Cytoplasmic			
15595617	PA0420	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1.5	9.90E-02	Citronellol	6.3	52478	10	Cytoplasmic	COG0161	Coenzyme metabolism	
15595620	PA0423	pasP	PasP	1.9	1.55E-01	Oktansaeure	6.5	20776	20	Periplasmic	COG2353	Function unknown	
15595621	PA0424	mexR	multidrug resistance operon repressor MexR	3.4	1.09E-02	Citronellol	5.9	16964	2	Cytoplasmic	COG1846	Transcription	
15595622	PA0425	mexA	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion pro	1.8	4.56E-03	Oktansaeure	9.2	40969	3	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15595623	PA0426	mexB	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB	1.9	2.59E-03	Citronellol	5.4	112790	8	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15595624	PA0427	oprM	Major intrinsic multiple antibiotic resistance efflux outer membrane protein Opr	1.2	6.75E-01	Oktansaeure	5.3	52598	6	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15595626	PA0429		hypothetical protein	5.4	5.06E-02	Oktansaeure	7.0	40872	2	Cytoplasmic			
15595627	PA0430	metF	5,10-methylenetetrahydrofolate reductase	1.3	2.99E-01	Citronellol	6.5	32196	17	Periplasmic	COG0685	Amino acid transport and metabolism	
15595628	PA0431		hypothetical protein	1.3	5.87E-01	Citronellol	6.8	20639	2	Unknown	COG0317	Signal transduction mechanisms	Transcription
15595629	PA0432	sahH	S-adenosyl-L-homocysteine hydrolase	1.5	5.78E-02	Citronellol	6.0	51400	32	Periplasmic	COG0499	Coenzyme metabolism	
15595631	PA0434		hypothetical protein	1.2	7.16E-01	Citronellol	5.8	81304	13	Periplasmic	COG1629	Inorganic ion transport and metabolism	
15595634	PA0437	codA	cytosine deaminase	1.5	9.60E-02	Citronellol	6.0	47074	6	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15595643	PA0446		conserved hypothetical protein	2.1	2.37E-02	Citronellol	5.3	43847	5	Cytoplasmic	COG1804	Energy production and conversion	
15595644	PA0447	gcdH	glutaryl-CoA dehydrogenase	1.6	6.46E-02	Citronellol	6.1	43311	7	Cytoplasmic	COG1960	Lipid metabolism	
15595646	PA0449		hypothetical protein	1.5	2.95E-02	Citronellol	10.5	19808	8	Cytoplasmic	COG1607	Lipid metabolism	
15595656	PA0459		probable ClpA/B protease ATP binding subunit	3.5	9.90E-02	Citronellol	6.7	94143	12	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15595659	PA0462		hypothetical protein	2.0	1.43E-01	Citronellol	10.6	26230	11	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones	
15595664	PA0467		conserved hypothetical protein	1.5	1.04E-01	Citronellol	7.5	23301	6	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15595665	PA0468		hypothetical protein	2.2	1.08E-03	Oktansaeure	4.8	33594	4	Periplasmic	COG4257	Defense mechanisms	
15595666	PA0469		hypothetical protein	1.2	6.10E-01	Citronellol	4.7	32137	12	Cytoplasmic			
15595670	PA0473		probable glutathione S-transferase	5.1	1.35E-05	Citronellol	5.8	28294	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15595675	PA0478		probable N-acetyltransferase	2.2	2.64E-02	Citronellol	4.6	18109	4	Cytoplasmic	COG0456	General function prediction only	
15595679	PA0482	glcB	malate synthase G	1.9	3.41E-02	Oktansaeure	5.5	78659	76	Periplasmic	COG2225	Energy production and conversion	
15595681	PA0484		conserved hypothetical protein	3.9	2.13E-02	Citronellol	4.5	18553	4	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15595684	PA0487		probable molybdenum transport regulator	3.7	2.16E-01	Oktansaeure	9.2	26948	2	Cytoplasmic	COG2005	General function prediction only	
15595697	PA0500	bioB	biotin synthase	2.9	7.22E-01	Oktansaeure	6.0	39113	6	Cytoplasmic	COG0502	Coenzyme metabolism	
15595699	PA0502		probable biotin biosynthesis protein bioH	2.2	4.99E-03	Citronellol	4.3	26494	2	Cytoplasmic	COG0596	General function prediction only	
15595700	PA0503		probable biotin synthesis protein BioC	3.9	1.11E-03	Oktansaeure	9.0	29712	2	Unknown	COG2226	Coenzyme metabolism	
15595701	PA0504	bioD	dethiobiotin synthase	1.2	5.70E-01	Citronellol	5.3	23337	7	Cytoplasmic	COG0132	Coenzyme metabolism	
15595703	PA0506		probable acyl-CoA dehydrogenase	1.3	3.18E-01	Citronellol	5.8	65358	40	Periplasmic	COG1960	Lipid metabolism	
15595704	PA0507		probable acyl-CoA dehydrogenase	4.6	1.36E-01	Citronellol	6.4	64349	4	Cytoplasmic	COG1960	Lipid metabolism	
15595705	PA0508		probable acyl-CoA dehydrogenase	1.2	5.66E-01	Citronellol	5.1	63628	49	Cytoplasmic	COG1960	Lipid metabolism	
15595716	PA0519	nirS	nitrite reductase precursor	32.7	2.04E-04	Oktansaeure	8.2	62653	4	Periplasmic	COG2010	Energy production and conversion	
15595732	PA0535		probable transcriptional regulator	2.4	5.08E-02	Oktansaeure	4.9	20231	2	Cytoplasmic	COG1396	Transcription	
15595734	PA0537		conserved hypothetical protein	2.2	6.08E-02	Citronellol	8.9	22180	8	Outer Membrane Vesicle	COG1704	Function unknown	
15595743	PA0546	metK	methionine adenosyltransferase	1.1	8.44E-01	Citronellol	5.2	42709	25	Cytoplasmic	COG0192	Coenzyme metabolism	
15595745	PA0548	tktA	transketolase	1.2	4.36E-02	Oktansaeure	5.0	72220	37	Periplasmic	COG0021	Carbohydrate transport and metabolism	
15595747	PA0550		conserved hypothetical protein	1.1	7.10E-01	Citronellol	5.4	29834	9	Cytoplasmic	COG3622	Carbohydrate transport and metabolism	
15595748	PA0551	epd	D-erythrose 4-phosphate dehydrogenase	2.0	1.96E-01	Citronellol	5.8	38743	4	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15595749	PA0552	pgk	phosphoglycerate kinase	1.2	3.14E-01	Citronellol	5.1	40404	22	Periplasmic	COG0126	Carbohydrate transport and metabolism	
15595752	PA0555	fda	fructose-1,6-bisphosphate aldolase	1.4	1.87E-01	Citronellol	5.3	38574	27	Cytoplasmic	COG0191	Carbohydrate transport and metabolism	
15595755	PA0558		conserved hypothetical protein	1.5	9.11E-03	Citronellol	6.2	27987	14	Cytoplasmic	COG2226	Coenzyme metabolism	
15595759	PA0562		probable hydrolase	3.1	2.79E-02	Oktansaeure	5.4	24232	8	Cytoplasmic	COG0637	General function prediction only	
15595765	PA0568		hypothetical protein	1.8	1.10E-01	Citronellol	4.2	17683	3	Cytoplasmic			
15595768	PA0571		hypothetical protein	1.6	2.38E-01	Oktansaeure	5.0	22501	5	Unknown			
15595773	PA0576	rpoD	sigma factor RpoD	1.4	3.09E-02	Oktansaeure	4.6	69643	27	Outer Membrane Vesicle	COG0568	Transcription	
15595775	PA0578		conserved hypothetical protein	2.8	7.42E-02	Citronellol	6.0	16842	2	Cytoplasmic	COG1610	Function unknown	
15595777	PA0580	gcp	O-sialoglycoprotein endopeptidase	2.8	9.78E-03	Oktansaeure	6.2	36561	4	Extracellular	COG0533	Posttranslational modification, protein turnover, chaperones	
15595780	PA0583		hypothetical protein	1.3	4.42E-01	Oktansaeure	5.6	20091	4	Cytoplasmic	COG0801	Coenzyme metabolism	
15595783	PA0586		conserved hypothetical protein	1.4	2.97E-01	Citronellol	5.1	60814	15	Cytoplasmic	COG2719	Function unknown	
15595784	PA0587		conserved hypothetical protein	1.4	2.62E-01	Citronellol	7.8	48742	13	Cytoplasmic	COG2718	Function unknown	
15595785	PA0588		conserved hypothetical protein	1.0	8.61E-01	Oktansaeure	5.5	73722	47	Outer Membrane Vesicle	COG2766	Signal transduction mechanisms	
15595787	PA0590	apaH	bis(5'-nucleosyl)-tetraphosphatase	1.2	2.42E-01	Citronellol	7.2	32019	4	Cytoplasmic			
15595789	PA0592	ksgA	rRNA (adenine-N6,N6)-dimethyltransferase	2.8	5.30E-02	Oktansaeure	7.4	30058	4	Cytoplasmic	COG0030	Translation, ribosomal structure and biogenesis	
15595790	PA0593	pdxA	pyridoxal phosphate biosynthetic protein PdxA	1.1	4.91E-01	Oktansaeure	6.6	34891	9	Cytoplasmic	COG1995	Coenzyme metabolism	
15595791	PA0594	surA	peptidyl-prolyl cis-trans isomerase SurA	1.1	6.52E-01	Oktansaeure	5.6	48441	24	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones	
15595792	PA0595	ostA	organic solvent tolerance protein OstA precursor	1.1	4.22E-01	Citronellol	5.3	104271	3	Periplasmic	COG1452	Cell envelope biogenesis, outer membrane	
15595793	PA0596		hypothetical protein	1.1	5.61E-01	Citronellol	5.1	38185	6	Cytoplasmic	COG3178	General function prediction only	

15595794	PA0597		probable nucleotidyl transferase	1.4	1.74E-02	Oktansaeure	6.1	24149	4	Cytoplasmic	COG1208	Cell envelope biogenesis, outer membrane	Translation, ribosomal structure and biogenesis
15595798	PA0601		probable two-component response regulator	1.5	5.94E-01	Citronellol	6.5	22868	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15595801	PA0604		probable binding protein component of ABC transporter	2.8	3.07E-02	Citronellol	5.6	38167	10	Periplasmic	COG0687	Amino acid transport and metabolism	
15595804	PA0607	rpe	ribulose-phosphate 3-epimerase	1.5	2.21E-02	Oktansaeure	5.1	24096	8	Cytoplasmic	COG0036	Carbohydrate transport and metabolism	
15595806	PA0609	trpE	anthranilate synthetase component I	1.2	3.86E-01	Citronellol	4.7	54555	15	Cytoplasmic	COG0147	Amino acid transport and metabolism	Coenzyme metabolism
15595830	PA0633		hypothetical protein	2.4	3.91E-01	Oktansaeure	4.7	17539	2	Outer Membrane Vesicle			
15595846	PA0649	trpG	anthranilate synthase component II	1.7	1.86E-01	Oktansaeure	6.0	22046	3	Cytoplasmic	COG0512	Amino acid transport and metabolism	Coenzyme metabolism
15595847	PA0650	trpD	anthranilate phosphoribosyltransferase	1.8	6.46E-02	Oktansaeure	5.6	37384	5	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15595848	PA0651	trpC	indole-3-glycerol-phosphate synthase	1.6	6.55E-02	Citronellol	4.6	30315	9	Cytoplasmic	COG0134	Amino acid transport and metabolism	
15595850	PA0653		conserved hypothetical protein	2.4	1.50E-02	Citronellol	6.4	15237	5	Cytoplasmic	COG1765	Posttranslational modification, protein turnover, chaperones	
15595852	PA0655		hypothetical protein	1.4	9.07E-02	Oktansaeure	5.3	23644	6	Unknown	COG2941	Coenzyme metabolism	
15595857	PA0660		hypothetical protein	1.9	1.72E-02	Citronellol	6.2	34814	21	Cytoplasmic	COG2070	General function prediction only	
15595859	PA0662	argC	N-acetyl-gamma-glutamyl-phosphate reductase	1.6	1.48E-01	Citronellol	6.7	36684	15	Cytoplasmic	COG0002	Amino acid transport and metabolism	
15595861	PA0664		hypothetical protein	1.9	3.65E-02	Oktansaeure	5.6	14790	2	Cytoplasmic	COG1664	Cell envelope biogenesis, outer membrane	
15595862	PA0665		conserved hypothetical protein	1.2	8.01E-01	Citronellol	4.0	12484	2	Cytoplasmic	COG0316	Posttranslational modification, protein turnover, chaperones	
15595863	PA0666		conserved hypothetical protein	1.3	3.94E-01	Citronellol	5.2	39087	2	Cytoplasmic	COG2377	Posttranslational modification, protein turnover, chaperones	
15595865	PA0668	tyrZ	tyrosyl-tRNA synthetase 2	1.5	2.37E-01	Citronellol	5.6	44129	22	Periplasmic	COG0162	Translation, ribosomal structure and biogenesis	
15595869	PA0672	hemO	heme oxygenase	3.7	1.54E-02	Oktansaeure	4.8	21953	10	Unknown	COG3230	Inorganic ion transport and metabolism	
15595901	PA0704		probable amidase	4.7	4.02E-03	Citronellol	6.9	50605	4	Cytoplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15595903	PA0706	cat	chloramphenicol acetyltransferase	1.2	3.57E-01	Oktansaeure	6.1	23524	3	Unknown	COG0110	General function prediction only	
15595912	PA0715		hypothetical protein	1.6	7.30E-03	Citronellol	9.9	36589	7	Cytoplasmic	COG3344	DNA replication, recombination, and repair	
15595938	PA0741		conserved hypothetical protein	1.2	5.35E-01	Citronellol	6.6	22687	7	Unknown	COG2910	General function prediction only	
15595940	PA0743		probable 3-hydroxyisobutyrate dehydrogenase	2.3	1.90E-01	Citronellol	5.3	30754	3	Cytoplasmic	COG2084	Lipid metabolism	
15595941	PA0744		probable enoyl-CoA hydratase/isomerase	2.2	1.41E-01	Citronellol	5.1	40589	5	Cytoplasmic	COG1024	Lipid metabolism	
15595942	PA0745		probable enoyl-CoA hydratase/isomerase	1.5	1.90E-01	Citronellol	6.4	29904	15	Cytoplasmic	COG1024	Lipid metabolism	
15595943	PA0746		probable acyl-CoA dehydrogenase	2.8	9.37E-02	Citronellol	5.3	42553	2	Cytoplasmic	COG1960	Lipid metabolism	
15595944	PA0747		probable aldehyde dehydrogenase	1.7	2.81E-01	Citronellol	6.1	54564	4	Cytoplasmic	COG1012	Energy production and conversion	
15595947	PA0750	ung	uracil-DNA glycosylase	1.0	6.74E-01	Oktansaeure	8.2	26010	7	Cytoplasmic	COG0692	DNA replication, recombination, and repair	
15595951	PA0754		hypothetical protein	1.4	3.20E-01	Citronellol	5.5	34918	17	Unknown	COG3181	Function unknown	
15595953	PA0756		probable two-component response regulator	1.3	3.35E-01	Oktansaeure	5.2	24431	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15595955	PA0758		hypothetical protein	1.7	4.43E-03	Oktansaeure	4.7	30875	9	Cytoplasmic	COG1639	Signal transduction mechanisms	
15595956	PA0759		conserved hypothetical protein	1.3	3.93E-02	Oktansaeure	5.2	33667	15	Unknown	COG0354	General function prediction only	
15595958	PA0761	nadB	L-aspartate oxidase	1.2	1.15E-01	Oktansaeure	6.3	60004	7	Cytoplasmic	COG0029	Coenzyme metabolism	
15595959	PA0762	algU	sigma factor AlgU	1.8	1.50E-01	Oktansaeure	5.4	22196	7	Cytoplasmic	COG1595	Transcription	
15595961	PA0764	mucB	negative regulator for alginate biosynthesis MucB	1.2	4.31E-01	Citronellol	6.1	34572	4	Periplasmic	COG3026	Signal transduction mechanisms	
15595963	PA0766	mucD	serine protease MucD precursor	1.7	5.08E-02	Oktansaeure	7.8	50321	7	Periplasmic	COG0265	Posttranslational modification, protein turnover, chaperones	
15595964	PA0767	lepA	GTP-binding protein LepA	5.3	2.82E-03	Oktansaeure	5.3	66263	8	Cytoplasmic Membrane	COG0481	Cell envelope biogenesis, outer membrane	
15595967	PA0770	rnc	ribonuclease III	1.2	3.41E-01	Citronellol	6.6	25474	4	Cytoplasmic	COG0571	Transcription	
15595968	PA0771	era	GTP-binding protein Era	1.2	4.86E-01	Oktansaeure	6.6	34550	6	Cytoplasmic Membrane	COG1159	General function prediction only	
15595970	PA0773	pdxJ	pyridoxal phosphate biosynthetic protein PdxJ	1.3	1.04E-01	Citronellol	5.6	27228	7	Cytoplasmic	COG0854	Coenzyme metabolism	
15595972	PA0775		conserved hypothetical protein	1.2	3.85E-01	Oktansaeure	5.3	27608	2	Cytoplasmic	COG4106	General function prediction only	
15595976	PA0779		probable ATP-dependent protease	1.7	4.56E-02	Citronellol	6.8	88574	10	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones	
15595979	PA0782	putA	proline dehydrogenase PutA	1.0	6.79E-01	Oktansaeure	6.0	115630	22	Periplasmic	COG4230	Energy production and conversion	
15595989	PA0792	prpD	propionate catabolic protein PrpD	1.9	2.80E-01	Oktansaeure	6.6	54881	11	Cytoplasmic	COG2079	General function prediction only	
15595991	PA0794		probable aconitate hydratase	2.8	3.09E-02	Citronellol	5.3	94890	11	Cytoplasmic	COG1048	Energy production and conversion	
15595992	PA0795	prpC	citrate synthase 2	1.8	1.03E-02	Citronellol	6.4	41689	17	Cytoplasmic	COG0372	Energy production and conversion	
15595993	PA0796	prpB	carboxyphosphonoenolpyruvate phosphonomutase	1.3	9.38E-02	Citronellol	5.2	32137	12	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15596001	PA0804		probable oxidoreductase	2.0	3.45E-02	Citronellol	4.8	30017	4	Cytoplasmic	COG0656	General function prediction only	
15596004	PA0807	ampDh3	AmpDh3	4.8	8.83E-04	Oktansaeure	6.3	28720	2	Outer Membrane Vesicle	COG3023	Cell envelope biogenesis, outer membrane	
15596017	PA0820		hypothetical protein	1.2	3.87E-01	Oktansaeure	6.9	30068	2	Cytoplasmic	COG3183	Defense mechanisms	
15596029	PA0832		conserved hypothetical protein	1.0	8.79E-01	Citronellol	6.2	23483	2	Cytoplasmic	COG0491	General function prediction only	
15596030	PA0833		hypothetical protein	1.1	6.15E-01	Oktansaeure	9.0	24713	8	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596032	PA0835	pta	phosphate acetyltransferase	1.2	3.10E-01	Oktansaeure	5.0	75696	21	Periplasmic	COG0280	Energy production and conversion	
15596033	PA0836	ackA	acetate kinase	1.1	6.58E-01	Oktansaeure	7.1	42421	9	Cytoplasmic	COG0282	Energy production and conversion	
15596034	PA0837	slyD	peptidyl-prolyl cis-trans isomerase SlyD	1.6	4.65E-01	Citronellol	4.2	17010	3	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones	
15596035	PA0838		probable glutathione peroxidase	2.8	2.41E-02	Citronellol	4.9	17264	6	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596037	PA0840		probable oxidoreductase	1.2	8.73E-01	Oktansaeure	5.5	40334	12	Cytoplasmic	COG1902	Energy production and conversion	
15596045	PA0848		probable alkyl hydroperoxide reductase	2.0	1.09E-01	Citronellol	5.1	21814	3	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15596048	PA0851		hypothetical protein	2.2	3.44E-01	Oktansaeure	6.8	34024	7	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15596049	PA0852	cbpD	chitin-binding protein CbpD precursor	3.0	2.59E-03	Oktansaeure	6.9	41917	9	Extracellular	COG3397	Function unknown	
15596050	PA0853		probable oxidoreductase	1.3	2.18E-01	Citronellol	8.3	23485	6	Cytoplasmic	COG2249	General function prediction only	
15596051	PA0854	fumC2	fumarate hydratase	1.8	4.23E-03	Citronellol	6.1	49122	20	Cytoplasmic	COG0114	Energy production and conversion	
15596053	PA0856		hypothetical protein	1.7	2.85E-01	Oktansaeure	10.1	19998	7	Unknown	COG3184	Function unknown	
15596055	PA0858		conserved hypothetical protein	10.0	2.31E-02	Oktansaeure	5.7	35420	5	Cytoplasmic	COG1054	General function prediction only	
15596056	PA0859		hypothetical protein	1.2	2.37E-01	Citronellol	4.6	21466	3	Unknown	COG3531	Posttranslational modification, protein turnover, chaperones	
15596059	PA0862		hypothetical protein	1.4	2.22E-01	Citronellol	6.5	29845	5	Cytoplasmic	COG5424	Coenzyme metabolism	
15596060	PA0863		probable oxidoreductase	1.5	2.18E-02	Citronellol	4.9	33368	4	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15596062	PA0865	hpd	4-hydroxyphenylpyruvate dioxygenase	10.6	1.12E-01	Oktansaeure	4.9	39913	5	Periplasmic	COG3185	Amino acid transport and metabolism	General function prediction only
15596064	PA0867	mliC	membrane-bound lysozyme inhibitor of c-type lysozyme MliC	2.1	4.00E-02	Oktansaeure	4.8	13695	7	Outer Membrane Vesicle	COG3895	General function prediction only	
15596067	PA0870	phhC	aromatic amino acid aminotransferase	1.2	1.65E-01	Citronellol	6.2	43273	6	Cytoplasmic	COG1448	Amino acid transport and metabolism	
15596068	PA0871	phhB	pterin-4-alpha-carbinolamine dehydratase	2.0	4.40E-02	Citronellol	6.4	13333	5	Cytoplasmic	COG2154	Coenzyme metabolism	
15596069	PA0872	phhA	phenylalanine-4-hydroxylase	5.1	1.78E-01	Oktansaeure	5.6	30322	3	Cytoplasmic	COG3186	Amino acid transport and metabolism	
15596084	PA0887	acsA	acetyl-coenzyme A synthetase	1.3	1.90E-01	Citronellol	6.3	71762	38	Cytoplasmic	COG0365	Lipid metabolism	
15596085	PA0888	aotJ	arginine/ornithine binding protein AotJ	1.0	8.35E-01	Oktansaeure	6.8	28010	20	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596088	PA0891		hypothetical protein	1.4	1.97E-01	Citronellol	4.9	40214	4	Cytoplasmic	COG3608	General function prediction only	
15596092	PA0895	aruC	N-succinylglutamate 5-semialdehyde dehydrogenase	1.2	4.21E-01	Citronellol	5.8	43747	26	Periplasmic	COG4992	Amino acid transport and metabolism	
15596093	PA0896	aruF	arginine/ornithine succinyltransferase AI subunit	1.8	1.50E-01	Citronellol	4.7	36930	6	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596094	PA0897	aruG	arginine/ornithine succinyltransferase AII subunit	1.6	8.00E-02	Citronellol	6.5	37245	9	Cytoplasmic	COG3138	Amino acid transport and metabolism	
15596096	PA0899	aruB	succinylarginine dihydrolase	1.8	2.18E-03	Citronellol	6.2	48875	11	Periplasmic	COG3724	Amino acid transport and metabolism	
15596098	PA0901	aruE	succinylglutamate desuccinylase	1.0	8.79E-01	Oktansaeure	6.0	36909	9	Cytoplasmic	COG2988	Amino acid transport and metabolism	
15596099	PA0902		hypothetical protein	1.1	7.59E-01	Oktansaeure	6.4	35430	11	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15596100	PA0903	alaS	alanyl-tRNA synthetase	1.3	1.88E-01	Citronellol	5.2	94701	40	Cytoplasmic	COG0013	Translation, ribosomal structure and biogenesis	
15596101	PA0904	lysC	aspartate kinase alpha and beta chain	1.8	4.56E-02	Citronellol	5.0	44388	25	Cytoplasmic	COG0527	Amino acid transport and metabolism	
15596112	PA0915		conserved hypothetical protein	3.5	4.45E-02	Oktansaeure	6.3	17514	4	Cytoplasmic	COG4807	Function unknown	
15596113	PA0916		conserved hypothetical protein	19.7	9.61E-03	Citronellol	4.6	48961	2	Cytoplasmic	COG0621	Translation, ribosomal structure and biogenesis	
15596129	PA0932	cysM	cysteine synthase B	1.6	1.52E-01	Citronellol	5.5	32448	10	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596131	PA0934	relA	GTP pyrophosphokinase	4.5	1.21E-03	Oktansaeure	7.6	83815	22	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15596132	PA0935		conserved hypothetical protein	1.6	2.90E-01	Oktansaeure	4.6	31250	2	Cytoplasmic	COG3956	General function prediction only	
15596134	PA0937		conserved hypothetical protein	1.9	2.20E-01	Oktansaeure	9.7	20789	4	Cytoplasmic	COG3122	Function unknown	
15596140	PA0943		hypothetical protein	1.3	3.76E-01	Citronellol	8.7	27183	15	Periplasmic			
15596142	PA0945	purM	phosphoribosylaminoimidazole synthetase	1.2	3.76E-01	Citronellol	4.5	37122	14	Cytoplasmic	COG0150	Nucleotide transport and metabolism	
15596144	PA0947		conserved hypothetical protein	3.9	5.37E-02	Oktansaeure	6.0	26843	3	Cytoplasmic	COG0593	DNA replication, recombination, and repair	
15596146	PA0949	wrbA	Trp repressor binding protein WrbA	1.5	5.21E-01	Citronellol	6.8	20744	6	Unknown	COG0655	General function prediction only	
15596153	PA0956	proS	prolyl-tRNA synthetase	1.5	4.25E-03	Oktansaeure	5.1	63103	33	Periplasmic	COG0442	Translation, ribosomal structure and biogenesis	
15596154	PA0957		hypothetical protein	8.3	2.10E-04	Citronellol	6.3	14622	6	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596155	PA0958	oprD	Basic amino acid, basic peptide and imipenem outer membrane porin OprD prec	3.3	7.40E-02	Citronellol	4.8	48360	10	Periplasmic			
15596156	PA0959		hypothetical protein	9.9	4.92E-01	Citronellol	6.5	23069	3	Cytoplasmic	COG0537	Nucleotide transport and metabolism	Carbohydrate transport and metabolism

15596159	PA0962		probable dna-binding stress protein	1.0	7.53E-01	Oktansaeure	4.7	17493	12	Cytoplasmic	COG0783	Inorganic ion transport and metabolism	
15596160	PA0963	aspS	aspartyl-tRNA synthetase	1.5	1.48E-02	Oktansaeure	5.2	66207	37	Periplasmic	COG0173	Translation, ribosomal structure and biogenesis	
15596161	PA0964	pmpR	pqsR-mediated PQS regulator, PmpR	1.0	8.62E-01	Oktansaeure	4.4	26557	4	Cytoplasmic	COG0217	Function unknown	
15596163	PA0966	ruvA	Holliday junction DNA helicase RuvA	1.0	9.05E-01	Citronellol	6.1	21927	9	Cytoplasmic	COG0632	DNA replication, recombination, and repair	
15596166	PA0969	tolQ	TolQ protein	1.4	8.86E-01	Citronellol	6.3	25250	5	Cytoplasmic Membrane	COG0811	Intracellular trafficking and secretion	
15596169	PA0972	tolB	TolB protein	1.2	3.53E-01	Citronellol	9.2	47720	20	Periplasmic	COG0823	Intracellular trafficking and secretion	
15596170	PA0973	oprL	Peptidoglycan associated lipoprotein OprL precursor	1.1	6.67E-01	Oktansaeure	6.3	17925	5	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane	
15596171	PA0974		conserved hypothetical protein	1.5	1.45E-01	Citronellol	8.7	29097	7	Outer Membrane Vesicle	COG1729	Function unknown	
15596173	PA0976		conserved hypothetical protein	2.0	1.49E-01	Citronellol	4.7	23900	2	Unknown	COG0603	General function prediction only	
15596178	PA0981		hypothetical protein	2.5	5.63E-02	Citronellol	6.4	21871	3	Unknown			
15596192	PA0995	ogt	methylated-DNA--protein-cysteine methyltransferase	11.3	1.83E-02	Oktansaeure	7.6	19253	3	Cytoplasmic	COG0350	DNA replication, recombination, and repair	
15596194	PA0997	pqsB	PqsB	6.1	9.35E-03	Oktansaeure	4.6	30501	10	Cytoplasmic	COG0332	acyl-carrier-protein	
15596195	PA0998	pqsC	PqsC	14.5	2.37E-03	Oktansaeure	4.9	38238	10	Cytoplasmic	COG0332	acyl-carrier-protein	
15596196	PA0999	pqsD	3-oxoacyl-[acyl-carrier-protein] synthase III	12.5	6.49E-03	Oktansaeure	5.3	36378	20	Cytoplasmic	COG0332	acyl-carrier-protein	
15596197	PA1000	pqsE	Quinolone signal response protein	4.2	5.49E-02	Oktansaeure	5.3	34306	7	Cytoplasmic	COG0491	General function prediction only	
15596201	PA1004	nadA	quinolinate synthetase A	1.2	8.15E-02	Citronellol	5.4	38418	6	Cytoplasmic	COG0379	Coenzyme metabolism	
15596202	PA1005		conserved hypothetical protein	1.3	5.13E-01	Citronellol	8.4	52994	6	Periplasmic	COG4783	General function prediction only	
15596205	PA1008	bcp	bacterioferritin comigratory protein	2.2	8.81E-04	Citronellol	7.3	17352	12	Unknown	COG1225	Posttranslational modification, protein turnover, chaperones	
15596206	PA1009		hypothetical protein	1.8	1.99E-01	Oktansaeure	5.6	20585	3	Cytoplasmic	COG2716	Amino acid transport and metabolism	
15596207	PA1010	dapA	dihydrodipicolinate synthase	1.2	4.28E-01	Citronellol	6.4	31449	23	Periplasmic	COG0329	Amino acid transport and metabolism	Cell envelope biogenesis, outer membrane
15596208	PA1011		hypothetical protein	1.4	2.58E-01	Citronellol	4.7	43055	6	Periplasmic	COG3317	Cell envelope biogenesis, outer membrane	
15596210	PA1013	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.5	9.86E-02	Citronellol	5.1	26831	20	Periplasmic	COG0152	Nucleotide transport and metabolism	
15596212	PA1015		probable transcriptional regulator	2.5	8.90E-04	Citronellol	7.0	28853	3	Cytoplasmic	COG1414	Transcription	
15596220	PA1023		probable short-chain dehydrogenase	1.9	1.36E-02	Citronellol	6.7	32821	8	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596223	PA1026		hypothetical protein	2.6	3.79E-02	Citronellol	4.8	17184	3	Cytoplasmic			
15596224	PA1027		probable aldehyde dehydrogenase	1.7	4.98E-02	Citronellol	6.8	57291	3	Cytoplasmic	COG1012	Energy production and conversion	
15596230	PA1033		probable glutathione S-transferase	2.2	1.36E-02	Citronellol	6.8	24527	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596233	PA1036		hypothetical protein	1.2	2.89E-01	Oktansaeure	4.6	19537	2	Unknown			
15596236	PA1039		conserved hypothetical protein	1.2	4.51E-01	Oktansaeure	6.7	17189	3	Unknown	COG3012	Function unknown	
15596237	PA1040		hypothetical protein	1.6	5.03E-02	Citronellol	6.0	18721	5	Unknown			
15596238	PA1041		probable outer membrane protein precursor	4.1	5.39E-02	Citronellol	5.1	21747	2	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane	
15596240	PA1043		hypothetical protein	3.3	4.02E-02	Oktansaeure	8.2	27276	3	Periplasmic			
15596244	PA1047		probable esterase	1.5	9.43E-02	Citronellol	6.1	42335	7	Periplasmic	COG1680	Defense mechanisms	
15596246	PA1049	pdxH	pyridoxine 5'-phosphate oxidase	1.0	9.78E-01	Citronellol	6.8	24860	8	Cytoplasmic	COG0259	Coenzyme metabolism	
15596250	PA1053		conserved hypothetical protein	1.0	5.24E-01	Oktansaeure	10.1	15649	2	Outer Membrane Vesicle	COG3133	Cell envelope biogenesis, outer membrane	
15596258	PA1061		conserved hypothetical protein	1.3	5.13E-02	Citronellol	6.6	39952	16	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15596259	PA1062		hypothetical protein	2.0	1.68E-01	Oktansaeure	6.5	19155	4	Cytoplasmic	COG1247	Cell envelope biogenesis, outer membrane	
15596261	PA1064		hypothetical protein	1.7	7.07E-01	Citronellol	5.1	24172	3	Periplasmic	COG3650	Function unknown	
15596262	PA1065		conserved hypothetical protein	5.6	7.20E-03	Citronellol	6.8	17989	2	Unknown	COG3189	Function unknown	
15596263	PA1066		probable short-chain dehydrogenase	1.2	5.09E-01	Citronellol	7.6	23376	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596265	PA1068		probable heat shock protein (hsp90 family)	3.8	4.97E-03	Oktansaeure	5.7	70659	15	Cytoplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596266	PA1069		hypothetical protein	1.5	7.86E-03	Oktansaeure	4.3	86114	25	Cytoplasmic			
15596267	PA1070	braG	branched-chain amino acid transport protein BraG	21.4	2.41E-02	Citronellol	6.6	25592	3	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
15596271	PA1074	braC	branched-chain amino acid transport protein BraC	3.1	2.26E-02	Citronellol	5.5	39769	27	Periplasmic	COG0683	Amino acid transport and metabolism	
15596285	PA1088		hypothetical protein	1.9	1.03E-01	Oktansaeure	4.8	28800	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15596286	PA1089		conserved hypothetical protein	1.3	3.83E-01	Oktansaeure	5.0	22471	2	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15596287	PA1090		hypothetical protein	1.4	5.39E-02	Citronellol	5.3	24703	5	Cytoplasmic	COG1213	Cell envelope biogenesis, outer membrane	
15596288	PA1091	fgtA	flagellar glycosyl transferase, FgtA	4.9	7.22E-02	Citronellol	5.2	187155	24	Cytoplasmic Membrane	COG1887	Cell envelope biogenesis, outer membrane	
15596289	PA1092	fliC	flagellin type B	3.4	3.04E-03	Citronellol	5.2	49242	20	Periplasmic	COG1344	Cell motility and secretion	
15596291	PA1094	fliD	flagellar capping protein FliD	2.1	2.17E-02	Citronellol	7.1	49449	11	Periplasmic	COG1345	Cell motility and secretion	
15596294	PA1097	fleQ	transcriptional regulator FleQ	1.1	6.69E-01	Oktansaeure	5.0	55277	10	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596321	PA1124	dgt	deoxyguanosinetriphosphate triphosphohydrolase	4.7	2.55E-01	Oktansaeure	6.5	56741	1	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15596324	PA1127		probable oxidoreductase	1.7	1.47E-01	Oktansaeure	5.2	36474	3	Cytoplasmic	COG0667	Energy production and conversion	
15596332	PA1135		conserved hypothetical protein	2.4	1.51E-02	Citronellol	6.4	31898	13	Cytoplasmic	COG0693	General function prediction only	
15596337	PA1140		conserved hypothetical protein	1.2	2.99E-01	Citronellol	6.3	31614	5	Cytoplasmic	COG3257	General function prediction only	
15596352	PA1155	nrdB	NrdB, tyrosyl radical-harboring component of class Ia ribonucleotide reductase	3.6	1.32E-02	Oktansaeure	4.5	47386	8	Periplasmic	COG0208	Nucleotide transport and metabolism	
15596353	PA1156	nrdA	NrdA, catalytic component of class Ia ribonucleotide reductase	1.6	4.24E-02	Oktansaeure	5.7	107105	47	Periplasmic	COG0209	Nucleotide transport and metabolism	
15596354	PA1157		probable two-component response regulator	1.2	5.06E-01	Oktansaeure	4.7	26373	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596358	PA1161	rrmA	rRNA methyltransferase	3.1	5.14E-03	Oktansaeure	7.9	29644	2	Cytoplasmic	COG2226	Coenzyme metabolism	
15596359	PA1162	dapE	succinyl-diaminopimelate desuccinylase	1.3	1.93E-01	Oktansaeure	5.0	41077	11	Cytoplasmic	COG0624	Amino acid transport and metabolism	
15596362	PA1165	pcpS	PcpS	1.1	7.54E-01	Citronellol	7.0	26715	4	Unknown	COG2977	Secondary metabolites biosynthesis, transport, and catabolism	
15596363	PA1166		hypothetical protein	2.1	5.40E-02	Citronellol	7.3	28156	8	Unknown	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596366	PA1169		probable lipoxygenase	161.6	3.78E-02	Oktansaeure	6.8	74803	3	Periplasmic			
15596368	PA1171		probable transglycolase	1.3	1.30E-01	Oktansaeure	9.3	42682	8	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane	
15596370	PA1173	napB	cytochrome c-type protein NapB precursor	19.3	3.16E-03	Citronellol	8.3	17918	3	Periplasmic	COG3043	Energy production and conversion	
15596371	PA1174	napA	periplasmic nitrate reductase protein NapA	6.6	8.87E-03	Citronellol	8.6	92942	28	Periplasmic	COG0243	Energy production and conversion	
15596376	PA1179	phoP	two-component response regulator PhoP	1.6	1.61E-01	Oktansaeure	5.2	25650	5	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15596384	PA1187		probable acyl-CoA dehydrogenase	5.6	1.17E-03	Citronellol	6.5	42350	10	Cytoplasmic	COG1960	Lipid metabolism	
15596385	PA1188		hypothetical protein	2.9	1.31E-02	Citronellol	6.0	42128	4	Cytoplasmic	COG1804	Energy production and conversion	
15596389	PA1192		conserved hypothetical protein	2.7	6.37E-02	Oktansaeure	6.5	31260	2	Cytoplasmic	COG0037	Cell cycle control, cell division, chromosome partitioning	
15596390	PA1193		hypothetical protein	1.2	6.62E-01	Oktansaeure	9.1	25292	3	Cytoplasmic	COG2818	DNA replication, recombination, and repair	
15596397	PA1200		conserved hypothetical protein	1.9	4.07E-02	Citronellol	5.1	24597	5	Cytoplasmic	COG4122	General function prediction only	
15596399	PA1202		probable hydrolase	2.7	2.47E-02	Citronellol	4.8	22471	13	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596401	PA1204		conserved hypothetical protein	1.1	8.75E-01	Citronellol	6.5	20224	4	Cytoplasmic	COG0431	General function prediction only	
15596403	PA1206		hypothetical protein	2.2	9.47E-04	Oktansaeure	4.4	17690	6	Cytoplasmic			
15596413	PA1216		hypothetical protein	1.4	4.59E-01	Oktansaeure	6.1	28573	9	Cytoplasmic	COG4976	General function prediction only	
15596422	PA1225		probable NAD(P)H dehydrogenase	3.2	3.21E-01	Oktansaeure	7.0	22551	2	Cytoplasmic	COG2249	General function prediction only	
15596457	PA1260		amino acid ABC transporter periplasmic binding protein	9.4	2.75E-03	Citronellol	5.2	29142	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596469	PA1272	cobO	cob(I)alamin adenosyltransferase	1.5	3.12E-01	Oktansaeure	8.0	22292	6	Cytoplasmic	COG2109	Coenzyme metabolism	
15596475	PA1278	cobP	cobinamide kinase	1.1	5.36E-01	Oktansaeure	5.4	18862	3	Cytoplasmic	COG2087	Coenzyme metabolism	
15596476	PA1279	cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.2	3.04E-01	Citronellol	6.6	36531	4	Cytoplasmic	COG2038	Coenzyme metabolism	
15596477	PA1280		hypothetical protein	1.1	8.62E-01	Citronellol	6.7	21591	4	Cytoplasmic	COG0406	General function prediction only	
15596480	PA1283		probable transcriptional regulator	2.5	3.79E-03	Oktansaeure	4.9	20307	3	Unknown	COG1309	Transcription	
15596484	PA1287		probable glutathione peroxidase	2.0	7.28E-02	Citronellol	8.3	20217	10	Periplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15596485	PA1288		probable outer membrane protein precursor	1.4	3.14E-01	Oktansaeure	6.0	45561	12	Periplasmic	COG2067	Lipid metabolism	
15596489	PA1292		probable 3-mercaptopyruvate sulfurtransferase	1.1	5.16E-01	Citronellol	5.3	30597	14	Periplasmic	COG2897	Inorganic ion transport and metabolism	
15596491	PA1294	rnd	ribonuclease D	1.2	4.84E-01	Citronellol	4.8	43066	8	Cytoplasmic	COG0349	Translation, ribosomal structure and biogenesis	
15596493	PA1296		probable 2-hydroxyacid dehydrogenase	3.5	2.02E-01	Oktansaeure	5.6	33730	2	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596501	PA1304		probable oligopeptidase	1.3	1.54E-01	Oktansaeure	4.7	75881	21	Periplasmic	COG1770	Amino acid transport and metabolism	
15596504	PA1307		conserved hypothetical protein	1.4	1.37E-01	Citronellol	5.7	28544	5	Cytoplasmic	COG0121	General function prediction only	
15596521	PA1324		hypothetical protein	1.9	1.22E-02	Citronellol	5.8	18303	5	Unknown			
15596532	PA1335		probable two-component response regulator	1.8	5.41E-03	Citronellol	6.9	46687	3	Cytoplasmic	COG2204	Signal transduction mechanisms	
15596534	PA1337	ansB	glutaminase-asparaginase	2.6	2.55E-03	Citronellol	7.3	38644	19	Periplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15596535	PA1338	ggt	gamma-glutamyltranspeptidase precursor	4.2	6.40E-03	Citronellol	6.2	59874	15	Periplasmic	COG0405	Amino acid transport and metabolism	
15596538	PA1341		amino acid ABC transporter membrane protein	3.4	6.43E-01	Citronellol	9.3	27593	3	Cytoplasmic Membrane	COG0765	Amino acid transport and metabolism	
15596539	PA1342		probable binding protein component of ABC transporter	2.4	2.09E-02	Citronellol	8.6	33054	43	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15596541	PA1344		probable short-chain dehydrogenase	1.4	3.74E-01	Citronellol	4.9	27397	9	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only

15596564	PA1367		hypothetical protein	2.5	1.52E-01	Oktansaeure	4.5	29789	2	Cytoplasmic	COG0384	General function prediction only	
15596568	PA1371		hypothetical protein	1.8	5.68E-02	Citronellol	5.2	27419	3	Unknown	COG5619	Function unknown	
15596569	PA1372		hypothetical protein	1.0	9.09E-01	Oktansaeure	5.5	79820	20	Cytoplasmic	COG3972	General function prediction only	
15596572	PA1375	pdxB	erythronate-4-phosphate dehydrogenase	1.2	1.91E-01	Oktansaeure	5.5	41001	5	Cytoplasmic	COG0111	Amino acid transport and metabolism	
15596573	PA1376	aceK	isocitrate dehydrogenase kinase/phosphatase	2.2	2.24E-02	Citronellol	5.0	66760	17	Cytoplasmic	COG4579	Signal transduction mechanisms	
15596574	PA1377		conserved hypothetical protein	1.6	5.62E-02	Oktansaeure	7.9	20068	4	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596599	PA1402		hypothetical protein	1.1	7.38E-01	Oktansaeure	4.7	23753	5	Cytoplasmic	COG4122	General function prediction only	
15596627	PA1430	lasR	transcriptional regulator LasR	3.7	4.71E-03	Oktansaeure	6.5	26618	9	Cytoplasmic	COG2771	Transcription	
15596637	PA1440		hypothetical protein	1.0	9.18E-01	Citronellol	3.9	22382	4	Cytoplasmic	COG3318	General function prediction only	
15596639	PA1442		conserved hypothetical protein	3.7	2.26E-02	Citronellol	10.3	18760	2	Cytoplasmic Membrane	COG1580	Cell motility and secretion	
15596640	PA1443	fliM	flagellar motor switch protein FliM	1.5	9.19E-02	Citronellol	5.0	36282	3	Cytoplasmic	COG1868	Cell motility and secretion	
15596641	PA1444	fliN	flagellar motor switch protein FliN	1.4	8.30E-01	Citronellol	4.0	16620	4	Cytoplasmic Membrane	COG1886	Cell motility and secretion	Intracellular trafficking and secretion
15596651	PA1454	fleN	flagellar synthesis regulator FleN	2.9	3.64E-03	Citronellol	8.7	30037	4	Cytoplasmic Membrane	COG0455	Cell motility	
15596652	PA1455	fliA	sigma factor FliA	1.6	1.64E-02	Citronellol	5.9	27522	4	Cytoplasmic	COG1191	Transcription	
15596654	PA1457	cheZ	chemotaxis protein CheZ	1.4	1.91E-02	Oktansaeure	4.6	29622	10	Cytoplasmic	COG3143	Cell motility and secretion	Signal transduction mechanisms
15596655	PA1458		probable two-component sensor	2.1	1.74E-01	Oktansaeure	4.3	79737	20	Cytoplasmic	COG0643	Cell motility and secretion	Signal transduction mechanisms
15596656	PA1459		probable methyltransferase	2.5	4.51E-03	Oktansaeure	8.6	39004	9	Cytoplasmic	COG2201	Cell motility and secretion	Signal transduction mechanisms
15596659	PA1462		probable plasmid partitioning protein	1.5	2.89E-01	Oktansaeure	10.1	28407	3	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning	
15596661	PA1464		probable purine-binding chemotaxis protein	1.9	2.24E-02	Citronellol	4.1	17536	12	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15596667	PA1470		probable short-chain dehydrogenase	3.6	2.35E-03	Citronellol	4.9	25365	8	Unknown	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596669	PA1472		conserved hypothetical protein	1.7	5.72E-03	Citronellol	5.8	21138	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15596690	PA1493	cysP	sulfate-binding protein of ABC transporter	1.2	3.49E-01	Oktansaeure	8.6	36485	19	Periplasmic	COG1613	Inorganic ion transport and metabolism	
15596692	PA1495		hypothetical protein	1.0	9.75E-01	Citronellol	5.9	23443	3	Unknown	COG4339	Function unknown	
15596706	PA1509		hypothetical protein	7.5	8.14E-04	Oktansaeure	6.8	42364	6	Cytoplasmic			
15596707	PA1510		hypothetical protein	49.5	3.76E-05	Oktansaeure	5.1	63320	11	Unknown			
15596708	PA1511		conserved hypothetical protein	17.5	8.02E-05	Oktansaeure	6.4	93635	9	Cytoplasmic	COG3501	Function unknown	
15596713	PA1516		hypothetical protein	1.0	7.77E-01	Oktansaeure	4.8	18896	7	Cytoplasmic	COG3195	Function unknown	
15596717	PA1520		probable transcriptional regulator	2.6	1.46E-01	Oktansaeure	7.9	28646	2	Cytoplasmic	COG1802	Transcription	
15596718	PA1521		probable guanine deaminase	2.2	1.01E-01	Citronellol	5.2	48311	3	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15596720	PA1523	xdhB	xanthine dehydrogenase	1.8	5.23E-01	Citronellol	6.3	87664	2	Cytoplasmic	COG4631	Nucleotide transport and metabolism	
15596723	PA1526		probable transcriptional regulator	1.2	4.18E-01	Oktansaeure	7.8	25070	3	Cytoplasmic	COG1802	Transcription	
15596724	PA1527		conserved hypothetical protein	6.7	1.68E-01	Citronellol	4.8	131580	12	Cytoplasmic	COG1196	Cell division and chromosome partitioning	
15596725	PA1528	zipA	cell division protein ZipA	1.4	3.84E-01	Oktansaeure	5.7	32236	4	Outer Membrane Vesicle	COG3115	Cell division and chromosome partitioning	
15596726	PA1529	lig	DNA ligase	1.2	4.01E-01	Citronellol	5.1	86767	19	Cytoplasmic	COG0272	DNA replication, recombination, and repair	
15596729	PA1532	dnaX	DNA polymerase subunits gamma and tau	9.0	1.98E-01	Oktansaeure	4.4	73309	5	Cytoplasmic	COG2812	DNA replication, recombination, and repair	
15596731	PA1534	recR	recombination protein RecR	1.4	7.69E-01	Oktansaeure	6.0	21173	6	Cytoplasmic	COG0353	DNA replication, recombination, and repair	
15596732	PA1535		citronellyl-CoA dehydrogenase	25.6	8.30E-05	Citronellol	5.6	42041	21	Cytoplasmic	COG1960	Lipid metabolism	
15596740	PA1543	apt	adenine phosphoribosyltransferase	1.5	1.86E-01	Citronellol	4.6	19804	7	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15596741	PA1544	anr	transcriptional regulator Anr	1.1	7.47E-01	Oktansaeure	5.2	27129	9	Cytoplasmic	COG0664	Signal transduction mechanisms	
15596747	PA1550		hypothetical protein	1.0	8.87E-01	Oktansaeure	5.1	20338	2	Outer Membrane Vesicle	COG3198	Function unknown	
15596750	PA1553	ccoO1	Cytochrome c oxidase, cbb3-type, CcoO subunit	1.5	6.16E-01	Citronellol	8.2	22758	6	Outer Membrane Vesicle	COG2993	Energy production and conversion	
15596759	PA1562	acnA	aconitate hydratase 1	3.4	4.94E-03	Citronellol	5.4	99147	39	Cytoplasmic	COG1048	Energy production and conversion	
15596773	PA1576		probable 3-hydroxyisobutyrate dehydrogenase	1.1	5.85E-01	Oktansaeure	5.2	30777	12	Cytoplasmic	COG2084	Lipid metabolism	
15596776	PA1579		hypothetical protein	1.1	6.38E-01	Oktansaeure	8.2	22110	13	Periplasmic			
15596777	PA1580	gltA	citrate synthase	1.1	3.60E-01	Oktansaeure	7.0	47695	33	Periplasmic	COG0372	Energy production and conversion	
15596778	PA1581	sdhC	succinate dehydrogenase (C subunit)	1.8	4.25E-02	Citronellol	10.4	13738	2	Outer Membrane Vesicle	COG2009	Energy production and conversion	
15596780	PA1583	sdhA	succinate dehydrogenase (A subunit)	2.2	2.45E-03	Oktansaeure	6.5	63532	27	Periplasmic	COG1053	Energy production and conversion	
15596781	PA1584	sdhB	succinate dehydrogenase (B subunit)	1.2	7.79E-01	Oktansaeure	6.9	26155	7	Outer Membrane Vesicle	COG0479	Energy production and conversion	
15596782	PA1585	sucA	2-oxoglutarate dehydrogenase (E1 subunit)	1.4	1.96E-01	Citronellol	6.5	105877	42	Outer Membrane Vesicle	COG0567	Energy production and conversion	
15596783	PA1586	sucB	dihydrolipoamide succinyltransferase (E2 subunit)	1.3	4.79E-01	Citronellol	5.2	42887	25	Periplasmic	COG0508	Energy production and conversion	
15596784	PA1587	lpdG	lipoamide dehydrogenase-glc	1.0	9.42E-01	Oktansaeure	7.0	50165	27	Periplasmic	COG1249	Energy production and conversion	
15596785	PA1588	sucC	succinyl-CoA synthetase beta chain	1.3	1.94E-01	Citronellol	6.1	41542	28	Periplasmic	COG0045	Energy production and conversion	
15596786	PA1589	sucD	succinyl-CoA synthetase alpha chain	1.2	2.62E-01	Citronellol	6.0	30266	24	Periplasmic	COG0074	Energy production and conversion	
15596790	PA1593		hypothetical protein	2.4	4.23E-02	Citronellol	6.3	16817	2	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596793	PA1596	htpG	heat shock protein HtpG	1.6	4.36E-03	Oktansaeure	4.9	71667	47	Periplasmic	COG0326	Posttranslational modification, protein turnover, chaperones	
15596794	PA1597		hypothetical protein	1.2	7.01E-01	Citronellol	5.9	25791	10	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15596806	PA1609	fabB	beta-ketoacyl-ACP synthase I	1.3	4.34E-01	Citronellol	5.3	42806	20	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15596807	PA1610	fabA	beta-hydroxydecanoyl-ACP dehydrase	2.3	9.48E-03	Citronellol	6.9	18747	10	Cytoplasmic	COG0764	Lipid metabolism	
15596811	PA1614	gpsA	glycerol-3-phosphate dehydrogenase, biosynthetic	1.1	5.69E-01	Citronellol	6.2	36773	14	Cytoplasmic	COG0240	Energy production and conversion	
15596813	PA1616		conserved hypothetical protein	1.7	3.61E-01	Oktansaeure	6.4	16715	4	Unknown	COG2062	Signal transduction mechanisms	
15596814	PA1617		probable AMP-binding enzyme	16.1	2.52E-02	Citronellol	7.2	61370	14	Cytoplasmic	COG1022	Lipid metabolism	
15596815	PA1618		conserved hypothetical protein	2.9	6.49E-01	Citronellol	7.0	15595	7	Unknown	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15596819	PA1622		probable hydrolase	5.3	3.76E-05	Citronellol	7.1	31290	11	Cytoplasmic	COG0596	General function prediction only	
15596820	PA1623		conserved hypothetical protein	1.1	6.00E-01	Citronellol	6.1	24924	11	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596821	PA1624		hypothetical protein	1.5	9.03E-02	Oktansaeure	6.4	29533	4	Periplasmic			
15596836	PA1639		hypothetical protein	2.1	1.40E-01	Oktansaeure	5.4	22457	5	Periplasmic			
15596839	PA1642	selD	selenophosphate synthetase	1.6	3.80E-01	Oktansaeure	4.7	36354	10	Cytoplasmic	COG0709	Amino acid transport and metabolism	
15596840	PA1643		conserved hypothetical protein	1.6	4.02E-01	Citronellol	7.0	41845	2	Cytoplasmic	COG2603	General function prediction only	
15596841	PA1644		conserved hypothetical protein	1.2	5.89E-01	Citronellol	5.5	21838	5	Unknown	COG1853	General function prediction only	
15596845	PA1648		probable oxidoreductase	1.8	3.21E-02	Citronellol	6.1	36168	6	Cytoplasmic	COG2130	General function prediction only	
15596846	PA1649		probable short-chain dehydrogenase	2.0	6.70E-01	Citronellol	5.8	25785	3	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15596852	PA1655		probable glutathione S-transferase	1.0	8.16E-01	Citronellol	5.3	22738	8	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15596854	PA1657		conserved hypothetical protein	11.5	5.30E-03	Oktansaeure	4.5	18165	8	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15596855	PA1658		conserved hypothetical protein	20.5	1.02E-03	Oktansaeure	5.1	55560	14	Cytoplasmic	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15596859	PA1662		probable ClpA/B-type protease	41.9	1.23E-04	Oktansaeure	5.5	95774	30	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15596863	PA1666		hypothetical protein	14.0	1.70E-03	Oktansaeure	7.4	18440	3	Unknown	COG3521	Intracellular trafficking, secretion, and vesicular transport	
15596864	PA1667		hypothetical protein	65.1	1.49E-03	Oktansaeure	6.5	49689	7	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15596870	PA1673		hypothetical protein	15.4	9.80E-03	Oktansaeure	6.2	17853	5	Cytoplasmic	COG2703	Inorganic ion transport and metabolism	
15596871	PA1674	folE2	GTP cyclohydrolase I precursor	1.1	6.37E-01	Oktansaeure	7.6	20236	12	Outer Membrane Vesicle	COG0302	Coenzyme metabolism	
15596874	PA1677		conserved hypothetical protein	1.2	4.38E-01	Oktansaeure	6.5	21034	10	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15596875	PA1678		probable DNA methylase	1.6	3.88E-01	Citronellol	4.4	34229	4	Cytoplasmic	COG2890	Translation, ribosomal structure and biogenesis	
15596878	PA1681	aroC	chorismate synthase	1.0	8.39E-01	Oktansaeure	6.6	38987	7	Cytoplasmic	COG0082	Amino acid transport and metabolism	
15596880	PA1683		probable sugar aldolase	1.3	2.02E-01	Citronellol	6.5	22868	4	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15596881	PA1684		1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase MtnD	1.0	8.11E-01	Oktansaeure	5.0	20552	7	Cytoplasmic	COG1791	Function unknown	
15596883	PA1686	alkA	DNA-3-methyladenine glycosidase II	5.5	3.44E-02	Oktansaeure	6.9	32211	3	Unknown	COG0122	DNA replication, recombination, and repair	
15596884	PA1687	speE	spermidine synthase	1.2	4.35E-01	Citronellol	4.9	32238	8	Periplasmic	COG0421	Amino acid transport and metabolism	
15596886	PA1689		conserved hypothetical protein	52.9	7.39E-04	Citronellol	6.5	77984	6	Outer Membrane Vesicle	COG1368	Cell envelope biogenesis, outer membrane	
15596923	PA1726	bglX	periplasmic beta-glucosidase	1.1	7.36E-01	Citronellol	7.1	83003	5	Periplasmic	COG1472	Carbohydrate transport and metabolism	
15596930	PA1733		conserved hypothetical protein	3.4	3.07E-03	Citronellol	5.3	26467	7	Unknown	COG3484	Posttranslational modification, protein turnover, chaperones	
15596931	PA1734		hypothetical protein	2.1	2.22E-01	Citronellol	8.2	30246	2	Unknown	COG2857	Energy production and conversion	
15596933	PA1736		probable acyl-CoA thiolase	7.1	4.90E-04	Citronellol	5.3	42102	20	Cytoplasmic	COG0183	Lipid metabolism	
15596934	PA1737		probable 3-hydroxyacyl-CoA dehydrogenase	4.2	8.64E-05	Citronellol	6.7	76666	38	Cytoplasmic	COG1250	Lipid metabolism	
15596939	PA1742	pauD2	Glutamine amidotransferase class I	5.7	8.85E-03	Oktansaeure	5.0	27361	5	Cytoplasmic	COG0518	Nucleotide transport and metabolism	
15596943	PA1746		hypothetical protein	41.1	1.64E-02	Oktansaeure	6.6	18189	5	Outer Membrane Vesicle	COG2110	General function prediction only	
15596945	PA1748		probable enoyl-CoA hydratase/isomerase	1.2	3.42E-01	Oktansaeure	7.8	24412	12	Cytoplasmic	COG1024	Lipid metabolism	
15596946	PA1749		hypothetical protein	1.1	6.50E-01	Citronellol	10.0	17672	3	Unknown	COG2388	General function prediction only	
15596947	PA1750		phospho-2-dehydro-3-deoxyheptonate aldolase	1.0	6.90E-01	Oktansaeure	6.5	39132	14	Cytoplasmic	COG0722	Amino acid transport and metabolism	

15596949	PA1752		hypothetical protein	1.6	1.56E-01	Oktansaeure	6.7	34141	11	Cytoplasmic	COG1893	Coenzyme metabolism
15596950	PA1753		conserved hypothetical protein	3.7	1.30E-01	Oktansaeure	4.7	18372	4	Cytoplasmic	COG0589	Signal transduction mechanisms
15596951	PA1754	cysB	transcriptional regulator CysB	1.1	6.30E-01	Oktansaeure	7.0	36110	11	Periplasmic	COG0583	Transcription
15596953	PA1756	cysH	3'-phosphoadenosine-5'-phosphosulfate reductase	2.1	2.88E-05	Citronellol	6.4	30215	7	Cytoplasmic	COG0175	Amino acid transport and metabolism
15596954	PA1757	thrH	homoserine kinase	1.2	1.66E-01	Citronellol	5.0	23501	8	Cytoplasmic	COG0560	Amino acid transport and metabolism
15596956	PA1759		probable transcriptional regulator	1.1	5.53E-01	Citronellol	6.3	101111	15	Unknown	COG2909	Transcription
15596957	PA1760		probable transcriptional regulator	1.0	5.39E-01	Oktansaeure	6.8	101628	5	Cytoplasmic	COG2909	Transcription
15596965	PA1768		hypothetical protein	1.4	1.81E-01	Citronellol	9.6	19720	7	Unknown	COG4067	Posttranslational modification, protein turnover, chaperones
15596966	PA1769		conserved hypothetical protein	1.2	8.37E-01	Citronellol	6.1	31074	11	Cytoplasmic	COG1806	Function unknown
15596967	PA1770	ppsA	phosphoenolpyruvate synthase	1.2	3.62E-01	Oktansaeure	4.8	85798	66	Cytoplasmic	COG0574	Carbohydrate transport and metabolism
15596969	PA1772		probable methyltransferase	1.6	1.51E-02	Citronellol	4.6	17404	8	Cytoplasmic	COG0684	Coenzyme metabolism
15596972	PA1775	cmpX	conserved cytoplasmic membrane protein, CmpX protein	1.2	8.02E-01	Citronellol	8.8	29019	3	Outer Membrane Vesicle		
15596974	PA1777	oprF	Major porin and structural outer membrane porin OprF precursor	1.8	1.21E-01	Oktansaeure	4.8	37639	15	Periplasmic	COG2885	Cell envelope biogenesis, outer membrane
15596984	PA1787	acnB	aconitate hydratase 2	1.7	5.97E-03	Citronellol	5.0	93595	73	Periplasmic	COG1049	Energy production and conversion
15596986	PA1789		hypothetical protein	2.0	1.24E-02	Oktansaeure	5.3	31273	14	Cytoplasmic	COG0589	Signal transduction mechanisms
15596987	PA1790		hypothetical protein	4.3	7.63E-03	Oktansaeure	6.7	23312	5	Cytoplasmic	COG4445	Nucleotide transport and metabolism
15596990	PA1793	ppiB	peptidyl-prolyl cis-trans isomerase B	1.7	2.22E-02	Citronellol	6.2	18126	12	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones
15596991	PA1794	glnS	glutaminyl-tRNA synthetase	1.3	2.57E-01	Oktansaeure	5.6	62912	27	Periplasmic	COG0008	Translation, ribosomal structure and biogenesis
15596992	PA1795	cysS	cysteinyl-tRNA synthetase	1.8	1.32E-01	Citronellol	5.4	51245	21	Periplasmic	COG0215	Translation, ribosomal structure and biogenesis
15596993	PA1796	folD	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolase	1.2	1.87E-01	Citronellol	5.8	30549	12	Periplasmic	COG0190	Coenzyme metabolism
15596997	PA1800	tig	trigger factor	1.5	3.74E-02	Citronellol	4.5	48582	29	Periplasmic	COG0544	Posttranslational modification, protein turnover, chaperones
15596998	PA1801	clpP	ClpP	1.1	7.24E-01	Oktansaeure	6.4	23502	18	Periplasmic	COG0740	Posttranslational modification, protein turnover, chaperones
15596999	PA1802	clpX	ClpX	1.0	7.38E-01	Citronellol	4.8	46991	23	Cytoplasmic	COG1219	Posttranslational modification, protein turnover, chaperones
15597000	PA1803	lon	Lon protease	1.3	2.99E-01	Oktansaeure	6.0	88647	31	Cytoplasmic	COG0466	Posttranslational modification, protein turnover, chaperones
15597001	PA1804	hupB	DNA-binding protein HU	4.4	1.89E-02	Oktansaeure	10.8	9054	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair
15597002	PA1805	ppiD	peptidyl-prolyl cis-trans isomerase D	2.1	5.10E-02	Oktansaeure	4.7	68741	6	Periplasmic	COG0760	Posttranslational modification, protein turnover, chaperones
15597003	PA1806	fabI	NADH-dependent enoyl-ACP reductase	1.2	8.95E-02	Citronellol	5.7	28006	8	Cytoplasmic Membrane	COG0623	acyl-carrier-protein
15597007	PA1810		probable binding protein component of ABC transporter	1.4	9.16E-02	Oktansaeure	6.5	70473	13	Periplasmic	COG4166	Amino acid transport and metabolism
15597010	PA1813		probable hydroxyacylglutathione hydrolase	2.0	1.43E-02	Citronellol	6.3	28865	5	Cytoplasmic	COG0491	General function prediction only
15597012	PA1815	rnhA	ribonuclease H	1.4	2.09E-01	Citronellol	8.7	16697	5	Unknown	COG0328	DNA replication, recombination, and repair
15597013	PA1816	dnaQ	DNA polymerase III, epsilon chain	1.8	1.22E-02	Oktansaeure	5.0	26814	6	Cytoplasmic	COG0847	DNA replication, recombination, and repair
15597015	PA1818	ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase, LdcA	1.2	4.06E-01	Citronellol	6.1	82757	14	Cytoplasmic	COG1982	Amino acid transport and metabolism
15597018	PA1821		probable enoyl-CoA hydratase/isomerase	5.3	2.01E-02	Citronellol	5.4	29957	10	Cytoplasmic	COG1024	Lipid metabolism
15597019	PA1822	fimL	hypothetical protein	139.3	1.29E-01	Citronellol	4.9	60868	2	Cytoplasmic		
15597020	PA1823		conserved hypothetical protein	1.5	8.42E-02	Citronellol	4.9	31356	6	Cytoplasmic	COG2816	DNA replication, recombination, and repair
15597025	PA1828		probable short-chain dehydrogenase	1.8	1.25E-02	Citronellol	7.4	26919	15	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15597026	PA1829		hypothetical protein	1.3	1.86E-01	Citronellol	5.9	40833	10	Cytoplasmic	COG3173	General function prediction only
15597028	PA1831		hypothetical protein	1.2	4.28E-01	Citronellol	6.3	26378	7	Cytoplasmic	COG0406	General function prediction only
15597030	PA1833		probable oxidoreductase	1.1	2.17E-01	Citronellol	5.2	34552	17	Cytoplasmic	COG0604	Energy production and conversion
15597033	PA1836		probable transcriptional regulator	2.9	1.61E-01	Oktansaeure	7.0	21316	2	Cytoplasmic	COG1309	Transcription
15597034	PA1837		hypothetical protein	1.5	2.13E-01	Citronellol	4.7	18765	3	Cytoplasmic	COG3749	Function unknown
15597035	PA1838	cysI	sulfite reductase	1.5	3.01E-01	Citronellol	5.9	62132	22	Periplasmic	COG0155	Inorganic ion transport and metabolism
15597038	PA1841		hypothetical protein	15.2	1.72E-02	Oktansaeure	5.1	18654	3	Cytoplasmic	COG3760	Function unknown
15597040	PA1843	metH	methionine synthase	4.1	9.78E-02	Citronellol	4.6	135062	43	Periplasmic	COG1410	Amino acid transport and metabolism
15597041	PA1844	tse1	Tse1	10.5	2.71E-03	Oktansaeure	8.8	16443	2	Extracellular		
15597042	PA1845		hypothetical protein	1.3	4.88E-01	Oktansaeure	4.6	18757	2	Unknown		
15597043	PA1846	cti	cis/trans isomerase	8.4	1.14E-03	Oktansaeure	6.0	86517	10	Periplasmic		
15597044	PA1847	nfuA	NfuA	1.1	7.85E-01	Citronellol	4.2	21136	6	Cytoplasmic	COG0694	Posttranslational modification, protein turnover, chaperones
15597060	PA1863	modA	molybdate-binding periplasmic protein precursor ModA	2.3	1.14E-01	Citronellol	6.8	26377	3	Periplasmic	COG0725	Inorganic ion transport and metabolism
15597071	PA1874		hypothetical protein	10.2	2.63E-02	Citronellol	3.1	238414	2	Unknown		
15597077	PA1880		probable oxidoreductase	3.9	3.50E-03	Citronellol	7.4	77656	22	Cytoplasmic Membrane	COG1529	Energy production and conversion
15597078	PA1881		probable oxidoreductase	23.1	1.13E-03	Citronellol	7.7	15959	6	Cytoplasmic	COG2080	Energy production and conversion
15597084	PA1887		hypothetical protein	1.5	6.83E-01	Oktansaeure	8.0	24376	4	Unknown		
15597087	PA1890		probable glutathione S-transferase	1.0	9.91E-01	Citronellol	7.0	23440	10	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15597091	PA1894		hypothetical protein	4.2	1.13E-02	Oktansaeure	5.3	26179	10	Unknown		
15597099	PA1902	phzD2	phenazine biosynthesis protein PhzD	6.4	3.82E-01	Oktansaeure	5.6	23195	2	Unknown	COG1535	Secondary metabolites biosynthesis, transport, and catabolism
15599411	PA1905	phzG2	probable pyridoxamine 5'-phosphate oxidase	13.2	2.23E-03	Oktansaeure	6.4	24367	3	Cytoplasmic	COG0259	Coenzyme metabolism
15597109	PA1913		hypothetical protein	6.8	4.31E-03	Oktansaeure	8.4	25410	2	Unknown		
15597110	PA1914		conserved hypothetical protein	7.5	1.54E-03	Citronellol	6.9	46125	7	Extracellular		
15597123	PA1927	metE	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	5.3	1.50E-03	Oktansaeure	5.7	86211	22	Cytoplasmic	COG0620	Amino acid transport and metabolism
15597126	PA1930		probable chemotaxis transducer	1.8	4.60E-01	Oktansaeure	6.5	47801	3	Cytoplasmic Membrane	COG0840	Cell motility and secretion
15597142	PA1946	rbsB	binding protein component precursor of ABC ribose transporter	3.6	6.19E-02	Citronellol	8.4	33860	16	Periplasmic	COG1879	Carbohydrate transport and metabolism
15597145	PA1949	rbsR	ribose operon repressor RbsR	1.4	4.49E-02	Citronellol	7.2	36446	6	Cytoplasmic	COG1609	Transcription
15597146	PA1950	rbsK	ribokinase	1.7	1.55E-02	Citronellol	4.9	31846	8	Cytoplasmic	COG0524	Carbohydrate transport and metabolism
15597160	PA1964		probable ATP-binding component of ABC transporter	2.3	1.29E-02	Oktansaeure	4.8	57917	7	Cytoplasmic	COG0488	General function prediction only
15597178	PA1982	exaA	quinoprotein ethanol dehydrogenase	11.7	5.94E-04	Citronellol	7.1	68123	6	Periplasmic	COG4993	Carbohydrate transport and metabolism
15597183	PA1987	pqqC	pyrroloquinoline quinone biosynthesis protein C	4.0	1.77E-03	Citronellol	7.4	29449	4	Cytoplasmic	COG5424	Coenzyme metabolism
15597190	PA1994		hypothetical protein	2.0	1.54E-01	Citronellol	4.7	21561	6	Cytoplasmic	COG3554	Function unknown
15597193	PA1997		probable AMP-binding enzyme	1.5	1.95E-01	Citronellol	6.5	71929	11	Cytoplasmic	COG0365	Lipid metabolism
15597195	PA1999	dhcA	DhcA, dehydrocarnitine CoA transferase, subunit A	2.1	5.80E-03	Citronellol	5.0	25244	5	Cytoplasmic	COG1788	Lipid metabolism
15597196	PA2000	dhcB	DhcB, dehydrocarnitine CoA transferase, subunit B	2.0	2.81E-02	Citronellol	4.6	23187	17	Cytoplasmic	COG2057	Lipid metabolism
15597197	PA2001	atoB	acetyl-CoA acetyltransferase	1.8	2.20E-02	Citronellol	6.4	40405	26	Cytoplasmic	COG0183	Lipid metabolism
15597199	PA2003	bdhA	3-hydroxybutyrate dehydrogenase	1.2	4.16E-01	Citronellol	5.6	26727	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism
15597203	PA2007	maiA	maleylacetoacetate isomerase	2.7	1.39E-02	Citronellol	6.9	23685	7	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15597204	PA2008	fahA	fumarylacetoacetase	1.3	3.85E-01	Citronellol	6.0	46341	6	Cytoplasmic	COG0179	Secondary metabolites biosynthesis, transport, and catabolism
15597207	PA2011	liuE	3-hydroxy-3-methylglutaryl-CoA lyase	17.2	1.50E-05	Citronellol	6.0	31837	12	Cytoplasmic	COG0119	Amino acid transport and metabolism
15597208	PA2012	liuD	methylcrotonyl-CoA carboxylase, alpha-subunit (biotin-containing)	21.2	7.73E-06	Citronellol	5.6	71282	29	Cytoplasmic	COG4770	Lipid metabolism
15597209	PA2013	liuC	putative 3-methylglutaconyl-CoA hydratase	39.5	4.53E-08	Citronellol	5.2	28947	10	Cytoplasmic	COG1024	Lipid metabolism
15597210	PA2014	liuB	methylcrotonyl-CoA carboxylase, beta-subunit	45.2	1.78E-05	Citronellol	6.7	57433	29	Cytoplasmic	COG4799	Lipid metabolism
15597211	PA2015	liuA	putative isovaleryl-CoA dehydrogenase	31.1	6.41E-05	Citronellol	5.5	42209	36	Cytoplasmic	COG1960	Lipid metabolism
15597212	PA2016	liuR	regulator of liu genes	19.9	6.01E-02	Citronellol	5.4	15631	5	Extracellular	COG0789	Transcription
15597216	PA2020		probable transcriptional regulator	3.9	7.55E-02	Oktansaeure	7.1	23695	2	Cytoplasmic	COG1309	Transcription
15597219	PA2023	galU	UTP--glucose-1-phosphate uridylyltransferase	1.1	7.02E-01	Citronellol	5.1	31236	23	Periplasmic	COG1210	Cell envelope biogenesis, outer membrane
15597220	PA2024		probable ring-cleaving dioxygenase	2.0	1.04E-01	Citronellol	5.6	15373	5	Unknown	COG0346	Amino acid transport and metabolism
15597221	PA2025	gor	glutathione reductase	1.2	3.72E-01	Citronellol	6.3	49237	16	Cytoplasmic	COG1249	Energy production and conversion
15597229	PA2033		hypothetical protein	1.4	8.22E-01	Oktansaeure	4.9	33646	3	Cytoplasmic	COG2375	Inorganic ion transport and metabolism
15597230	PA2034		hypothetical protein	13.7	9.74E-03	Oktansaeure	6.3	24525	6	Cytoplasmic	COG2242	Coenzyme metabolism
15597240	PA2044		hypothetical protein	1.5	4.45E-02	Oktansaeure	6.1	70083	8	Periplasmic	COG1305	Amino acid transport and metabolism
15597267	PA2071	fusA2	elongation factor G	1.8	1.34E-01	Citronellol	4.9	77574	24	Cytoplasmic	COG0480	Translation, ribosomal structure and biogenesis
15597272	PA2076		probable transcriptional regulator	61.7	1.06E-02	Oktansaeure	6.0	32458	2	Cytoplasmic	COG0583	Transcription
15597276	PA2080	kynU	kynureninase KynU	1.1	3.46E-01	Citronellol	5.3	46294	9	Cytoplasmic	COG3844	Amino acid transport and metabolism
15597277	PA2081	kynB	kynurenine formamidase, KynB	2.5	1.17E-01	Citronellol	5.2	23152	4	Cytoplasmic	COG1878	Amino acid transport and metabolism
15597278	PA2082	kynR	KynR	1.5	1.19E-01	Citronellol	6.5	17846	4	Cytoplasmic	COG1522	Transcription
15597315	PA2119		alcohol dehydrogenase (Zn-dependent)	9.4	1.95E-02	Oktansaeure	5.4	38561	4	Cytoplasmic	COG1063	Amino acid transport and metabolism
15597365	PA2169		hypothetical protein	7.4	9.21E-03	Citronellol	4.9	16843	2	Cytoplasmic		
15597380	PA2184		conserved hypothetical protein	2.4	6.75E-02	Citronellol	4.7	18990	3	Cytoplasmic	COG3685	Function unknown
15597393	PA2197		conserved hypothetical protein	1.0	7.85E-01	Oktansaeure	6.3	37135	15	Cytoplasmic	COG2130	General function prediction only

Translation, ribosomal structure and biogenesis
Intracellular trafficking and secretion
General function prediction only
General function prediction only
Signal transduction mechanisms

15597394	PA2198		hypothetical protein	1.3	3.84E-01	Citronellol	5.2	12944	5	Cytoplasmic	COG1359	Function unknown	
15597395	PA2199		probable dehydrogenase	1.1	5.73E-01	Citronellol	5.4	30886	12	Cytoplasmic	COG2084	Lipid metabolism	
15597400	PA2204		probable binding protein component of ABC transporter	3.5	2.10E-03	Oktansaeure	9.7	29309	17	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15597418	PA2222		hypothetical protein	2.1	3.98E-02	Citronellol	5.0	23441	7	Unknown			
15597425	PA2229		conserved hypothetical protein	1.1	4.15E-01	Oktansaeure	6.5	26560	7	Cytoplasmic	COG2258	Function unknown	
15597428	PA2232	pslB	PslB	2.6	8.84E-03	Oktansaeure	6.0	53515	17	Periplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15597449	PA2253	ansA	L-asparaginase I	1.1	6.16E-01	Citronellol	5.3	34755	4	Cytoplasmic	COG0252	Amino acid transport and metabolism	Translation, ribosomal structure and biogenesis
15597467	PA2271		probable acetyltransferase	1.1	8.74E-01	Citronellol	6.2	19165	3	Cytoplasmic			
15597486	PA2290	gcd	glucose dehydrogenase	1.5	8.48E-01	Citronellol	6.2	86218	3	Outer Membrane Vesicle	COG4993	Carbohydrate transport and metabolism	
15597496	PA2300	chiC	chitinase	18.3	3.49E-04	Oktansaeure	5.1	53042	8	Extracellular	COG3469	Carbohydrate transport and metabolism	
15597497	PA2301		hypothetical protein	2.8	3.90E-02	Oktansaeure	6.5	19330	10	Cytoplasmic	COG2606	Function unknown	
15597498	PA2302	ambE	AmbE	3.5	5.26E-03	Citronellol	4.8	229041	102	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597499	PA2303	ambD	AmbD	1.3	2.12E-01	Oktansaeure	6.6	38657	7	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597500	PA2304	ambC	AmbC	1.5	3.04E-01	Citronellol	6.8	40696	8	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15597501	PA2305	ambB	AmbB	3.9	2.46E-01	Citronellol	6.3	134446	28	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597519	PA2323		probable glyceraldehyde-3-phosphate dehydrogenase	3.2	6.39E-02	Citronellol	6.4	59960	5	Cytoplasmic	COG1012	Energy production and conversion	
15597526	PA2330		hypothetical protein	1.5	5.82E-01	Oktansaeure	6.6	37680	3	Unknown	COG1960	Lipid metabolism	
15597527	PA2331		hypothetical protein	6.0	3.34E-02	Oktansaeure	5.0	19904	8	Unknown	COG2128	Function unknown	
15597549	PA2353		conserved hypothetical protein	1.6	6.39E-02	Oktansaeure	6.2	43286	2	Cytoplasmic	COG1485	General function prediction only	
15597559	PA2363		hypothetical protein	4.5	3.33E-03	Citronellol	5.2	47778	2	Cytoplasmic	COG3522	Intracellular trafficking, secretion, and vesicular transport	
15597561	PA2365		conserved hypothetical protein	2.9	6.33E-02	Oktansaeure	4.4	20177	4	Cytoplasmic	COG3516	Intracellular trafficking, secretion, and vesicular transport	
15597562	PA2366		uricase PuuD	1.9	1.39E-01	Oktansaeure	5.7	55042	4	Cytoplasmic Membrane	COG3517	Intracellular trafficking, secretion, and vesicular transport	
15597563	PA2367		hypothetical protein	6.1	1.70E-04	Citronellol	4.6	17636	6	Extracellular	COG3157	Intracellular trafficking, secretion, and vesicular transport	
15597567	PA2371		probable ClpA/B-type protease	1.1	6.37E-01	Oktansaeure	5.1	92424	2	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597568	PA2372		hypothetical protein	6.1	3.93E-02	Citronellol	8.4	21241	2	Unknown			
15597574	PA2378		probable aldehyde dehydrogenase	6.7	5.22E-04	Citronellol	8.4	83665	16	Cytoplasmic Membrane	COG1529	Energy production and conversion	
15597581	PA2385	pvdQ	3-oxo-C12-homoserine lactone acylase PvdQ	1.8	1.72E-01	Oktansaeure	7.1	84039	32	Periplasmic	COG2366	General function prediction only	
15597582	PA2386	pvdA	L-ornithine N5-oxygenase	22.4	9.76E-05	Oktansaeure	6.5	49478	24	Cytoplasmic	COG3486	Secondary metabolites biosynthesis, transport, and catabolism	
15597590	PA2394	pvdN	PvdN	2.0	7.65E-02	Oktansaeure	7.3	47981	13	Unknown	COG0520	Posttranslational modification, protein turnover, chaperones	
15597591	PA2395	pvdO	PvdO	1.2	4.43E-01	Oktansaeure	5.4	31070	9	Periplasmic	COG1262	Function unknown	
15597592	PA2396	pvdF	pyoverdine synthetase F	2.1	7.73E-02	Oktansaeure	5.0	31039	23	Cytoplasmic	COG0299	Nucleotide transport and metabolism	
15597594	PA2398	fpvA	ferripyoverdine receptor	2.1	2.73E-03	Oktansaeure	5.3	91167	26	Periplasmic	COG4773	Inorganic ion transport and metabolism	
15597595	PA2399	pvdD	pyoverdine synthetase D	2.0	6.81E-02	Oktansaeure	5.0	273645	52	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
110645305	PA2400	pvdJ	PvdJ	2.0	6.66E-02	Oktansaeure	5.1	240213	9	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597598	PA2402		probable non-ribosomal peptide synthetase	2.7	9.87E-03	Oktansaeure	5.1	569179	197	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597603	PA2407		probable adhesion protein	1.4	9.77E-02	Oktansaeure	9.6	34309	8	Periplasmic	COG0803	Inorganic ion transport and metabolism	
15597606	PA2410		hypothetical protein	1.0	9.75E-01	Citronellol	5.0	31732	11	Unknown	COG0803	Inorganic ion transport and metabolism	
15597607	PA2411		probable thioesterase	34.8	3.80E-05	Oktansaeure	5.4	27846	12	Cytoplasmic	COG3208	Secondary metabolites biosynthesis, transport, and catabolism	
15597609	PA2413	pvdH	L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, PvdH	19.3	3.54E-04	Oktansaeure	6.5	50215	19	Cytoplasmic	COG0160	Amino acid transport and metabolism	
15597615	PA2419		probable hydrolase	2.4	2.15E-02	Citronellol	6.5	24272	2	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15597620	PA2424	pvdL	PvdL	4.4	4.04E-04	Oktansaeure	5.1	480292	173	Unknown	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15597638	PA2442	gcvT2	glycine cleavage system protein T2	1.0	1.00E+00	Oktansaeure	6.4	39882	19	Periplasmic	COG0404	Amino acid transport and metabolism	
15597640	PA2444	glyA2	serine hydroxymethyltransferase	1.4	5.01E-01	Oktansaeure	6.5	44974	5	Periplasmic	COG0112	Amino acid transport and metabolism	
15597641	PA2445	gcvP2	glycine cleavage system protein P2	2.7	2.02E-02	Oktansaeure	6.0	103918	36	Periplasmic	COG1003	Amino acid transport and metabolism	
15597644	PA2448		hypothetical protein	26.5	1.70E-01	Citronellol	6.6	62839	2	Periplasmic	COG1574	General function prediction only	
15597646	PA2450		hypothetical protein	1.3	5.36E-02	Oktansaeure	6.4	34331	5	Periplasmic			
15597651	PA2455		hypothetical protein	1.7	3.01E-02	Oktansaeure	5.6	20332	3	Cytoplasmic	COG3153	General function prediction only	
15597658	PA2462		hypothetical protein	6.3	6.23E-03	Citronellol	5.1	573168	46	Outer Membrane Vesicle	COG3210	Intracellular trafficking and secretion	
15597660	PA2464		hypothetical protein	1.0	9.40E-01	Citronellol	4.6	17626	5	Periplasmic			
15597672	PA2476	dsbG	thiol:disulfide interchange protein DsbG	1.0	9.87E-01	Oktansaeure	7.1	28053	3	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15597677	PA2481		hypothetical protein	3.8	1.31E-02	Citronellol	8.5	31249	2	Periplasmic	COG3258	Energy production and conversion	
15597679	PA2483		conserved hypothetical protein	1.1	8.32E-01	Oktansaeure	6.2	36102	7	Cytoplasmic	COG2141	Energy production and conversion	
15597687	PA2491		probable oxidoreductase	1.5	2.27E-01	Citronellol	5.3	36832	15	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15597689	PA2493	mexE	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion pro	1.6	1.57E-01	Citronellol	8.8	45031	8	Cytoplasmic Membrane	COG0845	Cell envelope biogenesis, outer membrane	
15597690	PA2494	mexF	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF	7.8	1.15E-02	Citronellol	5.4	115509	9	Cytoplasmic Membrane	COG0841	Defense mechanisms	
15597692	PA2496		hypothetical protein	3.1	1.35E-01	Oktansaeure	6.6	19483	2	Cytoplasmic	COG2318	Function unknown	
15597699	PA2503		hypothetical protein	1.5	1.93E-01	Oktansaeure	4.6	45895	3	Cytoplasmic			
15597700	PA2504		hypothetical protein	3.0	2.42E-02	Citronellol	4.3	22822	5	Cytoplasmic	COG4859	Function unknown	
15597703	PA2507	catA	catechol 1,2-dioxygenase	21.4	1.76E-04	Citronellol	5.1	34160	11	Cytoplasmic	COG3485	Secondary metabolites biosynthesis, transport, and catabolism	
15597711	PA2515	xylL	cis-1,2-dihydroxycyclohexa-3,4-diene carboxylate dehydrogenase	69.2	8.84E-02	Citronellol	5.2	27240	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597713	PA2517	xylY	toluate 1,2-dioxygenase beta subunit	78.2	1.40E-04	Citronellol	4.9	19191	2	Cytoplasmic	COG5517	Secondary metabolites biosynthesis, transport, and catabolism	
15597725	PA2529		hypothetical protein	1.1	6.01E-01	Citronellol	5.6	52681	2	Cytoplasmic	COG0312	General function prediction only	
15597726	PA2530		hypothetical protein	1.5	4.04E-01	Citronellol	5.7	48959	6	Unknown	COG0312	General function prediction only	
15597727	PA2531		probable aminotransferase	2.0	2.97E-01	Oktansaeure	9.4	40715	6	Unknown	COG0079	Amino acid transport and metabolism	
15597728	PA2532	tpx	thiol peroxidase	2.0	3.35E-02	Citronellol	4.9	17234	14	Periplasmic	COG2077	Posttranslational modification, protein turnover, chaperones	
15597741	PA2545	xthA	exodeoxyribonuclease III	1.3	6.60E-02	Citronellol	6.4	31003	9	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15597746	PA2550		probable acyl-CoA dehydrogenase	2.1	7.72E-01	Citronellol	6.6	45482	7	Cytoplasmic	COG1960	Lipid metabolism	
15597747	PA2551		probable transcriptional regulator	1.2	4.44E-01	Citronellol	9.9	35144	5	Cytoplasmic	COG0583	Transcription	
15597748	PA2552		probable acyl-CoA dehydrogenase	5.0	8.14E-05	Citronellol	5.6	40908	9	Cytoplasmic	COG1960	Lipid metabolism	
15597749	PA2553		probable acyl-CoA thiolase	5.0	6.79E-04	Citronellol	5.9	41400	17	Cytoplasmic	COG0183	Lipid metabolism	
15597750	PA2554		probable short-chain dehydrogenase	5.2	1.81E-03	Citronellol	6.6	26394	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15597751	PA2555		probable AMP-binding enzyme	3.5	5.15E-02	Citronellol	6.1	60159	5	Cytoplasmic	COG0365	Lipid metabolism	
15597753	PA2557		probable AMP-binding enzyme	25.7	3.40E-04	Citronellol	6.1	62629	25	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15597758	PA2562		hypothetical protein	1.2	9.22E-01	Citronellol	10.0	17384	2	Unknown			
15597763	PA2567		hypothetical protein	3.4	3.92E-01	Oktansaeure	4.8	65617	3	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15597768	PA2572		probable two-component response regulator	6.4	1.71E-01	Citronellol	5.4	50757	2	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15597771	PA2575		hypothetical protein	1.3	2.96E-01	Oktansaeure	6.4	22222	13	Unknown	COG3560	General function prediction only	
15597773	PA2577		probable transcriptional regulator	1.5	3.18E-02	Citronellol	8.0	16459	3	Cytoplasmic	COG1522	Transcription	
15597778	PA2582		hypothetical protein	1.4	3.49E-01	Oktansaeure	10.5	19446	7	Unknown	COG3109	Signal transduction mechanisms	
15597782	PA2586	gacA	response regulator GacA	5.1	6.10E-03	Oktansaeure	6.1	23576	1	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15597788	PA2592		probable periplasmic spermidine/putrescine-binding protein	3.0	3.82E-03	Oktansaeure	6.7	40725	8	Periplasmic	COG0687	Amino acid transport and metabolism	
15597790	PA2594		conserved hypothetical protein	1.7	8.36E-02	Oktansaeure	9.2	34686	6	Periplasmic	COG0715	Inorganic ion transport and metabolism	
15597797	PA2601		probable transcriptional regulator	1.4	9.83E-01	Oktansaeure	5.5	32375	2	Cytoplasmic	COG0583	Transcription	
15597805	PA2609		hypothetical protein	1.5	4.45E-01	Oktansaeure	6.7	36625	4	Cytoplasmic	COG0547	Amino acid transport and metabolism	
15597807	PA2611	cysG	siroheme synthase	6.1	4.75E-02	Oktansaeure	6.3	50370	6	Cytoplasmic	COG0007	Coenzyme metabolism	
15597808	PA2612	serS	seryl-tRNA synthetase	1.1	7.02E-01	Citronellol	5.3	47231	19	Periplasmic	COG0172	Translation, ribosomal structure and biogenesis	
15597809	PA2613		conserved hypothetical protein	2.1	3.15E-02	Oktansaeure	6.3	49047	2	Cytoplasmic	COG2256	DNA replication, recombination, and repair	
15597810	PA2614	lolA	periplasmic chaperone LolA	1.2	5.32E-01	Oktansaeure	5.8	23072	15	Periplasmic	COG2834	Cell envelope biogenesis, outer membrane	
15597812	PA2616	trxB1	thioredoxin reductase 1	1.8	1.57E-01	Oktansaeure	5.2	33818	10	Periplasmic	COG0492	Posttranslational modification, protein turnover, chaperones	
15597814	PA2618		hypothetical protein	2.1	4.53E-02	Citronellol	8.5	27826	6	Cytoplasmic	COG2935	Posttranslational modification, protein turnover, chaperones	
15597816	PA2620	clpA	ATP-binding protease component ClpA	3.2	1.54E-02	Oktansaeure	5.9	84010	29	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597818	PA2622	cspD	cold-shock protein CspD	1.7	1.86E-01	Citronellol	5.6	9600	4	Cytoplasmic	COG1278	Transcription	
15597819	PA2623	icd	isocitrate dehydrogenase	2.1	3.90E-02	Citronellol	4.9	45577	49	Periplasmic	COG0538	Energy production and conversion	
15597820	PA2624	idh	isocitrate dehydrogenase	2.0	1.72E-02	Oktansaeure	6.1	81633	39	Periplasmic	COG2838	Energy production and conversion	
15597821	PA2625		conserved hypothetical protein	2.1	7.43E-02	Citronellol	5.2	17525	6	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15597822	PA2626	trmU	tRNA methyltransferase	1.1	6.83E-01	Oktansaeure	5.9	41886	2	Cytoplasmic	COG0482	Translation, ribosomal structure and biogenesis	
15597823	PA2627		conserved hypothetical protein	2.5	9.02E-02	Oktansaeure	10.9	23030	3	Unknown	COG2915	General function prediction only	

15597825	PA2629	purB	adenylosuccinate lyase	1.3	3.96E-01	Citronellol	5.7	50500	22	Cytoplasmic	COG0015	Nucleotide transport and metabolism	
15597826	PA2630		conserved hypothetical protein	1.3	2.16E-01	Oktansaeure	4.1	44057	4	Cytoplasmic	COG2850	Function unknown	
15597827	PA2631		probable acetyl transferase	1.1	9.60E-01	Citronellol	4.8	16040	8	Cytoplasmic	COG2153	General function prediction only	
15597828	PA2632		hypothetical protein	2.5	5.45E-02	Oktansaeure	8.0	23249	2	Unknown			
15597830	PA2634	aceA	isocitrate lyase AceA	2.0	5.72E-04	Oktansaeure	5.9	58886	59	Periplasmic	COG2224	Energy production and conversion	
15597835	PA2639	nuoD	NADH dehydrogenase I chain C,D	1.7	1.53E-01	Oktansaeure	6.7	68323	7	Cytoplasmic	COG0649	Energy production and conversion	
15597836	PA2640	nuoE	NADH dehydrogenase I chain E	1.9	9.75E-02	Citronellol	4.8	18088	2	Cytoplasmic	COG1905	Energy production and conversion	
15597837	PA2641	nuoF	NADH dehydrogenase I chain F	1.8	4.66E-01	Oktansaeure	7.0	48678	3	Cytoplasmic	COG1894	Energy production and conversion	
15597838	PA2642	nuoG	NADH dehydrogenase I chain G	1.9	4.27E-01	Oktansaeure	6.0	98999	7	Outer Membrane Vesicle	COG1034	Energy production and conversion	
15597840	PA2644	nuoI	NADH Dehydrogenase I chain I	3.2	2.51E-01	Citronellol	6.7	20578	3	Cytoplasmic	COG1143	Energy production and conversion	
15597846	PA2650		conserved hypothetical protein	1.6	1.25E-01	Oktansaeure	5.7	29513	4	Cytoplasmic	COG2226	Coenzyme metabolism	
15597853	PA2657		probable two-component response regulator	1.4	4.24E-02	Oktansaeure	5.9	24729	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15597862	PA2666		probable 6-pyruvoyl tetrahydrobiopterin synthase	1.8	6.24E-02	Citronellol	6.4	13757	2	Cytoplasmic	COG0720	Coenzyme metabolism	
15597875	PA2679		hypothetical protein	1.4	1.92E-01	Citronellol	5.2	27641	5	Cytoplasmic	COG2226	Coenzyme metabolism	
15597878	PA2682		conserved hypothetical protein	5.1	3.36E-03	Citronellol	5.4	45495	3	Cytoplasmic	COG0412	Secondary metabolites biosynthesis, transport, and catabolism	
15597879	PA2683		probable serine/threonine dehydratase, degradative	1.2	4.13E-01	Oktansaeure	6.4	33957	3	Cytoplasmic	COG1171	Amino acid transport and metabolism	
15597880	PA2684		conserved hypothetical protein	1.6	3.19E-01	Citronellol	6.6	145819	6	Outer Membrane	COG3209	Cell envelope biogenesis, outer membrane	
15597881	PA2685	vgrG4	VgrG4	2.1	2.60E-02	Oktansaeure	6.3	81620	4	Cytoplasmic	COG3501	Function unknown	
15597888	PA2692		probable transcriptional regulator	1.4	3.96E-02	Oktansaeure	6.5	19143	5	Cytoplasmic	COG1959	Transcription	
15597895	PA2699		hypothetical protein	5.2	4.27E-02	Citronellol	6.2	67906	2	Unknown	COG1574	General function prediction only	
15597898	PA2702	tse2	Tse2	2.1	1.31E-01	Oktansaeure	6.8	17657	2	Extracellular			
15597901	PA2705		hypothetical protein	3.9	1.23E-01	Oktansaeure	7.1	45584	2	Cytoplasmic	COG3825	Function unknown	
15597903	PA2707		hypothetical protein	1.2	2.97E-01	Oktansaeure	6.1	32205	23	Cytoplasmic	COG0714	General function prediction only	
15597905	PA2709	cysK	cysteine synthase A	1.0	8.08E-01	Citronellol	6.6	34309	18	Cytoplasmic	COG0031	Amino acid transport and metabolism	
15597913	PA2717	cpo	chloroperoxidase precursor	3.0	3.17E-02	Citronellol	5.9	30435	9	Cytoplasmic	COG0596	General function prediction only	
15597916	PA2720		hypothetical protein	1.1	6.85E-01	Oktansaeure	4.7	23816	3	Cytoplasmic			
15597917	PA2721		hypothetical protein	11.5	1.27E-03	Citronellol	4.6	17356	3	Cytoplasmic	COG3865	Function unknown	
15597918	PA2722		hypothetical protein	1.1	5.96E-01	Citronellol	6.3	14641	2	Unknown	COG3791	Function unknown	
15597921	PA2725		probable chaperone	19.0	1.68E-01	Oktansaeure	6.2	68829	4	Cytoplasmic	COG0542	Posttranslational modification, protein turnover, chaperones	
15597928	PA2732		hypothetical protein	5.1	1.17E-01	Citronellol	6.2	128671	24	Cytoplasmic	COG0610	Defense mechanisms	
15597930	PA2734		hypothetical protein	1.1	6.20E-01	Citronellol	6.1	48703	11	Cytoplasmic	COG0732	Defense mechanisms	
15597931	PA2735		probable restriction-modification system protein	1.4	5.37E-02	Oktansaeure	5.4	89570	30	Cytoplasmic	COG0286	Defense mechanisms	
15597933	PA2737		conserved hypothetical protein	7.5	1.08E-01	Oktansaeure	10.2	10254	2	Unknown	COG0789	Transcription	
15597935	PA2739	pheT	phenylalanyl-tRNA synthetase, beta subunit	1.1	5.19E-01	Oktansaeure	5.1	86799	35	Periplasmic	COG0072	Translation, ribosomal structure and biogenesis	
15597936	PA2740	pheS	phenylalanyl-tRNA synthetase, alpha-subunit	1.3	3.12E-01	Citronellol	5.8	38063	14	Periplasmic	COG0016	Translation, ribosomal structure and biogenesis	
15597937	PA2741	rplT	50S ribosomal protein L20	1.3	5.48E-01	Oktansaeure	12.3	13365	7	Outer Membrane Vesicle	COG0292	Translation, ribosomal structure and biogenesis	
15597939	PA2743	infC	translation initiation factor IF-3	2.5	3.68E-02	Oktansaeure	10.3	20864	8	Cytoplasmic	COG0290	Translation, ribosomal structure and biogenesis	
15597940	PA2744	thrS	threonyl-tRNA synthetase	1.3	3.40E-02	Oktansaeure	6.3	73080	38	Periplasmic	COG0441	Translation, ribosomal structure and biogenesis	
15597951	PA2755	eco	ecotin precursor	1.9	1.20E-01	Citronellol	6.5	17228	8	Periplasmic	COG4574	General function prediction only	
15597956	PA2760	oprQ	OprQ	1.3	5.67E-01	Citronellol	5.5	46850	15	Periplasmic			
15597960	PA2764		hypothetical protein	2.4	5.94E-04	Citronellol	6.0	24519	10	Cytoplasmic			
15597961	PA2765		hypothetical protein	2.0	1.89E-02	Citronellol	4.5	32396	13	Unknown	COG2837	Inorganic ion transport and metabolism	
15597966	PA2770		hypothetical protein	1.0	8.87E-01	Citronellol	4.7	28258	9	Cytoplasmic	COG0384	General function prediction only	
15597988	PA2792		hypothetical protein	1.9	1.31E-01	Oktansaeure	6.4	22070	2	Unknown			
15597990	PA2794		pseudaminidase	2.6	1.17E-03	Citronellol	6.2	47151	7	Unknown			
15597992	PA2796	tal	transaldolase	1.2	9.91E-02	Citronellol	4.9	33946	22	Cytoplasmic	COG0176	Carbohydrate transport and metabolism	
15597993	PA2797		hypothetical protein	2.8	1.18E-02	Oktansaeure	4.6	17710	4	Cytoplasmic	COG1366	Signal transduction mechanisms	
15597994	PA2798		probable two-component response regulator	1.0	8.54E-01	Oktansaeure	4.6	43485	5	Cytoplasmic	COG2208	Signal transduction mechanisms	Transcription
15597996	PA2800		conserved hypothetical protein	1.5	3.80E-01	Oktansaeure	5.3	26148	2	Periplasmic	COG2853	Cell envelope biogenesis, outer membrane	
15598002	PA2806		conserved hypothetical protein	1.1	9.06E-01	Citronellol	5.4	30848	6	Cytoplasmic	COG2904	Function unknown	
15598005	PA2809	copR	two-component response regulator, CopR	1.4	3.70E-01	Oktansaeure	4.6	25716	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15598008	PA2812		probable ATP-binding component of ABC transporter	2.9	1.98E-01	Citronellol	6.3	34540	5	Cytoplasmic Membrane	COG1131	Defense mechanisms	
15598009	PA2813		probable glutathione S-transferase	1.4	4.96E-01	Citronellol	4.8	23405	13	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598011	PA2815		probable acyl-CoA dehydrogenase	1.7	2.75E-01	Oktansaeure	5.9	88762	5	Outer Membrane Vesicle	COG1960	Lipid metabolism	
15598017	PA2821		probable glutathione S-transferase	1.0	9.88E-01	Citronellol	6.1	24716	4	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15598018	PA2822		conserved hypothetical protein	1.6	9.36E-03	Citronellol	4.4	17129	2	Unknown	COG1956	Signal transduction mechanisms	
15598019	PA2823		conserved hypothetical protein	1.2	4.86E-01	Oktansaeure	5.7	33760	10	Cytoplasmic	COG2607	General function prediction only	
15598022	PA2826		probable glutathione peroxidase	6.7	1.58E-04	Citronellol	8.3	17659	6	Cytoplasmic	COG0386	Posttranslational modification, protein turnover, chaperones	
15598024	PA2828		probable aminotransferase	1.1	8.20E-01	Oktansaeure	6.1	44799	7	Periplasmic	COG0436	Amino acid transport and metabolism	
15598025	PA2829		hypothetical protein	1.5	4.71E-01	Citronellol	5.2	16432	2	Unknown			
15598027	PA2831		conserved hypothetical protein	2.6	1.44E-01	Citronellol	5.3	42933	7	Cytoplasmic	COG2866	Amino acid transport and metabolism	
15598028	PA2832	tpm	thiopurine methyltransferase	1.5	4.09E-02	Citronellol	4.7	24875	4	Cytoplasmic			
15598037	PA2841		probable enoyl-CoA hydratase/isomerase	3.4	1.28E-04	Citronellol	5.4	28612	7	Cytoplasmic	COG1024	Lipid metabolism	
15598046	PA2850	ohr	organic hydroperoxide resistance protein	279.4	3.52E-02	Citronellol	7.4	14522	2	Cytoplasmic	COG1764	Secondary metabolites biosynthesis, transport and catabolism	
15598047	PA2851	efp	translation elongation factor P	1.2	3.16E-01	Citronellol	4.5	20985	9	Periplasmic	COG0231	Translation, ribosomal structure and biogenesis	
15598049	PA2853	oprI	Outer membrane lipoprotein OprI precursor	2.1	4.24E-02	Citronellol	8.5	8835	2	Outer Membrane			
15598050	PA2854		conserved hypothetical protein	1.1	5.44E-01	Citronellol	5.6	34799	7	Periplasmic	COG1376	Function unknown	
15598052	PA2856	tesA	acyl-CoA thioesterase I precursor	2.3	1.10E-01	Citronellol	5.9	21037	7	Periplasmic	COG2755	Amino acid transport and metabolism	
15598058	PA2862	lipA	lactonizing lipase precursor	47.3	5.27E-03	Citronellol	6.9	32723	6	Extracellular	COG1075	General function prediction only	
15598062	PA2866	mttC	secretion protein MttC	1.1	5.73E-01	Oktansaeure	6.1	29544	2	Cytoplasmic	COG0084	DNA replication, recombination, and repair	
15598065	PA2869		hypothetical protein	3.0	1.39E-02	Citronellol	8.7	18206	4	Cytoplasmic Membrane	COG3915	Function unknown	
15598067	PA2871		hypothetical protein	1.5	4.00E-02	Citronellol	5.4	28695	15	Unknown	COG1946	Lipid metabolism	
15598072	PA2876	pyrF	orotidine 5'-phosphate decarboxylase	1.1	6.86E-01	Citronellol	5.3	24394	11	Cytoplasmic	COG0284	Nucleotide transport and metabolism	
15598081	PA2885	atuR	putative repressor of atu genes	3.1	1.70E-02	Citronellol	4.9	22057	5	Unknown	COG1309	Transcription	
15598082	PA2886	atuA	expressed protein with apparent function in citronellol catabolism	64.0	2.57E-05	Citronellol	5.1	64435	28	Cytoplasmic			
15598083	PA2887	atuB	putative dehydrogenase involved in catabolism of citronellol	79.9	1.99E-06	Citronellol	7.3	30751	23	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598084	PA2888	atuC	geranyl-CoA carboxylase, beta-subunit	45.9	1.17E-04	Citronellol	6.5	57328	26	Cytoplasmic	COG4799	Lipid metabolism	
15598085	PA2889	atuD	citronellyl-CoA dehydrogenase, AtuD	61.5	6.27E-06	Citronellol	6.3	42714	45	Cytoplasmic	COG1960	Lipid metabolism	
15598086	PA2890	atuE	putative isohexenylglutaconyl-CoA hydratase	35.4	2.06E-07	Citronellol	5.2	27717	15	Cytoplasmic	COG1024	Lipid metabolism	
15598087	PA2891	atuF	geranyl-CoA carboxylase, alpha-subunit (biotin-containing)	27.5	1.76E-04	Citronellol	6.1	71747	32	Cytoplasmic	COG4770	Lipid metabolism	
15598088	PA2892	atuG	GCase, alpha-subunit (biotin-containing)	87.6	4.56E-07	Citronellol	7.2	29631	22	Cytoplasmic	COG4221	General function prediction only	
15598095	PA2899		probable transcriptional regulator	2.5	3.39E-02	Oktansaeure	7.6	23250	9	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598098	PA2902		hypothetical protein	1.1	4.98E-01	Oktansaeure	4.8	30448	3	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598100	PA2904	cobI	precorrin-2 methyltransferase CobI	1.7	3.04E-03	Citronellol	6.3	27275	3	Cytoplasmic	COG2243	Coenzyme metabolism	
15598101	PA2905	cobH	precorrin isomerase CobH	1.6	4.44E-02	Citronellol	5.7	21650	4	Cytoplasmic	COG2082	Coenzyme metabolism	
15598114	PA2918		probable short-chain dehydrogenase	2.4	3.96E-03	Citronellol	7.2	26738	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598135	PA2939		probable aminopeptidase	13.6	6.94E-04	Citronellol	4.8	57511	18	Extracellular	COG2234	General function prediction only	
15598136	PA2940		probable acyl-CoA thiolase	15.7	1.26E-02	Citronellol	5.5	39211	2	Cytoplasmic	COG0183	Lipid metabolism	
15598140	PA2944	cobN	cobalamin biosynthetic protein CobN	1.3	9.54E-01	Citronellol	5.2	138499	3	Cytoplasmic	COG1429	Coenzyme metabolism	
15598141	PA2945		conserved hypothetical protein	1.6	3.28E-01	Citronellol	4.9	41175	3	Cytoplasmic	COG0523	General function prediction only	
15598146	PA2950	pfmß	proton motive force protein, PMF	2.0	3.62E-02	Citronellol	4.8	43528	17	Cytoplasmic	COG3007	Function unknown	
15598147	PA2951	etfA	electron transfer flavoprotein alpha-subunit	1.1	1.14E-01	Oktansaeure	4.8	31423	20	Periplasmic	COG2025	Energy production and conversion	
15598148	PA2952	etfB	electron transfer flavoprotein beta-subunit	1.0	9.43E-01	Citronellol	9.6	26377	25	Outer Membrane Vesicle	COG2086	Energy production and conversion	
15598149	PA2953		electron transfer flavoprotein-ubiquinone oxidoreductase	1.5	1.65E-01	Citronellol	5.6	59896	14	Outer Membrane Vesicle	COG0644	Energy production and conversion	
15598150	PA2954		hypothetical protein	1.5	2.29E-01	Oktansaeure	4.9	21240	6	Cytoplasmic	COG3816	Function unknown	
15598154	PA2958		hypothetical protein	1.0	9.53E-01	Oktansaeure	6.3	42109	2	Cytoplasmic	COG0520	Posttranslational modification, protein turnover, chaperones	
15598155	PA2959		conserved hypothetical protein	1.1	4.80E-01	Oktansaeure	5.3	28114	5	Cytoplasmic	COG0084	DNA replication, recombination, and repair	

15598158	PA2962	tmk	thymidylate kinase	1.0	5.35E-01	Oktansaeure	4.9	23077	5	Cytoplasmic	COG0125	Nucleotide transport and metabolism	
15598160	PA2964	pabC	4-amino-4-deoxychorismate lyase	2.0	6.05E-02	Citronellol	5.7	29886	4	Cytoplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15598161	PA2965	fabF1	beta-ketoacyl-acyl carrier protein synthase II	1.0	8.39E-01	Citronellol	5.8	43465	10	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598162	PA2966	acpP	acyl carrier protein	2.3	2.44E-01	Citronellol	3.8	8741	3	Cytoplasmic	COG0236	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598163	PA2967	fabG	3-oxoacyl-[acyl-carrier-protein] reductase	1.1	5.26E-01	Citronellol	6.6	25585	13	Periplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598164	PA2968	fabD	malonyl-CoA-[acyl-carrier-protein] transacylase	1.1	6.26E-01	Citronellol	4.8	32444	11	Periplasmic	COG0331	Lipid metabolism	
15598168	PA2972		conserved hypothetical protein	1.3	6.09E-01	Citronellol	6.0	21054	8	Cytoplasmic	COG0424	Cell division and chromosome partitioning	
15598172	PA2976	rne	ribonuclease E	1.2	3.67E-01	Oktansaeure	4.6	117463	37	Outer Membrane Vesicle	COG1530	Translation, ribosomal structure and biogenesis	
15598173	PA2977	murB	UDP-N-acetylpyruvoylglucosamine reductase	1.4	1.54E-01	Oktansaeure	6.7	37595	3	Cytoplasmic	COG0812	Cell envelope biogenesis, outer membrane	
15598174	PA2978	ptpA	phosphotyrosine protein phosphatase	1.4	1.88E-01	Citronellol	6.1	17152	6	Cytoplasmic	COG0394	Signal transduction mechanisms	
15598175	PA2979	kdsB	3-deoxy-manno-octulosonate cytidylyltransferase	1.2	5.06E-01	Citronellol	5.4	27646	10	Cytoplasmic	COG1212	Cell envelope biogenesis, outer membrane	
15598187	PA2991	sth	soluble pyridine nucleotide transhydrogenase	1.1	4.67E-01	Oktansaeure	6.7	51161	15	Cytoplasmic	COG1249	Energy production and conversion	
15598197	PA3001		probable glyceraldehyde-3-phosphate dehydrogenase	2.1	2.98E-02	Citronellol	8.0	50111	7	Periplasmic	COG0057	Carbohydrate transport and metabolism	
15598198	PA3002	mfd	transcription-repair coupling protein Mfd	3.9	1.52E-01	Citronellol	5.7	128763	36	Periplasmic	COG1197	DNA replication, recombination, and repair	Transcription
15598199	PA3003		hypothetical protein	1.4	4.40E-02	Oktansaeure	4.5	22474	4	Periplasmic			
15598200	PA3004		5'-methylthioinosine phosphorylase	1.5	1.02E-01	Citronellol	6.6	26266	7	Cytoplasmic	COG0005	Nucleotide transport and metabolism	
15598201	PA3005	nagZ	beta-N-acetyl-D-glucosaminidase	1.3	3.04E-01	Oktansaeure	6.2	36101	10	Cytoplasmic	COG1472	Carbohydrate transport and metabolism	
15598202	PA3006	psrA	transcriptional regulator PsrA	1.0	8.80E-01	Oktansaeure	9.9	25784	5	Cytoplasmic	COG1309	Transcription	
15598203	PA3007	lexA	repressor protein LexA	1.5	7.63E-02	Citronellol	6.5	22506	3	Cytoplasmic	COG1974	Transcription	Signal transduction mechanisms
15598207	PA3011	topA	DNA topoisomerase I	1.6	1.25E-01	Citronellol	8.7	97282	47	Cytoplasmic	COG0550	DNA replication, recombination, and repair	
15598209	PA3013	foaB	fatty-acid oxidation complex beta-subunit	1.2	4.35E-01	Oktansaeure	6.8	41643	32	Cytoplasmic	COG0183	Lipid metabolism	
15598210	PA3014	faoA	fatty-acid oxidation complex alpha-subunit	1.5	5.37E-02	Oktansaeure	5.6	76954	53	Periplasmic	COG1250	Lipid metabolism	
15598211	PA3015		hypothetical protein	4.4	4.64E-02	Citronellol	5.9	30469	5	Unknown			
15598215	PA3019		probable ATP-binding component of ABC transporter	3.3	4.70E-04	Oktansaeure	5.0	71155	16	Cytoplasmic	COG0488	General function prediction only	
15598217	PA3021		hypothetical protein	2.0	4.99E-02	Oktansaeure	7.8	14206	7	Unknown	COG3755	Function unknown	
15598218	PA3022		hypothetical protein	1.2	3.99E-01	Oktansaeure	5.9	29579	13	Cytoplasmic	COG3217	General function prediction only	
15598219	PA3023		conserved hypothetical protein	1.5	1.13E-01	Citronellol	4.7	31504	11	Cytoplasmic	COG1597	Lipid metabolism	General function prediction only
15598224	PA3028	moeA2	molybdenum cofactor biosynthesis protein A2	1.6	3.14E-02	Citronellol	5.0	43359	5	Cytoplasmic	COG0303	Coenzyme metabolism	
15598225	PA3029	moaB2	molybdopterin biosynthetic protein B2	1.4	4.48E-02	Citronellol	5.6	19224	11	Cytoplasmic	COG0521	Coenzyme metabolism	
15598226	PA3030	mobA	molybdopterin-guanine dinucleotide biosynthesis protein MobA	3.6	4.19E-02	Oktansaeure	7.6	21870	8	Cytoplasmic	COG0746	Coenzyme metabolism	
15598228	PA3032	snr1	cytochrome c Snr1	1.6	1.89E-01	Citronellol	6.8	52500	7	Cytoplasmic	COG1858	Inorganic ion transport and metabolism	
15598230	PA3034		probable transcriptional regulator	5.2	1.34E-02	Oktansaeure	8.5	20988	2	Cytoplasmic			
15598234	PA3038		probable porin	8.0	3.01E-02	Citronellol	7.1	46712	9	Periplasmic			
15598239	PA3043		conserved hypothetical protein	1.4	1.60E-01	Citronellol	6.5	50083	6	Cytoplasmic	COG0232	Nucleotide transport and metabolism	
15598244	PA3048		conserved hypothetical protein	1.1	4.39E-01	Oktansaeure	8.0	81155	11	Cytoplasmic	COG0116	DNA replication, recombination, and repair	
15598248	PA3052		hypothetical protein	1.4	7.51E-02	Oktansaeure	9.3	36362	2	Cytoplasmic			
15598249	PA3053		probable hydrolytic enzyme	1.0	6.75E-01	Citronellol	8.0	37485	3	Periplasmic	COG0596	General function prediction only	
15598250	PA3054		hypothetical protein	2.9	1.42E-02	Oktansaeure	6.6	71165	7	Periplasmic	COG2866	Amino acid transport and metabolism	
15598264	PA3068	gdhB	NAD-dependent glutamate dehydrogenase	3.9	1.43E-01	Citronellol	6.1	182637	12	Outer Membrane Vesicle	COG2902	Amino acid transport and metabolism	
15598266	PA3070		conserved hypothetical protein	2.3	1.48E-02	Citronellol	4.9	36148	2	Cytoplasmic	COG0714	General function prediction only	
15598276	PA3080		hypothetical protein	11.6	6.01E-04	Citronellol	4.8	38479	10	Unknown	COG4447	General function prediction only	
15598277	PA3081		conserved hypothetical protein	1.5	4.86E-02	Citronellol	9.2	50680	9	Periplasmic			
15598278	PA3082	gbt	glycine betaine transmethylase	1.7	2.19E-01	Oktansaeure	4.5	71403	7	Periplasmic			
15598279	PA3083	pepN	aminopeptidase N	1.8	5.10E-02	Citronellol	4.9	100046	46	Periplasmic	COG0308	Amino acid transport and metabolism	
15598284	PA3088		conserved hypothetical protein	1.2	5.02E-01	Citronellol	7.3	32140	8	Cytoplasmic	COG0061	Coenzyme metabolism	
15598288	PA3092	fadH1	2,4-dienoyl-CoA reductase FadH1	5.5	2.67E-03	Citronellol	7.2	72969	20	Cytoplasmic	COG1902	Energy production and conversion	
15598297	PA3101	xcpT	general secretion pathway protein G	1.2	4.57E-01	Oktansaeure	8.8	16112	2	Cytoplasmic Membrane	COG2165	Cell motility and secretion	Intracellular trafficking and secretion
15598302	PA3106		probable short-chain dehydrogenase	1.6	5.77E-02	Citronellol	4.6	26997	6	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598303	PA3107	metZ	o-succinylhomoserine sulfhydrylase	1.1	4.37E-01	Citronellol	6.3	43185	15	Periplasmic	COG0626	Amino acid transport and metabolism	
15598304	PA3108	purF	amidophosphoribosyltransferase	1.0	9.14E-01	Oktansaeure	6.8	55370	17	Outer Membrane Vesicle	COG0034	Nucleotide transport and metabolism	
15598307	PA3111	folC	folylpolyglutamate synthetase	1.1	8.03E-01	Citronellol	5.0	46505	3	Cytoplasmic	COG0285	Coenzyme metabolism	
15598308	PA3112	accD	acetyl-CoA carboxylase beta subunit	1.1	8.94E-01	Citronellol	7.1	31843	12	Periplasmic	COG0777	Lipid metabolism	
15598309	PA3113	trpF	N-(5'phosphoribosyl)anthranilate (PRA) isomerase	1.6	2.65E-01	Oktansaeure	6.8	22280	4	Cytoplasmic	COG0135	Amino acid transport and metabolism	
15598310	PA3114	truA	tRNA-pseudouridine synthase I	1.1	6.43E-01	Oktansaeure	9.3	31483	2	Cytoplasmic	COG0101	Translation, ribosomal structure and biogenesis	
15598311	PA3115	fimV	Motility protein FimV	8.5	1.40E-01	Oktansaeure	4.0	96928	2	Outer Membrane Vesicle	COG3170	Cell motility and secretion	Intracellular trafficking and secretion
15598313	PA3117	asd	aspartate semialdehyde dehydrogenase	1.1	6.34E-01	Oktansaeure	5.5	40494	24	Periplasmic	COG0136	Amino acid transport and metabolism	
15598314	PA3118	leuB	3-isopropylmalate dehydrogenase	1.1	8.01E-01	Citronellol	4.8	39120	15	Cytoplasmic	COG0473	Amino acid transport and metabolism	
15598316	PA3120	leuD	3-isopropylmalate dehydratase small subunit	1.5	4.72E-02	Citronellol	4.7	24011	13	Cytoplasmic	COG0066	Amino acid transport and metabolism	
15598317	PA3121	leuC	3-isopropylmalate dehydratase large subunit	1.6	4.63E-02	Citronellol	6.3	51042	15	Cytoplasmic	COG0065	Amino acid transport and metabolism	
15598318	PA3122		probable transcriptional regulator	1.2	4.97E-01	Oktansaeure	6.4	32835	5	Cytoplasmic	COG0583	Transcription	
15598319	PA3123		conserved hypothetical protein	3.0	3.90E-02	Citronellol	4.6	13516	7	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
15598322	PA3126	ibpA	heat-shock protein IbpA	4.7	4.83E-02	Oktansaeure	6.1	16583	3	Cytoplasmic	COG0071	Posttranslational modification, protein turnover, chaperones	
15598323	PA3127		hypothetical protein	2.1	5.47E-03	Citronellol	5.0	29403	12	Unknown			
15598324	PA3128		probable short-chain dehydrogenase	1.9	1.02E-03	Citronellol	6.8	26219	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598326	PA3130		hypothetical protein	2.5	1.14E-02	Oktansaeure	5.2	16555	7	Unknown	COG0824	General function prediction only	
15598327	PA3131		probable aldolase	1.1	7.19E-01	Oktansaeure	5.3	22852	7	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598330	PA3134	gltX	glutamyl-tRNA synthetase	1.5	1.18E-01	Citronellol	6.7	56749	18	Cytoplasmic	COG0008	Translation, ribosomal structure and biogenesis	
15598334	PA3138	uvrB	excinuclease ABC subunit B	1.3	1.09E-01	Oktansaeure	5.1	76067	11	Cytoplasmic	COG0556	DNA replication, recombination, and repair	
15598335	PA3139		probable amino acid aminotransferase	1.4	1.03E-01	Citronellol	6.6	43319	19	Periplasmic	COG1448	Amino acid transport and metabolism	
15598344	PA3148	wbpI	UDP-N-acetylglucosamine 2-epimerase WbpI	1.3	1.51E-01	Oktansaeure	5.8	38907	18	Cytoplasmic	COG0381	Cell envelope biogenesis, outer membrane	
15598347	PA3151	hisF2	imidazoleglycerol-phosphate synthase, cyclase subunit	1.2	1.52E-01	Citronellol	5.7	27448	6	Cytoplasmic	COG0107	Amino acid transport and metabolism	
15598348	PA3152	hisH2	glutamine amidotransferase	1.5	2.53E-02	Oktansaeure	7.1	22663	10	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15598351	PA3155	wbpE	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3-uluronic acid transaminase, wbpE	1.1	3.62E-01	Citronellol	6.0	38924	17	Periplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598352	PA3156	wbpD	UDP-2-acetamido-3-amino-2,3-dideoxy-d-glucuronic acid N-acetyltransferase, W	1.2	6.38E-01	Oktansaeure	7.8	20562	5	Cytoplasmic	COG1045	Amino acid transport and metabolism	
15598354	PA3158	wbpB	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	1.4	1.98E-01	Oktansaeure	6.6	35717	20	Cytoplasmic	COG0673	General function prediction only	
15598355	PA3159	wbpA	UDP-N-acetyl-d-glucosamine 6-Dehydrogenase	1.2	3.45E-01	Citronellol	5.2	48155	35	Periplasmic	COG0677	Cell envelope biogenesis, outer membrane	
15598358	PA3162	rpsA	30S ribosomal protein S1	1.1	4.61E-01	Oktansaeure	4.6	61869	32	Cytoplasmic	COG0539	Translation, ribosomal structure and biogenesis	
15598359	PA3163	cmk	cytidylate kinase	1.1	6.27E-01	Citronellol	4.8	24637	11	Cytoplasmic	COG0283	Nucleotide transport and metabolism	
15598361	PA3165	hisC2	histidinol-phosphate aminotransferase	11.5	7.55E-05	Oktansaeure	4.8	39483	7	Cytoplasmic	COG0079	Amino acid transport and metabolism	
15598362	PA3166	pheA	chorismate mutase	1.2	4.64E-01	Citronellol	6.3	40632	9	Cytoplasmic	COG0077	Amino acid transport and metabolism	
15598363	PA3167	serC	3-phosphoserine aminotransferase	1.4	2.11E-01	Citronellol	4.7	39917	15	Periplasmic	COG1932	Coenzyme metabolism	Amino acid transport and metabolism
15598364	PA3168	gyrA	DNA gyrase subunit A	1.3	2.72E-01	Citronellol	4.6	101134	45	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15598365	PA3169		5-methylthioribose-1-phosphate isomerase MtnA	1.2	1.48E-01	Oktansaeure	5.1	39425	8	Cytoplasmic	COG0182	Translation, ribosomal structure and biogenesis	
15598366	PA3170		conserved hypothetical protein	1.7	3.60E-02	Citronellol	5.5	48493	6	Cytoplasmic	COG0402	Nucleotide transport and metabolism	General function prediction only
15598367	PA3171	ubiG	3-demethylubiquinone-9 3-methyltransferase	2.8	1.17E-02	Oktansaeure	6.3	25860	7	Cytoplasmic	COG2227	Coenzyme metabolism	
15598368	PA3172		probable hydrolase	1.1	6.44E-01	Oktansaeure	5.0	24944	9	Cytoplasmic	COG0546	General function prediction only	
15598369	PA3173		probable short-chain dehydrogenase	1.0	7.16E-01	Oktansaeure	4.9	26332	7	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598376	PA3180		hypothetical protein	6.4	1.14E-02	Oktansaeure	4.7	16863	2	Unknown	COG1051	Nucleotide transport and metabolism	
15598377	PA3181		2-keto-3-deoxy-6-phosphogluconate aldolase	2.7	2.35E-02	Citronellol	7.6	23953	3	Cytoplasmic	COG0800	Carbohydrate transport and metabolism	
15598378	PA3182	pgl	6-phosphogluconolactonase	1.7	4.28E-02	Citronellol	6.5	25571	3	Unknown	COG0363	Carbohydrate transport and metabolism	
15598386	PA3190		probable binding protein component of ABC sugar transporter	2.4	9.50E-02	Citronellol	5.8	45131	7	Periplasmic	COG1653	Carbohydrate transport and metabolism	
15598389	PA3193	glk	glucokinase	1.3	7.38E-01	Citronellol	5.0	34606	3	Cytoplasmic	COG0837	Carbohydrate transport and metabolism	
15598390	PA3194	edd	phosphogluconate dehydratase	5.1	4.74E-02	Citronellol	6.7	65182	6	Cytoplasmic	COG0129	Amino acid transport and metabolism	Carbohydrate transport and metabolism
15598391	PA3195	gapA	glyceraldehyde 3-phosphate dehydrogenase	1.6	3.96E-01	Citronellol	6.6	36170	7	Cytoplasmic	COG0057	Carbohydrate transport and metabolism	
15598392	PA3196		hypothetical protein	3.5	1.09E-02	Citronellol	3.9	19293	2	Unknown			
15598395	PA3199		conserved hypothetical protein	1.4	5.62E-01	Citronellol	6.7	23144	4	Cytoplasmic	COG0009	Translation, ribosomal structure and biogenesis	
15598401	PA3205		hypothetical protein	7.6	7.72E-03	Citronellol	10.5	16696	3	Unknown	COG3678	Intracellular trafficking and secretion	Cell motility and secretio

15598404	PA3208		conserved hypothetical protein	1.2	9.63E-01	Citronellol	6.5	19948	12	Cytoplasmic Membrane	COG0778	Energy production and conversion	
15598410	PA3214		hypothetical protein	1.5	3.38E-01	Oktansaeure	10.4	23214	3	Unknown	COG3218	General function prediction only	
15598421	PA3225		probable transcriptional regulator	1.2	1.37E-01	Citronellol	7.4	34098	8	Cytoplasmic	COG0583	Transcription	
15598423	PA3227	ppiA	peptidyl-prolyl cis-trans isomerase A	1.7	1.67E-01	Citronellol	8.5	20104	11	Periplasmic	COG0652	Posttranslational modification, protein turnover, chaperones	
15598429	PA3233		hypothetical protein	3.9	4.87E-02	Citronellol	6.3	66563	2	Cytoplasmic	COG2905	Signal transduction mechanisms	
15598439	PA3243	minC	cell division inhibitor MinC	1.2	2.29E-01	Oktansaeure	6.5	28124	10	Cytoplasmic	COG0850	Cell division and chromosome partitioning	
15598440	PA3244	minD	cell division inhibitor MinD	1.2	2.21E-01	Oktansaeure	5.5	29617	21	Periplasmic	COG2894	Cell division and chromosome partitioning	
15598443	PA3247		hypothetical protein	2.4	6.91E-02	Citronellol	6.0	46658	12	Cytoplasmic	COG1362	Amino acid transport and metabolism	
15598446	PA3250		hypothetical protein	2.8	5.09E-02	Citronellol	6.2	38285	14	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15598451	PA3255		hypothetical protein	1.7	1.09E-02	Citronellol	4.4	21635	7	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15598452	PA3256		probable oxidoreductase	1.1	4.32E-01	Citronellol	5.2	33387	14	Cytoplasmic Membrane	COG0604	Energy production and conversion	General function prediction only
15598453	PA3257	prc	periplasmic tail-specific protease	1.1	4.55E-01	Oktansaeure	6.6	78182	37	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15598458	PA3262		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.1	6.61E-01	Oktansaeure	4.8	26845	11	Outer Membrane Vesicle	COG0545	Posttranslational modification, protein turnover, chaperones	
15598459	PA3263		conserved hypothetical protein	1.2	2.63E-02	Oktansaeure	4.7	34015	17	Cytoplasmic	COG2974	DNA replication, recombination, and repair	
15598473	PA3277		probable short-chain dehydrogenase	2.0	7.69E-02	Citronellol	6.5	29251	3	Cytoplasmic	COG0300	General function prediction only	
15598482	PA3286		hypothetical protein	1.1	4.24E-01	Citronellol	6.4	38139	15	Periplasmic	COG0332	acyl-carrier-protein	
15598483	PA3287		conserved hypothetical protein	1.9	2.76E-02	Citronellol	5.5	18194	3	Periplasmic	COG0666	General function prediction only	
15598493	PA3297		probable ATP-dependent helicase	2.6	1.16E-01	Oktansaeure	8.5	149907	2	Cytoplasmic Membrane	COG1643	DNA replication, recombination, and repair	
15598495	PA3299	fadD1	long-chain-fatty-acid--CoA ligase	3.3	6.72E-03	Citronellol	7.5	61654	24	Outer Membrane Vesicle	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598496	PA3300	fadD2	long-chain-fatty-acid--CoA ligase	3.1	1.57E-02	Citronellol	7.2	61736	11	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15598498	PA3302		conserved hypothetical protein	1.2	6.40E-01	Citronellol	5.0	16901	7	Unknown	COG2030	Lipid metabolism	
15598504	PA3308	hepA	RNA helicase HepA	1.3	3.08E-01	Citronellol	4.8	106839	19	Periplasmic	COG0553	Transcription	DNA replication, recombination, and repair
15598505	PA3309		conserved hypothetical protein	3.0	6.85E-02	Oktansaeure	5.4	16496	16	Periplasmic	COG0589	Signal transduction mechanisms	
15598508	PA3312		probable 3-hydroxyisobutyrate dehydrogenase	1.0	9.87E-01	Oktansaeure	5.5	30908	7	Cytoplasmic	COG2084	Lipid metabolism	
15598509	PA3313		hypothetical protein	1.2	3.56E-01	Citronellol	10.2	36539	22	Periplasmic	COG3221	Inorganic ion transport and metabolism	
15598522	PA3326	clpP2	ClpP2	3.1	3.44E-02	Oktansaeure	5.4	22142	13	Cytoplasmic	COG0740	Posttranslational modification, protein turnover, chaperones	Intracellular trafficking and secretion
15598523	PA3327		probable non-ribosomal peptide synthetase	1.7	7.46E-02	Oktansaeure	5.5	259403	99	Cytoplasmic	COG1020	Secondary metabolites biosynthesis, transport, and catabolism	
15598524	PA3328		probable FAD-dependent monooxygenase	16.3	3.52E-04	Oktansaeure	8.3	42498	3	Unknown	COG0654	Coenzyme metabolism	Energy production and conversion
15598525	PA3329		hypothetical protein	2.8	1.51E-03	Oktansaeure	6.2	49134	11	Cytoplasmic			
15598526	PA3330		probable short chain dehydrogenase	28.8	3.35E-04	Oktansaeure	8.8	32031	11	Cytoplasmic	COG4221	General function prediction only	
15598527	PA3331		cytochrome P450	4.5	6.44E-04	Oktansaeure	5.7	46345	10	Cytoplasmic Membrane	COG2124	Secondary metabolites biosynthesis, transport, and catabolism	
15598528	PA3332		conserved hypothetical protein	3.2	4.26E-03	Oktansaeure	5.5	15920	10	Cytoplasmic	COG3631	General function prediction only	
15598529	PA3333	fabH2	3-oxoacyl-[acyl-carrier-protein] synthase III	6.3	5.44E-05	Oktansaeure	5.0	34003	11	Cytoplasmic	COG0332	acyl-carrier-protein	
15598531	PA3335		hypothetical protein	41.4	9.27E-04	Oktansaeure	5.2	27632	6	Cytoplasmic			
15598533	PA3337	rfaD	ADP-L-glycero-D-mannoheptose 6-epimerase	171.0	7.61E-03	Oktansaeure	6.5	37384	3	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15598537	PA3341		probable transcriptional regulator	1.6	2.53E-01	Oktansaeure	8.6	16071	2	Cytoplasmic	COG1846	Transcription	
15598540	PA3344	recQ	ATP-dependent DNA helicase RecQ	2.2	4.81E-02	Oktansaeure	5.8	79449	2	Cytoplasmic	COG0514	DNA replication, recombination, and repair	
15598544	PA3348		probable chemotaxis protein methyltransferase	1.2	3.85E-01	Citronellol	9.6	30615	9	Cytoplasmic	COG1352	Cell motility and secretion	Signal transduction mechanisms
15598545	PA3349		probable chemotaxis protein	1.7	6.16E-02	Oktansaeure	6.1	34402	15	Cytoplasmic	COG0835	Cell motility and secretion	Signal transduction mechanisms
15598549	PA3353		hypothetical protein	1.0	9.22E-01	Oktansaeure	6.8	29852	11	Cytoplasmic	COG5581	Signal transduction mechanisms	
15598553	PA3357	dsdA	D-serine dehydratase	1.2	3.95E-01	Oktansaeure	6.0	48200	6	Cytoplasmic	COG3048	Amino acid transport and metabolism	
15598593	PA3397	fpr	NADPH-dependent ferredoxin reductase	1.4	1.41E-01	Oktansaeure	5.9	29518	23	Periplasmic	COG1018	Energy production and conversion	
15598610	PA3414		hypothetical protein	2.4	9.94E-02	Oktansaeure	8.1	20918	2	Unknown			
15598611	PA3415		probable dihydrolipoamide acetyltransferase	3.8	2.01E-01	Oktansaeure	5.5	39521	6	Cytoplasmic	COG0508	Energy production and conversion	
15598612	PA3416		probable pyruvate dehydrogenase E1 component, beta chain	117.0	2.81E-02	Oktansaeure	5.7	36143	2	Unknown	COG0022	Energy production and conversion	
15598613	PA3417		probable pyruvate dehydrogenase E1 component, alpha subunit	26.0	1.61E-02	Oktansaeure	5.2	40414	4	Cytoplasmic	COG1071	Energy production and conversion	
15598614	PA3418	ldh	leucine dehydrogenase	2.7	9.50E-02	Citronellol	5.9	35633	7	Cytoplasmic	COG0334	Amino acid transport and metabolism	
15598617	PA3421		conserved hypothetical protein	7.4	6.43E-03	Citronellol	9.2	50690	3	Unknown			
15598622	PA3426		probable enoyl CoA-hydratase/isomerase	2.8	3.96E-04	Citronellol	4.5	26998	4	Cytoplasmic	COG1024	Lipid metabolism	
15598623	PA3427		probable short-chain dehydrogenases	2.0	1.39E-01	Citronellol	5.8	32323	10	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15598626	PA3430		probable aldolase	2.7	2.54E-02	Citronellol	6.6	27993	7	Cytoplasmic	COG0235	Carbohydrate transport and metabolism	
15598634	PA3438	folE1	GTP cyclohydrolase I precursor	2.3	5.68E-03	Oktansaeure	7.6	20833	6	Cytoplasmic	COG0302	Coenzyme metabolism	
15598636	PA3440		conserved hypothetical protein	3.1	2.37E-02	Citronellol	5.7	11637	2	Unknown	COG3492	Function unknown	
15598641	PA3445		conserved hypothetical protein	115.0	1.90E-02	Oktansaeure	9.0	35184	4	Unknown	COG0715	Inorganic ion transport and metabolism	
15598646	PA3450		probable antioxidant protein	6.0	1.13E-03	Oktansaeure	5.2	24164	15	Cytoplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598649	PA3453		conserved hypothetical protein	1.2	2.88E-01	Citronellol	5.4	24160	9	Unknown	COG3132	Function unknown	
15598650	PA3454		probable acyl-CoA thiolase	32.3	1.30E-01	Citronellol	5.1	42050	2	Cytoplasmic	COG0183	Lipid metabolism	
15598652	PA3456		hypothetical protein	2.4	2.79E-03	Oktansaeure	7.2	70517	6	Cytoplasmic	COG4121	Function unknown	
15598654	PA3458		probable transcriptional regulator	1.9	8.26E-03	Oktansaeure	5.6	17599	3	Unknown	COG1846	Transcription	
15598657	PA3461		conserved hypothetical protein	3.9	1.81E-04	Citronellol	5.1	43294	8	Cytoplasmic	COG1363	Carbohydrate transport and metabolism	
15598667	PA3471		probable malic enzyme	1.5	3.37E-02	Oktansaeure	5.2	62420	15	Periplasmic	COG0281	Energy production and conversion	
15598671	PA3475	pheC	cyclohexadienyl dehydratase precursor	1.3	1.87E-01	Citronellol	6.9	30448	5	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15598672	PA3476	rhlI	autoinducer synthesis protein RhlI	3.3	4.91E-01	Oktansaeure	5.3	22630	3	Unknown	COG3916	Signal transduction mechanisms	Secondary metabolites biosynthesis, transport, and catabolism
15598673	PA3477	rhlR	transcriptional regulator RhlR	1.3	7.97E-01	Oktansaeure	7.2	27577	3	Cytoplasmic	COG2771	Transcription	
15598676	PA3480		probable deoxycytidine triphosphate deaminase	1.1	9.90E-01	Citronellol	6.3	21154	8	Cytoplasmic	COG0717	Nucleotide transport and metabolism	
15598677	PA3481		conserved hypothetical protein	1.1	6.88E-01	Citronellol	5.1	38889	9	Cytoplasmic Membrane	COG0489	Cell division and chromosome partitioning	
15598678	PA3482	metG	methionyl-tRNA synthetase	1.2	1.75E-01	Oktansaeure	5.4	74903	28	Periplasmic	COG0143	Translation, ribosomal structure and biogenesis	
15598682	PA3486		conserved hypothetical protein	9.6	2.57E-02	Oktansaeure	6.3	90635	6	Cytoplasmic	COG3501	Function unknown	
15598683	PA3487	pldA	phospholipase D	29.4	3.86E-04	Oktansaeure	6.7	122340	7	Periplasmic	COG1502	Lipid metabolism	
15598704	PA3508		probable transcriptional regulator	1.2	6.16E-01	Citronellol	5.8	30877	2	Cytoplasmic	COG1414	Transcription	
15598720	PA3524	gloA1	lactoylglutathione lyase	2.2	7.76E-01	Citronellol	4.7	14251	2	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15598721	PA3525	argG	argininosuccinate synthase	1.1	5.38E-01	Oktansaeure	5.3	45297	17	Periplasmic	COG0137	Amino acid transport and metabolism	
15598723	PA3527	pyrC	dihydroorotase	1.2	4.86E-01	Citronellol	6.6	38406	12	Cytoplasmic	COG0418	Nucleotide transport and metabolism	
15598724	PA3528	rnt	ribonuclease T	1.1	9.57E-01	Citronellol	4.8	24723	9	Cytoplasmic	COG0847	DNA replication, recombination, and repair	
15598725	PA3529		alkylhydroperoxide reductase C	1.4	9.72E-02	Citronellol	5.3	21822	14	Periplasmic	COG0450	Posttranslational modification, protein turnover, chaperones	
15598727	PA3531	bfrB	bacterioferritin	14.8	6.64E-02	Oktansaeure	4.8	18553	3	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15598733	PA3537	argF	ornithine carbamoyltransferase, anabolic	1.3	9.59E-02	Citronellol	5.7	33924	13	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15598735	PA3539		conserved hypothetical protein	1.3	9.02E-02	Oktansaeure	6.7	29560	13	Cytoplasmic	COG3022	Function unknown	
15598748	PA3552	arnB	ArnB	1.8	1.31E-02	Citronellol	8.0	41867	2	Cytoplasmic	COG0399	Cell envelope biogenesis, outer membrane	
15598750	PA3554	arnA	ArnA	2.6	4.45E-02	Oktansaeure	6.7	74360	11	Outer Membrane Vesicle	COG0223	Translation, ribosomal structure and biogenesis	
15598758	PA3562	fruI	phosphotransferase system transporter enzyme I, FruI	6.4	2.39E-02	Citronellol	4.8	101572	2	Cytoplasmic	COG1080	Carbohydrate transport and metabolism	
15598759	PA3563	fruR	fructose transport system repressor FruR	1.3	6.56E-02	Citronellol	6.4	36369	3	Cytoplasmic	COG1609	Transcription	
15598763	PA3567		probable oxidoreductase	1.1	9.38E-01	Oktansaeure	6.6	36678	5	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15598764	PA3568		probable acetyl-coa synthetase	1.1	6.84E-01	Citronellol	6.7	68990	8	Cytoplasmic	COG0365	Lipid metabolism	
15598765	PA3569	mmsB	3-hydroxyisobutyrate dehydrogenase	2.0	1.94E-01	Citronellol	6.2	30486	3	Cytoplasmic	COG2084	Lipid metabolism	
15598766	PA3570	mmsA	methylmalonate-semialdehyde dehydrogenase	2.0	1.67E-01	Citronellol	6.4	53663	7	Cytoplasmic	COG1012	Energy production and conversion	
15598774	PA3578		conserved hypothetical protein	1.4	7.88E-02	Citronellol	4.9	28906	6	Cytoplasmic Membrane	COG0384	General function prediction only	
15598775	PA3579		probable carbohydrate kinase	1.2	6.92E-01	Oktansaeure	5.6	54207	2	Cytoplasmic	COG0554	Energy production and conversion	
15598776	PA3580		conserved hypothetical protein	1.3	4.97E-01	Oktansaeure	10.1	16493	4	Cytoplasmic	COG2606	Function unknown	
15598778	PA3582	glpK	glycerol kinase	2.6	3.44E-02	Citronellol	5.9	55966	25	Cytoplasmic	COG0554	Energy production and conversion	
15598783	PA3587	metR	transcriptional regulator MetR	1.5	4.19E-02	Oktansaeure	5.6	34216	4	Cytoplasmic	COG0583	Transcription	
15598800	PA3604	erdR	response regulator ErdR	1.1	4.75E-01	Citronellol	4.8	23531	12	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15598806	PA3610	potD	polyamine transport protein PotD	6.0	3.08E-01	Oktansaeure	5.5	39260	3	Periplasmic	COG0687	Amino acid transport and metabolism	
15598809	PA3613		hypothetical protein	2.2	2.51E-02	Oktansaeure	6.4	88379	24	Periplasmic	COG3957	Carbohydrate transport and metabolism	
15598810	PA3614		hypothetical protein	1.4	2.66E-01	Citronellol	7.0	51921	6	Cytoplasmic	COG1236	Translation, ribosomal structure and biogenesis	
15598811	PA3615		hypothetical protein	1.2	1.35E-01	Citronellol	6.0	40465	9	Cytoplasmic	COG1611	General function prediction only	
15598813	PA3617	recA	RecA protein	1.1	8.01E-01	Citronellol	5.2	36879	14	Cytoplasmic	COG0468	DNA replication, recombination, and repair	

15598814	PA3618		conserved hypothetical protein	2.9	5.26E-02	Oktansaeure	5.0	17715	5	Unknown	COG1546	General function prediction only
15598816	PA3620	mutS	DNA mismatch repair protein MutS	1.4	3.43E-02	Oktansaeure	6.1	94977	19	Cytoplasmic	COG0249	DNA replication, recombination, and repair
15598817	PA3621	fdxA	ferredoxin I	1.9	1.13E-01	Citronellol	3.7	12159	3	Cytoplasmic	COG1146	Energy production and conversion
15598818	PA3622	rpoS	sigma factor RpoS	2.7	1.08E-01	Oktansaeure	5.1	38235	4	Cytoplasmic	COG0568	Transcription
15598820	PA3624	pcm	L-isoaspartate protein carboxylmethyltransferase type II	1.7	4.73E-03	Oktansaeure	6.1	23407	3	Cytoplasmic	COG2518	Posttranslational modification, protein turnover, chaperones
15598821	PA3625	surE	survival protein SurE	1.1	4.95E-01	Oktansaeure	5.2	26368	5	Unknown	COG0496	General function prediction only
15598824	PA3628		probable esterase	1.9	5.98E-02	Citronellol	6.3	31243	8	Unknown	COG0627	General function prediction only
15598825	PA3629	adhC	alcohol dehydrogenase class III	2.3	1.37E-02	Citronellol	5.4	39208	8	Cytoplasmic	COG1062	Energy production and conversion
15598829	PA3633	ybtP	4-diphosphocytidyl-2-C-methylerythritol synthase	1.6	2.94E-01	Oktansaeure	5.2	25613	3	Cytoplasmic	COG1211	Lipid metabolism
15598831	PA3635	eno	enolase	1.4	6.70E-02	Citronellol	4.8	45195	22	Cytoplasmic	COG0148	Carbohydrate transport and metabolism
15598832	PA3636	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	1.4	1.02E-01	Citronellol	6.5	31143	20	Cytoplasmic	COG2877	Cell envelope biogenesis, outer membrane
15598833	PA3637	pyrG	CTP synthase	1.2	4.16E-01	Oktansaeure	5.4	59617	30	Periplasmic	COG0504	Nucleotide transport and metabolism
15598835	PA3639	accA	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)	1.3	1.94E-01	Oktansaeure	5.2	34947	23	Outer Membrane Vesicle	COG0825	Lipid metabolism
15598836	PA3640	dnaE	DNA polymerase III, alpha chain	1.8	6.81E-01	Citronellol	5.1	130904	38	Cytoplasmic	COG0587	DNA replication, recombination, and repair
15598838	PA3642	rnhB	ribonuclease HII	1.3	5.51E-01	Oktansaeure	6.5	21771	2	Cytoplasmic	COG0164	DNA replication, recombination, and repair
15598840	PA3644	lpxA	UDP-N-acetylglucosamine acyltransferase	1.6	2.80E-02	Citronellol	7.1	28010	8	Cytoplasmic	COG1043	acyl carrier protein
15598841	PA3645	fabZ	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	2.3	7.59E-02	Citronellol	7.6	16774	5	Cytoplasmic	COG0764	Lipid metabolism
15598842	PA3646	lpxD	UDP-3-O-[3-hydroxylauroyl] glucosamine N-acyltransferase	1.1	8.43E-01	Citronellol	6.2	36191	3	Cytoplasmic	COG1044	3-hydroxymyristoyl
15598843	PA3647		probable outer membrane protein precursor	2.0	6.50E-02	Citronellol	10.0	19058	9	Unknown	COG2825	Cell envelope biogenesis, outer membrane
15598846	PA3650	dxr	1-deoxy-d-xylulose 5-phosphate reductoisomerase	1.2	6.72E-02	Oktansaeure	5.7	42508	4	Unknown	COG0743	Lipid metabolism
15598849	PA3653	frr	ribosome recycling factor	1.0	8.13E-01	Oktansaeure	5.9	20485	17	Cytoplasmic	COG0233	Translation, ribosomal structure and biogenesis
15598850	PA3654	pyrH	uridylate kinase	1.1	5.77E-01	Citronellol	5.4	26272	11	Periplasmic	COG0528	Nucleotide transport and metabolism
15598851	PA3655	tsf	elongation factor Ts	1.2	2.03E-01	Citronellol	5.0	30653	29	Periplasmic	COG0264	Translation, ribosomal structure and biogenesis
15598852	PA3656	rpsB	30S ribosomal protein S2	1.6	8.81E-02	Oktansaeure	9.0	27336	15	Periplasmic	COG0052	Translation, ribosomal structure and biogenesis
15598853	PA3657	map	methionine aminopeptidase	1.3	1.32E-01	Oktansaeure	6.3	29086	10	Cytoplasmic	COG0024	Translation, ribosomal structure and biogenesis
15598854	PA3658	glnD	protein-PII uridylyltransferase	1.4	5.92E-01	Citronellol	5.5	103403	4	Cytoplasmic	COG2844	Posttranslational modification, protein turnover, chaperones
15598855	PA3659		probable aminotransferase	2.1	1.53E-02	Oktansaeure	5.5	44544	7	Cytoplasmic	COG0436	Amino acid transport and metabolism
15598862	PA3666	dapD	tetrahydrodipicolinate succinylase	1.0	7.41E-01	Citronellol	6.0	35973	12	Periplasmic	COG2171	Amino acid transport and metabolism
15598871	PA3675		hypothetical protein	1.0	9.88E-01	Oktansaeure	9.4	23645	7	Unknown		
15598874	PA3678		probable transcriptional regulator	1.5	4.78E-01	Citronellol	6.3	23150	9	Cytoplasmic	COG1309	Transcription
15598878	PA3682		hypothetical protein	1.5	5.84E-02	Citronellol	5.0	29150	8	Cytoplasmic	COG2513	Carbohydrate transport and metabolism
15598881	PA3685		conserved hypothetical protein	1.2	3.06E-01	Citronellol	4.8	24180	5	Cytoplasmic Membrane	COG1214	Posttranslational modification, protein turnover, chaperones
15598882	PA3686	adk	adenylate kinase	1.2	2.64E-01	Citronellol	6.4	23107	19	Cytoplasmic	COG0563	Nucleotide transport and metabolism
15598883	PA3687	ppc	phosphoenolpyruvate carboxylase	1.5	7.82E-02	Citronellol	6.2	97839	23	Cytoplasmic	COG2352	Energy production and conversion
15598887	PA3691		hypothetical protein	1.6	6.97E-01	Citronellol	8.5	14468	3	Outer Membrane Vesicle		
15598888	PA3692	lptF	Lipotoxon F, LptF	1.3	4.85E-01	Oktansaeure	9.9	28514	9	Outer Membrane	COG2885	Cell envelope biogenesis, outer membrane
15598889	PA3693		conserved hypothetical protein	1.7	9.39E-01	Citronellol	7.0	18219	3	Unknown	COG2110	General function prediction only
15598892	PA3696		conserved hypothetical protein	2.3	1.25E-01	Oktansaeure	5.4	26551	2	Unknown	COG2013	Function unknown
15598894	PA3698		hypothetical protein	1.4	2.20E-01	Citronellol	4.5	20351	5	Unknown		
15598896	PA3700	lysS	lysyl-tRNA synthetase	1.0	7.79E-01	Citronellol	5.0	57329	35	Periplasmic	COG1190	Translation, ribosomal structure and biogenesis
15598897	PA3702	wspR	WspR	2.1	7.60E-02	Citronellol	5.6	37887	2	Cytoplasmic	COG3706	Signal transduction mechanisms
15598911	PA3716		hypothetical protein	2.1	1.28E-01	Oktansaeure	4.1	60503	7	Outer Membrane Vesicle		
15598918	PA3723		probable FMN oxidoreductase	1.8	1.88E-01	Citronellol	6.3	40319	15	Cytoplasmic	COG1902	Energy production and conversion
15598921	PA3726		conserved hypothetical protein	1.1	5.09E-01	Oktansaeure	4.8	20596	5	Cytoplasmic	COG4681	Function unknown
15598922	PA3727		hypothetical protein	3.1	3.11E-03	Oktansaeure	4.9	26461	6	Cytoplasmic	COG1502	Lipid metabolism
15598923	PA3728		hypothetical protein	1.3	7.88E-01	Citronellol	4.9	197133	63	Cytoplasmic Membrane	COG1196	Cell division and chromosome partitioning
15598924	PA3729		conserved hypothetical protein	1.6	2.04E-01	Oktansaeure	4.9	75882	2	Outer Membrane Vesicle	COG2268	Function unknown
15598926	PA3731		conserved hypothetical protein	1.9	3.35E-02	Oktansaeure	7.5	24893	10	Cytoplasmic	COG1842	Transcription Signal transduction mechanisms
15598927	PA3732		conserved hypothetical protein	1.3	1.11E-01	Citronellol	4.0	15959	3	Unknown	COG3789	Function unknown
15598928	PA3733		hypothetical protein	1.2	4.29E-01	Oktansaeure	5.9	44766	3	Cytoplasmic	COG1804	Energy production and conversion
15598930	PA3735	thrC	threonine synthase	1.4	1.23E-01	Citronellol	6.6	51795	21	Periplasmic	COG0498	Amino acid transport and metabolism
15598931	PA3736	hom	homoserine dehydrogenase	1.0	4.25E-01	Citronellol	5.1	46192	14	Cytoplasmic	COG0460	Amino acid transport and metabolism
15598932	PA3737	dsbC	thiol:disulfide interchange protein DsbC	1.7	3.82E-03	Oktansaeure	8.8	26095	7	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones
15598937	PA3742	rplS	50S ribosomal protein L19	1.9	2.33E-01	Oktansaeure	11.1	13032	2	Cytoplasmic	COG0335	Translation, ribosomal structure and biogenesis
15598941	PA3746	ffh	signal recognition particle protein Ffh	1.6	1.90E-01	Oktansaeure	10.3	49359	5	Cytoplasmic Membrane	COG0541	Intracellular trafficking and secretion
15598946	PA3751	purT	phosphoribosylglycinamide formyltransferase 2	1.3	9.16E-02	Citronellol	6.1	42342	18	Periplasmic	COG0027	Nucleotide transport and metabolism
15598948	PA3753		conserved hypothetical protein	3.0	7.74E-05	Citronellol	7.0	18509	5	Cytoplasmic	COG0663	General function prediction only
15598949	PA3754		hypothetical protein	1.8	1.18E-01	Citronellol	4.5	22855	3	Cytoplasmic		
15598950	PA3755		conserved hypothetical protein	1.3	9.69E-01	Citronellol	4.6	20829	5	Cytoplasmic	COG1051	Nucleotide transport and metabolism
15598954	PA3759		probable aminotransferase	2.2	1.73E-01	Citronellol	5.7	36123	4	Cytoplasmic	COG2222	Cell envelope biogenesis, outer membrane
15598955	PA3760		N-Acetyl-D-Glucosamine phosphotransferase system transporter	2.9	9.14E-03	Citronellol	5.4	89195	2	Cytoplasmic	COG1080	Carbohydrate transport and metabolism
15598958	PA3763	purL	phosphoribosylformylglycinamidine synthase	2.9	1.02E-01	Citronellol	4.8	140646	54	Periplasmic	COG0046	Nucleotide transport and metabolism
15598960	PA3765		hypothetical protein	1.1	5.10E-01	Oktansaeure	6.3	20903	4	Unknown	COG3644	Function unknown
15598962	PA3767		conserved hypothetical protein	1.1	7.48E-01	Oktansaeure	9.2	19906	2	Cytoplasmic	COG0590	Nucleotide transport and metabolism Translation, ribosomal structure and biogenesis
15598964	PA3769	guaA	GMP synthase	1.5	9.76E-02	Citronellol	5.6	57959	30	Periplasmic	COG0519	Nucleotide transport and metabolism
15598965	PA3770	guaB	inosine-5'-monophosphate dehydrogenase	1.0	8.35E-01	Citronellol	6.7	51707	35	Periplasmic	COG0516	Nucleotide transport and metabolism
15598974	PA3779		hypothetical protein	2.8	5.36E-02	Citronellol	5.3	37696	5	Periplasmic	COG1638	Carbohydrate transport and metabolism
15598978	PA3783		hypothetical protein	1.2	3.48E-01	Citronellol	6.4	23091	7	Unknown	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15598980	PA3785		conserved hypothetical protein	2.2	1.11E-01	Citronellol	6.8	17000	11	Periplasmic	COG2847	Inorganic ion transport and metabolism
15598985	PA3790	oprC	Putative copper transport outer membrane porin OprC precursor	1.8	8.00E-02	Oktansaeure	6.4	79303	16	Periplasmic	COG1629	Inorganic ion transport and metabolism
15598990	PA3795		probable oxidoreductase	1.2	2.00E-01	Citronellol	5.3	34803	8	Cytoplasmic	COG0667	Energy production and conversion
15598992	PA3797		conserved hypothetical protein	1.1	7.03E-01	Citronellol	5.8	29996	5	Cytoplasmic	COG0388	General function prediction only
15598993	PA3798		probable aminotransferase	1.2	2.92E-01	Citronellol	6.2	42594	8	Cytoplasmic	COG0436	Amino acid transport and metabolism
15598994	PA3799		conserved hypothetical protein	4.4	7.15E-02	Oktansaeure	9.6	55006	2	Cytoplasmic Membrane	COG1160	General function prediction only
15598996	PA3801		conserved hypothetical protein	1.6	7.16E-01	Citronellol	4.8	23108	5	Outer Membrane Vesicle	COG2976	Function unknown
15598997	PA3802	hisS	histidyl-tRNA synthetase	2.0	5.67E-02	Citronellol	5.0	47480	14	Cytoplasmic	COG0124	Translation, ribosomal structure and biogenesis
15598998	PA3803	gcpE	probable isoprenoid biosynthetic protein GcpE	1.4	2.28E-01	Citronellol	6.4	40056	11	Cytoplasmic	COG0821	Lipid metabolism
15599002	PA3807	ndk	nucleoside diphosphate kinase	1.3	6.54E-01	Citronellol	5.3	15592	11	Cytoplasmic	COG0105	Nucleotide transport and metabolism
15599004	PA3809	fdx2	ferredoxin [2Fe-2S]	1.7	1.53E-01	Citronellol	4.0	12241	4	Cytoplasmic	COG0633	Energy production and conversion
15599005	PA3810	hscA	heat shock protein HscA	1.5	1.52E-02	Oktansaeure	4.6	66446	17	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones
15599006	PA3811	hscB	heat shock protein HscB	1.5	3.09E-01	Oktansaeure	4.6	20203	2	Cytoplasmic	COG1076	Posttranslational modification, protein turnover, chaperones
15599008	PA3813	iscU	probable iron-binding protein IscU	2.1	3.58E-01	Citronellol	5.8	13753	4	Cytoplasmic	COG0822	Energy production and conversion
15599009	PA3814	iscS	L-cysteine desulfurase (pyridoxal phosphate-dependent)	1.6	7.05E-03	Citronellol	5.9	44666	23	Cytoplasmic	COG1104	Amino acid transport and metabolism
15599010	PA3815	iscR	IscR	1.1	7.46E-01	Citronellol	6.9	17853	6	Unknown	COG1959	Transcription
15599012	PA3817		probable methyltransferase	1.2	2.46E-01	Citronellol	6.2	28493	8	Cytoplasmic	COG0565	Translation, ribosomal structure and biogenesis
15599013	PA3818		extragenic suppressor protein SuhB	1.3	1.50E-01	Oktansaeure	6.6	29521	10	Periplasmic	COG0483	Carbohydrate transport and metabolism
15599016	PA3821	secD	secretion protein SecD	3.2	5.55E-01	Citronellol	9.4	67674	3	Outer Membrane Vesicle	COG0342	Intracellular trafficking and secretion
15599017	PA3822		conserved hypothetical protein	2.0	1.69E-02	Citronellol	9.6	11862	2	Outer Membrane Vesicle	COG1862	Intracellular trafficking and secretion
15599027	PA3832	holC	DNA polymerase III, chi subunit	1.3	1.54E-01	Oktansaeure	5.7	16109	2	Cytoplasmic	COG2927	DNA replication, recombination, and repair
15599029	PA3834	valS	valyl-tRNA synthetase	1.5	2.05E-01	Citronellol	5.2	107707	42	Periplasmic	COG0525	Translation, ribosomal structure and biogenesis
15599031	PA3836		hypothetical protein	1.7	2.54E-02	Citronellol	8.7	34220	21	Periplasmic	COG2984	General function prediction only
15599039	PA3844		hypothetical protein	1.0	9.93E-01	Citronellol	4.8	22795	6	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones
15599041	PA3846		hypothetical protein	1.1	9.53E-01	Citronellol	5.1	19892	5	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism
15599044	PA3849		conserved hypothetical protein	1.5	2.19E-01	Citronellol	5.1	37930	6	Cytoplasmic	COG3081	General function prediction only
15599045	PA3850		hypothetical protein	4.1	2.67E-01	Oktansaeure	4.4	33613	2	Unknown		
15599047	PA3852		hypothetical protein	1.4	1.94E-01	Citronellol	5.4	33979	7	Periplasmic	COG0625	Posttranslational modification, protein turnover, chaperones
15599050	PA3855		hypothetical protein	1.7	2.22E-01	Oktansaeure	7.9	26286	2	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones

15599051	PA3856		hypothetical protein	1.4	1.96E-01	Citronellol	9.9	18327	2	Unknown			
15599053	PA3858		probable amino acid-binding protein	2.4	6.96E-03	Citronellol	7.9	37043	12	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599054	PA3859		carboxylesterase	2.1	2.33E-01	Oktansaeure	4.9	23420	7	Unknown	COG0400	General function prediction only	
15599055	PA3860		probable AMP-binding enzyme	2.6	4.29E-03	Citronellol	6.2	68986	25	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599060	PA3865		probable amino acid binding protein	1.2	6.31E-01	Citronellol	6.1	28433	3	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599061	PA3866		pyocin protein	3.8	6.05E-02	Citronellol	8.8	80731	6	Extracellular			
15599074	PA3879	narL	two-component response regulator NarL	1.1	6.96E-01	Citronellol	4.8	24255	3	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599081	PA3886		hypothetical protein	1.1	5.37E-01	Citronellol	4.9	32290	4	Cytoplasmic	COG0647	Carbohydrate transport and metabolism	
15599091	PA3896		probable 2-hydroxyacid dehydrogenase	1.5	3.37E-01	Oktansaeure	8.2	35632	9	Cytoplasmic	COG1052	Energy production and conversion	Coenzyme metabolism
15599098	PA3903	prfC	peptide chain release factor 3	1.1	5.91E-01	Citronellol	5.7	59865	15	Cytoplasmic	COG4108	Translation, ribosomal structure and biogenesis	
15599100	PA3905		hypothetical protein	5.9	8.97E-03	Oktansaeure	7.7	20024	4	Unknown			
15599103	PA3908		hypothetical protein	1.6	1.45E-02	Oktansaeure	5.0	27294	10	Cytoplasmic			
15599111	PA3916	moaE	molybdopterin converting factor, large subunit	1.8	1.26E-01	Citronellol	6.1	16686	2	Cytoplasmic	COG0314	Coenzyme metabolism	
15599113	PA3918	moaC	molybdopterin biosynthetic protein C	1.5	2.73E-02	Citronellol	7.0	17306	11	Cytoplasmic	COG0315	Coenzyme metabolism	
15599114	PA3919		conserved hypothetical protein	1.9	1.77E-02	Oktansaeure	6.3	51700	18	Cytoplasmic	COG1875	General function prediction only	
15599117	PA3922		conserved hypothetical protein	7.0	4.22E-03	Citronellol	9.0	51229	36	Periplasmic			
15599118	PA3923		hypothetical protein	3.8	9.85E-03	Citronellol	4.7	69590	12	Outer Membrane			
15599119	PA3924		probable medium-chain acyl-CoA ligase	2.4	1.96E-02	Citronellol	6.0	62315	25	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599120	PA3925		probable acyl-CoA thiolase	1.0	8.84E-01	Oktansaeure	6.4	40553	34	Cytoplasmic	COG0183	Lipid metabolism	
15599126	PA3931		conserved hypothetical protein	2.1	1.76E-02	Oktansaeure	8.6	28101	14	Periplasmic	COG1464	Inorganic ion transport and metabolism	
15599130	PA3935	tauD	taurine dioxygenase	20.8	2.72E-03	Oktansaeure	6.4	31029	3	Cytoplasmic	COG2175	Secondary metabolites biosynthesis, transport, and catabolism	
15599133	PA3938		probable periplasmic taurine-binding protein precursor	9.5	1.12E-03	Oktansaeure	7.9	35859	13	Unknown	COG4521	Inorganic ion transport and metabolism	
15599135	PA3940		probable DNA binding protein	2.3	3.78E-01	Oktansaeure	9.2	9892	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
15599136	PA3941		hypothetical protein	1.3	7.39E-01	Citronellol	5.8	22025	3	Cytoplasmic	COG0546	General function prediction only	
15599137	PA3942	tesB	acyl-CoA thioesterase II	1.1	9.78E-01	Citronellol	5.8	32934	6	Cytoplasmic	COG1946	Lipid metabolism	
15599139	PA3944		conserved hypothetical protein	1.5	1.47E-01	Oktansaeure	5.3	21857	4	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15599140	PA3945		conserved hypothetical protein	1.2	4.39E-01	Citronellol	5.7	22403	2	Cytoplasmic	COG1670	Translation, ribosomal structure and biogenesis	
15599143	PA3948	rocA1	Two-component response regulator RocA1	3.2	1.15E-01	Oktansaeure	6.8	22996	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599151	PA3956		hypothetical protein	2.5	1.67E-01	Citronellol	5.1	15453	3	Unknown	COG0346	Amino acid transport and metabolism	
15599160	PA3965		probable transcriptional regulator	2.0	8.98E-02	Citronellol	5.7	19289	8	Cytoplasmic	COG1522	Transcription	
15599167	PA3972		probable acyl-CoA dehydrogenase	4.9	5.90E-04	Citronellol	6.4	60338	32	Cytoplasmic	COG1960	Lipid metabolism	
15599171	PA3976	thiE	thiamin-phosphate pyrophosphorylase	1.3	4.24E-01	Oktansaeure	7.1	22146	6	Unknown	COG0352	Coenzyme metabolism	
15599172	PA3977	hemL	glutamate-1-semialdehyde 2,1-aminomutase	1.1	7.35E-01	Citronellol	5.6	45398	24	Cytoplasmic	COG0001	Coenzyme metabolism	
15599173	PA3978		hypothetical protein	1.7	8.63E-02	Citronellol	4.3	19636	2	Unknown	COG0790	General function prediction only	
15599178	PA3983		conserved hypothetical protein	1.2	2.15E-02	Oktansaeure	4.6	31549	6	Cytoplasmic Membrane	COG4535	Inorganic ion transport and metabolism	
15599182	PA3987	leuS	leucyl-tRNA synthetase	1.1	8.69E-01	Citronellol	5.5	97647	38	Periplasmic	COG0495	Translation, ribosomal structure and biogenesis	
15599183	PA3988		hypothetical protein	1.1	9.88E-01	Citronellol	5.0	22884	4	Periplasmic	COG2980	Cell envelope biogenesis, outer membrane	
15599187	PA3992		hypothetical protein	3.5	6.63E-03	Oktansaeure	8.2	47761	2	Periplasmic	COG2951	Cell envelope biogenesis, outer membrane	
15599191	PA3996	lis	lipoate synthase	2.3	3.85E-01	Oktansaeure	6.9	36733	2	Cytoplasmic	COG0320	Coenzyme metabolism	
15599192	PA3997	lipB	lipoate-protein ligase B	2.0	2.20E-02	Oktansaeure	6.0	23856	3	Cytoplasmic	COG0321	Coenzyme metabolism	
15599199	PA4004		conserved hypothetical protein	1.1	4.10E-01	Oktansaeure	9.2	17791	2	Cytoplasmic	COG1576	Function unknown	
15599202	PA4007	proA	gamma-glutamyl phosphate reductase	1.1	3.33E-01	Citronellol	5.2	45044	15	Periplasmic	COG0014	Amino acid transport and metabolism	
15599205	PA4010		hypothetical protein	1.5	2.23E-02	Citronellol	8.8	26949	6	Cytoplasmic	COG2094	DNA replication, recombination, and repair	
15599207	PA4012		hypothetical protein	1.7	3.00E-02	Citronellol	4.3	21808	3	Cytoplasmic	COG2802	General function prediction only	
15599210	PA4015		conserved hypothetical protein	3.4	2.14E-02	Citronellol	5.6	16700	13	Cytoplasmic	COG2030	Lipid metabolism	
15599212	PA4017		conserved hypothetical protein	2.3	2.31E-02	Oktansaeure	7.1	23164	5	Cytoplasmic	COG0702	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599214	PA4019		probable aromatic acid decarboxylase	1.5	5.79E-01	Citronellol	4.8	22367	3	Cytoplasmic	COG0163	Coenzyme metabolism	
15599215	PA4020	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate liga	1.3	3.30E-01	Oktansaeure	6.4	48469	5	Cytoplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599220	PA4025		probable ethanolamine ammonia-lyase light chain	1.8	5.37E-01	Oktansaeure	6.6	30144	2	Cytoplasmic	COG4302	Amino acid transport and metabolism	
15599221	PA4026		probable acetyltransferase	3.4	1.55E-03	Citronellol	7.0	18049	10	Cytoplasmic	COG0456	General function prediction only	
15599226	PA4031	ppa	inorganic pyrophosphatase	1.8	4.72E-02	Oktansaeure	4.9	19396	11	Cytoplasmic	COG0221	Energy production and conversion	
15599227	PA4032		probable two-component response regulator	1.5	2.87E-02	Oktansaeure	5.7	27422	3	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599230	PA4035		hypothetical protein	2.2	1.36E-03	Citronellol	6.3	35895	4	Periplasmic	COG4254	Function unknown	
15599238	PA4043	ispA	geranyltranstransferase	1.8	4.31E-01	Oktansaeure	5.1	31464	6	Cytoplasmic	COG0142	Coenzyme metabolism	
15599239	PA4044	dxs	1-deoxyxylulose-5-phosphate synthase	4.5	7.02E-04	Oktansaeure	5.5	68049	8	Cytoplasmic	COG1154	Coenzyme metabolism	Lipid metabolism
15599243	PA4048		hypothetical protein	1.2	7.76E-01	Citronellol	9.4	23085	3	Unknown	COG3577	General function prediction only	
15599244	PA4049		hypothetical protein	1.4	2.00E-01	Citronellol	8.2	28328	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599247	PA4052	nusB	NusB protein	1.3	6.63E-01	Citronellol	8.5	17675	5	Unknown	COG0781	Transcription	
15599248	PA4053	ribE	6,7-dimethyl-8-ribityllumazine synthase	5.7	7.20E-01	Citronellol	5.8	16413	2	Cytoplasmic	COG0054	Coenzyme metabolism	
15599249	PA4054	ribB	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	1.0	9.96E-01	Citronellol	5.1	39438	13	Cytoplasmic	COG0108	Coenzyme metabolism	
15599250	PA4055	ribC	riboflavin synthase alpha chain	2.9	4.30E-02	Oktansaeure	6.4	23469	4	Cytoplasmic	COG0307	Coenzyme metabolism	
15599252	PA4057	nrdR	NrdR	1.0	9.49E-01	Citronellol	8.0	17925	7	Cytoplasmic	COG1327	Transcription	
15599256	PA4061		probable thioredoxin	1.1	9.00E-01	Citronellol	4.4	31878	15	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15599262	PA4067	oprG	Outer membrane protein OprG precursor	12.0	4.52E-02	Oktansaeure	4.7	25193	5	Periplasmic	COG3047	Cell envelope biogenesis, outer membrane	
15599263	PA4068		probable epimerase	1.1	6.04E-01	Citronellol	5.7	33310	12	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15599264	PA4069		hypothetical protein	1.3	1.47E-01	Oktansaeure	6.3	32939	6	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15599274	PA4079		probable dehydrogenase	1.6	3.38E-02	Citronellol	5.1	24319	8	Extracellular	COG0300	General function prediction only	
15599310	PA4115		conserved hypothetical protein	1.5	1.91E-02	Oktansaeure	7.1	51130	7	Cytoplasmic	COG1611	General function prediction only	
15599324	PA4129		hypothetical protein	46.5	1.52E-03	Oktansaeure	5.3	18122	6	Unknown	COG3749	Function unknown	
15599346	PA4151	acoB	acetoin catabolism protein AcoB	11.6	2.39E-02	Citronellol	4.8	36437	3	Cytoplasmic	COG0022	Energy production and conversion	
15599357	PA4162		probable short-chain dehydrogenase	1.3	5.85E-01	Oktansaeure	8.0	24857	11	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599358	PA4163		hypothetical protein	1.2	3.65E-01	Citronellol	4.7	60494	17	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis	
15599375	PA4180		probable acetolactate synthase large subunit	2.7	2.27E-02	Oktansaeure	6.3	59806	8	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
15599385	PA4190	pqsL	probable FAD-dependent monooxygenase	6.3	2.48E-02	Oktansaeure	6.3	43975	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15599386	PA4191		probable iron/ascorbate oxidoreductase	8.5	3.24E-01	Oktansaeure	5.8	37441	2	Cytoplasmic	COG3491	General function prediction only	
15599390	PA4195		probable binding protein component of ABC transporter	4.1	5.38E-04	Oktansaeure	7.9	29539	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15599393	PA4198		probable AMP-binding enzyme	2.6	2.21E-01	Oktansaeure	6.2	59548	2	Cytoplasmic	COG0318	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15599394	PA4199		probable acyl-CoA dehydrogenase	2.1	1.20E-01	Citronellol	5.0	63926	8	Cytoplasmic	COG1960	Lipid metabolism	
15599396	PA4201	ddlA	D-alanine-D-alanine ligase A	1.1	5.01E-01	Citronellol	4.9	36533	5	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599397	PA4202		hypothetical protein	1.3	9.39E-02	Citronellol	8.1	36782	8	Cytoplasmic	COG2070	General function prediction only	
15599399	PA4204	pgpL	periplasmic gluconolactonase, PgpL	1.2	9.61E-01	Citronellol	7.4	41616	11	Periplasmic	COG2706	Carbohydrate transport and metabolism	
15599406	PA4211	phzB1	probable phenazine biosynthesis protein	15.6	1.13E-03	Oktansaeure	5.9	18888	5	Cytoplasmic			
15599413	PA4217	phzS	flavin-containing monooxygenase	2.5	1.37E-01	Oktansaeure	5.9	43644	4	Cytoplasmic	COG0654	Coenzyme metabolism	Energy production and conversion
15599428	PA4232	ssb	single-stranded DNA-binding protein	1.1	5.91E-01	Oktansaeure	5.3	18557	9	Cytoplasmic	COG0629	DNA replication, recombination, and repair	
15599430	PA4234	uvrA	excinuclease ABC subunit A	1.7	1.40E-01	Citronellol	6.6	104456	31	Cytoplasmic	COG0178	DNA replication, recombination, and repair	
15599431	PA4235	bfrA	bacterioferritin	1.5	3.34E-01	Oktansaeure	4.8	17940	11	Outer Membrane Vesicle	COG2193	Inorganic ion transport and metabolism	
15599432	PA4236	katA	catalase	2.1	3.31E-02	Citronellol	6.7	55589	28	Periplasmic	COG0753	Inorganic ion transport and metabolism	
15599433	PA4237	rplQ	50S ribosomal protein L17	1.6	3.54E-01	Citronellol	11.1	14504	3	Outer Membrane Vesicle	COG0203	Translation, ribosomal structure and biogenesis	
15599434	PA4238	rpoA	DNA-directed RNA polymerase alpha chain	1.1	4.83E-01	Oktansaeure	4.6	36649	19	Outer Membrane Vesicle	COG0202	Transcription	
15599435	PA4239	rpsD	30S ribosomal protein S4	1.3	4.78E-01	Oktansaeure	10.5	23277	12	Outer Membrane Vesicle	COG0522	Translation, ribosomal structure and biogenesis	
15599436	PA4240	rpsK	30S ribosomal protein S11	4.2	4.11E-02	Oktansaeure	11.5	13630	5	Outer Membrane Vesicle	COG0100	Translation, ribosomal structure and biogenesis	
15599437	PA4241	rpsM	30S ribosomal protein S13	1.3	5.40E-01	Oktansaeure	11.5	13265	7	Cytoplasmic	COG0099	Translation, ribosomal structure and biogenesis	
15599440	PA4244	rplO	50S ribosomal protein L15	1.5	5.00E-01	Citronellol	11.6	15174	5	Cytoplasmic	COG0200	Translation, ribosomal structure and biogenesis	
15599442	PA4246	rpsE	30S ribosomal protein S5	1.7	1.30E-01	Oktansaeure	10.6	17625	13	Cytoplasmic	COG0098	Translation, ribosomal structure and biogenesis	
15599444	PA4248	rplF	50S ribosomal protein L6	1.4	5.02E-01	Oktansaeure	10.5	19099	9	Cytoplasmic	COG0097	Translation, ribosomal structure and biogenesis	
15599445	PA4249	rpsH	30S ribosomal protein S8	3.4	6.73E-02	Oktansaeure	10.2	14171	5	Cytoplasmic	COG0096	Translation, ribosomal structure and biogenesis	
15599446	PA4250	rpsN	30S ribosomal protein S14	3.3	5.81E-02	Oktansaeure	11.9	11565	4	Cytoplasmic	COG0199	Translation, ribosomal structure and biogenesis	

15599447	PA4251	rplE	50S ribosomal protein L5	1.0	8.47E-01	Citronellol	10.3	20392	15	Outer Membrane Vesicle	COG0094	Translation, ribosomal structure and biogenesis	
15599449	PA4253	rplN	50S ribosomal protein L14	1.7	3.06E-01	Oktansaeure	11.4	13412	6	Outer Membrane Vesicle	COG0093	Translation, ribosomal structure and biogenesis	
15599452	PA4256	rplP	50S ribosomal protein L16	1.2	6.41E-01	Oktansaeure	11.8	15401	6	Cytoplasmic	COG0197	Translation, ribosomal structure and biogenesis	
15599453	PA4257	rpsC	30S ribosomal protein S3	1.5	1.96E-01	Oktansaeure	10.8	25838	16	Outer Membrane Vesicle	COG0092	Translation, ribosomal structure and biogenesis	
15599456	PA4260	rplB	50S ribosomal protein L2	1.3	5.33E-01	Oktansaeure	11.8	29579	6	Cytoplasmic	COG0090	Translation, ribosomal structure and biogenesis	
15599458	PA4262	rplD	50S ribosomal protein L4	1.3	5.98E-01	Oktansaeure	10.6	21640	6	Outer Membrane Vesicle	COG0088	Translation, ribosomal structure and biogenesis	
15599459	PA4263	rplC	50S ribosomal protein L3	1.2	7.98E-01	Oktansaeure	10.6	22592	5	Cytoplasmic	COG0087	Translation, ribosomal structure and biogenesis	
15599461	PA4265	tufA	elongation factor Tu	1.3	1.35E-01	Citronellol	5.0	43337	53	Cytoplasmic	COG0050	Translation, ribosomal structure and biogenesis	
15599462	PA4266	fusA1	elongation factor G	1.0	9.30E-01	Citronellol	4.8	77752	75	Periplasmic	COG0480	Translation, ribosomal structure and biogenesis	
15599463	PA4267	rpsG	30S ribosomal protein S7	1.2	7.58E-01	Citronellol	10.9	17504	18	Outer Membrane Vesicle	COG0049	Translation, ribosomal structure and biogenesis	
15599464	PA4268	rpsL	30S ribosomal protein S12	1.1	6.02E-01	Oktansaeure	11.6	13799	6	Cytoplasmic	COG0048	Translation, ribosomal structure and biogenesis	
15599465	PA4269	rpoC	DNA-directed RNA polymerase beta* chain	3.7	1.63E-01	Citronellol	7.1	154364	99	Outer Membrane Vesicle	COG0086	Transcription	
15599466	PA4270	rpoB	DNA-directed RNA polymerase beta chain	4.5	1.80E-01	Citronellol	5.6	150837	111	Periplasmic	COG0085	Transcription	
15599468	PA4272	rplJ	50S ribosomal protein L10	1.6	7.76E-02	Citronellol	9.5	17602	9	Cytoplasmic	COG0244	Translation, ribosomal structure and biogenesis	
15599469	PA4273	rplA	50S ribosomal protein L1	1.2	1.79E-01	Citronellol	10.3	24234	17	Outer Membrane Vesicle	COG0081	Translation, ribosomal structure and biogenesis	
15599470	PA4274	rplK	50S ribosomal protein L11	2.2	1.51E-01	Oktansaeure	10.4	14907	5	Outer Membrane Vesicle	COG0080	Translation, ribosomal structure and biogenesis	
15599471	PA4275	nusG	transcription antitermination protein NusG	1.2	4.94E-01	Oktansaeure	5.8	20130	8	Cytoplasmic	COG0250	Transcription	
15599474	PA4278		hypothetical protein	1.2	4.18E-01	Oktansaeure	5.9	26077	3	Unknown			
15599475	PA4279		hypothetical protein	1.5	3.93E-02	Citronellol	5.4	26758	4	Cytoplasmic	COG1521	Transcription	
15599478	PA4282		probable exonuclease	3.1	6.73E-01	Citronellol	5.5	138959	10	Extracellular	COG0419	DNA replication, recombination, and repair	
15599479	PA4283	recD	exodeoxyribonuclease V alpha chain	1.4	1.62E-01	Citronellol	6.7	79084	8	Cytoplasmic	COG0507	DNA replication, recombination, and repair	
15599480	PA4284	recB	exodeoxyribonuclease V beta chain	9.8	8.41E-02	Citronellol	5.5	139379	14	Unknown	COG1074	DNA replication, recombination, and repair	
15599481	PA4285	recC	exodeoxyribonuclease V gamma chain	2.2	4.95E-03	Citronellol	5.3	132646	8	Cytoplasmic	COG1330	DNA replication, recombination, and repair	
15599482	PA4286		hypothetical protein	1.5	6.81E-02	Citronellol	5.2	24815	4	Unknown	COG0095	Coenzyme metabolism	
15599492	PA4296	pprB	two-component response regulator, PprB	2.5	1.99E-01	Oktansaeure	6.7	30557	6	Cytoplasmic	COG2197	Signal transduction mechanisms	Transcription
15599504	PA4308		conserved hypothetical protein	1.9	2.27E-02	Citronellol	6.5	53246	14	Unknown	COG0433	Replication, recombination, and repair	
15599506	PA4310	pctB	chemotactic transducer PctB	3.0	4.85E-01	Oktansaeure	4.8	68076	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion	Signal transduction mechanisms
15599510	PA4314	purU1	formyltetrahydrofolate deformylase	1.1	4.45E-01	Oktansaeure	6.5	32410	9	Periplasmic	COG0788	Nucleotide transport and metabolism	
15599511	PA4315	mvaT	transcriptional regulator MvaT, P16 subunit	1.8	2.65E-01	Oktansaeure	10.1	14180	3	Cytoplasmic			
15599512	PA4316	sbcB	exodeoxyribonuclease I	1.9	3.39E-02	Citronellol	5.4	55449	3	Cytoplasmic	COG2925	DNA replication, recombination, and repair	
15599513	PA4317		hypothetical protein	2.3	6.68E-01	Citronellol	9.2	26709	2	Cytoplasmic Membrane			
15599518	PA4322		conserved hypothetical protein	1.5	5.18E-03	Citronellol	6.2	36661	8	Cytoplasmic	COG0714	General function prediction only	
15599525	PA4329	pykA	pyruvate kinase II	1.0	8.52E-01	Oktansaeure	6.7	52252	26	Periplasmic	COG0469	Carbohydrate transport and metabolism	
15599526	PA4330		probable enoyl-CoA hydratase/isomerase	17.6	2.02E-06	Citronellol	6.7	28152	17	Cytoplasmic	COG1024	Lipid metabolism	
15599527	PA4331		probable ferredoxin reductase	2.5	3.90E-03	Citronellol	7.3	33842	2	Cytoplasmic	COG0543	Coenzyme metabolism	Energy production and conversion
15599529	PA4333		probable fumarase	2.5	1.49E-01	Citronellol	5.2	54763	16	Periplasmic	COG1951	Energy production and conversion	
15599532	PA4336		conserved hypothetical protein	2.9	1.06E-01	Citronellol	6.0	20993	6	Cytoplasmic	COG0693	General function prediction only	
15599536	PA4340		hypothetical protein	1.0	9.00E-01	Oktansaeure	6.1	20988	7	Periplasmic			
15599541	PA4345		hypothetical protein	1.9	4.64E-01	Oktansaeure	4.8	22161	2	Unknown	COG2353	Function unknown	
15599544	PA4348		conserved hypothetical protein	15.5	1.77E-02	Oktansaeure	5.5	29475	2	Cytoplasmic	COG0426	Energy production and conversion	
15599545	PA4349		hypothetical protein	1.4	1.70E-01	Oktansaeure	6.2	31671	10	Unknown	COG1960	Lipid metabolism	
15599548	PA4352		conserved hypothetical protein	11.6	1.49E-03	Oktansaeure	6.2	30972	14	Outer Membrane Vesicle	COG0589	Signal transduction mechanisms	
15599549	PA4353		conserved hypothetical protein	2.1	3.01E-01	Oktansaeure	8.5	22029	2	Cytoplasmic	COG3124	Function unknown	
15599552	PA4356	xenB	xenobiotic reductase	1.3	9.47E-02	Oktansaeure	4.9	37796	23	Periplasmic	COG1902	Energy production and conversion	
15599562	PA4366	sodB	superoxide dismutase	2.3	1.14E-02	Citronellol	5.2	21351	7	Periplasmic	COG0605	Inorganic ion transport and metabolism	
15599566	PA4370	icmP	Insulin-cleaving metalloproteinase outer membrane protein precursor	1.0	8.70E-01	Citronellol	4.5	47230	26	Outer Membrane	COG3487	Inorganic ion transport and metabolism	
15599568	PA4372		hypothetical protein	2.3	2.53E-01	Oktansaeure	6.0	38323	7	Outer Membrane Vesicle	COG3489	General function prediction only	
15599572	PA4376	pncB2	nicotinate phosphoribosyltransferase	1.3	1.59E-01	Citronellol	6.7	45690	5	Cytoplasmic	COG1488	Coenzyme metabolism	
15599577	PA4381		probable two-component response regulator	1.9	2.59E-01	Oktansaeure	5.9	25235	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599581	PA4385	groEL	GroEL protein	1.2	1.78E-01	Oktansaeure	4.8	57086	57	Periplasmic	COG0459	Posttranslational modification, protein turnover, chaperones	
15599582	PA4386	groES	GroES protein	1.6	4.51E-03	Citronellol	4.9	10267	6	Periplasmic	COG0234	Posttranslational modification, protein turnover, chaperones	
15599584	PA4388		hypothetical protein	1.4	3.15E-02	Citronellol	6.4	26982	7	Cytoplasmic	COG0748	Inorganic ion transport and metabolism	
15599585	PA4389		probable short-chain dehydrogenase	1.2	5.61E-01	Citronellol	7.3	26720	26	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599591	PA4395		conserved hypothetical protein	1.2	6.24E-01	Citronellol	8.2	18044	14	Cytoplasmic	COG1666	Function unknown	
15599595	PA4399		conserved hypothetical protein	1.4	1.04E-01	Oktansaeure	6.1	21065	5	Cytoplasmic	COG2096	Coenzyme transport and metabolism	
15599596	PA4400		probable pyrophosphohydrolase	2.0	5.21E-02	Citronellol	5.1	34022	4	Cytoplasmic	COG0352	Coenzyme metabolism	
15599597	PA4401		probable glutathione S-transferase	2.2	1.47E-02	Citronellol	5.4	23789	11	Unknown	COG0625	Posttranslational modification, protein turnover, chaperones	
15599598	PA4402	argJ	glutamate N-acetyltransferase	1.4	2.40E-01	Citronellol	5.3	41762	20	Cytoplasmic	COG1364	Amino acid transport and metabolism	
15599599	PA4403	secA	secretion protein SecA	1.2	3.97E-01	Oktansaeure	5.4	103854	37	Outer Membrane Vesicle	COG0653	Intracellular trafficking and secretion	
15599602	PA4406	lpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.1	5.28E-01	Citronellol	5.0	33435	15	Periplasmic	COG0774	Cell envelope biogenesis, outer membrane	
15599603	PA4407	ftsZ	cell division protein FtsZ	10.1	2.87E-04	Oktansaeure	4.7	41218	10	Periplasmic	COG0206	Cell division and chromosome partitioning	
15599604	PA4408	ftsA	cell division protein FtsA	5.7	6.53E-03	Oktansaeure	5.0	44646	13	Cytoplasmic	COG0849	Cell division and chromosome partitioning	
15599606	PA4410	ddlB	D-alanine--D-alanine ligase	1.2	1.78E-01	Citronellol	4.7	34363	12	Cytoplasmic	COG1181	Cell envelope biogenesis, outer membrane	
15599607	PA4411	murC	UDP-N-acetylmuramate--alanine ligase	1.4	1.04E-01	Citronellol	6.1	51949	7	Periplasmic	COG0773	Cell envelope biogenesis, outer membrane	
15599608	PA4412	murG	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-und	5.4	6.02E-02	Oktansaeure	10.0	37799	2	Cytoplasmic Membrane	COG0707	Cell envelope biogenesis, outer membrane	
15599610	PA4414	murD	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1.5	5.39E-02	Citronellol	5.7	48080	16	Cytoplasmic	COG0771	Cell envelope biogenesis, outer membrane	
15599612	PA4416	murF	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alan	1.1	4.57E-01	Citronellol	6.5	47412	16	Cytoplasmic	COG0770	Cell envelope biogenesis, outer membrane	
15599613	PA4417	murE	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	1.5	7.28E-02	Citronellol	5.1	51263	17	Cytoplasmic	COG0769	Cell envelope biogenesis, outer membrane	
15599616	PA4420		conserved hypothetical protein	1.3	2.32E-01	Citronellol	7.7	34640	12	Cytoplasmic	COG0275	Cell envelope biogenesis, outer membrane	
15599617	PA4421		conserved hypothetical protein	1.8	1.29E-01	Citronellol	4.9	17079	2	Cytoplasmic	COG2001	Function unknown	
15599619	PA4423		conserved hypothetical protein	1.9	2.29E-01	Citronellol	7.2	65629	3	Periplasmic	COG3107	General function prediction only	
15599621	PA4425		sedoheptulose 7-phosphate isomerase GmhA	2.1	6.98E-02	Oktansaeure	4.7	21413	8	Cytoplasmic	COG0279	Carbohydrate transport and metabolism	
15599622	PA4426		conserved hypothetical protein	2.9	2.92E-04	Citronellol	9.8	20619	4	Outer Membrane Vesicle	COG2823	General function prediction only	
15599624	PA4428	sspA	stringent starvation protein A	1.6	3.51E-02	Citronellol	6.1	23615	5	Cytoplasmic	COG0625	Posttranslational modification, protein turnover, chaperones	
15599625	PA4429		probable cytochrome c1 precursor	1.1	6.10E-01	Oktansaeure	7.5	28993	4	Outer Membrane Vesicle	COG2857	Energy production and conversion	
15599627	PA4431		probable iron-sulfur protein	1.3	4.70E-01	Citronellol	6.5	20828	4	Outer Membrane Vesicle	COG0723	Energy production and conversion	
15599628	PA4432	rpsI	30S ribosomal protein S9	1.0	9.23E-01	Citronellol	11.8	14615	4	Outer Membrane Vesicle	COG0103	Translation, ribosomal structure and biogenesis	
15599629	PA4433	rplM	50S ribosomal protein L13	1.1	8.49E-01	Citronellol	10.4	16029	4	Cytoplasmic	COG0102	Translation, ribosomal structure and biogenesis	
15599630	PA4434		probable oxidoreductase	1.1	6.01E-01	Citronellol	5.7	38644	8	Periplasmic	COG0667	Energy production and conversion	
15599631	PA4435		probable acyl-CoA dehydrogenase	12.7	6.23E-04	Citronellol	6.1	42128	20	Cytoplasmic	COG1960	Lipid metabolism	
15599634	PA4438		conserved hypothetical protein	3.2	2.58E-03	Oktansaeure	6.2	41993	3	Cytoplasmic	COG1485	General function prediction only	
15599635	PA4439	trpS	tryptophanyl-tRNA synthetase	1.1	4.01E-01	Oktansaeure	5.8	48961	16	Periplasmic	COG0180	Translation, ribosomal structure and biogenesis	
15599636	PA4440		hypothetical protein	1.0	7.44E-01	Oktansaeure	6.2	22315	6	Unknown	COG2945	General function prediction only	
15599637	PA4441		hypothetical protein	2.9	8.39E-03	Citronellol	6.3	16386	2	Outer Membrane Vesicle	COG3105	Function unknown	
15599638	PA4442	cysN	ATP sulfurylase GTP-binding subunit/APS kinase	2.5	5.53E-03	Oktansaeure	5.6	69268	28	Periplasmic	COG2895	Inorganic ion transport and metabolism	
15599639	PA4443	cysD	ATP sulfurylase small subunit	2.1	2.69E-03	Oktansaeure	7.1	35478	11	Cytoplasmic	COG0175	Amino acid transport and metabolism	Coenzyme metabolism
15599641	PA4445		conserved hypothetical protein	1.6	1.03E-01	Citronellol	5.3	27360	7	Cytoplasmic	COG0327	Function unknown	
15599643	PA4447	hisC1	histidinol-phosphate aminotransferase	1.1	2.89E-02	Citronellol	6.0	38655	8	Periplasmic	COG0079	Amino acid transport and metabolism	
15599644	PA4448	hisD	histidinol dehydrogenase	1.6	4.76E-02	Citronellol	4.9	47179	19	Periplasmic	COG0141	Amino acid transport and metabolism	
15599645	PA4449	hisG	ATP-phosphoribosyltransferase	1.0	9.30E-01	Citronellol	9.3	22844	15	Cytoplasmic	COG0040	Amino acid transport and metabolism	
15599646	PA4450	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.0	8.92E-01	Oktansaeure	5.5	44645	17	Periplasmic	COG0766	Cell envelope biogenesis, outer membrane	
15599649	PA4453		conserved hypothetical protein	1.4	1.49E-01	Citronellol	9.7	23760	16	Periplasmic	COG2854	Secondary metabolites biosynthesis, transport, and catabolism	
15599650	PA4454		conserved hypothetical protein	1.4	2.73E-01	Oktansaeure	4.7	16557	2	Outer Membrane Vesicle	COG1463	Secondary metabolites biosynthesis, transport, and catabolism	
15599653	PA4457		arabinose-5-phosphate isomerase KdsD	1.1	4.99E-01	Citronellol	5.6	34179	9	Cytoplasmic	COG0794	Cell envelope biogenesis, outer membrane	
15599654	PA4458		conserved hypothetical protein	1.8	1.59E-02	Citronellol	5.6	19334	12	Cytoplasmic	COG1778	General function prediction only	
15599656	PA4460		conserved hypothetical protein	1.2	7.90E-01	Citronellol	9.6	19126	9	Periplasmic	COG1934	Function unknown	
15599657	PA4461		probable ATP-binding component of ABC transporter	1.7	1.75E-01	Oktansaeure	6.7	26450	2	Outer Membrane Vesicle	COG1137	General function prediction only	

15599658	PA4462	rpoN	RNA polymerase sigma-54 factor	1.4	4.04E-01	Oktansaeure	4.4	56054	6	Cytoplasmic	COG1508	Transcription
15599661	PA4465		conserved hypothetical protein	1.1	5.13E-01	Citronellol	5.7	32218	5	Cytoplasmic	COG1660	General function prediction only
15599664	PA4468	sodM	superoxide dismutase	1.7	1.86E-01	Oktansaeure	6.2	22506	6	Periplasmic	COG0605	Inorganic ion transport and metabolism
15599666	PA4470	fumC1	fumarate hydratase	1.4	4.09E-01	Oktansaeure	5.9	48695	25	Cytoplasmic	COG0114	Energy production and conversion
15599668	PA4472	pmbA	PmbA protein	2.1	2.08E-02	Citronellol	5.5	47908	11	Cytoplasmic	COG0312	General function prediction only
15599670	PA4474		conserved hypothetical protein	1.5	3.60E-03	Citronellol	5.0	50266	8	Cytoplasmic	COG0312	General function prediction only
15599671	PA4475		conserved hypothetical protein	1.7	3.52E-02	Citronellol	6.8	30724	13	Cytoplasmic	COG0388	General function prediction only
15599673	PA4477	cafA	cytoplasmic axial filament protein	1.4	1.89E-02	Citronellol	5.0	54665	15	Cytoplasmic	COG1530	Translation, ribosomal structure and biogenesis
15599674	PA4478		conserved hypothetical protein	1.1	6.09E-01	Oktansaeure	4.7	20974	7	Cytoplasmic	COG0424	Cell division and chromosome partitioning
15599677	PA4481	mreB	rod shape-determining protein MreB	2.2	5.26E-02	Oktansaeure	5.1	36976	15	Outer Membrane Vesicle	COG1077	Cell division and chromosome partitioning
15599679	PA4483	gatA	Glu-tRNA(Gln) amidotransferase subunit A	1.2	3.66E-01	Citronellol	5.5	51862	22	Periplasmic	COG0154	Translation, ribosomal structure and biogenesis
15599680	PA4484	gatB	Glu-tRNA(Gln) amidotransferase subunit B	1.1	4.47E-01	Citronellol	5.1	53081	25	Periplasmic	COG0064	Translation, ribosomal structure and biogenesis
15599685	PA4489		conserved hypothetical protein	1.2	6.00E-01	Citronellol	5.3	167428	27	Outer Membrane Vesicle	COG2373	General function prediction only
15599686	PA4490		conserved hypothetical protein	4.8	1.31E-02	Oktansaeure	10.3	23969	5	Cytoplasmic Membrane	COG3234	Function unknown
15599689	PA4493	roxR	RoxR	1.8	1.81E-01	Oktansaeure	5.3	20616	8	Cytoplasmic	COG4567	Signal transduction mechanisms Transcription
15599691	PA4495		hypothetical protein	1.2	5.00E-01	Citronellol	5.9	24879	11	Periplasmic	COG3471	Function unknown
15599692	PA4496		probable binding protein component of ABC transporter	3.9	4.63E-03	Citronellol	7.6	60077	26	Periplasmic	COG0747	Amino acid transport and metabolism
15599693	PA4497		probable binding protein component of ABC transporter	7.9	3.88E-02	Citronellol	7.0	59496	2	Periplasmic	COG0747	Amino acid transport and metabolism
15599694	PA4498		probable metallopeptidase	4.5	2.48E-01	Citronellol	6.2	44126	4	Cytoplasmic	COG0006	Amino acid transport and metabolism
15599695	PA4499		probable transcriptional regulator	2.4	5.30E-01	Oktansaeure	6.2	20435	4	Cytoplasmic	COG1396	Transcription
15599698	PA4502		probable binding protein component of ABC transporter	3.3	2.76E-02	Citronellol	6.6	58611	3	Periplasmic	COG0747	Amino acid transport and metabolism
15599704	PA4508		probable transcriptional regulator	2.9	7.84E-02	Citronellol	6.7	17334	3	Cytoplasmic	COG1522	Transcription
15599711	PA4515		conserved hypothetical protein	1.6	1.43E-01	Oktansaeure	6.6	25616	3	Cytoplasmic	COG3128	Function unknown
15599715	PA4519	speC	ornithine decarboxylase	1.2	1.74E-01	Citronellol	4.7	43559	16	Cytoplasmic	COG0019	Amino acid transport and metabolism
15599718	PA4522	ampD	beta-lactamase expression regulator AmpD	1.0	8.42E-01	Citronellol	5.5	21028	3	Cytoplasmic	COG3023	Cell envelope biogenesis, outer membrane
15599719	PA4523		hypothetical protein	20.3	4.57E-03	Oktansaeure	5.5	83588	2	Cytoplasmic		
15599720	PA4524	nadC	nicotinate-nucleotide pyrophosphorylase	1.1	9.32E-01	Citronellol	5.1	30552	13	Cytoplasmic	COG0157	Coenzyme metabolism
15599721	PA4525	pilA	type 4 fimbrial precursor PilA	3.8	3.36E-04	Citronellol	6.6	15512	6	Outer Membrane Vesicle	COG4969	Cell motility and secretion Intracellular trafficking and secretion
15599722	PA4526	pilB	type 4 fimbrial biogenesis protein PilB	2.2	3.49E-04	Oktansaeure	5.7	62328	6	Cytoplasmic	COG2804	Cell motility and secretion Intracellular trafficking and secretion
15599725	PA4529	coaE	dephosphocoenzyme A kinase	1.3	3.42E-01	Oktansaeure	6.8	22843	7	Cytoplasmic	COG0237	Coenzyme metabolism
15599729	PA4533		hypothetical protein	1.3	3.90E-01	Oktansaeure	9.5	17613	4	Periplasmic		
15599738	PA4542	clpB	ClpB protein	1.7	9.65E-03	Oktansaeure	5.1	95005	45	Periplasmic	COG0542	Posttranslational modification, protein turnover, chaperones
15599739	PA4543		conserved hypothetical protein	1.4	5.84E-02	Citronellol	7.5	26047	4	Unknown	COG1496	Secondary metabolites biosynthesis, transport and catabolism
15599743	PA4547	pilR	two-component response regulator PilR	3.1	7.63E-02	Oktansaeure	5.9	49737	2	Cytoplasmic	COG2204	Signal transduction mechanisms
15599744	PA4548		probable D-amino acid oxidase	2.4	1.03E-02	Oktansaeure	6.5	39413	5	Cytoplasmic Membrane	COG0665	Amino acid transport and metabolism
15599750	PA4554	pilY1	type 4 fimbrial biogenesis protein PilY1	2.4	5.90E-03	Citronellol	6.4	126583	8	Periplasmic	COG3419	Cell motility and secretion Intracellular trafficking and secretion
15599753	PA4557	lytB	LytB protein	1.1	8.03E-01	Citronellol	5.2	34762	4	Cytoplasmic	COG0761	Lipid metabolism
15599754	PA4558		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.4	5.64E-02	Oktansaeure	4.3	15984	6	Cytoplasmic	COG1047	Posttranslational modification, protein turnover, chaperones
15599756	PA4560	ileS	isoleucyl-tRNA synthetase	1.5	1.24E-01	Citronellol	6.1	105464	37	Cytoplasmic	COG0060	Translation, ribosomal structure and biogenesis
15599757	PA4561	ribF	riboflavin kinase/FAD synthase	1.2	7.90E-02	Citronellol	9.1	34340	8	Cytoplasmic	COG0196	Coenzyme metabolism
15599760	PA4564		conserved hypothetical protein	1.4	4.99E-01	Oktansaeure	9.2	16724	2	Periplasmic	COG3045	Function unknown
15599761	PA4565	proB	glutamate 5-kinase	1.0	7.35E-01	Oktansaeure	7.3	39845	6	Cytoplasmic	COG0263	Amino acid transport and metabolism
15599762	PA4566	obg	GTP-binding protein Obg	1.3	4.25E-01	Oktansaeure	4.5	44338	5	Cytoplasmic	COG0536	General function prediction only
15599764	PA4568	rplU	50S ribosomal protein L21	3.2	7.29E-01	Citronellol	10.6	11654	2	Outer Membrane Vesicle	COG0261	Translation, ribosomal structure and biogenesis
15599765	PA4569	ispB	octaprenyl-diphosphate synthase	1.2	3.63E-01	Citronellol	4.6	34851	15	Cytoplasmic	COG0142	Coenzyme metabolism
15599768	PA4572	fklB	peptidyl-prolyl cis-trans isomerase FklB	1.0	8.34E-01	Oktansaeure	4.5	21795	6	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones
15599772	PA4576		probable ATP-dependent protease	1.2	3.43E-01	Oktansaeure	4.7	90222	39	Periplasmic	COG1067	Posttranslational modification, protein turnover, chaperones
15599776	PA4580		conserved hypothetical protein	1.2	4.86E-01	Oktansaeure	8.2	20498	2	Cytoplasmic	COG3236	Function unknown
15599783	PA4587	ccpR	cytochrome c551 peroxidase precursor	20.3	8.16E-03	Oktansaeure	6.7	37403	7	Periplasmic	COG1858	Inorganic ion transport and metabolism
15599784	PA4588	gdhA	glutamate dehydrogenase	1.1	4.79E-01	Oktansaeure	6.0	48856	22	Unknown	COG0334	Amino acid transport and metabolism
15599791	PA4595		probable ATP-binding component of ABC transporter	2.1	1.57E-03	Oktansaeure	5.4	61302	31	Periplasmic	COG0488	General function prediction only
15599798	PA4602	glyA3	serine hydroxymethyltransferase	1.7	2.36E-01	Citronellol	6.0	45157	18	Periplasmic	COG0112	Amino acid transport and metabolism
15599809	PA4613	katB	catalase	32.7	1.87E-03	Citronellol	8.6	57131	4	Cytoplasmic	COG0753	Inorganic ion transport and metabolism
15599810	PA4614	mscL	conductance mechanosensitive channel	1.1	6.69E-01	Oktansaeure	4.6	14432	4	Outer Membrane Vesicle	COG1970	Cell envelope biogenesis, outer membrane
15599811	PA4615		probable oxidoreductase	1.1	4.47E-01	Citronellol	5.2	29377	10	Cytoplasmic	COG1018	Energy production and conversion
15599821	PA4625	cdrA	cyclic diguanylate-regulated TPS partner A, CdrA	5.1	3.63E-02	Oktansaeure	4.7	219755	2	Extracellular		
15599822	PA4626	hprA	glycerate dehydrogenase	1.3	8.15E-02	Citronellol	6.7	34285	13	Cytoplasmic	COG1052	Energy production and conversion Coenzyme metabolism
15599828	PA4632		hypothetical protein	1.2	6.06E-01	Citronellol	7.6	29159	3	Periplasmic	COG0501	Posttranslational modification, protein turnover, chaperones
15599829	PA4633		probable chemotaxis transducer	1.5	1.07E-01	Citronellol	4.5	76623	2	Cytoplasmic Membrane	COG0840	Cell motility and secretion Signal transduction mechanisms
15599830	PA4634		hypothetical protein	2.8	3.08E-01	Oktansaeure	8.7	22996	2	Unknown	COG2135	Function unknown
15599835	PA4639		hypothetical protein	1.8	1.42E-02	Citronellol	9.8	20736	8	Outer Membrane Vesicle		
15599836	PA4640	mqoB	malate:quinone oxidoreductase	1.9	1.06E-02	Oktansaeure	7.0	55498	6	Cytoplasmic	COG0579	General function prediction only
15599839	PA4644		hypothetical protein	49.3	1.33E-02	Oktansaeure	5.9	17109	2	Unknown		
15599840	PA4645		probable purine/pyrimidine phosphoribosyl transferase	1.6	3.84E-01	Citronellol	5.6	20639	12	Cytoplasmic	COG0634	Nucleotide transport and metabolism
15599841	PA4646	upp	uracil phosphoribosyltransferase	1.3	2.73E-01	Citronellol	7.0	22938	16	Cytoplasmic	COG0035	Nucleotide transport and metabolism
15599846	PA4651	cupE4	Pilin assembly chaperone CupE4	2.5	5.30E-02	Citronellol	9.7	28981	5	Unknown	COG3121	Cell motility and secretion Intracellular trafficking and secretion
15599851	PA4656		conserved hypothetical protein	3.3	2.99E-03	Oktansaeure	8.3	33852	5	Cytoplasmic	COG1090	General function prediction only
15599852	PA4657		hypothetical protein	1.2	5.26E-01	Oktansaeure	6.8	35913	10	Unknown	COG3380	General function prediction only
15599854	PA4659		probable transcriptional regulator	11.6	6.85E-04	Oktansaeure	8.0	33959	2	Cytoplasmic	COG0789	Transcription
15599857	PA4662	murI	glutamate racemase	1.6	3.34E-02	Citronellol	5.2	28274	3	Cytoplasmic	COG0796	Cell envelope biogenesis, outer membrane
15599858	PA4663	moeB	molybdopterin biosynthesis MoeB protein	1.6	2.35E-01	Oktansaeure	5.6	26686	5	Cytoplasmic	COG0476	Coenzyme metabolism
15599860	PA4665	prfA	peptide chain release factor 1	2.0	9.73E-03	Citronellol	4.8	40040	5	Cytoplasmic	COG0216	Translation, ribosomal structure and biogenesis
15599864	PA4669	ipk	isopentenyl monophosphate kinase	1.9	1.93E-01	Oktansaeure	6.6	30843	3	Unknown	COG1947	Lipid metabolism
15599865	PA4670	prs	ribose-phosphate pyrophosphokinase	1.1	4.07E-01	Oktansaeure	6.5	34008	23	Periplasmic	COG0462	Nucleotide transport and metabolism Amino acid transport and metabolism
15599866	PA4671		probable ribosomal protein L25	1.0	8.54E-01	Oktansaeure	6.2	21962	12	Periplasmic	COG1825	Translation, ribosomal structure and biogenesis
15599867	PA4672		peptidyl-tRNA hydrolase	3.7	2.49E-02	Oktansaeure	9.8	20772	3	Cytoplasmic	COG0193	Translation, ribosomal structure and biogenesis
15599868	PA4673		conserved hypothetical protein	1.7	1.91E-02	Citronellol	4.8	40078	14	Cytoplasmic	COG0012	Translation, ribosomal structure and biogenesis
15599870	PA4675		probable TonB-dependent receptor	2.1	1.75E-02	Oktansaeure	5.2	80952	6	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599871	PA4676		probable carbonic anhydrase	1.1	5.54E-01	Citronellol	6.0	24223	13	Cytoplasmic	COG0288	Inorganic ion transport and metabolism
15599873	PA4678	rimI	peptide n-acetyltransferase RimI	1.0	8.03E-01	Oktansaeure	6.2	17095	3	Cytoplasmic	COG0456	General function prediction only
15599874	PA4679		hypothetical protein	7.4	1.10E-01	Oktansaeure	5.0	24841	2	Unknown		
15599881	PA4686		hypothetical protein	6.4	5.75E-02	Oktansaeure	5.3	106827	5	Periplasmic	COG1196	Cell division and chromosome partitioning
15599882	PA4687	hitA	ferric iron-binding periplasmic protein HitA	2.4	2.96E-02	Oktansaeure	5.5	36149	17	Periplasmic	COG1840	Inorganic ion transport and metabolism
15599888	PA4694	ilvC	ketol-acid reductoisomerase	1.5	2.10E-02	Oktansaeure	5.7	36424	33	Periplasmic	COG0059	Amino acid transport and metabolism Coenzyme metabolism
15599889	PA4695	ilvH	acetolactate synthase isozyme III small subunit	1.7	1.50E-01	Oktansaeure	6.3	17784	8	Cytoplasmic	COG0440	Amino acid transport and metabolism
15599890	PA4696	ilvI	acetolactate synthase large subunit	1.3	2.49E-01	Oktansaeure	6.8	62986	29	Cytoplasmic	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase
15599895	PA4701		conserved hypothetical protein	1.5	9.92E-02	Citronellol	6.0	58344	29	Periplasmic	COG2187	Function unknown
15599898	PA4704	cbpA	cAMP-binding protein A	1.7	6.94E-02	Citronellol	5.2	29671	2	Cytoplasmic	COG0664	Signal transduction mechanisms
15599902	PA4708	phuT	Heme-transport protein, PhuT	2.0	1.94E-03	Oktansaeure	7.8	31037	17	Periplasmic	COG4558	Inorganic ion transport and metabolism
15599903	PA4709		probable hemin degrading factor	2.3	3.91E-02	Oktansaeure	5.6	39057	11	Cytoplasmic	COG3720	Inorganic ion transport and metabolism
15599904	PA4710	phuR	Heme/Hemoglobin uptake outer membrane receptor PhuR precursor	2.1	1.59E-01	Oktansaeure	5.9	84724	11	Periplasmic	COG1629	Inorganic ion transport and metabolism
15599909	PA4715		probable aminotransferase	4.2	9.30E-03	Oktansaeure	8.1	46064	4	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599910	PA4716		hypothetical protein	1.1	9.64E-01	Citronellol	5.0	30850	3	Cytoplasmic	COG0384	General function prediction only
15599911	PA4717		conserved hypothetical protein	1.5	3.39E-01	Citronellol	6.1	31861	3	Unknown	COG2321	General function prediction only
15599914	PA4720	trmA	tRNA (uracil-5-)-methyltransferase	1.1	8.15E-01	Oktansaeure	7.0	41206	3	Cytoplasmic	COG2265	Translation, ribosomal structure and biogenesis
15599916	PA4722		probable aminotransferase	1.0	9.90E-01	Citronellol	5.7	42567	8	Cytoplasmic	COG0436	Amino acid transport and metabolism
15599917	PA4723	dksA	suppressor protein DksA	1.5	9.79E-02	Citronellol	4.8	17344	12	Periplasmic	COG1734	Signal transduction mechanisms

15599920	PA4726	cbrB	two-component response regulator CbrB	2.7	1.22E-04	Oktansaeure	5.5	52286	17	Cytoplasmic	COG2204	Signal transduction mechanisms	
15599922	PA4728	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	7.6	1.05E-02	Oktansaeure	4.6	18014	2	Cytoplasmic	COG0801	Coenzyme metabolism	
15599923	PA4729	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.1	1.88E-01	Oktansaeure	5.8	27874	10	Periplasmic	COG0413	Coenzyme metabolism	
15599924	PA4730	panC	pantoate--beta-alanine ligase	1.1	5.55E-01	Oktansaeure	6.5	30836	10	Cytoplasmic	COG0414	Coenzyme metabolism	
15599926	PA4732	pgi	glucose-6-phosphate isomerase	1.3	1.71E-01	Citronellol	6.6	61944	16	Periplasmic	COG0166	Carbohydrate transport and metabolism	
15599927	PA4733	acsB	acetyl-coenzyme A synthetase	3.4	7.96E-03	Citronellol	6.2	71624	18	Cytoplasmic	COG0365	Lipid metabolism	
15599934	PA4740	pnp	polyribonucleotide nucleotidyltransferase	1.0	7.69E-01	Oktansaeure	4.8	75421	58	Periplasmic	COG1185	Translation, ribosomal structure and biogenesis	
15599936	PA4742	truB	tRNA pseudouridine 55 synthase	2.1	1.06E-01	Oktansaeure	6.9	33378	5	Cytoplasmic	COG0130	Translation, ribosomal structure and biogenesis	
15599938	PA4744	infB	translation initiation factor IF-2	1.3	1.88E-01	Oktansaeure	6.0	90912	31	Periplasmic	COG0532	Translation, ribosomal structure and biogenesis	
15599939	PA4745	nusA	N utilization substance protein A	1.8	6.77E-03	Oktansaeure	4.3	54658	27	Periplasmic	COG0195	Transcription	
15599940	PA4746		conserved hypothetical protein	3.8	2.67E-02	Oktansaeure	4.3	17139	2	Cytoplasmic	COG0779	Function unknown	
15599941	PA4747	secG	secretion protein SecG	1.3	3.88E-01	Oktansaeure	5.1	13207	2	Outer Membrane Vesicle	COG1314	Intracellular trafficking and secretion	
15599942	PA4748	tpiA	triosephosphate isomerase	2.3	5.86E-03	Oktansaeure	5.3	25621	10	Cytoplasmic	COG0149	Carbohydrate transport and metabolism	
15599943	PA4749	glmM	phosphoglucosamine mutase	1.2	5.52E-01	Citronellol	6.0	47796	8	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15599944	PA4750	folP	dihydropteroate synthase	1.2	3.95E-02	Citronellol	5.4	30490	6	Cytoplasmic	COG0294	Coenzyme metabolism	
15599945	PA4751	ftsH	cell division protein FtsH	1.0	7.97E-01	Citronellol	5.6	69955	2	Outer Membrane Vesicle	COG0465	Posttranslational modification, protein turnover, chaperones	
15599949	PA4755	greA	transcription elongation factor GreA	1.5	1.22E-01	Oktansaeure	4.7	17158	12	Periplasmic	COG0782	Function unknown	
15599950	PA4756	carB	carbamoylphosphate synthetase large subunit	3.8	9.20E-02	Citronellol	4.8	117330	68	Periplasmic	COG0458	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599952	PA4758	carA	carbamoyl-phosphate synthase small chain	1.1	5.42E-01	Citronellol	5.2	40810	12	Cytoplasmic	COG0505	Amino acid transport and metabolism	Nucleotide transport and metabolism
15599953	PA4759	dapB	dihydrodipicolinate reductase	1.1	3.97E-01	Citronellol	6.0	28324	15	Periplasmic	COG0289	Amino acid transport and metabolism	
15599954	PA4760	dnaJ	DnaJ protein	2.9	2.30E-03	Oktansaeure	7.4	40260	5	Cytoplasmic	COG0484	Posttranslational modification, protein turnover, chaperones	
15599955	PA4761	dnaK	DnaK protein	1.7	3.09E-02	Oktansaeure	4.5	68403	56	Periplasmic	COG0443	Posttranslational modification, protein turnover, chaperones	
15599956	PA4762	grpE	heat shock protein GrpE	1.1	6.06E-01	Oktansaeure	4.2	20702	11	Cytoplasmic	COG0576	Posttranslational modification, protein turnover, chaperones	
15599958	PA4764	fur	ferric uptake regulation protein	1.1	8.41E-01	Citronellol	5.9	15234	9	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15599962	PA4768	smpB	SmpB protein	11.9	1.96E-02	Oktansaeure	10.4	18032	2	Unknown	COG0691	Posttranslational modification, protein turnover, chaperones	
15599970	PA4776	pmrA	PmrA: two-component regulator system response regulator PmrA	2.4	1.59E-01	Oktansaeure	5.6	24394	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15599975	PA4781		cyclic di-GMP phosphodiesterase	5.1	2.01E-01	Citronellol	5.0	43628	5	Cytoplasmic	COG3437	Transcription	Signal transduction mechanisms
15599978	PA4784		probable transcriptional regulator	1.4	6.64E-01	Citronellol	6.5	16733	2	Cytoplasmic	COG1522	Transcription	
15599980	PA4786		probable short-chain dehydrogenase	5.2	8.08E-02	Oktansaeure	9.9	47182	2	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15599986	PA4792		conserved hypothetical protein	1.5	4.30E-01	Citronellol	9.6	34152	2	Unknown	COG0584	Energy production and conversion	
15599987	PA4793		hypothetical protein	1.9	2.50E-02	Citronellol	8.4	21281	2	Periplasmic			
15599989	PA4795		hypothetical protein	1.6	7.46E-02	Citronellol	4.7	13527	3	Cytoplasmic	COG2044	General function prediction only	
15599990	PA4796		hypothetical protein	2.3	3.11E-03	Citronellol	4.8	17129	4	Unknown	COG0509	Amino acid transport and metabolism	
15600006	PA4813	lipC	lipase LipC	70.7	7.37E-04	Citronellol	5.8	32341	2	Extracellular	COG1075	General function prediction only	
15600032	PA4839	speA	arginine decarboxylase (ADC)	1.1	1.75E-01	Oktansaeure	5.2	70667	12	Periplasmic	COG1166	Amino acid transport and metabolism	
15600034	PA4841		conserved hypothetical protein	1.2	6.08E-01	Oktansaeure	4.4	19733	4	Unknown	COG1443	Lipid metabolism	
15600040	PA4847	accB	biotin carboxyl carrier protein (BCCP)	1.3	1.63E-01	Oktansaeure	4.7	16455	6	Unknown	COG0511	Lipid metabolism	
15600041	PA4848	accC	biotin carboxylase	1.1	6.27E-01	Citronellol	6.3	48888	17	Periplasmic	COG0439	Lipid metabolism	
15600043	PA4850	prmA	ribosomal protein L11 methyltransferase	1.2	6.86E-02	Citronellol	4.2	32000	4	Periplasmic	COG2264	Translation, ribosomal structure and biogenesis	
15600047	PA4854	purH	phosphoribosylaminoimidazolecarboxamide formyltransferase	1.5	2.05E-01	Citronellol	6.5	57665	31	Periplasmic	COG0138	Nucleotide transport and metabolism	
15600048	PA4855	purD	phosphoribosylamine--glycine ligase	2.0	6.95E-02	Citronellol	4.7	45212	20	Periplasmic	COG0151	Nucleotide transport and metabolism	
15600059	PA4866		conserved hypothetical protein	1.5	1.98E-01	Citronellol	6.3	18743	2	Unknown	COG1247	Cell envelope biogenesis, outer membrane	
15600061	PA4868	ureC	urease alpha subunit	2.2	1.98E-02	Oktansaeure	6.2	60611	12	Cytoplasmic	COG0804	Amino acid transport and metabolism	
15600065	PA4872		hypothetical protein	1.0	9.74E-01	Citronellol	5.4	31320	6	Cytoplasmic	COG2513	Carbohydrate transport and metabolism	
15600067	PA4874		conserved hypothetical protein	6.6	5.17E-02	Citronellol	10.3	14433	6	Periplasmic			
15600069	PA4876	osmE	osmotically inducible lipoprotein OsmE	4.2	6.95E-01	Citronellol	8.8	12523	1	Outer Membrane Vesicle			
15600073	PA4880		probable bacterioferritin	5.2	2.40E-03	Citronellol	4.4	20217	8	Cytoplasmic	COG2193	Inorganic ion transport and metabolism	
15600077	PA4884		hypothetical protein	1.7	5.15E-01	Oktansaeure	9.7	21561	3	Periplasmic			
15600083	PA4890	desT	DesT	1.5	3.19E-01	Oktansaeure	9.1	22899	4	Cytoplasmic	COG1309	Transcription	
15600086	PA4893	ureG	urease accessory protein UreG	4.1	2.32E-04	Oktansaeure	4.6	21991	8	Cytoplasmic	COG0378	Posttranslational modification, protein turnover, chaperones	Transcription
15600092	PA4899		probable aldehyde dehydrogenase	3.5	7.47E-03	Citronellol	5.8	52697	6	Cytoplasmic	COG1012	Energy production and conversion	
15600100	PA4907		probable short-chain dehydrogenase	1.3	1.02E-01	Citronellol	5.1	27384	11	Cytoplasmic	COG4221	General function prediction only	
15600102	PA4909		probable ATP-binding component of ABC transporter	31.0	1.41E-03	Citronellol	7.8	26262	3	Cytoplasmic Membrane	COG0410	Amino acid transport and metabolism	
15600106	PA4913		probable binding protein component of ABC transporter	6.1	2.42E-02	Citronellol	6.6	39798	17	Periplasmic	COG0683	Amino acid transport and metabolism	
15600109	PA4916		hypothetical protein	3.1	1.70E-01	Oktansaeure	6.5	25457	2	Unknown	COG1051	Nucleotide transport and metabolism	
15600111	PA4918		hypothetical protein	2.9	7.24E-03	Citronellol	4.7	23821	8	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15600112	PA4919	pncB1	nicotinate phosphoribosyltransferase	1.7	1.01E-01	Citronellol	6.3	46095	9	Cytoplasmic	COG1488	Coenzyme metabolism	
15600113	PA4920	nadE	NH3-dependent NAD synthetase	1.5	9.14E-02	Citronellol	5.4	29696	15	Periplasmic	COG0171	Coenzyme metabolism	
15600115	PA4922	azu	azurin precursor	1.9	4.63E-03	Oktansaeure	6.9	16008	17	Periplasmic	COG3241	Energy production and conversion	
15600116	PA4923		conserved hypothetical protein	1.1	9.90E-01	Citronellol	5.2	20725	4	Unknown	COG1611	General function prediction only	
15600124	PA4931	dnaB	replicative DNA helicase	1.2	3.29E-01	Citronellol	4.7	51589	2	Cytoplasmic	COG0305	DNA replication, recombination, and repair	
15600125	PA4932	rplI	50S ribosomal protein L9	2.0	1.60E-02	Oktansaeure	5.3	15532	6	Periplasmic	COG0359	Translation, ribosomal structure and biogenesis	
15600128	PA4935	rpsF	30S ribosomal protein S6	1.4	2.57E-01	Oktansaeure	4.6	16165	17	Periplasmic	COG0360	Translation, ribosomal structure and biogenesis	
15600129	PA4936		probable rRNA methylase	2.5	1.01E-01	Oktansaeure	7.2	27081	2	Cytoplasmic	COG0566	Translation, ribosomal structure and biogenesis	
15600131	PA4938	purA	adenylosuccinate synthetase	1.1	2.97E-01	Citronellol	6.0	46814	18	Periplasmic	COG0104	Nucleotide transport and metabolism	
15600132	PA4939		conserved hypothetical protein	1.0	8.66E-01	Citronellol	4.8	42546	11	Cytoplasmic	COG3705	Amino acid transport and metabolism	
15600139	PA4946	mutL	DNA mismatch repair protein MutL	2.1	3.00E-02	Oktansaeure	6.5	69748	5	Cytoplasmic	COG0323	DNA replication, recombination, and repair	
15600141	PA4948		conserved hypothetical protein	3.7	9.89E-04	Oktansaeure	4.7	16463	3	Cytoplasmic	COG0802	General function prediction only	
15600142	PA4949		conserved hypothetical protein	1.0	8.51E-01	Oktansaeure	7.6	51550	3	Unknown	COG0063	Carbohydrate transport and metabolism	
15600144	PA4951	orn	oligoribonuclease	2.4	1.85E-02	Citronellol	5.6	20826	4	Cytoplasmic	COG1949	RNA processing and modification	
15600148	PA4955		hypothetical protein	1.2	3.44E-01	Citronellol	10.0	56255	3	Cytoplasmic Membrane			
15600149	PA4956	rhdA	thiosulfate:cyanide sulfurtransferase	1.3	2.14E-02	Oktansaeure	5.3	29391	9	Cytoplasmic	COG2897	Inorganic ion transport and metabolism	
15600152	PA4959	fimX	FimX	1.7	1.01E-01	Oktansaeure	4.9	75992	14	Cytoplasmic Membrane	COG2200	Signal transduction mechanisms	
15600153	PA4960		probable phosphoserine phosphatase	1.1	4.17E-01	Oktansaeure	4.9	46438	9	Cytoplasmic	COG0560	Amino acid transport and metabolism	
15600157	PA4964	parC	topoisomerase IV subunit A	1.6	3.61E-02	Oktansaeure	5.9	83364	20	Cytoplasmic	COG0188	DNA replication, recombination, and repair	
15600160	PA4967	parE	topoisomerase IV subunit B	2.1	7.90E-03	Oktansaeure	5.9	69178	7	Cytoplasmic	COG0187	DNA replication, recombination, and repair	
15600161	PA4968		conserved hypothetical protein	1.2	5.93E-01	Citronellol	6.8	22645	3	Unknown	COG3150	General function prediction only	
15600162	PA4969	cpdA	Cyclic AMP (cAMP) Phosphodiesterase, CpdA	1.9	2.78E-01	Oktansaeure	4.8	30498	2	Cytoplasmic	COG1409	General function prediction only	
15600164	PA4971	aspP	adenosine diphosphate sugar pyrophosphatase	1.5	8.23E-02	Citronellol	4.7	23133	7	Cytoplasmic			
15600166	PA4973	thiC	thiamin biosynthesis protein ThiC	1.1	7.76E-01	Citronellol	5.8	69784	12	Cytoplasmic	COG0422	Coenzyme metabolism	
15600167	PA4974		probable outer membrane protein precursor	1.1	5.22E-01	Citronellol	5.9	53405	5	Periplasmic	COG1538	Cell envelope biogenesis, outer membrane	Intracellular trafficking and secretion
15600168	PA4975		NAD(P)H quinone oxidoreductase	1.0	8.92E-01	Citronellol	6.0	26315	2	Cytoplasmic	COG2249	General function prediction only	
15600180	PA4987		probable transcriptional regulator	1.1	8.98E-01	Citronellol	5.6	22368	3	Cytoplasmic	COG1917	Function unknown	
15600184	PA4991		hypothetical protein	1.6	7.87E-02	Oktansaeure	8.0	42109	2	Cytoplasmic	COG0578	Energy production and conversion	
15600185	PA4992		hypothetical protein	1.2	1.14E-01	Citronellol	6.4	29030	7	Cytoplasmic	COG0667	Energy production and conversion	
15600189	PA4996	rfaE	LPS biosynthesis protein RfaE	1.2	1.22E-01	Citronellol	6.2	50348	18	Periplasmic	COG2870	Cell envelope biogenesis, outer membrane	
15600191	PA4998		conserved hypothetical protein	1.7	3.32E-01	Oktansaeure	10.0	24986	2	Cytoplasmic			
15600194	PA5001		hypothetical protein	1.1	4.35E-01	Oktansaeure	8.7	36625	3	Cytoplasmic	COG0438	Cell envelope biogenesis, outer membrane	
15600198	PA5005		probable carbamoyl transferase	2.9	2.59E-02	Oktansaeure	6.9	66047	8	Outer Membrane Vesicle	COG2192	Posttranslational modification, protein turnover, chaperones	
15600206	PA5013	ilvE	branched-chain amino acid transferase	1.0	7.44E-01	Citronellol	6.2	34084	24	Periplasmic	COG0115	Amino acid transport and metabolism	Coenzyme metabolism
15600207	PA5014	glnE	glutamate-ammonia-ligase adenylyltransferase	1.6	3.96E-02	Citronellol	5.2	110102	27	Cytoplasmic	COG1391	Posttranslational modification, protein turnover, chaperones	Signal transduction mechanisms
15600208	PA5015	aceE	pyruvate dehydrogenase	1.5	3.50E-02	Citronellol	5.6	99563	49	Periplasmic	COG2609	Energy production and conversion	
15600209	PA5016	aceF	dihydrolipoamide acetyltransferase	1.2	3.72E-01	Oktansaeure	5.0	56676	24	Periplasmic	COG0508	Energy production and conversion	
15600211	PA5018	msrA	peptide methionine sulfoxide reductase	1.1	8.32E-01	Oktansaeure	5.0	23517	7	Unknown	COG0225	Posttranslational modification, protein turnover, chaperones	
15600212	PA5019		conserved hypothetical protein	1.2	7.77E-01	Oktansaeure	6.0	31882	9	Cytoplasmic	COG2961	General function prediction only	
15600213	PA5020		probable acyl-CoA dehydrogenase	2.0	7.69E-01	Citronellol	6.2	66235	2	Cytoplasmic	COG1960	Lipid metabolism	
15600218	PA5025	metY	homocysteine synthase	2.4	8.18E-04	Oktansaeure	6.5	45177	14	Cytoplasmic	COG2873	Amino acid transport and metabolism	

15600219	PA5026		hypothetical protein	15.4	3.28E-03	Citronellol	6.3	16786	3	Cytoplasmic	COG2050	Secondary metabolites biosynthesis, transport, and catabolism	
15600227	PA5034	hemE	uroporphyrinogen decarboxylase	1.1	7.21E-01	Citronellol	6.3	38792	10	Cytoplasmic	COG0407	Coenzyme metabolism	
15600228	PA5035	gltD	glutamate synthase small chain	1.1	5.38E-01	Oktansaeure	6.4	52625	18	Cytoplasmic	COG0493	Amino acid transport and metabolism	General function prediction only
15600229	PA5036	gltB	glutamate synthase large chain precursor	3.0	1.30E-01	Citronellol	6.0	161607	63	Cytoplasmic	COG0069	Amino acid transport and metabolism	
15600231	PA5038	aroB	3-dehydroquinate synthase	1.1	6.68E-01	Citronellol	5.6	40109	11	Cytoplasmic	COG0337	Amino acid transport and metabolism	
15600232	PA5039	aroK	shikimate kinase	1.6	2.60E-01	Oktansaeure	8.8	19205	3	Cytoplasmic	COG0703	Amino acid transport and metabolism	
15600239	PA5046		malic enzyme	1.9	5.35E-02	Citronellol	4.8	45428	33	Periplasmic	COG0281	Energy production and conversion	
15600244	PA5051	argS	arginyl-tRNA synthetase	1.5	2.22E-01	Citronellol	5.2	65199	18	Periplasmic	COG0018	Translation, ribosomal structure and biogenesis	
15600246	PA5053	hslV	heat shock protein HslV	1.5	2.78E-01	Citronellol	6.7	18767	7	Cytoplasmic	COG5405	Posttranslational modification, protein turnover, chaperones	
15600247	PA5054	hslU	heat shock protein HslU	1.3	1.98E-01	Citronellol	5.4	50082	13	Cytoplasmic	COG1220	Posttranslational modification, protein turnover, chaperones	
15600253	PA5060	phaF	polyhydroxyalkanoate synthesis protein PhaF	1.1	7.29E-01	Oktansaeure	11.1	30577	3	Cytoplasmic	COG3937	Function unknown	
15600256	PA5063	ubiE	ubiquinone biosynthesis methyltransferase UbiE	2.4	3.35E-02	Oktansaeure	9.5	28254	11	Cytoplasmic	COG2226	Coenzyme metabolism	
15600257	PA5064		hypothetical protein	1.5	1.24E-01	Oktansaeure	6.0	22767	7	Cytoplasmic	COG3165	Function unknown	
15600259	PA5066	hisI	phosphoribosyl-AMP cyclohydrolase	1.2	3.19E-01	Citronellol	6.0	15375	8	Cytoplasmic	COG0139	Amino acid transport and metabolism	
15600261	PA5068	tatA	translocation protein TatA	4.4	1.84E-01	Citronellol	7.7	9190	2	Cytoplasmic Membrane	COG1826	Intracellular trafficking and secretion	
15600264	PA5071		conserved hypothetical protein	1.6	3.33E-01	Oktansaeure	9.1	26065	3	Cytoplasmic	COG1385	Function unknown	
15600269	PA5076		probable binding protein component of ABC transporter	1.8	4.41E-03	Citronellol	7.6	29736	20	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600270	PA5077	mdoH	periplasmic glucans biosynthesis protein MdoH	2.8	2.88E-01	Oktansaeure	8.9	96994	2	Outer Membrane Vesicle	COG2943	Cell envelope biogenesis, outer membrane	
15600271	PA5078		conserved hypothetical protein	1.9	4.81E-02	Citronellol	7.0	59444	15	Periplasmic	COG3131	Inorganic ion transport and metabolism	
15600272	PA5079		conserved hypothetical protein	1.1	9.70E-01	Citronellol	6.3	15530	3	Unknown	COG1490	Translation, ribosomal structure and biogenesis	
15600273	PA5080		prolyl aminopeptidase	1.1	6.00E-01	Citronellol	6.2	36515	17	Cytoplasmic	COG0596	General function prediction only	
15600274	PA5081		hypothetical protein	3.1	2.54E-03	Citronellol	4.7	17918	4	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600275	PA5082		probable binding protein component of ABC transporter	3.0	7.10E-02	Citronellol	8.2	32866	2	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600283	PA5090		conserved hypothetical protein	58.6	6.02E-04	Oktansaeure	5.8	87821	5	Cytoplasmic	COG3501	Function unknown	
15600284	PA5091	hutG	N-formylglutamate amidohydrolase	1.3	3.86E-01	Citronellol	5.9	29791	5	Cytoplasmic	COG3741	Amino acid transport and metabolism	
15600285	PA5092	hutI	imidazolone-5-propionate hydrolase HutI	2.2	6.46E-02	Citronellol	6.0	43425	2	Cytoplasmic	COG1228	Secondary metabolites biosynthesis, transport, and catabolism	
15600289	PA5096		probable binding protein component of ABC transporter	2.0	3.14E-01	Oktansaeure	5.2	35496	3	Periplasmic	COG2113	Amino acid transport and metabolism	
15600291	PA5098	hutH	histidine ammonia-lyase	3.5	1.10E-01	Oktansaeure	5.8	53779	3	Cytoplasmic	COG2986	Amino acid transport and metabolism	
15600293	PA5100	hutU	urocanase	27.2	5.42E-02	Citronellol	6.3	61161	4	Cytoplasmic	COG2987	Amino acid transport and metabolism	
15600296	PA5103		hypothetical protein	1.6	4.68E-01	Oktansaeure	6.2	37890	2	Periplasmic	COG2113	Amino acid transport and metabolism	
15600297	PA5104		conserved hypothetical protein	1.3	8.80E-01	Citronellol	5.6	21415	5	Unknown	COG3758	Function unknown	
15600298	PA5105	hutC	histidine utilization repressor HutC	1.5	2.61E-01	Citronellol	7.4	27779	2	Cytoplasmic	COG2188	Transcription	
15600302	PA5109		hypothetical protein	1.4	4.58E-01	Citronellol	5.1	22697	6	Cytoplasmic	COG3803	Function unknown	
15600303	PA5110	fbp	fructose-1,6-bisphosphatase	1.4	4.91E-01	Oktansaeure	5.9	37216	13	Periplasmic	COG0158	Carbohydrate transport and metabolism	
15600304	PA5111	gloA3	lactoylglutathione lyase	1.5	3.27E-01	Citronellol	4.8	20215	3	Cytoplasmic	COG0346	Amino acid transport and metabolism	
15600305	PA5112	estA	esterase EstA	1.7	7.33E-01	Citronellol	4.5	69608	5	Periplasmic	COG3240	Lipid metabolism	General function prediction only
15600308	PA5115		conserved hypothetical protein	1.5	2.78E-01	Oktansaeure	5.2	20998	6	Cytoplasmic			
15600310	PA5117	typA	regulatory protein TypA	1.2	1.80E-01	Oktansaeure	5.0	66903	17	Periplasmic	COG1217	Signal transduction mechanisms	
15600311	PA5118	thiI	thiazole biosynthesis protein ThiI	4.8	2.52E-01	Oktansaeure	6.7	54849	2	Cytoplasmic	COG0301	Coenzyme metabolism	
15600312	PA5119	glnA	glutamine synthetase	1.3	5.04E-01	Oktansaeure	5.0	51944	23	Outer Membrane Vesicle	COG0174	Amino acid transport and metabolism	
15600315	PA5122		hypothetical protein	1.0	7.18E-01	Oktansaeure	6.4	18427	2	Unknown			
15600321	PA5128	secB	secretion protein SecB	2.3	4.29E-02	Citronellol	4.2	18146	11	Periplasmic	COG1952	Intracellular trafficking and secretion	
15600324	PA5131	pgm	phosphoglycerate mutase	1.2	5.61E-01	Oktansaeure	4.9	55601	22	Periplasmic	COG0696	Carbohydrate transport and metabolism	
15600327	PA5134		probable carboxyl-terminal protease	2.1	5.59E-02	Oktansaeure	5.4	46018	5	Periplasmic	COG0793	Cell envelope biogenesis, outer membrane	
15600330	PA5137		hypothetical protein	4.8	1.79E-03	Citronellol	7.5	27991	6	Unknown	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600331	PA5138		hypothetical protein	1.3	8.31E-02	Citronellol	4.9	27915	11	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600332	PA5139		hypothetical protein	2.0	3.78E-02	Citronellol	5.8	27565	7	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600334	PA5141	hisA	phosphoribosylformimino-5-aminoimidazole carboxamide	1.3	9.16E-02	Citronellol	4.7	25938	4	Cytoplasmic	COG0106	Amino acid transport and metabolism	
15600335	PA5142	hisH1	glutamine amidotransferase	2.6	1.95E-02	Citronellol	6.3	23666	10	Cytoplasmic	COG0118	Amino acid transport and metabolism	
15600336	PA5143	hisB	imidazoleglycerol-phosphate dehydratase	1.4	7.35E-02	Citronellol	6.5	21937	6	Cytoplasmic	COG0131	Amino acid transport and metabolism	
15600339	PA5146		hypothetical protein	1.0	9.57E-01	Citronellol	8.3	80849	6	Outer Membrane Vesicle	COG2982	Cell envelope biogenesis, outer membrane	
15600343	PA5150		probable short-chain dehydrogenase	1.2	3.80E-01	Oktansaeure	6.2	26191	12	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600346	PA5153		amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter peripl	2.8	1.31E-02	Citronellol	4.9	27561	21	Periplasmic	COG0834	Amino acid transport and metabolism	Signal transduction mechanisms
15600354	PA5161	rmlB	dTDP-D-glucose 4,6-dehydratase	1.2	2.87E-01	Citronellol	5.9	39542	14	Cytoplasmic	COG1088	Cell envelope biogenesis, outer membrane	
15600355	PA5162	rmlD	dTDP-4-dehydrorhamnose reductase	1.1	2.91E-01	Citronellol	6.1	33106	12	Cytoplasmic	COG1091	Cell envelope biogenesis, outer membrane	
15600356	PA5163	rmlA	glucose-1-phosphate thymidylyltransferase	1.2	2.22E-01	Citronellol	5.0	32457	17	Cytoplasmic	COG1209	Cell envelope biogenesis, outer membrane	
15600357	PA5164	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	1.2	4.91E-02	Oktansaeure	6.0	20766	10	Unknown	COG1898	Cell envelope biogenesis, outer membrane	
15600359	PA5166	dctD	DctD	1.1	6.81E-01	Oktansaeure	5.5	50864	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600360	PA5167	dctP	DctP	2.3	1.73E-02	Citronellol	8.8	37051	21	Periplasmic	COG1638	Carbohydrate transport and metabolism	
15600364	PA5171	arcA	arginine deiminase	1.5	1.70E-01	Citronellol	5.5	46436	33	Cytoplasmic	COG2235	Amino acid transport and metabolism	
15600365	PA5172	arcB	ornithine carbamoyltransferase, catabolic	1.1	9.34E-01	Oktansaeure	6.6	38108	27	Cytoplasmic	COG0078	Amino acid transport and metabolism	
15600366	PA5173	arcC	carbamate kinase	1.3	3.14E-01	Oktansaeure	5.0	33080	20	Cytoplasmic	COG0549	Amino acid transport and metabolism	
15600367	PA5174		probable beta-ketoacyl synthase	1.4	8.98E-02	Oktansaeure	6.0	68763	7	Periplasmic	COG0304	Lipid metabolism	Secondary metabolites biosynthesis, transport, and catabolism
15600368	PA5175	cysQ	3,5-bisphosphate nucleotidase CysQ	1.2	3.99E-01	Oktansaeure	4.8	29779	6	Cytoplasmic	COG1218	Inorganic ion transport and metabolism	
15600369	PA5176		conserved hypothetical protein	1.6	1.31E-02	Citronellol	4.5	20983	9	Cytoplasmic	COG1051	Nucleotide transport and metabolism	
15600370	PA5177		probable hydrolase	5.0	3.85E-02	Oktansaeure	5.9	25629	4	Cytoplasmic	COG1011	General function prediction only	
15600372	PA5179		probable transcriptional regulator	2.7	1.53E-02	Oktansaeure	6.4	32533	2	Cytoplasmic	COG0583	Transcription	
15600377	PA5184		hypothetical protein	1.2	1.36E-01	Citronellol	8.8	20417	11	Periplasmic	COG1605	Amino acid transport and metabolism	
15600379	PA5186		probable iron-containing alcohol dehydrogenase	1.6	7.31E-02	Oktansaeure	5.4	40354	4	Cytoplasmic	COG1454	Energy production and conversion	
15600380	PA5187		probable acyl-CoA dehydrogenase	75.7	1.49E-02	Oktansaeure	5.3	64558	6	Cytoplasmic	COG1960	Lipid metabolism	
15600381	PA5188		probable 3-hydroxyacyl-CoA dehydrogenase	1.5	4.69E-02	Oktansaeure	5.2	44810	12	Cytoplasmic	COG1250	Lipid metabolism	
15600383	PA5190		probable nitroreductase	1.3	4.68E-01	Oktansaeure	6.0	22450	6	Cytoplasmic	COG0778	Energy production and conversion	
15600385	PA5192	pckA	phosphoenolpyruvate carboxykinase	1.1	8.56E-01	Citronellol	5.1	55732	34	Periplasmic	COG1866	Energy production and conversion	
15600386	PA5193	yrfI	heat shock protein HSP33	1.6	4.54E-02	Oktansaeure	4.5	32834	7	Cytoplasmic	COG1281	Posttranslational modification, protein turnover, chaperones	
15600393	PA5200	amgR	AmgR	1.3	6.70E-02	Oktansaeure	6.6	27924	13	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600394	PA5201		conserved hypothetical protein	1.3	6.58E-02	Oktansaeure	6.3	84963	35	Periplasmic	COG2183	Transcription	
15600396	PA5203	gshA	glutamate--cysteine ligase	1.4	2.71E-01	Citronellol	4.9	59205	16	Cytoplasmic	COG2918	Coenzyme metabolism	
15600397	PA5204	argA	N-acetylglutamate synthase	1.3	1.95E-02	Oktansaeure	6.5	47858	10	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600399	PA5206	argE	acetylornithine deacetylase	1.2	2.83E-01	Citronellol	5.3	42163	2	Cytoplasmic	COG0624	Amino acid transport and metabolism	
15600401	PA5208		conserved hypothetical protein	3.1	3.88E-03	Oktansaeure	5.2	25644	3	Cytoplasmic	COG1392	Inorganic ion transport and metabolism	
15600403	PA5210		probable secretion pathway ATPase	1.9	1.76E-01	Oktansaeure	6.5	65981	6	Cytoplasmic	COG2804	Cell motility and secretion	Intracellular trafficking and secretion
15600406	PA5213	gcvP1	glycine cleavage system protein P1	3.0	5.82E-02	Citronellol	6.5	104710	15	Cytoplasmic	COG1003	Amino acid transport and metabolism	
15600407	PA5214	gcvH1	glycine cleavage system protein H1	6.1	1.91E-01	Citronellol	3.9	13642	2	Unknown	COG0509	Amino acid transport and metabolism	
15600408	PA5215	gcvT1	glycine-cleavage system protein T1	1.3	2.29E-01	Citronellol	5.4	38907	8	Periplasmic	COG0404	Amino acid transport and metabolism	
15600410	PA5217		probable binding protein component of ABC iron transporter	1.3	3.40E-01	Citronellol	6.4	36292	7	Periplasmic	COG1840	Inorganic ion transport and metabolism	
15600413	PA5220		hypothetical protein	1.7	9.57E-01	Oktansaeure	6.2	30542	3	Unknown			
15600417	PA5224	pepP	aminopeptidase P	1.1	6.19E-01	Citronellol	5.1	49710	16	Cytoplasmic	COG0006	Amino acid transport and metabolism	
15600418	PA5225		hypothetical protein	1.1	5.83E-01	Citronellol	4.0	19358	4	Unknown	COG3079	Function unknown	
15600421	PA5228		conserved hypothetical protein	1.9	1.20E-01	Oktansaeure	12.0	23077	3	Unknown	COG0212	Coenzyme metabolism	
15600422	PA5229		conserved hypothetical protein	1.8	1.84E-02	Citronellol	7.5	16871	6	Unknown	COG2947	Function unknown	
15600427	PA5234		probable oxidoreductase	1.1	9.33E-01	Oktansaeure	7.0	34011	9	Cytoplasmic	COG0604	Energy production and conversion	General function prediction only
15600432	PA5239	rho	transcription termination factor Rho	1.2	3.95E-01	Oktansaeure	6.8	47069	21	Periplasmic	COG1158	Transcription	
15600433	PA5240	trxA	thioredoxin	1.5	1.66E-01	Citronellol	4.5	11870	9	Cytoplasmic	COG3118	Posttranslational modification, protein turnover, chaperones	
15600434	PA5241	ppx	exopolyphosphatase	1.2	4.13E-01	Citronellol	6.7	56419	12	Cytoplasmic	COG0248	Nucleotide transport and metabolism	Inorganic ion transport and metabolism
15600435	PA5242	ppk	polyphosphate kinase	1.2	3.08E-01	Oktansaeure	7.7	83151	27	Cytoplasmic Membrane	COG0855	Inorganic ion transport and metabolism	
15600436	PA5243	hemB	delta-aminolevulinic acid dehydratase	1.1	6.47E-01	Citronellol	4.8	37005	7	Cytoplasmic	COG0113	Coenzyme metabolism	
15600438	PA5245		conserved hypothetical protein	1.5	3.01E-01	Citronellol	4.7	23426	14	Cytoplasmic	COG3155	Secondary metabolites biosynthesis, transport, and catabolism	

15600445	PA5252		probable ATP-binding component of ABC transporter	14.0	5.03E-04	Oktansaeure	5.9	70871	9	Cytoplasmic	COG0488	General function prediction only	
15600447	PA5254		probable peptidyl-prolyl cis-trans isomerase, FkbP-type	1.5	2.51E-01	Oktansaeure	5.4	23047	2	Outer Membrane	COG0545	Posttranslational modification, protein turnover, chaperones	
15600452	PA5259	hemD	uroporphyrinogen-III synthetase	1.3	1.42E-01	Citronellol	4.8	27247	4	Unknown	COG1587	Coenzyme metabolism	
15600453	PA5260	hemC	porphobilinogen deaminase	1.4	2.01E-01	Citronellol	5.3	33641	5	Cytoplasmic	COG0181	Coenzyme metabolism	
15600454	PA5261	algR	alginate biosynthesis regulatory protein AlgR	2.5	9.85E-03	Citronellol	7.3	27608	12	Cytoplasmic	COG3279	Transcription	Signal transduction mechanisms
15600456	PA5263	argH	argininosuccinate lyase	1.6	1.24E-01	Citronellol	5.5	51640	20	Periplasmic	COG0165	Amino acid transport and metabolism	
15600459	PA5266		conserved hypothetical protein	30.0	8.05E-04	Oktansaeure	6.4	76707	11	Cytoplasmic	COG3501	Function unknown	
15600470	PA5277	lysA	diaminopimelate decarboxylase	1.6	1.13E-01	Citronellol	5.4	45490	17	Periplasmic	COG0019	Amino acid transport and metabolism	
15600471	PA5278	dapF	diaminopimelate epimerase	1.1	3.23E-01	Oktansaeure	7.7	30320	9	Cytoplasmic	COG0253	Amino acid transport and metabolism	
15600472	PA5279		conserved hypothetical protein	1.8	1.03E-01	Oktansaeure	5.3	25767	3	Cytoplasmic	COG3159	Function unknown	
15600474	PA5281		probable hydrolase	3.9	2.97E-03	Oktansaeure	5.9	25852	3	Cytoplasmic	COG1011	General function prediction only	
15600481	PA5288	glnK	nitrogen regulatory protein P-II 2	4.0	4.87E-02	Citronellol	5.2	12286	2	Cytoplasmic Membrane	COG0347	Amino acid transport and metabolism	
15600485	PA5292	pchP	phosphorylcholine phosphatase	1.1	6.69E-01	Oktansaeure	5.8	39117	3	Periplasmic			
15600490	PA5297	poxB	pyruvate dehydrogenase (cytochrome)	17.6	9.08E-04	Oktansaeure	6.0	62320	3	Cytoplasmic Membrane	COG0028	acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase	
15600491	PA5298		xanthine phosphoribosyltransferase	1.5	1.87E-01	Oktansaeure	6.6	20575	6	Cytoplasmic	COG0503	Nucleotide transport and metabolism	
15600492	PA5299		hypothetical protein	1.8	1.75E-02	Oktansaeure	5.7	68673	3	Cytoplasmic	COG0427	Energy production and conversion	
15600494	PA5301	pauR	probable transcriptional regulator	1.3	5.32E-01	Citronellol	5.3	19944	6	Cytoplasmic	COG1396	Transcription	
15600501	PA5308	lrp	leucine-responsive regulatory protein	2.9	3.96E-02	Citronellol	8.3	18868	2	Cytoplasmic	COG1522	Transcription	
15600505	PA5312	pauC	Aldehyde dehydrogenase	1.3	1.25E-01	Citronellol	5.3	53143	25	Periplasmic	COG1012	Energy production and conversion	
15600506	PA5313	gabT2	Transaminase	1.5	2.16E-01	Citronellol	6.7	48347	3	Cytoplasmic	COG0161	Coenzyme metabolism	
15600510	PA5317		probable binding protein component of ABC dipeptide transporter	2.3	6.29E-02	Oktansaeure	7.0	57880	9	Periplasmic	COG0747	Amino acid transport and metabolism	
15600513	PA5320	coaC	Phosphopantothenoylcysteine synthase/(R)-4'-phospho-N-pantothenoylcysteine	1.2	1.61E-01	Citronellol	6.3	43133	10	Cytoplasmic	COG0452	Coenzyme metabolism	
15600515	PA5322	algC	phosphomannomutase AlgC	1.0	7.47E-01	Citronellol	5.0	50295	26	Cytoplasmic	COG1109	Carbohydrate transport and metabolism	
15600516	PA5323	argB	acetylglutamate kinase	1.1	7.81E-01	Citronellol	6.8	31849	18	Cytoplasmic	COG0548	Amino acid transport and metabolism	
15600522	PA5329		conserved hypothetical protein	2.1	1.83E-02	Citronellol	5.0	17712	7	Cytoplasmic	COG0824	General function prediction only	
15600523	PA5330		hypothetical protein	1.5	3.17E-01	Citronellol	9.4	22434	9	Unknown			
15600524	PA5331	pyrE	orotate phosphoribosyltransferase	2.2	7.11E-02	Citronellol	5.1	23320	11	Cytoplasmic	COG0461	Nucleotide transport and metabolism	
15600525	PA5332	crc	catabolite repression control protein	1.4	6.55E-02	Oktansaeure	5.2	29844	8	Cytoplasmic	COG0708	DNA replication, recombination, and repair	
15600527	PA5334	rph	ribonuclease PH	1.0	7.57E-01	Oktansaeure	5.9	25654	7	Cytoplasmic	COG0689	Translation, ribosomal structure and biogenesis	
15600528	PA5335		conserved hypothetical protein	1.3	1.04E-01	Citronellol	5.8	31708	14	Cytoplasmic	COG1561	Function unknown	
15600529	PA5336	gmk	guanylate kinase	1.3	2.19E-01	Citronellol	5.3	23102	10	Cytoplasmic	COG0194	Nucleotide transport and metabolism	
15600531	PA5338	spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.8	4.46E-03	Oktansaeure	9.4	78861	18	Cytoplasmic	COG0317	Signal transduction mechanisms	Transcription
15600532	PA5339		conserved hypothetical protein	1.7	9.72E-01	Citronellol	4.8	13610	6	Cytoplasmic	COG0251	Translation, ribosomal structure and biogenesis	
15600536	PA5343		hypothetical protein	1.1	4.99E-01	Oktansaeure	6.2	30778	10	Unknown	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15600537	PA5344	oxyR	OxyR	1.7	5.75E-04	Oktansaeure	6.7	34295	12	Cytoplasmic	COG0583	Transcription	
15600538	PA5345	recG	ATP-dependent DNA helicase RecG	2.0	7.55E-03	Oktansaeure	7.3	76178	4	Cytoplasmic	COG1200	DNA replication, recombination, and repair	Transcription
15600539	PA5346	sadB	SadB	62.0	5.41E-03	Oktansaeure	6.0	51427	2	Cytoplasmic	COG1639	Signal transduction mechanisms	
15600540	PA5347		hypothetical protein	6.4	1.68E-03	Oktansaeure	11.1	14726	5	Unknown			
15600541	PA5348		probable DNA-binding protein	69.5	4.55E-03	Citronellol	11.3	9695	2	Cytoplasmic	COG0776	DNA replication, recombination, and repair	
15600542	PA5349		probable rubredoxin reductase	1.1	6.75E-01	Citronellol	5.5	40617	10	Cytoplasmic	COG1251	Energy production and conversion	
15600550	PA5357		hypothetical protein	1.1	6.21E-01	Citronellol	4.7	19512	8	Cytoplasmic	COG3161	Coenzyme metabolism	
15600552	PA5359		hypothetical protein	9.7	2.04E-02	Citronellol	8.0	16472	5	Periplasmic	COG4315	Function unknown	
15600553	PA5360	phoB	two-component response regulator PhoB	2.1	6.29E-03	Oktansaeure	5.1	25711	2	Cytoplasmic	COG0745	Signal transduction mechanisms	Transcription
15600557	PA5364		probable two-component response regulator	1.1	4.08E-01	Oktansaeure	9.4	32401	4	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600558	PA5365	phoU	phosphate uptake regulatory protein PhoU	2.2	6.45E-04	Oktansaeure	5.0	27487	5	Cytoplasmic	COG0704	Inorganic ion transport and metabolism	
15600562	PA5369	pstS	phosphate ABC transporter, periplasmic phosphate-binding protein, PstS	1.1	6.31E-01	Citronellol	9.5	34473	8	Periplasmic	COG0226	Inorganic ion transport and metabolism	
15600564	PA5371		conserved hypothetical protein	2.5	2.29E-02	Citronellol	4.5	14555	2	Unknown	COG1607	Lipid metabolism	
15600566	PA5373	betB	betaine aldehyde dehydrogenase	1.1	9.75E-01	Oktansaeure	5.0	53332	6	Cytoplasmic	COG1012	Energy production and conversion	
15600567	PA5374	betI	transcriptional regulator BetI	1.8	3.10E-01	Citronellol	9.0	21861	5	Unknown	COG1309	Transcription	
15600571	PA5378		hypothetical protein	1.8	1.98E-03	Citronellol	7.3	34427	12	Periplasmic	COG2113	Amino acid transport and metabolism	
15600588	PA5395		conserved hypothetical protein	2.7	8.93E-04	Citronellol	7.8	18513	3	Unknown	COG3558	Function unknown	
15600606	PA5413	ltaA	low specificity l-threonine aldolase	1.1	5.36E-01	Citronellol	5.0	38213	6	Cytoplasmic	COG2008	Amino acid transport and metabolism	
15600614	PA5421	fdhA	glutathione-independent formaldehyde dehydrogenase	7.8	1.92E-03	Citronellol	6.8	42008	2	Cytoplasmic	COG1063	Amino acid transport and metabolism	General function prediction only
15600615	PA5422		hypothetical protein	1.2	1.25E-01	Citronellol	5.1	36107	12	Cytoplasmic	COG0676	Carbohydrate transport and metabolism	
15600616	PA5423		hypothetical protein	1.1	9.43E-01	Citronellol	5.7	20002	3	Periplasmic	COG3495	Function unknown	
15600618	PA5425	purK	phosphoribosylaminoimidazole carboxylase	1.2	2.66E-01	Citronellol	5.4	38496	6	Cytoplasmic Membrane	COG0026	Nucleotide transport and metabolism	
15600619	PA5426	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	1.4	8.97E-02	Citronellol	6.2	16889	9	Unknown	COG0041	Nucleotide transport and metabolism	
15600620	PA5427	adhA	alcohol dehydrogenase	6.5	1.42E-02	Oktansaeure	5.8	35911	12	Outer Membrane Vesicle	COG1064	General function prediction only	
15600622	PA5429	aspA	aspartate ammonia-lyase	1.0	9.88E-01	Citronellol	5.6	51069	10	Periplasmic	COG1027	Amino acid transport and metabolism	
15600626	PA5433		conserved hypothetical protein	2.0	1.30E-02	Citronellol	9.0	25584	2	Unknown	COG1670	Translation, ribosomal structure and biogenesis	
15600628	PA5435		probable transcarboxylase subunit	1.3	2.49E-01	Citronellol	5.7	66095	31	Cytoplasmic	COG5016	Energy production and conversion	
15600629	PA5436		probable biotin carboxylase subunit of a transcarboxylase	1.9	1.65E-02	Citronellol	6.6	51816	11	Cytoplasmic	COG0439	Lipid metabolism	
15600631	PA5438		probable transcriptional regulator	1.4	3.01E-01	Oktansaeure	7.2	31648	5	Cytoplasmic	COG1737	Transcription	
15600632	PA5439		probable glucose-6-phosphate dehydrogenase	1.7	1.31E-01	Citronellol	7.2	54573	3	Cytoplasmic	COG0364	Carbohydrate transport and metabolism	
15600634	PA5441		hypothetical protein	1.4	1.75E-01	Oktansaeure	4.6	80036	35	Periplasmic			
15600636	PA5443	uvrD	DNA helicase II	2.0	1.87E-02	Oktansaeure	5.7	81494	13	Cytoplasmic	COG0210	DNA replication, recombination, and repair	
15600645	PA5452	wbpW	phosphomannose isomerase/GDP-mannose WbpW	16.8	2.67E-02	Oktansaeure	6.4	52574	2	Cytoplasmic	COG0836	Cell envelope biogenesis, outer membrane	
15600646	PA5453	gmd	GDP-mannose 4,6-dehydratase	1.5	1.86E-01	Citronellol	6.5	36399	13	Cytoplasmic	COG1089	Cell envelope biogenesis, outer membrane	
15600647	PA5454	rmd	oxidoreductase Rmd	2.4	2.50E-04	Citronellol	6.7	33910	7	Cytoplasmic	COG0451	Cell envelope biogenesis, outer membrane	Carbohydrate transport and metabolism
15600650	PA5457		hypothetical protein	1.4	7.52E-01	Citronellol	6.2	31744	3	Cytoplasmic	COG2227	Coenzyme metabolism	
15600652	PA5459		hypothetical protein	1.2	3.79E-01	Citronellol	4.7	30701	8	Cytoplasmic	COG2226	Coenzyme metabolism	
15600668	PA5475		hypothetical protein	13.9	1.98E-02	Oktansaeure	4.8	21000	7	Cytoplasmic			
15600674	PA5481		hypothetical protein	1.5	3.71E-01	Citronellol	5.2	17366	4	Periplasmic			
15600676	PA5483	algB	two-component response regulator AlgB	1.1	3.99E-01	Oktansaeure	5.2	49323	7	Cytoplasmic	COG2204	Signal transduction mechanisms	
15600682	PA5489	dsbA	thiol:disulfide interchange protein DsbA	1.1	7.08E-01	Oktansaeure	6.4	23375	10	Periplasmic	COG1651	Posttranslational modification, protein turnover, chaperones	
15600683	PA5490	cc4	cytochrome c4 precursor	2.1	2.65E-01	Citronellol	7.6	20735	5	Outer Membrane Vesicle	COG2863	Energy production and conversion	
15600685	PA5492		conserved hypothetical protein	3.7	9.13E-02	Oktansaeure	7.1	23786	6	Unknown	COG0218	General function prediction only	
15600686	PA5493	polA	DNA polymerase I	1.5	5.98E-02	Citronellol	4.8	99792	45	Periplasmic	COG0749	DNA replication, recombination, and repair	
15600689	PA5496	nrdJb	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, N	3.2	3.65E-02	Oktansaeure	6.4	24886	3	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
15600690	PA5497	nrdJa	class II (cobalamin-dependent) ribonucleotide-diphosphate reductase subunit, N	5.1	2.02E-02	Oktansaeure	6.0	82741	7	Cytoplasmic	COG0209	Nucleotide transport and metabolism	
15600692	PA5499	np20	transcriptional regulator np20	1.1	9.08E-01	Citronellol	6.9	18216	2	Cytoplasmic	COG0735	Inorganic ion transport and metabolism	
15600698	PA5505		probable TonB-dependent receptor	1.3	7.70E-02	Oktansaeure	8.7	28065	15	Periplasmic	COG1464	Inorganic ion transport and metabolism	
15600700	PA5507		hypothetical protein	1.2	2.62E-01	Oktansaeure	6.4	24262	8	Cytoplasmic	COG1335	Secondary metabolites biosynthesis, transport, and catabolism	
15600709	PA5516	pdxY	pyridoxamine kinase	1.1	3.59E-01	Citronellol	6.0	31285	5	Cytoplasmic	COG2240	Coenzyme metabolism	
15600712	PA5519		conserved hypothetical protein	2.4	1.37E-03	Citronellol	7.5	21215	3	Unknown	COG1607	Lipid metabolism	
15600713	PA5520		hypothetical protein	1.5	2.65E-02	Citronellol	5.1	26250	3	Unknown			
15600714	PA5521		probable short-chain dehydrogenase	1.2	2.43E-01	Citronellol	5.8	26894	13	Cytoplasmic	COG1028	Secondary metabolites biosynthesis, transport, and catabolism	General function prediction only
15600716	PA5523		probable aminotransferase	5.0	3.42E-03	Citronellol	6.7	48908	3	Cytoplasmic	COG0001	Coenzyme metabolism	
15600721	PA5528		hypothetical protein	1.2	3.38E-01	Oktansaeure	6.5	30414	2	Cytoplasmic Membrane	COG4395	Function unknown	
15600735	PA5542		hypothetical protein	3.9	2.10E-04	Citronellol	6.3	45872	9	Unknown	COG1680	Defense mechanisms	
15600738	PA5545		conserved hypothetical protein	3.9	1.59E-02	Citronellol	7.8	33627	15	Periplasmic	COG2358	General function prediction only	
15600739	PA5546		conserved hypothetical protein	1.7	1.88E-02	Citronellol	5.7	44096	12	Cytoplasmic	COG2230	Cell envelope biogenesis, outer membrane	
15600742	PA5549	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.8	3.98E-03	Oktansaeure	5.9	66294	24	Periplasmic	COG0449	Cell envelope biogenesis, outer membrane	
15600745	PA5552	glmU	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate u	2.0	6.73E-02	Citronellol	6.2	48851	15	Periplasmic	COG1207	Cell envelope biogenesis, outer membrane	
15600747	PA5554	atpD	ATP synthase beta chain	2.4	1.11E-03	Citronellol	4.7	49499	43	Periplasmic	COG0055	Energy production and conversion	
15600748	PA5555	atpG	ATP synthase gamma chain	1.8	2.03E-01	Citronellol	8.1	31553	16	Outer Membrane Vesicle	COG0224	Energy production and conversion	
15600749	PA5556	atpA	ATP synthase alpha chain	2.6	1.40E-03	Citronellol	5.1	55393	29	Periplasmic	COG0056	Energy production and conversion	

15600750	PA5557	atpH	ATP synthase delta chain	3.1	6.67E-02	Citronellol	5.9	19260	10	Outer Membrane Vesicle	COG0712	Energy production and conversion
15600751	PA5558	atpF	ATP synthase B chain	2.3	5.61E-04	Citronellol	5.8	16924	9	Outer Membrane Vesicle	COG0711	Energy production and conversion
15600755	PA5562	spoOJ	chromosome partitioning protein Spo0J	1.7	7.20E-02	Oktansaeure	10.0	31969	6	Cytoplasmic	COG1475	Transcription
15600756	PA5563	soj	chromosome partitioning protein Soj	3.8	1.62E-02	Oktansaeure	6.1	28609	2	Cytoplasmic Membrane	COG1192	Cell division and chromosome partitioning
15600757	PA5564	gidB	glucose inhibited division protein B	1.5	4.32E-02	Citronellol	6.3	23735	4	Unknown	COG0357	Cell envelope biogenesis, outer membrane
15600758	PA5565	gidA	glucose-inhibited division protein A	2.6	9.07E-03	Oktansaeure	6.5	69605	5	Cytoplasmic	COG0445	Cell cycle control, cell division, chromosome partitioning
15600760	PA5567		conserved hypothetical protein	1.1	4.29E-01	Oktansaeure	4.9	48744	2	Cytoplasmic	COG0486	General function prediction only
15600762	PA5569	rnpA	ribonuclease P protein component	1.8	3.16E-02	Citronellol	11.5	15282	5	Unknown	COG0594	Translation, ribosomal structure and biogenesis
375041995				1.5	1.83E-01	Oktansaeure			76			
375041914				7.7	2.81E-04	Citronellol			27			
22001796				1.4	5.35E-01	Oktansaeure			29			
313111914				1.1	5.84E-01	Oktansaeure			25			
296388504				1.2	1.51E-01	Citronellol			30			
254242706				2.2	1.20E-01	Citronellol			24			
282403590				46.4	5.83E-02	Citronellol			20			
313110180				1.4	5.42E-02	Citronellol			24			
347307435				1.6	4.60E-03	Oktansaeure			14			
239949862				1.2	3.95E-01	Citronellol			16			
239949861				1.0	9.76E-01	Oktansaeure			15			
254236126				1.4	7.85E-01	Oktansaeure			13			
118572621				1.8	2.90E-03	Citronellol			12			
107103488				1.5	1.80E-01	Citronellol			12			
355641798				8.3	5.70E-03	Oktansaeure			12			
375044686				12.3	3.25E-01	Oktansaeure			10			
308198348				1.4	6.00E-02	Citronellol			11			
334834247				1.0	9.08E-01	Citronellol			12			
308154506				17.5	3.80E-02	Oktansaeure			10			
375041918				1.2	4.96E-01	Oktansaeure			11			
99032099				1.1	8.29E-01	Oktansaeure			10			
344189438				1.6	2.69E-01	Oktansaeure			8			
116053335				2.7	1.28E-01	Citronellol			7			
107099078				1.0	8.41E-01	Citronellol			8			
107100575				1.1	7.63E-01	Citronellol			7			
107104196				6.3	1.36E-01	Oktansaeure			6			
107101116				1.1	2.09E-01	Citronellol			7			
107099288				2.2	3.08E-02	Oktansaeure			6			
359783701				3.9	1.61E-02	Oktansaeure			4			
296389665				1.5	3.66E-02	Oktansaeure			5			
107102888				1.0	9.54E-01	Oktansaeure			5			
107102668				1.2	1.73E-01	Citronellol			5			
107101938				1.0	8.30E-01	Citronellol			4			
107103573				1.0	7.74E-01	Oktansaeure			4			
107102801				1.8	5.27E-02	Citronellol			4			
70732985				3.5	7.15E-02	Oktansaeure			3			
359782167				1.9	2.36E-01	Oktansaeure			3			
107102789				8.8	2.54E-02	Oktansaeure			3			
107104298				2.4	7.13E-02	Oktansaeure			3			
347305107				1.3	5.71E-01	Citronellol			2			
254240896				9.7	8.37E-03	Citronellol			2			
312386137				1.1	6.88E-01	Citronellol			2			
56459460				2.9	1.26E-02	Oktansaeure			2			
111017917				1.5	2.46E-02	Oktansaeure			2			
302186668				3.0	1.20E-01	Oktansaeure			2			
379708778				4.0	9.14E-02	Oktansaeure			3			
359394219				3.0	2.74E-01	Oktansaeure			2			
339494273				2.0	9.45E-02	Oktansaeure			3			
77456237				1.3	5.01E-01	Oktansaeure			1			
182677049				2.9	1.92E-01	Oktansaeure			3			
374702386				1.6	5.44E-01	Oktansaeure			2			
226944916				2.6	1.21E-01	Oktansaeure			3			
327479614				2.5	3.39E-02	Oktansaeure			2			
330807576				3.3	2.53E-02	Citronellol			2			
88798958				2.7	7.85E-02	Oktansaeure			2			
104782430				30.7	1.07E-03	Citronellol			3			
254481764				1.6	7.20E-02	Oktansaeure			2			
107101092				Infinity	1.34E-05	Oktansaeure			2			
116052531				1.3	3.90E-01	Citronellol			2			
152998459				4.2	1.29E-05	Citronellol			1			
93007153				1.0	4.92E-01	Citronellol			1			
244539066				1.5	1.14E-01	Citronellol			2			
146306154				2.1	1.28E-02	Oktansaeure			1			
330808408				5.2	3.76E-02	Citronellol			2			
357405980				1.3	3.38E-01	Oktansaeure			2			
330502104				1.1	5.24E-01	Oktansaeure			2			
218891628				1.6	1.85E-01	Oktansaeure			2			
359782718				1.8	2.58E-01	Oktansaeure			2			
317969623				1.3	1.44E-01	Oktansaeure			2			
355639818				1.2	6.98E-01	Citronellol			3			
104781332				2.0	9.51E-02	Citronellol			3			
116049588				4.5	1.64E-02	Citronellol			2			
169634113				18.3	8.62E-03	Citronellol			2			
313110099				4.1	1.38E-01	Citronellol			2			

5.5 Selected Reaction Monitoring

					Glucose 1		Glucose 2		Glucose 3		Vanillin 1		Vanillin 2		Vanillin 3			Glucose 1	Glucose 2	Glucose 3	Vanillin 1	Vanillin 2	Vanillin 3	Mittelwert Glucose	Mittelwert Vanillin	Vanillin/Glucose	MW Regulation
Protein	Peptid	Fragment	Q1/Q3	Retentionszeit (erwartet)	Fläche	Retentionszeit	Fläche	Retentionszei	Area	Retention Time	Area	Retention Tir	Area	Retention Tir	Area	Retention Time	Korrekturfaktor:	1.47	0.79	0.61	1.06	0.84	1.00				
3-dehydrog synthase KT2440	ELSAGLAEVIK	2/y10	565.3 / 1000.6	24.85	594.41	24.85	27095.79	24.32	31261.54	24.18	598.35	24.28	22146.75	24.59	14831.23	24.22		876	21540	18925	636	18628	14831	13780	11365	0.82	
3-dehydrog synthase KT2440	ELSAGLAEVIK	2/y7	565.3 / 729.5	24.86	68590.26	24.86	469579.68	24.31	590505.12	24.17	116551.86	24.24	419736.09	24.58	343120.14	24.21		101120	373290	357477	123815	353055	343120	277296	273330	0.99	
3-dehydrog synthase KT2440	ELSAGLAEVIK	2/y8	565.3 / 800.5	24.22	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
3-dehydrog synthase KT2440	AVLIDTTSLK	2/y5	530.8 / 549.3	26.06	N/A	N/A	50595.65	26.08	57495.08	25.96	31112.96	26.10	32782.29	26.55	39502.70	25.99			40221	34806	33052	27574	39503	37513	33376	0.89	0.93
3-dehydrog synthase KT2440	AVLIDTTSLK	2/y6	530.8 / 664.3	26.08	N/A	N/A	145678.94	26.09	190237.64	25.96	134950.26	26.10	138407.77	26.53	142194.84	25.97			115807	115165	143359	116420	142195	115486	133991	1.16	
3-dehydrog synthase KT2440	AVLIDTTSLK	2/y7	530.8 / 777.4	26.10	N/A	N/A	165314.05	26.10	233964.77	25.97	142081.56	26.09	148098.60	26.54	157842.46	25.98			131416	141636	150935	124571	157842	136526	144449	1.06	
3-dehydrog synthase KT2440	ALDSAALTEAIR	2/y9	615.8 / 931.5	27.28	N/A	N/A	35782.20	27.27	51728.38	27.13	24404.13	27.31	N/A	N/A	27560.41	27.14			28445	31315	25925		27560	29880	26743	0.90	
3-dehydrog synthase KT2440	ALDSAALTEAIR	2/y7	615.8 / 773.5	27.28	N/A	N/A	120622.39	27.27	174708.91	27.13	60127.47	27.30	N/A	N/A	83702.21	27.14			95888	105764	63874		83702	100826	73788	0.73	
3-dehydrog synthase KT2440	ALDSAALTEAIR	2/y8	615.8 / 844.5	27.28	N/A	N/A	37160.03	27.28	55459.02	27.13	24585.47	27.30	N/A	N/A	31747.55	27.16			29540	33573	26117		31748	31557	28933	0.92	
3-oxoadipa CoA-transf KT2440	LSGVPLIK	2/y4	413.8 / 470.3	25.78	N/A	N/A	N/A	N/A	N/A	N/A	665810.72	25.77	615414.57	26.17	636290.93	25.66					707300	517647	636291		620412	infinity	infinity
3-oxoadipa CoA-transf KT2440	LSGVPLIK	2/y5	413.8 / 569.4	25.22	N/A	N/A	N/A	N/A	N/A	N/A	25965.81	25.77	32860.15	26.19	26669.44	25.65					27584	27640	26669		27298	infinity	infinity
3-oxoadipa CoA-transf KT2440	LSGVPLIK	2/y6	413.8 / 626.4	25.78	N/A	N/A	N/A	N/A	N/A	N/A	848673.89	25.77	910934.59	26.17	798738.12	25.66					901557	766219	798738		822171	infinity	infinity
4-aminobut aminotrans KT2440	NSTVIDVEGR	2/y6	545.3 / 688.4	23.29	132462.02	23.79	358056.89	23.29	446347.96	23.15	367997.09	23.25	469284.74	23.53	402376.36	23.22		195284	284636	270208	390928	394732	402376	250043	396012	1.58	
4-aminobut aminotrans KT2440	NSTVIDVEGR	2/y7	545.3 / 787.4	23.79	101854.81	23.79	232978.95	23.28	302236.63	23.14	256600.36	23.25	317407.37	23.52	277975.03	23.22		150161	185206	182966	272590	266982	277975	172778	272516	1.58	
4-aminobut aminotrans KT2440	NSTVIDVEGR	2/y8	545.3 / 888.5	23.79	64044.63	23.79	131789.06	23.29	175273.00	23.14	175823.39	23.24	194556.70	23.52	164375.08	23.22		94419	104765	106106	186780	163648	164375	101763	171601	1.69	1.59
4-aminobut aminotrans KT2440	VVAAVQEQLTK	2/y7	593.3 / 845.5	23.97	82218.74	23.97	217717.79	23.46	313202.11	23.31	241227.84	23.41	292516.77	23.70	262161.91	23.37		121212	173074	189605	256260	246046	262162	161297	254822	1.58	
4-aminobut aminotrans KT2440	VVAAVQEQLTK	2/y9	593.3 / 987.5	23.98	183557.63	23.98	510450.77	23.45	646678.94	23.31	556054.69	23.42	665011.22	23.71	563816.46	23.37		270612	405781	391483	590704	559364	563816	355959	571295	1.60	
4-aminobut aminotrans KT2440	VVAAVQEQLTK	2/y8	593.3 / 916.5	23.97	62325.66	23.97	177826.86	23.46	230438.69	23.32	179610.62	23.41	219518.60	23.70	185552.98	23.38		91884	141363	139502	190803	184645	185553	124250	187000	1.51	
4-aminobut aminotrans KT2440	ILVPLTAEDALLDK	2/y8	755.9 / 874.5	30.53	N/A	N/A	21516.73	31.48	35057.55	30.98	23559.54	31.35	N/A	N/A	22664.05	31.06											
4-aminobut aminotrans KT2440	ILVPLTAEDALLDK	2/y9	755.9 / 975.5	31.49	N/A	N/A	91869.57	31.49	75723.88	30.98	51860.12	31.35	N/A	N/A	50601.77	31.06											
4-aminobut aminotrans KT2440	ILVPLTAEDALLDK	2/y7	755.9 / 803.4	31.55	N/A	N/A	24115.60	31.54	16966.16	30.99	12039.61	31.35	N/A	N/A	13456.36	31.05											
4-hydroxyb 3-monooxyg KT2440	QSIPEGVLK	2/y6	485.8 / 642.4	21.47	121534.24	21.93	185294.60	21.47	197873.86	21.35	102018.42	21.47	184621.37	21.72	142345.66	21.47		179174	147299	119788	108376	155291	142346	148754	135338	0.91	
4-hydroxyb 3-monooxyg KT2440	QSIPEGVLK	2/y7	485.8 / 755.5	21.47	27420.06	21.93	40773.49	21.48	50088.08	21.35	23879.53	21.47	48115.94	21.72	33089.38	21.46		40424	32413	30322	25368	40472	33089	34386	32976	0.96	0.99
4-hydroxyb 3-monooxyg KT2440	QSIPEGVLK	2/y8	485.8 / 842.5	21.50	15816.12	21.95	24327.56	21.50	22287.57	21.37	17357.91	21.48	27226.54	21.74	20048.10	21.49		23317	19339	13492	18440	22901	20048	18716	20463	1.09	
4-hydroxyb 3-monooxyg KT2440	QTAEYVLGR	2/y5	518.8 / 607.4	23.72	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
4-hydroxyb 3-monooxyg KT2440	QTAEYVLGR	2/y6	518.8 / 736.4	23.57	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
4-hydroxyb 3-monooxyg KT2440	QTAEYVLGR	2/y7	518.8 / 807.4	23.57	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
4-hydroxyb 3-monooxyg KT2440	AGIDNIIVER	2/y6	550.3 / 743.4	24.26	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
4-hydroxyb 3-monooxyg KT2440	AGIDNIIVER	2/y7	550.3 / 858.5	24.87	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
4-hydroxyb 3-monooxyg KT2440	AGIDNIIVER	2/y5	550.3 / 629.4	24.48	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
5,10-methy dehydrogen KT2440	VISAIHPSK	2/y6	476.3 / 652.4	21.53	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
5,10-methy dehydrogen KT2440	VISAIHPSK	2/y7	476.3 / 739.4	21.11	128044.13	21.55	221207.96	21.11	279064.95	20.98	144613.39	21.11	209864.88	21.37	157672.57	21.13		188771	175848	168939	153625	176525	157673	177853	162607	0.91	0.91
5,10-methy dehydrogen KT2440	LPNGR	2/y4	278.7 / 443.2	22.65	143900.59	23.14	195581.76	22.66	262883.20	22.52	222962.18	22.65	132014.59	22.90	130619.69	22.61		212147	155477	159143	236856	111042	130620	175589	159506	0.91	
5,10-methy dehydrogen KT2440	DVDGFNPLNVGR	2/y9	651.8 / 973.5	29.09	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
ABC transporte KT2440	LAQQK	2/y4	294.2 / 474.3	23.83	N/A	N/A	4120609.80	23.86	5468343.04	23.72	1631158.14	23.83	2688967.70	24.10	1752231.46	23.78											
ABC transporte KT2440	LAQQK	2/b4	294.2 / 441.3	23.84	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
ABC transporte KT2440	FEAEK	2/y4	312.2 / 476.2	24.68	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
ABC transporte KT2440	FEAEK	2/b4	312.2 / 477.2	24.35	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
ABC transporte KT2440	FEAEK	2/b3	312.2 / 348.2	24.35	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											5.45
ABC transporte KT2440	GTWEDLASK	2/y5	503.8 / 533.3	25.51	N/A	N/A	22007.85	25.49	19651.16	25.37	69272.38	25.49	104166.51	25.86	80305.25	25.39			17495	11896	73589	87618	80305	14696	80504	5.48	
ABC transporte KT2440	GTWEDLASK	2/y6	503.8 / 662.3	25.66	N/A	N/A	26913.01	25.51	75712.93	25.48	157361.47	25.50	159296.01	25.86	163525.32	25.39			21394	45835	167167	133989	163525	33615	154894	4.61	
ABC transporte KT2440	GTWEDLASK	2/y7	503.8 / 848.4	25.49	N/A	N/A	38301.43	25.50	36403.73	25.36	155995.53	25.49	193468.10	25.85	164675.71	25.38			30448	22038	165716	162733	164676	26243	164375	6.26	
adenylosuc synthetase KT2440	TLEELPQAAR	2/y7	564.3 / 784.4	24.00	N/A	N/A	525523.08	24.01	751978.10	23.87	344749.66	23.98	428021.27	24.27	401303.60	23.91			417762	455229	366232	360024	401304	436495	375853	0.86	
adenylosuc synthetase KT2440	TLEELPQAAR	2/y6	564.3 / 655.4	24.02	N/A	N/A	357270.74	24.01	471007.30	23.86	268768.74	23.97	299703.78	24.26	274919.16	23.91			284011	285136	285517	252091	274919	284573	270842	0.95	
adenylosuc synthetase KT2440	TLEELPQAAR	2/y8	564.3 / 913.5	24.00	N/A	N/A	1109210.23	24.01	1487093.65	23.86	760609.06	23.98	796783.55	24.27	835773.96	23.91			881762	900249	808005	670202	835774	891006	771327	0.87	
adenylosuc synthetase KT2440	NVVVLGTQWGDEGK	2/y8	751.4 / 920.4	28.00	N/A	N/A	29291.43	28.00	32522.40	27.75	11003.32	27.97	11962.42	28.55	12776.81	27.78			23285	19688	11689	10062	12777	21487	11509	0.54	0.71
adenylosuc synthetase KT2440	NVVVLGTQWGDEGK	2/y9	751.4 / 977.4	27.92	N/A	N/A	112227.93	27.93	162995.41	27.75	61058.60	27.96	54725.18	28.55	55089.62	27.78			89215	98673	64863	46031	55090	93944	55328	0.59	
adenylosuc synthetase KT2440	NVVVLGTQWGDEGK	2/y7	751.4 / 819.4	27.92	N/A	N/A	16313.72	27.93	24347.17	27.74	8862.58	27.96	7411.49	28.55	9670.77	27.78			12969	14739	9415	6234	9671	13854	8440	0.61	
adenylosuc synthetase KT2440	TVLHLIPSGILR	2/y8	659.9 / 868.6	28.64	N/A	N/A	N/A	N/A	386784.62	28.45	89582.36	28.68	N/A	N/A	110425.14	28.45											
adenylosuc synthetase KT2440	TVLHLIPSGILR	2/y7	659.9 / 755.5	28.64	N/A	N/A	205068.09	28.64	466105.91	28.37	98613.39	28.67	N/A	N/A	134920.01	28.46			163018	282169	104758		134920	222593	119839	0.54	
aldehyde dehydrogen KT2440	LIAEFPR	2/y5	423.3 / 619.3	22.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
aldehyde dehydrogen KT2440	LIAEFPR	2/y6	423.3 / 732.4	22.46	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
aldehyde dehydrogen KT2440	LIAEFPR	2/y4	423.3 / 548.3	22.92	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A											
aldehyde dehydrogen KT2440	EEGAQLLTGGGAER	2/y9	694.3 / 873.5	24.88	8977.08	24.88	17484.09	24.29	25863.93	24.15	86871.12	24.27	72902.99	24.58	49912.09	24.20		13235	13899	15657	92284	61321	49912	14264	67839	4.76	
aldehyde dehydrogen KT2440	EEGAQLLTGGGAER	2/y8	694.3 / 760.4	24.88	17477.74	24.88	37982.41	24.30	52965.13	24.16	166823.75	24.27	144955.34	24.58	119078.11	24.20		25767	30194	32064	177219	121927	119078	29342	139408	4.75	
aldehyde dehydrogen KT2440	EEGAQLLTGGGAER	2/y7	694.3 / 647.3	24.88	16092.40	24.88	40243.29	24.30	52938.45	24.15	187884.57	24.28	155784.05	24.57	124548.33	24.19		23724	31991	32048	199592	131035	124548	29254	151725	5.19	
aldehyde dehydrogen KT2440	ETLNADVPLAADHFR	2/y8	834.9 / 926.5	27.03	N/A	N/A	N/A	N/A	N/A	N/A	34881.67	26.46	22472.23	26.98	22255.86	26.31					37055	18902	22256		26071	infinity	
aldehyde dehydrogen KT2440	ETLNADVPLAADHFR	2/y9	834.9 / 1025.6	27.00	N/A	N/A	N/A	N/A	N/A	N/A	5506.20	26.47	5171.24	26.99	4879.27	26.35					5849	4350	4879		5026	infinity	3.64 (Infinity Van)
aldehyde dehydrogen KT2440	ETLNADVPLAADHFR	2/y10	834.9 / 1140.6	27.14	N/A	N/A	N/A	N/A	N/A	N/A	4256.46	26.48	3401.23	26.98	2481.45	26.33					4522	2861	2481		3288	infinity	
aldehyde dehydrogen KT2440	YGNYIGGEFVTPVK	2/y8	772.4 / 876.5	28.80	4518.14	28.80	18034.26	27.81	23923.03	27.60	39447.59	27.84	19905.41	28.42	27753.63	27.63		6661	14336	14482	41906	16743	27754	11827	28801	2.44	
aldehyde dehydrogen KT2440	YGNYIGGEFVTPVK	2/y9	772.4 / 933.5	28.86	31727.00	28.86	107830.36	27.80	142229.32	27.61	269679.56	27.83	127462.02	28.42	167295.12	27.65		46774	85719	86102	286484	107213	167295	72865	186997	2.57	
aldehyde dehydrogen KT2440	YGNYIGGEFVTPVK	2/y6	772.4 / 690.4	28.83	3834.62	28.83	11593.17	27.81	15623.95	27.59	22409.61	27.83	14281.03	28.42	16186.55	27.66		5653	9216	9458	23806	12012	16187	8109	17335	2.14	
aldo/keto reductase KT2440	TAIAGLPK	2/y5	385.7 / 485.3	21.59	228522.95	22.04	347760.64	21.59	431932.93	21.46	194047.71	21.58	200082.48	21.83	179019.57	21.59		336903	276451	261481	206139	168296	179020	291612	184485	0.63	
aldo/keto reductase KT2440	TAIAGLPK	2/y6	385.7 / 598.4	21.57	49783.42	22.04	81473.15	21.59	101002.50	21.46	43133.87	21.58	50261.47	21.83	42337.93	21.59		73394	64767	61144	45822	42277	42338	66435	43479	0.65	0.64 (Infinity Van)
aldo/keto reductase KT2440	QALDVGYR	2/y5	461.2 / 609.3	23.31	N/A	N/A	N/A	N/A	N/A	N/A	131806.50	23.27	167726.54	23.55	150872.21	23.24					140020	141081	150872		143991	infinity	
aldo/keto reductase KT2440	QALDVGYR	2/y6	461.2 / 722.4	21.82	N/A	N/A	N/A	N/A	N/A	N/A	81771.03	23.27	113657.64	23.54	103880.94	23.24					86866	95601	103881		95450	infinity	
aldo/keto reductase KT2440	HIGVANFPLGLLR	3/y6	469.6 / 668.5	30.25	N/A	N/A	N/A	N/A	N/A	N/A																	
aldo/keto reductase KT2440	HIGVANFPLGLLR	3/b6	469.6 / 592.3	29.38	N/A	N/A	N/A	N/A	N/A	N/A																	
aldo/keto reductase KT2440	HIGVANFPLGLLR	3/y5	469.6 / 571.4	30.26	N/A	N/A	N/A	N/A	N/A	N/A																	
aminomethy [Pseudomon KT2440	VYEAIVSAGR	2/y7	532.8 / 673.4	23.93	N/A	N/A	N/A	N/A	N/A	N/A	516633.78	23.88	609522.80	24.17	595122.21	23.81					548827	512691	595122		552213	infinity	
aminomethy [Pseudomon KT2440	VYEAIVSAGR	2/y8	532.8 / 802.4	23.89	N/A	N/A	N/A	N/A	N/A	N/A	901860.37	23.88	1093719.05	24.16	1057981.11	23.81					958058	919965	1057981		978668	infinity	
aminomethy [Pseudomon KT2440	VYEAIVSAGR	2/y9	532.8 / 965.5	24.04	N/A	N/A	N/A	N/A	N/A	N/A	88542.22	23.87	107990.80	24.17	99384.28	23.82					94060	90835	99384		94760	infinity	69.13 (Infinity Van)
aminomethy [Pseudomon KT2440	SPVELGWAK	2/y8	493.8 / 899.5	24.43	N/A	N/A	257100.96	24.42	313785.77	24.27	142067.65	24.41	129661.40	24.71	149844.08	24.30											
aminomethy [Pseudomon KT2440	LAEDEFLLFGR	2/y8	655.3 / 996.5	31.71	N/A	N/A	2077.04	31.75	6555.79	31.18	113755.96	32.23	N/A	N/A	135408.23	31.88			1651	3969	120844		135408	2810	128126	45.60	
aminomethy [Pseudomon KT2440	LAEDEFLLFGR	2/y7	655.3 / 881.5	31.17	N/A	N/A	557.09	31.73	1340.13	31.21	62157.33	32.17	N/A	N/A	116680.46	31.89			443	811	66031		116680	627	91356	145.69	
aminomethy [Pseudomon KT2440	LAEDEFLLFGR	2/y6	655.3 / 752.5	31.79	N/A	N/A	13906.29	31.78	18562.48	31.21	127455.06	32.17	N/A	N/A	223569.34	31.89			11055	11237	135397		223569	11146	179483	16.10	
aminotrans [Pseudomon KT2440	LSLLHESGQPR	2/y7	618.8 / 810.4	22.62	N/A	N/A	163724.17	22.65	273835.05	22.51	N/A	N/A	N/A	N/A	N/A	N/A			130152	165773				147962		0.00	
aminotrans [Pseudomon KT2440	LSLLHESGQPR	2/y8	618.8 / 923.5	22.60	N/A	N/A	25806.29	22.65	35231.09	22.50	N/A	N/A	N/A	N/A	N/A	N/A			20515	21328				20921		0.00	
aminotrans [Pseudomon KT2440	LSLLHESGQPR	2/y6	618.8 / 673.3	22.65	N/A	N/A	135110.77	22.65	208369.29	22.52	N/A	N/A	N/A	N/A	N/A	N/A			107406	126142				116774		0.00	
aminotrans [Pseudomon KT2440	LLIVNYPNNPTGK	2/y7	721.9 / 727.4	26.78	N/A	N/A	464621.94	26.76	611763.56	26.61	31435.91	26.78	N/A	N/A	46051.21	26.64			369349	370346	33395		46051	369848	39723	0.11	0.07
aminotrans [Pseudomon KT2440	LLIVNYPNNPTGK	2/y8	721.9 / 890.4	26.74	N/A	N/A	152336.12	26.75	174001.39	26.62	11546.60	26.75	N/A	N/A	11406.56	26.61			121099	105336	12266		11407	113218	11836	0.10	
aminotrans [Pseudomon KT2440	LLIVNYPNNPTGK	3/y7	481.6 / 727.4	26.74	N/A	N/A	14491.35	26.73	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A			11520					11520		0.00	
aminotrans [Pseudomon KT2440	ETSLAPDSDDFFK	2/y8	736.3 / 970.4	28.55	N/A	N/A	167777.55	28.54	224204.70	28.34	13855.14	28.56	23916.36	29.21	18495.50	28.37			133374	135728	14718	20117	18495	134551	17777	0.13	
aminotrans [Pseudomon KT2440	ETSLAPDSDDFFK	2/y6	736.3 / 758.3	28.54	N/A	N/A	20130.39	28.55	28111.05	28.34	2849.75	28.56	3695.86	29.19	4526.37	28.38			16003	17018	3027	3109	4526	16510	3554	0.22	
aminotrans [Pseudomon KT2440	ETSLAPDSDDFFK	2/y7	736.3 / 873.4	28.53	N/A	N/A	6999.06	28.55	9118.71	28.34	359.20	28.64	1104.54	29.25	411.39	28.35			5564	5520	382	929	411	5542	574	0.10	
arginine deiminase KT2440	VVETGGNSFAAER	2/y7	668.8 / 794.4	22.41	10123.19	22.89	18242.15	22.43	24727.82	22.30	84412.84	22.42	100636.33	22.66	84160.82	22.39		14924	14502	14970	89673	84649	84161	14798	86161	5.82	
arginine deiminase KT2440	VVETGGNSFAAER	2/y9	668.8 / 908.4	22.44	35849.27	22.89	97759.23	22.42	121222.53	22.29	404085.20	22.41	512478.94	22.65	451213.68	22.39		52851	77713	73385	429265	431064	451214	67983	437181	6.43	
arginine deiminase KT2440	VVETGGNSFAAER	2/y6	668.8 / 680.3	22.41	12622.49	22.90	37914.26	22.42	45169.11	22.29	156489.08	22.41	201924.45	22.66	168636.18	22.39		18609	30140	27344	166240	169846	168636	25364	168241	6.63	6.88
arginine deiminase KT2440	NTYTNTLLR	2/y6	548.3 / 717.4	25.21	60846.61	25.21	139429.76	24.59	201202.94	24.45	680132.40	24.58	854554.80	24.88	773975.12	24.49		89704	110839	121803	722514	718796	773975	107449	738428	6.87	
arginine deiminase KT2440	NTYTNTLLR	2/y7	548.3 / 880.5	25.22	73089.44	25.22	148026.58	24.59	200647.94	24.45	759776.85	24.58	902830.90	24.88	807113.22	24.48		107753	117673	121467	807121	759402	807113	115631	791212	6.84	
arginine deiminase KT2440	NTYTNTLLR	2/y8	548.3 / 981.5	25.21	1758.90	25.21	2716.92	24.59	3024.91	24.47	20917.63	24.59	20516.44	24.88	17105.26	24.49		2593	2160	1831	22221	17257	17105	2195	18861	8.59	
arginine deiminase KT2440	EVIVAGLPK	2/y6	463.3 / 584.4	26.20	63916.59	26.20	81312.69	25.47	90323.63	25.34	460911.64	25.47	576268.09	25.84	464230.13	25.36		94230	64639	54680	489633	484719	464230	71183	479527	6.74	
arginine deiminase KT2440	EVIVAGLPK	2/y5	463.3 / 485.3	26.20	82702.82	26.20	121244.43	25.47	134739.49	25.34	696073.25	25.47	858419.69	25.84	657393.79	25.36		121926	96383	81568	739448	722047	657394	99959	706296	7.07	
arginine deiminase KT2440	EVIVAGLPK	2/y7	463.3 / 697.5	26.19	49440.98	26.19	71625.30	25.48	76649.31	25.34	380208.05	25.47	524436.31	25.84	380441.97	25.36		72889	56938	46402	403900	441122	380442	58743	408488	6.95	
arginyl-tR synthetase KT2440	STIIGDSVAR	2/y6	509.8 / 604.3	23.84	255524.95	23.84	536354.30	23.33	660645.80	23.19	359568.58	23.30	461897.17	23.57	401398.90	23.26		376711	426373	399938	381974	388518	401399	401007	390630	0.97	
arginyl-tR synthetase KT2440	STIIGDSVAR	2/y7	509.8 / 717.4	23.84	187924.45	23.84	383298.79	23.32	530301.84	23.19	278426.45	23.30	347616.00	23.57	284715.90	23.26		277050	304702	321031	295776	292392	284716	300928	290961	0.97	
arginyl-tR synthetase KT2440	STIIGDSVAR	2/y8	509.8 / 830.5	23.84	48844.43	23.84	104246.85	23.33	122098.43	23.19	67980.76	23.30	92221.23	23.58	75645.51	23.26		72010	82871	73915	72217	77570	75646	76265	75144	0.99	0.91
arginyl-tR synthetase KT2440	LINALPASADISK	2/y8	656.9 / 788.4	26.26	N/A	N/A	480063.86	26.25	627562.43	26.11	307800.43	26.24	290358.16	26.71	289618.89	26.12			381625	379911	326980	244230	289619	380768	286943	0.75	
arginyl-tR synthetase KT2440	LINALPASADISK	2/y9	656.9 / 901.5	26.24	N/A	N/A	42194.83	26.23	59545.23	26.11	25751.70	26.24	25570.35	26.69	27766.60	26.12			33543	36047	27356	21508	27767	34795	25544	0.73	
arginyl-tR synthetase KT2440	LINALPASADISK	2/y10	656.9 / 972.5	26.24	N/A	N/A	17229.02	26.24	24164.27	26.09	9214.46	26.24	10155.32	26.71	9934.85	26.15			13696	14628	9789	8542	9935	14162	9422	0.67	
arginyl-tR synthetase KT2440	TYELLNVK	2/y5	490.3 / 586.4	26.91	34659.66	26.91	51136.89	26.13	58455.14	25.98	45347.92	26.12	54322.59	26.57	44041.30	26.00		51097	40651	35387	48174	45693	44041	42379	45969	1.08	
arginyl-tR synthetase KT2440	TYELLNVK	2/y6	490.3 / 715.4	26.91	131949.44	26.91	235649.56	26.13	280554.23	25.99	193148.98	26.12	217851.94	26.56	183212.54	26.01		194528	187329	169840	205185	183243	183213	183899	190547	1.04	
arginyl-tR synthetase KT2440	TYELLNVK	2/y7	490.3 / 878.5	26.93	6396.36	26.93	14451.46	26.13	15102.43	25.98	8333.21	26.13	12952.42	26.55	9789.00	26.00		9430	11488	9143	8852	10895	9789	10020	9845	0.98	
aromatic amino KT2440	YYDAPTNDVNR	2/y7	664.3 / 815.4	22.25	420041.91	22.71	1003009.35	22.25	1363751.49	22.11	491038.39	22.23	634445.36	22.48	583185.01	22.21		619253	797338	825581	521637	533654	583185	747390	546159	0.73	
aromatic amino KT2440	YYDAPTNDVNR	2/y8	664.3 / 886.4	22.25	96292.27	22.71	237115.53	22.24	302168.23	22.11	113643.45	22.23	144827.55	22.47	126884.51	22.22		141960	188494	182925	120725	121819	126885	171126	123143	0.72	
aromatic amino KT2440	YYDAPTNDVNR	2/y6	664.3 / 718.3	22.23	28961.79	22.72	87060.05	22.24	107495.15	22.11	40395.17	22.23	49037.50	22.47	47165.77	22.21		42697	69208	65075	42912	41247	47166	58993	43775	0.74	
aromatic amino KT2440	VVTVQAVGGTGALK	2/y9	650.4 / 773.5	25.10	206161.20	25.10	507329.06	24.47	683152.54	24.33	311686.48	24.46	358400.16	24.78	297089.20	24.37		303936	403299	413563	331109	301463	297089	373599	309887	0.83	0.70
aromatic amino KT2440	VVTVQAVGGTGALK	2/y10	650.4 / 901.5	25.09	234359.39	25.09	539848.63	24.48	732426.18	24.33	314781.29	24.47	354252.78	24.77	287838.22	24.37		345508	429150	443392	334396	297974	287838	406017	306736	0.76	
aromatic amino KT2440	VVTVQAVGGTGALK	2/y8	650.4 / 702.4	25.10	140297.37	25.10	378439.31	24.47	466360.26	24.33	193319.44	24.46	227667.69	24.77	188242.05	24.36		206835	300839	282323	205366	191499	188242	263332	195036	0.74	
aromatic amino KT2440	LLFGAESPLLAAGR	2/y8	707.9 / 784.5	31.25	N/A	N/A	435407.57	31.25	640076.77	30.78	190070.38	31.14	N/A	N/A	223060.16	30.85			346125	387486	201914		223060	366806	212487	0.58	
aromatic amino KT2440	LLFGAESPLLAAGR	2/y9	707.9 / 913.5	31.26	N/A	N/A	278191.57	31.26	423583.94	30.78	127503.82	31.14	N/A	N/A	145131.81	30.85			221147	256427	135449		145132	238787	140290	0.59	
aromatic amino KT2440	LLFGAESPLLAAGR	2/y10	707.9 / 984.5	31.25	N/A	N/A	104332.02	31.26	153947.66	30.78	45648.18	31.15	N/A	N/A	58814.06	30.83			82938	93196	48493		58814	88067	53653	0.61	
carbamate kinase KT2440	VSTEKPGISYR	2/y6	618.8 / 692.4	20.73	13060.42	21.20	28795.51	20.74	41116.47	20.61	144115.65	20.74	187795.98	21.02	162886.32	20.77		19255	22891	24891	153096	157962	162886	22345	157981	7.07	

carbamate kinase KT2440	VSTEKPGISYR	2/y7	618.8 / 820.5	21.20	1514.67	21.20	4269.33	20.73	5295.27	20.61	21921.43	20.74	27389.48	21.02	21967.61	20.77	2233	3394	3206	23287	23038	21968	2944	22764	7.73	
carbamate kinase KT2440	VSTEKPGISYR	2/y8	618.8 / 949.5	20.73	641.68	21.20	2165.97	20.73	2478.04	20.61	7892.11	20.74	10310.34	21.02	9126.11	20.77	946	1722	1500	8384	8672	9126	1389	8727	6.28	8.18
carbamate kinase KT2440	FIGPVYSK	2/y5	455.8 / 593.3	24.94	458.74	24.94	4666.47	24.29	3979.44	24.16	22679.74	24.28	26587.47	24.59	22711.61	24.20	676	3710	2409	24093	22364	22712	2265	23056	10.18	
carbamate kinase KT2440	FIGPVYSK	2/y6	455.8 / 650.3	24.89	49794.34	24.89	122789.57	24.30	155032.53	24.17	682206.63	24.28	679656.01	24.59	701984.17	24.20	73410	97611	93853	724717	571682	701984	88291	666128	7.54	
carbamate kinase KT2440	FIGPVYSK	2/y7	455.8 / 763.4	24.92	1688.81	24.92	5938.42	24.32	9196.41	24.18	42737.40	24.27	52372.97	24.58	41670.23	24.21	2490	4721	5567	45401	44053	41670	4259	43708	10.26	
carbamate kinase KT2440	VAVISSLENIEDIVK	2/y7	815.0 / 830.5	32.91	N/A	N/A	14065.18	32.92	10125.03	32.41	45125.07	32.75	N/A	N/A	49191.40	32.50										
carbamate kinase KT2440	VAVISSLENIEDIVK	2/y8	815.0 / 959.5	32.89	N/A	N/A	14519.65	32.92	13770.31	32.43	58175.16	32.75	N/A	N/A	55136.68	32.50										
carbamate kinase KT2440	VAVISSLENIEDIVK	2/b9	815.0 / 913.5	32.90	N/A	N/A	1181.07	32.93	899.36	32.41	3516.20	32.75	N/A	N/A	3401.13	32.50										
cysteine desulfuras KT2440	VEIDLQK	2/y6	422.7 / 745.4	23.57	N/A	N/A	3593723.20	23.58	2768943.62	23.44	4257729.40	23.55	3350048.56	23.83	3601403.73	23.51										
cysteine desulfuras KT2440	FTTEEEVDYAAQK	2/y8	765.8 / 923.5	24.54	N/A	N/A	40139.86	24.55	48407.57	24.40	32488.59	24.52	42306.00	24.84	34780.98	24.44		31909	29305	34513	35585	34781	30607	34960	1.14	
cysteine desulfuras KT2440	FTTEEEVDYAAQK	2/y7	765.8 / 794.4	24.44	N/A	N/A	50406.08	24.55	67823.37	24.41	38664.84	24.52	48198.72	24.84	43689.33	24.42		40070	41059	41074	40542	43689	40564	41768	1.03	
cysteine desulfuras KT2440	FTTEEEVDYAAQK	2/b7	765.8 / 836.4	24.52	N/A	N/A	8252.70	24.56	12149.71	24.41	6518.07	24.53	8781.91	24.84	7810.70	24.43		6560	7355	6924	7387	7811	6958	7374	1.06	1.15
cysteine desulfuras KT2440	QVAELINADPR	2/y7	613.3 / 798.5	24.94	N/A	N/A	137519.68	24.91	177962.76	24.78	107754.28	24.91	133589.41	25.24	126612.95	24.81		109321	107734	114469	112367	126613	108527	117816	1.09	
cysteine desulfuras KT2440	QVAELINADPR	2/y8	613.3 / 927.5	24.94	N/A	N/A	51571.29	24.91	66464.81	24.78	41036.97	24.90	52485.14	25.24	47626.20	24.80		40996	40236	43594	44147	47626	40616	45122	1.11	
cysteine desulfuras KT2440	QVAELINADPR	2/y9	613.3 / 998.5	24.90	N/A	N/A	164141.25	24.92	208070.40	24.78	129603.48	24.91	146147.81	25.24	137686.00	24.79		130483	125961	137679	122930	137686	128222	132765	1.04	
cysteine desulfuras KT2440	GIGALYVSR	2/y5	468.3 / 637.4	25.22	N/A	N/A	200159.90	25.23	239317.75	25.10	191244.62	25.23	234616.05	25.58	180529.04	25.12		159116	144877	203162	197344	180529	151997	193678	1.27	
cysteine desulfuras KT2440	GIGALYVSR	2/y6	468.3 / 708.4	25.24	N/A	N/A	50293.52	25.24	60717.53	25.10	42958.61	25.23	58926.69	25.58	54131.11	25.12		39981	36757	45635	49565	54131	38369	49777	1.30	
cysteine desulfuras KT2440	GIGALYVSR	2/y7	468.3 / 765.4	25.22	N/A	N/A	614302.01	25.24	716336.26	25.10	599569.56	25.23	715161.75	25.58	577012.53	25.12		488337	433652	636931	601547	577013	460994	605164	1.31	
D-3-phosph dehydrogen KT2440	SAANSFEIR	2/y5	497.8 / 651.3	23.76	N/A	N/A	665327.59	23.76	810790.17	23.63	597051.22	23.73	935373.29	24.01	797103.42	23.68		528899	490832	634255	786775	797103	509866	739378	1.45	
D-3-phosph dehydrogen KT2440	SAANSFEIR	2/y6	497.8 / 765.4	23.76	N/A	N/A	871862.96	23.76	1044435.93	23.62	783816.56	23.73	1171109.25	24.01	1077454.20	23.68		693084	632275	832659	985061	1077454	662679	965058	1.46	
D-3-phosph dehydrogen KT2440	SAANSFEIR	2/y7	497.8 / 836.4	23.76	N/A	N/A	935784.61	23.76	1115794.16	23.62	856975.70	23.73	1359041.52	24.01	1150251.33	23.68		743898	675474	910377	1143137	1150251	709686	1067922	1.50	
D-3-phosph dehydrogen KT2440	SNDEEFESPLR	2/y7	661.8 / 877.4	25.54	N/A	N/A	520135.42	25.54	729610.43	25.40	467196.02	25.53	706859.87	25.91	588002.24	25.42		413479	441688	496309	594564	588002	427584	559625	1.31	1.34
D-3-phosph dehydrogen KT2440	SNDEEFESPLR	2/y6	661.8 / 748.4	25.54	N/A	N/A	962986.67	25.53	1207629.31	25.40	828582.50	25.53	1250673.23	25.91	1046507.44	25.42		765522	731068	880214	1051985	1046507	748295	992902	1.33	
D-3-phosph dehydrogen KT2440	GIAVFNAPYSNTR	2/y6	705.4 / 737.4	26.76	N/A	N/A	1088814.35	26.76	1284545.91	26.61	825360.17	26.77	N/A	N/A	1117265.14	26.63		865548	777632	876791		1117265	821590	997028	1.21	
D-3-phosph dehydrogen KT2440	GIAVFNAPYSNTR	2/y7	705.4 / 808.4	26.76	N/A	N/A	395215.71	26.76	493301.13	26.62	327166.29	26.77	N/A	N/A	394934.14	26.63		314175	298632	347553		394934	306404	371244	1.21	
D-3-phosph dehydrogen KT2440	GIAVFNAPYSNTR	2/y8	705.4 / 922.4	26.76	N/A	N/A	428601.17	26.76	537520.28	26.62	365578.94	26.77	N/A	N/A	439732.89	26.63		340715	325401	388359		439733	333058	414046	1.24	
delta-amin acid KT2440	LLAQEIER	2/y5	486.3 / 674.3	23.84	N/A	N/A	122824.23	23.85	149458.28	23.71	114193.65	23.82	132217.10	24.12	109447.98	23.77		97639	90478	121309	111212	109448	94058	113990	1.21	
delta-amin acid KT2440	LLAQEIER	2/y6	486.3 / 745.4	23.86	N/A	N/A	555475.08	23.85	696254.38	23.72	556557.90	23.83	664687.96	24.12	659214.78	23.77		441573	421495	591239	559092	659215	431534	603182	1.40	
delta-amin acid KT2440	LLAQEIER	2/y7	486.3 / 858.5	23.84	N/A	N/A	59930.57	23.86	81536.73	23.72	59822.91	23.84	81215.34	24.12	64768.36	23.77		47642	49360	63551	68313	64768	48501	65544	1.35	1.32
delta-amin acid KT2440	FGGLAGAIDEGR	2/y6	581.8 / 660.3	26.37	N/A	N/A	35694.21	26.38	37426.96	26.22	45705.21	26.37	26072.43	26.84	29270.36	26.25		28375	22657	48553	21930	29270	25516	33251	1.30	
delta-amin acid KT2440	FGGLAGAIDEGR	2/y7	581.8 / 717.3	26.37	N/A	N/A	219645.79	26.37	249732.21	26.24	279567.29	26.38	195091.50	26.84	164493.30	26.25		174606	151182	296988	164098	164493	162894	208527	1.28	
delta-amin acid KT2440	FGGLAGAIDEGR	2/y8	581.8 / 788.4	26.37	N/A	N/A	218132.08	26.37	250536.24	26.23	313877.32	26.37	191478.81	26.84	169971.27	26.25		173403	151668	333436	161059	169971	162536	221489	1.36	
delta-amin acid KT2440	TIFQETEFR	2/y6	585.8 / 809.4	26.86	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
delta-amin acid KT2440	TIFQETEFR	2/y7	585.8 / 956.5	26.93	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
delta-amin acid KT2440	TIFQETEFR	3/y4	390.9 / 552.3	27.24	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
dihydrolip acetyltran KT2440	FGEVEEVALTR	2/y8	625.3 / 916.5	27.57	252159.90	27.57	407041.34	26.68	461465.05	26.55	140297.43	26.70	125240.39	27.20	90041.75	26.56	371750	323576	279359	149040	105344	90042	324895	114809	0.35	
dihydrolip acetyltran KT2440	FGEVEEVALTR	2/y6	625.3 / 688.4	27.56	307604.65	27.56	434074.33	26.68	550504.59	26.55	175752.51	26.70	140520.03	27.20	108659.50	26.56	453490	345066	333262	186704	118196	108659	377273	137853	0.37	
dihydrolip acetyltran KT2440	FGEVEEVALTR	2/y7	625.3 / 817.4	27.56	682886.22	27.56	1075107.94	26.69	1272134.41	26.55	372391.87	26.70	312393.20	27.20	247621.76	26.57	1006754	854652	770118	395597	262765	247622	877175	301994	0.34	0.36
dihydrolip acetyltran KT2440	ELPDFNSSLAPSGK	2/y9	731.4 / 860.5	28.20	52176.73	28.20	107433.03	27.27	154514.40	27.11	26096.54	27.29	36593.07	27.83	24689.73	27.13	76922	85403	93539	27723	30780	24690	85288	27731	0.33	
dihydrolip acetyltran KT2440	ELPDFNSSLAPSGK	2/y8	731.4 / 746.4	28.21	54352.34	28.21	108912.20	27.25	156128.41	27.10	20460.14	27.29	33514.14	27.83	27242.94	27.12	80130	86579	94516	21735	28190	27243	87075	25723	0.30	
dihydrolip acetyltran KT2440	LTVLPLLLK	2/y5	505.4 / 583.4	32.84	383347.24	32.84	930605.59	32.25	1143398.57	31.74	226608.60	32.11	323546.18	32.79	231711.30	31.82	565155	739781	692185	240729	272146	231711	665707	248196	0.37	
dihydrolip acetyltran KT2440	LTVLPLLLK	2/y8	505.4 / 896.6	32.84	118257.32	32.84	298766.69	32.26	337105.34	31.74	67615.95	32.11	107719.08	32.79	64733.72	31.81	174342	237503	204075	71829	90606	64734	205307	75723	0.37	
dihydrolip acetyltran KT2440	SLLQLAAEAAALAEK	2/y10	749.9 / 944.5	35.50	27895.26	35.88	230662.42	35.50	306172.52	35.29	51495.58	35.52	71371.20	35.87	52917.61	35.37	41125	183364	185349	54704	60033	52918	136613	55885	0.41	
dihydrolip acetyltran KT2440	SLLQLAAEAAALAEK	2/y8	749.9 / 802.4	35.48	15568.92	35.91	87607.23	35.48	123350.87	35.24	21588.59	35.47	30351.99	35.80	24473.16	35.37	22953	69643	74674	22934	25530	24473	55756	24312	0.44	
dihydrooro [Pseudomon KT2440	LSSGPAAALR	2/y9	471.8 / 829.5	22.16	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
dihydrooro [Pseudomon KT2440	LSSGPAAALR	2/y8	471.8 / 742.4	22.43	24944.04	22.17	43475.42	21.72	46568.12	21.58	27017.73	21.71	33509.85	21.94	34554.01	21.72	36774	34561	28191	28701	28186	34554	33175	30481	0.92	
dihydrooro [Pseudomon KT2440	LSSGPAAALR	2/y7	471.8 / 655.4	22.43	54643.81	22.17	98330.09	21.71	107632.67	21.58	66268.68	21.71	82513.23	21.95	80175.88	21.71	80559	78167	65158	70398	69405	80176	74628	73326	0.98	0.86
dihydrooro [Pseudomon KT2440	IVAIGAAPAGFSASR	2/y8	694.4 / 792.4	26.52	N/A	N/A	160327.37	26.51	212913.81	26.37	112670.63	26.51	69873.76	27.00	113809.27	26.39		127452	128893	119692	58773	113809	128172	97425	0.76	
dihydrooro [Pseudomon KT2440	IVAIGAAPAGFSASR	2/y11	694.4 / 991.5	26.49	N/A	N/A	81648.16	26.50	106782.65	26.37	62912.99	26.52	50295.98	27.00	62754.37	26.37		64906	64644	66833	42306	62754	64775	57298	0.88	
dihydrooro [Pseudomon KT2440	IVAIGAAPAGFSASR	2/y10	694.4 / 934.5	26.50	N/A	N/A	20456.01	26.51	26548.95	26.38	16405.43	26.50	9395.05	27.01	15187.23	26.38		16261	16072	17428	7903	15187	16167	13506	0.84	
dihydrooro [Pseudomon KT2440	GLEGEQLAELVALR	2/y7	749.4 / 771.5	30.25	N/A	N/A	24052.22	31.94	46936.92	31.43	15918.08	31.80	N/A	N/A	20669.06	31.50		19120	28414	16910		20669	23767	18790	0.79	
dihydrooro [Pseudomon KT2440	GLEGEQLAELVALR	2/y8	749.4 / 884.6	30.46	N/A	N/A	11711.36	31.97	23603.13	31.43	9329.45	31.80	N/A	N/A	10859.27	31.50		9310	14289	9911		10859	11799	10385	0.88	
dihydroxy- dehydratas KT2440	IFESQDSAVR	2/y7	576.3 / 762.4	22.71	241447.80	23.18	511491.13	22.70	637686.12	22.57	342424.32	22.68	427859.08	22.94	340969.86	22.66	355958	406608	386039	363762	359887	340970	382868	354873	0.93	
dihydroxy- dehydratas KT2440	IFESQDSAVR	2/y8	576.3 / 891.4	22.71	368931.02	23.18	742351.06	22.70	895189.31	22.57	463487.15	22.68	569922.89	22.93	487456.77	22.66	543902	590129	541925	492369	479382	487457	558652	486402	0.87	
dihydroxy- dehydratas KT2440	IFESQDSAVR	2/y6	576.3 / 675.3	22.71	45590.49	23.18	100936.81	22.71	122157.16	22.57	60272.03	22.69	85552.34	22.93	66824.21	22.66	67212	80239	73951	64028	71961	66824	73801	67604	0.92	0.87
dihydroxy- dehydratas KT2440	AYALLATSADK	2/y7	562.3 / 705.4	25.84	89288.59	25.84	262633.40	25.17	365167.75	25.04	153253.58	25.17	189721.49	25.51	131438.13	25.06	131635	208779	221063	162803	159581	131438	187159	151274	0.81	
dihydroxy- dehydratas KT2440	AYALLATSADK	2/y8	562.3 / 818.5	25.86	54139.29	25.86	157370.93	25.17	217780.67	25.03	95881.93	25.16	112911.24	25.51	80252.86	25.06	79816	125101	131839	101857	94974	80253	112252	92361	0.82	
dihydroxy- dehydratas KT2440	AYALLATSADK	2/y9	562.3 / 889.5	25.86	87679.96	25.86	227906.24	25.17	318029.23	25.04	145642.29	25.17	158583.47	25.51	133115.44	25.06	129263	181173	192527	154718	133390	133115	167654	140408	0.84	
dihydroxy- dehydratas KT2440	VLIDIPNR	2/y5	470.3 / 614.3	26.94	79047.74	26.94	158519.61	26.14	197953.51	26.00	113045.18	26.15	108571.92	26.57	96536.65	26.02	116537	126014	119836	120089	91324	96537	120796	102650	0.85	
dihydroxy- dehydratas KT2440	VLIDIPNR	2/y6	470.3 / 727.4	26.93	141221.35	26.93	286891.22	26.15	360678.43	26.00	202055.78	26.13	236354.23	26.58	180006.42	26.02	208198	228063	218346	214647	198806	180006	218202	197820	0.91	
dihydroxy- dehydratas KT2440	VLIDIPNR	2/y7	470.3 / 840.5	26.96	11640.19	26.96	21148.73	26.14	31267.69	26.00	16776.41	26.13	18760.02	26.59	15060.98	26.05	17161	16812	18929	17822	15780	15061	17634	16221	0.92	
elongation factor KT2440	TTLTAALTR	2/y6	474.3 / 632.4	24.57	N/A	N/A	14492687.73	24.56	18176571.18	24.41	11336962.88	24.54	12087764.10	24.84	11970778.82	24.45		11520900	11003640	12043406	10167439	11970779	11262270	11393874	1.01	
elongation factor KT2440	TTLTAALTR	2/y7	474.3 / 745.5	24.54	N/A	N/A	16111145.08	24.56	19121560.63	24.42	11797336.31	24.54	13158949.96	24.85	12933012.79	24.45		12807485	11575713	12532466	11068450	12933013	12191599	12177977	1.00	0.85
elongation factor KT2440	TTLTAALTR	2/y8	474.3 / 846.5	24.54	N/A	N/A	678271.73	24.56	803807.33	24.41	516612.27	24.54	549151.37	24.85	540049.45	24.45		539189	486605	548804	461910	540049	512897	516921	1.01	
elongation factor KT2440	FTAEVYVLSK	2/y6	578.8 / 708.4	27.11	N/A	N/A	3288847.86	27.14	2832215.28	27.01	1362142.80	27.17	N/A	N/A	1977439.68	27.01		2614455	1714552	1447022		1977440	2164504	1712231	0.79	
elongation factor KT2440	FTAEVYVLSK	2/y7	578.8 / 837.5	27.11	N/A	N/A	3942196.08	27.14	3214001.17	27.01	1472127.60	27.16	N/A	N/A	2181570.57	27.01		3133832	1945676	1563861		2181571	2539754	1872716	0.74	
elongation factor KT2440	FTAEVYVLSK	2/y8	578.8 / 908.5	27.11	N/A	N/A	10879174.32	27.14	10221586.39	27.00	4593034.19	27.16	N/A	N/A	5803692.24	27.01		8648353	6187892	4879241		5803692	7418122	5341467	0.72	
elongation factor KT2440	LVETLDAYIPEPVR	2/y8	807.9 / 944.5	30.56	N/A	N/A	889708.66	30.56	1234768.82	30.13	438713.84	30.49	N/A	N/A	608653.55	30.21		707270	747498	466052		608654	727384	537353	0.74	
elongation factor KT2440	LVETLDAYIPEPVR	2/y7	807.9 / 873.5	30.56	N/A	N/A	1229264.93	30.56	1694469.66	30.13	840219.33	30.53	N/A	N/A	808331.31	30.21		977199	1025789	892576		808331	1001494	850454	0.85	
elongation factor KT2440	LVETLDAYIPEPVR	2/b8	807.9 / 905.5	30.56	N/A	N/A	468459.95	30.56	610524.47	30.14	252077.32	30.49	N/A	N/A	325214.69	30.21		372400	369596	267785		325215	370998	296500	0.80	
extracellu ligand-bin KT2440	VAEAIHK	2/y4	384.2 / 468.3	22.19	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
extracellu ligand-bin KT2440	VAEAIHK	2/y5	384.2 / 597.3	21.89	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
extracellu ligand-bin KT2440	QAVAVANK	2/y5	400.7 / 502.3	23.21	N/A	N/A	392842.79	23.21	451858.32	23.07	199799.41	23.19	216762.55	23.46	184740.24	23.16		312289	273544	212250	182327	184740	292916	193105	0.66	0.73
extracellu ligand-bin KT2440	QAVAVANK	2/y6	400.7 / 601.4	23.28	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
extracellu ligand-bin KT2440	QAVAVANK	2/y7	400.7 / 672.4	22.86	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
extracellu ligand-bin KT2440	QQYGEGIATAVK	2/y7	632.8 / 659.4	23.70	N/A	N/A	199951.85	23.69	322157.55	23.56	117912.22	23.67	128386.73	23.96	138628.36	23.61		158951	195026	125260	107991	138628	176988	123960	0.70	
extracellu ligand-bin KT2440	QQYGEGIATAVK	2/y8	632.8 / 788.5	23.68	N/A	N/A	51668.28	23.70	67487.08	23.56	29569.91	23.66	34178.66	23.96	32454.27	23.61		41073	40855	31413	28749	32454	40964	30872	0.75	
extracellu ligand-bin KT2440	QQYGEGIATAVK	2/y9	632.8 / 845.5	23.70	N/A	N/A	171050.95	23.70	287608.55	23.55	128477.18	23.67	98273.64	23.95	151011.56	23.61		135976	174111	136483	82661	151012	155044	123385	0.80	
formyltetr deformylas KT2440	DSAEDLVR	2/y7	452.7 / 789.4	23.99	N/A	N/A	N/A	N/A	N/A	N/A	9076.17	23.25	10269.58	23.52	13382.28	23.27				9642	8638	13382		10554	infinity	
formyltetr deformylas KT2440	DSAEDLVR	2/y5	452.7 / 631.3	23.61	N/A	N/A	N/A	N/A	N/A	N/A	499195.25	23.27	639604.20	23.53	563902.39	23.24				530302	537993	563902		544066	infinity	
formyltetr deformylas KT2440	DSAEDLVR	2/y4	452.7 / 502.3	23.97	N/A	N/A	N/A	N/A	N/A	N/A	439770.69	23.27	550055.16	23.53	476229.14	23.24				467174	462671	476229		468691	infinity	
formyltetr deformylas KT2440	AVLLFLEDR	2/y6	538.3 / 792.4	30.83	N/A	N/A	6356.78	30.57	12191.89	30.40	385802.73	30.75	N/A	N/A	548431.22	30.48		5053	7381	409843		548431	6217	479137	77.07	
formyltetr deformylas KT2440	AVLLFLEDR	2/y7	538.3 / 905.5	30.56	N/A	N/A	39765.57	30.56	45482.07	30.13	307195.85	30.75	N/A	N/A	430506.83	30.48		31611	27534	326338		430507	29573	378423	12.80	75.41 (Infinity Van)
formyltetr deformylas KT2440	AVLLFLEDR	2/y5	538.3 / 679.3	30.83	N/A	N/A	1938.64	30.39	16878.36	30.41	635786.83	30.75	N/A	N/A	928241.89	30.48		1541	10218	675405		928242	5879	801823	136.38	
formyltetr deformylas KT2440	NIVTQSQADLIVLAR	2/y9	821.0 / 998.6	30.87	N/A	N/A	N/A	N/A	N/A	N/A	17756.06	30.80	N/A	N/A	35065.18	30.54				18863		35065		26964	infinity	
formyltetr deformylas KT2440	NIVTQSQADLIVLAR	2/y10	821.0 / 1085.6	30.94	N/A	N/A	N/A	N/A	N/A	N/A	27627.68	30.80	N/A	N/A	60788.39	30.52				29349		60788		45069	infinity	
formyltetr deformylas KT2440	NIVTQSQADLIVLAR	2/y8	821.0 / 870.5	29.72	N/A	N/A	N/A	N/A	N/A	N/A	23483.02	30.79	N/A	N/A	44828.93	30.50				24946		44829		34888	infinity	
fructose-1 aldolase KT2440	YEAFGTAGNASK	2/y10	608.3 / 923.5	22.41	375531.02	22.86	939479.14	22.40	1183284.07	22.27	778502.75	22.39	912565.99	22.63	846959.35	22.38	553632	746835	716330	827014	767591	846959	672266	813855	1.21	
fructose-1 aldolase KT2440	YEAFGTAGNASK	2/y8	608.3 / 705.3	22.41	346023.36	22.86	835253.45	22.40	1121290.55	22.27	702521.14	22.39	862068.31	22.63	788254.86	22.38	510130	663981	678801	746297	725116	788255	617637	753223	1.22	
fructose-1 aldolase KT2440	YEAFGTAGNASK	2/y9	608.3 / 852.4	22.39	232992.06	22.86	604514.13	22.40	750619.40	22.27	486871.89	22.39	580157.67	22.63	526355.37	22.37	343492	480556	454406	517210	487991	526355	426151	510519	1.20	1.16
fructose-1 aldolase KT2440	FTKPPTGDVLAIDR	2/y9	765.4 / 959.5	25.26	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
fructose-1 aldolase KT2440	FTKPPTGDVLAIDR	2/y8	765.4 / 858.5	25.29	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
fructose-1 aldolase KT2440	YAGAPFLR	2/y5	447.8 / 603.4	25.89	N/A	N/A	11975.65	25.91	16138.20	25.79	7559.63	25.92	N/A	N/A	8119.14	25.81										
fructose-1 aldolase KT2440	YAGAPFLR	2/y6	447.8 / 660.4	25.95	N/A	N/A	293292.75	25.93	380432.33	25.78	220568.35	25.92	N/A	N/A	237723.82	25.81		233152	230304	234313		237724	231728	236018	1.02	
fructose-1 aldolase KT2440	YAGAPFLR	2/y7	447.8 / 731.4	25.91	N/A	N/A	108941.08	25.93	146548.35	25.79	80837.85	25.92	N/A	N/A	91333.13	25.81										
gamma-amin dehydrogen KT2440	LYVQDGIYER	2/y6	628.3 / 752.4	25.35	N/A	N/A	24384.67	25.38	32429.43	25.25	59188.25	25.37	94382.50	25.75	65602.46	25.27		19384	19632	62876	79388	65602	19508	69289	3.55	
gamma-amin dehydrogen KT2440	LYVQDGIYER	2/y7	628.3 / 880.4	25.40	N/A	N/A	29088.17	25.38	28875.50	25.25	78645.37	25.38	97623.06	25.75	82716.46	25.26		23124	17481	83546	82114	82716	20302	82792	4.08	3.83
gamma-amin dehydrogen KT2440	LYVQDGIYER	2/y8	628.3 / 979.5	25.42	N/A	N/A	25009.31	25.38	30597.34	25.25	69542.00	25.38	93897.12	25.75	68717.14	25.27		19881	18523	73875	78980	68717	19202	73858	3.85	
gamma-glut phosphate KT2440	YVVIGDGQLR	2/y6	560.3 / 645.3	25.71	N/A	N/A	198196.02	25.69	261477.73	25.56	199741.00	25.69	204135.30	26.09	202967.43	25.58		157555	158292	212188	171705	202967	157924	195620	1.24	
gamma-glut phosphate KT2440	YVVIGDGQLR	2/y7	560.3 / 758.4	25.71	N/A	N/A	188835.47	25.70	216163.95	25.55	186044.26	25.69	177323.20	26.09	158057.54	25.58		150114	130860	197637	149153	158058	140487	168283	1.20	1.22
gamma-glut phosphate KT2440	YVVIGDGQLR	2/y8	560.3 / 857.5	25.67	N/A	N/A	167829.41	25.69	217001.84	25.56	163231.82	25.68	185362.86	26.09	162273.09	25.58		133415	131367	173403	155915	162273	132391	163864	1.24	
gamma-glut phosphate KT2440	AELTAANELDLAAGR	2/y9	757.9 / 958.5	27.43	N/A	N/A	8160.48	27.44	21536.92	27.29	12233.18	27.47	N/A	N/A	14939.82	27.31										
gamma-glut phosphate KT2440	AELTAANELDLAAGR	2/y10	757.9 / 1029.5	27.43	N/A	N/A	11618.57	27.43	26728.61	27.37	12550.50	27.48	N/A	N/A	11959.74	27.33										
gamma-glut phosphate KT2440	AELTAANELDLAAGR	2/y8	757.9 / 844.5	27.46	N/A	N/A	7193.72	27.43	9157.26	27.30	5802.60	27.47	N/A	N/A	4265.35	27.31										
glycine cleavage KT2440	VGLLPQER	2/y5	456.3 / 642.4	24.46	N/A	N/A	33853.64	24.47	61165.56	24.32	151366.33	24.43	77133.39	24.75	76121.58	24.36		26912	37028	160798	64880	76122	31970	100600	3.15	
glycine cleavage KT2440	VGLLPQER	2/y7	456.3 / 812.5	24.46	N/A	N/A	31025.81	24.45	41899.65	24.31	162083.23	24.44	77636.14	24.75	75293.41	24.36		24664	25365	172183	65302	75293	25014	104260	4.17	
glycine cleavage KT2440	VGLLPQER	2/y6	456.3 / 755.4	24.46	N/A	N/A	11348.10	24.47	17061.64	24.31	48218.55	24.42	28089.71	24.75	26870.20	24.36		9021	10329	51223	23627	26870	9675	33907	3.50	3.08
glycine cleavage KT2440	ALLALQGPAAVK	2/y8	576.4 / 783.5	26.89	N/A	N/A	172233.43	26.91	195677.74	26.78	314233.17	26.94	333306.21	27.45	347302.53	26.79		136916	118458	333814	280355	347303	127687	320491	2.51	
glycine cleavage KT2440	ALLALQGPAAVK	2/y9	576.4 / 854.5	26.93	N/A	N/A	146381.73	26.92	181370.40	26.78	272902.31	26.94	365290.80	27.45	287637.19	26.79		116366	109797	289908	307259	287637	113081	294935	2.61	
glycine cleavage KT2440	ALLALQGPAAVK	2/y10	576.4 / 967.6	26.93	N/A	N/A	55428.71	26.93	60578.45	26.78	101957.34	26.93	113786.78	27.45	107192.16	26.79		44063	36673	108311	95710	107192	40368	103738	2.57	
glycine cleavage KT2440	AAGFPGAEAIFAHVR	2/y11	757.4 / 1167.6	28.92	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
glycine cleavage KT2440	AAGFPGAEAIFAHVR	2/y7	757.4 / 813.5	28.91	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
glycine cleavage KT2440	AAGFPGAEAIFAHVR	2/y8	757.4 / 942.5	28.91	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
heat shock KT2440	APSAAQPSINEK	2/y6	606.8 / 687.4	21.05	279772.15	21.05	733324.60	20.58	996259.88	20.46	360182.90	20.59	368469.05	20.90	372784.54	20.64	412458	582953	603111	382627	309932	372785	532841	355115	0.67	
heat shock KT2440	APSAAQPSINEK	2/y8	606.8 / 886.5	21.05	79201.51	21.05	205655.98	20.58	278894.68	20.46	101022.11	20.59	103294.00	20.89	101054.38	20.64	116764	163485	168836	107317	86884	101054	149695	98419	0.66	0.77

5.5. SRM Analyse Vanillin KT2440

heat shock KT2440	APSAAQPSINEK	2/y9	606.8 / 957.5	20.58	36675.36	21.05	98789.05	20.58	131840.43	20.46	47292.81	20.59	50205.60	20.89	49161.95	20.64	54069	78532	79813	50240	42230	49162	70805	47210	0.67	
heat shock KT2440	AVADLQNVR	2/y5	493.3 / 629.4	22.82	N/A	N/A	928757.58	22.83	1121655.21	22.69	621524.30	22.81	698517.27	23.06	651114.55	22.78		738312	679022	660253	587547	651115	708667	632972	0.89	
heat shock KT2440	AVADLQNVR	2/y6	493.3 / 744.4	22.82	N/A	N/A	964292.45	22.82	1210641.13	22.69	640095.99	22.81	726923.19	23.06	660827.91	22.78		766560	732892	679982	611440	660828	749726	650750	0.87	
heat shock KT2440	AVADLQNVR	2/y7	493.3 / 815.4	22.82	N/A	N/A	2865202.97	22.82	3540167.94	22.69	2001698.06	22.80	2164274.18	23.06	2040249.60	22.78		2277681	2143129	2126430	1820446	2040250	2210405	1995709	0.90	
heat shock KT2440	VLELEEQLAAAK	2/y9	657.4 / 972.5	27.78	N/A	N/A	795989.41	27.78	1087823.24	27.59	400955.95	27.80	N/A	N/A	546554.53	27.63		632768	658541	425941		546555	645655	486248	0.75	
heat shock KT2440	VLELEEQLAAAK	2/y7	657.4 / 730.4	27.78	N/A	N/A	724401.38	27.78	973010.25	27.59	374117.70	27.80	N/A	N/A	501828.06	27.63		575860	589036	397430		501828	582448	449629	0.77	
heat shock KT2440	VLELEEQLAAAK	2/y8	657.4 / 859.5	27.78	N/A	N/A	1108892.92	27.78	1492340.68	27.60	575431.81	27.80	N/A	N/A	792236.19	27.63		881510	903426	611289		792236	892468	701763	0.79	
hypothetic protein KT2440	AVGTYVEPK	2/y6	482.3 / 736.4	24.90	N/A	N/A	206192.04	24.91	269162.90	24.77	162934.23	24.90	174213.55	25.23	165825.95	24.80										
hypothetic protein KT2440	HPINAQER	2/y7	482.8 / 827.4	24.94	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
hypothetic protein KT2440	EIVTLGVPGVDPNK	2/y8	719.4 / 825.5	28.34	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
inosine/ur nucleoside KT2440	AITTVAGNVR	2/y6	501.3 / 615.4	22.71	N/A	N/A	N/A	N/A	314454.94	22.94	14435.17	22.22	20817.89	22.45	12213.36	22.21			190363	15335	17511	12213	190363	15020	0.08	
inosine/ur nucleoside KT2440	AITTVAGNVR	2/y7	501.3 / 716.4	22.69	N/A	N/A	N/A	N/A	219602.86	23.07	13889.64	22.22	22768.34	22.47	15533.10	22.20			132942	14755	19151	15533	132942	16480	0.12	0.10
inosine/ur nucleoside KT2440	AITTVAGNVR	2/y8	501.3 / 817.5	22.67	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
inosine/ur nucleoside KT2440	QLAAVNNQASK	2/y7	572.3 / 760.4	29.43	N/A	N/A	13869.68	29.43	12196.98	29.15	10534.68	29.49	N/A	N/A	12338.76	29.22										
inosine/ur nucleoside KT2440	QLAAVNNQASK	2/y8	572.3 / 831.4	29.41	N/A	N/A	24630.68	29.44	20528.37	29.14	20054.06	29.48	N/A	N/A	23105.14	29.20										
inosine/ur nucleoside KT2440	QLAAVNNQASK	2/y9	572.3 / 902.5	29.84	N/A	N/A	39530.97	29.43	33005.76	29.14	26258.00	29.47	N/A	N/A	29508.87	29.20										
inosine/ur nucleoside KT2440	LLTSNAR	2/y5	387.7 / 548.3	30.23	N/A	N/A	N/A	N/A	431759.73	29.87	167781.69	30.21	157095.08	30.84	167474.11	29.95										
inosine/ur nucleoside KT2440	LLTSNAR	2/y6	387.7 / 661.4	30.23	N/A	N/A	21281.24	30.22	35902.64	29.87	13878.62	30.21	14102.70	30.85	13622.27	29.94										
isocitrate dehydrogen KT2440	SLNVALR	2/y5	386.7 / 572.3	23.70	N/A	N/A	247340.24	23.69	334323.66	23.55	732528.45	23.66	828857.60	23.94	774639.41	23.61		196622	202391	778175	697181	774639	199507	749998	3.76	
isocitrate dehydrogen KT2440	SLNVALR	2/y6	386.7 / 685.4	23.31	N/A	N/A	1303.54	23.67	2608.19	23.55	5648.62	23.67	6445.30	23.93	3688.26	23.62		1036	1579	6001	5421	3688	1308	5037	3.85	
isocitrate dehydrogen KT2440	SLNVALR	2/y4	386.7 / 458.3	23.70	N/A	N/A	53043.29	23.68	66508.55	23.55	158776.37	23.66	211658.96	23.95	155760.81	23.62		42167	40263	168670	178034	155761	41215	167488	4.06	3.65
isocitrate dehydrogen KT2440	GPLTTPVGGGIR	2/y7	562.8 / 655.4	24.59	N/A	N/A	643934.32	24.61	911542.96	24.47	1817803.04	24.60	2058018.14	24.91	1998964.10	24.50		511893	551825	1931076	1731071	1998964	531859	1887037	3.55	
isocitrate dehydrogen KT2440	GPLTTPVGGGIR	2/y9	562.8 / 857.5	24.59	N/A	N/A	319302.28	24.61	379986.46	24.47	771988.06	24.60	868963.28	24.92	840032.49	24.50		253828	230034	820093	730915	840032	241931	797014	3.29	
isocitrate dehydrogen KT2440	GPLTTPVGGGIR	2/y10	562.8 / 970.6	24.59	N/A	N/A	48700.32	24.60	78928.99	24.47	142177.10	24.59	166488.09	24.91	147008.11	24.50		38714	47782	151037	140039	147008	43248	146028	3.38	
isocitrate dehydrogen KT2440	ENSEDIYAGIEWK	2/y8	777.4 / 979.5	28.83	N/A	N/A	1821.58	28.84	2926.10	28.63	3198.88	28.89	N/A	N/A	3034.66	28.69										
isocitrate dehydrogen KT2440	ENSEDIYAGIEWK	2/y9	777.4 / 1094.6	28.84	N/A	N/A	1558.46	28.86	1397.68	28.64	2220.98	28.90	N/A	N/A	3542.40	28.66										
isocitrate dehydrogen KT2440	ENSEDIYAGIEWK	2/y7	777.4 / 866.4	28.88	N/A	N/A	9993.64	28.87	14866.82	28.61	18171.04	28.89	N/A	N/A	24572.32	28.67										
isopropylm isomerase KT2440	DIVLAVIGK	2/y6	464.3 / 600.4	24.28	79566.62	24.28	223537.98	23.75	310634.86	23.61	141598.97	23.72	167821.95	24.00	140977.43	23.67	117302	177701	188051	150422	141161	140977	161018	144187	0.90	
isopropylm isomerase KT2440	DIVLAVIGK	2/y5	464.3 / 487.3	24.27	243919.63	24.27	612604.23	23.75	851917.72	23.61	401522.50	23.72	401702.82	23.99	377591.75	23.67	359602	486987	515730	426543	337886	377592	454106	380674	0.84	0.87
isopropylm isomerase KT2440	DIVLAVIGK	2/y7	464.3 / 699.5	24.23	32287.69	24.23	62387.70	23.72	87069.70	23.58	43204.55	23.69	42076.91	23.95	45185.24	23.63										
isopropylm isomerase KT2440	VPDPAAETDLVK	2/y9	627.8 / 943.5	25.96	47794.55	25.96	136829.10	25.24	182431.94	25.11	52578.31	25.25	61078.36	25.59	62541.49	25.14										
isopropylm isomerase KT2440	VPDPAAETDLVK	2/y7	627.8 / 775.4	25.96	12065.36	25.96	65004.20	25.23	88982.18	25.11	27397.94	25.23	33171.67	25.61	27745.78	25.11										
isopropylm isomerase KT2440	VPDPAAETDLVK	2/y8	627.8 / 846.5	25.98	13215.92	25.98	44608.69	25.25	56542.00	25.09	20366.65	25.23	22591.48	25.60	16664.91	25.12										
oligopepti ABC KT2440	QRPPLDPQAHSLVR	2/y11	807.5 / 1232.7	26.08	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
oligopepti ABC KT2440	QRPPLDPQAHSLVR	2/y8	807.5 / 907.5	25.64	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
oligopepti ABC KT2440	QRPPLDPQAHSLVR	2/y9	807.5 / 1022.5	26.26	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
oligopepti ABC KT2440	LATLPGIVPGR	2/y7	547.3 / 695.4	27.31	N/A	N/A	65139.32	27.31	96919.54	27.14	76427.53	27.33	N/A	N/A	85602.85	27.17		51782	58673	81190		85603	55227	83396	1.51	1.31
oligopepti ABC KT2440	LATLPGIVPGR	3/y7	365.2 / 695.4	27.32	N/A	N/A	148.01	27.32	157.83	27.19	N/A	N/A	N/A	N/A	157.72	27.18										
oligopepti ABC KT2440	LATLPGIVPGR	2/y8	547.3 / 808.5	26.98	N/A	N/A	3645.31	27.32	6020.12	27.11	2663.67	27.31	N/A	N/A	4473.98	27.19		2898	3644	2830		4474	3271	3652	1.12	
oligopepti ABC KT2440	VEIPAAESR	2/y6	486.3 / 630.3	29.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
oligopepti ABC KT2440	VEIPAAESR	2/y7	486.3 / 743.4	29.19	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
oligopepti ABC KT2440	VEIPAAESR	2/y8	486.3 / 872.5	29.23	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
polyamine ABC KT2440	IAAVQK	2/y4	315.2 / 445.3	23.66	3732.18	23.43	1379814.58	23.67	1781071.50	23.53	481447.24	23.64	467480.18	23.92	404760.42	23.61										
polyamine ABC KT2440	IAAVQK	2/y5	315.2 / 516.3	23.84	128621.96	24.34	205301.38	23.82	273307.86	23.68	188054.18	23.77	214926.89	24.06	207061.41	23.73										
polyamine ABC KT2440	AFYEPWEK	2/y4	535.3 / 559.3	27.23	N/A	N/A	79016.16	27.23	118097.24	27.08	137259.82	27.26	170593.03	27.80	149917.93	27.10		62814	71493	145813	143492	149918	67153	146408	2.18	
polyamine ABC KT2440	AFYEPWEK	2/y5	535.3 / 688.3	27.23	N/A	N/A	23199.53	27.23	32549.18	27.09	41154.90	27.26	54090.59	27.80	45019.42	27.12		18442	19704	43719	45497	45019	19073	44745	2.35	2.36
polyamine ABC KT2440	AFYEPWEK	2/y6	535.3 / 851.4	27.23	N/A	N/A	117548.57	27.23	144197.33	27.09	226106.36	27.26	256758.24	27.79	237575.14	27.10		93445	87293	240196	215968	237575	90369	231246	2.56	
polyamine ABC KT2440	TAPTSWADFWDTK	2/y7	763.3 / 882.4	31.29	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
polyamine ABC KT2440	TAPTSWADFWDTK	2/y8	763.3 / 1068.5	31.33	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
porin B KT2440	LSGSGTK	2/y5	325.2 / 449.2	23.66	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
porin B KT2440	LSGSGTK	2/y6	325.2 / 536.3	23.57	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
porin B KT2440	LSGSGTK	2/b6	325.2 / 503.3	23.55	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										(Infinity Glu)
porin B KT2440	YFDGALDVK	2/y6	514.3 / 602.3	26.32	1141.48	26.32	85227.38	26.47	99695.32	26.33	N/A	N/A	N/A	N/A	N/A	N/A	1683	67751	60353				43262		infinity	
porin B KT2440	YFDGALDVK	2/y7	514.3 / 717.4	26.45	295666.31	26.31	369570.42	26.45	497968.05	26.32	N/A	N/A	N/A	N/A	N/A	N/A	435890	293788	301457				343712		infinity	
porin B KT2440	YFDGALDVK	2/y8	514.3 / 864.5	26.29	1820.19	26.29	55341.45	26.45	81152.76	26.32	N/A	N/A	N/A	N/A	N/A	N/A	2683	43993	49128				31935		infinity	
putrescine ABC KT2440	AGVYEELDR	2/y5	526.3 / 661.3	24.84	322619.46	24.84	485849.17	24.26	613578.10	24.12	979179.63	24.23	571231.03	24.53	605363.71	24.16	475626	386224	371445	1040195	480482	605364	411098	708680	1.72	
putrescine ABC KT2440	AGVYEELDR	2/y6	526.3 / 824.4	24.84	671205.23	24.84	942404.18	24.26	1162619.02	24.12	1955361.58	24.24	1126998.31	24.54	1146545.84	24.16	989533	749160	703820	2077206	947957	1146546	814171	1390570	1.71	
putrescine ABC KT2440	AGVYEELDR	2/y7	526.3 / 923.5	24.85	29702.04	24.85	38821.35	24.25	45496.66	24.11	71955.54	24.24	40802.45	24.54	48823.24	24.17	43789	30861	27543	76439	34320	48823	34064	53194	1.56	
putrescine ABC KT2440	QLYAIAAPDASVQR	2/y7	751.9 / 772.4	26.14	N/A	N/A	257179.73	26.13	310338.79	26.00	283404.60	26.13	349081.42	26.58	328403.85	26.00		204444	187871	301064	293625	328404	196158	307698	1.57	1.71
putrescine ABC KT2440	QLYAIAAPDASVQR	2/y8	751.9 / 843.4	26.14	N/A	N/A	138686.57	26.13	162545.85	25.99	149022.37	26.13	205559.35	26.58	171869.47	26.00		110248	98401	158308	172903	171869	104325	167694	1.61	
putrescine ABC KT2440	QLYAIAAPDASVQR	2/y9	751.9 / 914.5	26.12	N/A	N/A	220741.18	26.13	265564.89	25.99	248335.26	26.12	318154.72	26.58	277130.69	26.01		175477	160766	263810	267611	277131	168122	269517	1.60	
putrescine ABC KT2440	NLDPDLLK	2/y5	464.3 / 585.4	26.28	N/A	N/A	446257.75	26.27	542953.78	26.13	582022.88	26.27	716232.04	26.71	629130.50	26.15		354751	328691	618291	602448	629130	341721	616623	1.80	
putrescine ABC KT2440	NLDPDLLK	2/y6	464.3 / 700.4	26.26	N/A	N/A	688556.94	26.26	838442.87	26.12	822359.68	26.26	1057180.06	26.71	1083829.46	26.14		547365	507572	873604	889231	1083829	527469	948888	1.80	
putrescine ABC KT2440	NLDPDLLK	2/f823	464.3 / 823.3	26.28	N/A	N/A	124513.85	26.26	141297.63	26.13	164351.70	26.26	226985.60	26.71	187371.71	26.15		98982	85538	174593	190925	187372	92260	184297	2.00	
Rieske (2Fe-2S) KT2440	NFAAHDQTLTDNIR	2/y8	808.4 / 960.5	24.02	15466.09	24.02	47395.84	23.49	74089.73	23.36	97005.10	23.62	82684.53	23.92	77084.43	23.57	22801	37677	44852	103050	69549	77084	35110	83228	2.37	
Rieske (2Fe-2S) KT2440	NFAAHDQTLTDNIR	2/y7	808.4 / 832.5	23.76	N/A	N/A	N/A	N/A	N/A	N/A	50877.54	23.63	69795.00	23.93	59490.05	23.59				54048	58707	59490		57415		
Rieske (2Fe-2S) KT2440	NFAAHDQTLTDNIR	2/b9	808.4 / 998.5	24.09	11639.83	24.09	23018.89	23.51	43192.94	23.39	35674.00	23.49	51671.34	23.79	32265.67	23.47	17160	18299	26148	37897	43463	32266	20536	37875	1.84	2.11
Rieske (2Fe-2S) KT2440	GNGLADDVPVDR	2/y7	614.3 / 815.4	24.06	N/A	N/A	N/A	N/A	N/A	N/A	550657.65	24.43	605636.01	24.74	579709.12	24.34				584971	509422	579709		558034		
Rieske (2Fe-2S) KT2440	GNGLADDVPVDR	2/y8	614.3 / 886.4	24.44	N/A	N/A	N/A	N/A	N/A	N/A	782123.00	24.43	726245.93	24.74	788660.44	24.34				830860	610871	788660		743464		
Rieske (2Fe-2S) KT2440	GNGLADDVPVDR	2/y9	614.3 / 999.5	23.72	N/A	N/A	N/A	N/A	N/A	N/A	28864.45	24.44	23737.54	24.74	27949.20	24.34				30663	19966	27949		26193		
Rieske (2Fe-2S) KT2440	QQQNLLAHPER	2/y7	667.3 / 835.5	25.03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
Rieske (2Fe-2S) KT2440	QQQNLLAHPER	2/y8	667.3 / 949.5	25.49	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
Rieske (2Fe-2S) KT2440	QQQNLLAHPER	2/y6	667.3 / 722.4	24.54	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
serine protein KT2440	IALNEELEK	2/y6	529.8 / 761.4	23.86	520895.96	23.86	1051404.78	23.35	1453638.04	23.21	571063.15	23.32	692705.45	23.60	597610.02	23.28										
serine protein KT2440	IALNEELEK	2/y7	529.8 / 874.5	23.87	530655.39	23.87	1131464.95	23.35	1438928.49	23.22	665221.91	23.33	804138.10	23.59	684954.04	23.28										
serine protein KT2440	IALNEELEK	2/y8	529.8 / 945.5	24.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
serine protein KT2440	LLVNSSLSK	2/y6	480.8 / 635.3	24.29	47458.75	24.29	104359.64	23.76	138282.53	23.61	368331.63	23.73	357925.98	24.02	303716.49	23.68										
serine protein KT2440	LLVNSSLSK	2/y7	480.8 / 734.4	24.31	185621.16	24.31	506279.03	23.76	684846.20	23.63	1068778.47	23.73	1380645.80	24.02	1175935.60	23.68										1.98
serine protein KT2440	LLVNSSLSK	2/y8	480.8 / 847.5	24.34	29038.83	24.34	96332.65	23.77	108638.43	23.63	135411.02	23.74	201179.85	24.02	187392.14	23.68										
serine protein KT2440	LQEFGGDISK	2/y7	547.3 / 723.4	24.70	161082.12	24.70	462579.70	24.12	523561.75	23.98	499091.86	24.10	527739.11	24.39	443535.94	24.02	237478	367726	316951	530192	443900	443536	307385	472543	1.54	
serine protein KT2440	LQEFGGDISK	2/y8	547.3 / 852.4	24.69	198333.80	24.69	442751.16	24.12	565711.03	23.98	701221.12	24.09	1000144.10	24.38	800022.20	24.02	292396	351963	342467	744916	841256	800022	328942	795398	2.42	
serine protein KT2440	LQEFGGDISK	2/y9	547.3 / 980.5	24.67	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
S-formylgl hydrolase KT2440	YLGEDR	2/y4	376.7 / 476.2	22.97	49090.98	23.41	104317.91	22.95	130243.69	22.81	88033.44	22.93	82373.24	23.18	86943.45	22.90	72373	82927	78846	93519	69287	86943	78049	83250	1.07	
S-formylgl hydrolase KT2440	YLGEDR	2/y5	376.7 / 589.3	23.38	14808.50	23.38	35537.19	22.94	35670.54	22.81	22156.87	22.93	27472.51	23.16	23217.80	22.91	21832	28250	21594	23538	23108	23218	23892	23288	0.97	
S-formylgl hydrolase KT2440	QLKPEALEQAAR	2/y9	677.4 / 984.5	24.67	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
S-formylgl hydrolase KT2440	QLKPEALEQAAR	2/y7	677.4 / 758.4	24.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										0.95
S-formylgl hydrolase KT2440	QLKPEALEQAAR	2/y8	677.4 / 887.5	24.54	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
S-formylgl hydrolase KT2440	DDFLEK	2/y5	383.7 / 651.3	23.54	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
S-formylgl hydrolase KT2440	DDFLEK	2/y4	383.7 / 536.3	24.31	29904.50	24.31	65685.71	23.76	62995.77	23.62	34055.98	23.71	43149.53	24.00	34309.01	23.67	44087	52217	38136	36178	36295	34309	44813	35594	0.79	
S-formylgl hydrolase KT2440	DDFLEK	2/b5	383.7 / 620.3	23.53	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
succinate dehydrogen KT2440	ALSEGVEYR	2/y5	512.3 / 623.3	22.54	356757.31	23.03	608131.99	22.55	762668.60	22.42	926288.03	22.54	1196621.80	22.78	936876.82	22.52	525954	483432	461700	984008	1006520	936877	490362	975802	1.99	
succinate dehydrogen KT2440	ALSEGVEYR	2/y6	512.3 / 752.4	22.54	150248.28	23.03	287335.31	22.55	340531.42	22.42	399874.26	22.54	499061.84	22.78	406939.94	22.52	221506	228416	206149	424792	419778	406940	218690	417170	1.91	
succinate dehydrogen KT2440	ALSEGVEYR	2/y7	512.3 / 839.4	22.54	737618.05	23.03	1277089.90	22.55	1506148.33	22.42	1908031.63	22.54	2473354.98	22.78	1987334.77	22.52	1087444	1015217	911784	2026927	2080425	1987335	1004815	2031562	2.02	1.95
succinate dehydrogen KT2440	DASDTDVDVALNR	2/y7	695.8 / 786.5	26.09	34134.73	26.09	80881.06	25.37	106258.81	25.24	97932.42	25.37	146240.30	25.73	118404.81	25.27	50324	64296	64326	104035	123008	118405	59649	115149	1.93	
succinate dehydrogen KT2440	DASDTDVDVALNR	2/y8	695.8 / 901.5	26.07	35963.46	26.07	74991.93	25.38	105652.41	25.25	102285.63	25.37	143380.36	25.74	102996.66	25.26	53020	59615	63959	108659	120602	102997	58864	110753	1.88	
succinate dehydrogen KT2440	GIEQLAGLR	2/y6	478.8 / 657.4	28.15	91539.91	28.15	212645.51	27.23	262576.18	27.08	300750.70	27.25	361333.21	27.79	312730.35	27.10	134954	169042	158957	319491	303930	312730	154318	312051	2.02	
succinate dehydrogen KT2440	GIEQLAGLR	2/y7	478.8 / 786.5	28.15	151163.22	28.15	417403.40	27.23	455895.75	27.08	517935.70	27.25	595951.26	27.78	502088.10	27.10	222854	331813	275988	550210	501275	502088	276885	517858	1.87	
succinate dehydrogen KT2440	GIEQLAGLR	2/y5	478.8 / 529.3	28.16	119231.32	28.16	241868.25	27.22	284573.01	27.08	342515.06	27.25	448458.08	27.79	337678.35	27.10	175778	192272	172273	363858	377214	337678	180108	359583	2.00	
TonB-depen receptor KT2440	GENLTDQTVR	2/y8	566.8 / 946.5	21.62	68131.77	22.07	147508.52	21.62	179497.62	21.49	37007.70	21.62	45505.07	21.86	41556.04	21.63	100444	117261	108663	39314	38276	41556	108790	39715	0.37	
TonB-depen receptor KT2440	GENLTDQTVR	2/y6	566.8 / 719.4	21.60	424628.65	22.07	866680.21	21.62	1042335.62	21.49	216823.59	21.62	310921.13	21.86	210309.02	21.62	626015	688964	631004	230335	261527	210309	648661	234057	0.36	
TonB-depen receptor KT2440	GENLTDQTVR	2/y7	566.8 / 832.5	21.62	86839.89	22.07	172273.18	21.62	216427.80	21.49	45487.14	21.62	57699.97	21.86	44526.27	21.63	128025	136948	131020	48322	48533	44526	131998	47127	0.36	
TonB-depen receptor KT2440	FYGIEAQDR	2/y6	549.8 / 731.4	25.59	10974.76	25.59	32974.44	24.87	45401.38	24.73	9564.33	24.88	3958.76	25.23	2192.62	24.84	16180	26213	27485	10160	3330	2193	23292	5228	0.22	0.33
TonB-depen receptor KT2440	FYGIEAQDR	2/y7	549.8 / 788.4	25.49	82354.35	25.49	301689.82	24.85	439884.21	24.71	67840.73	24.84	69640.57	25.17	66211.82	24.74	121412	239827	266295	72068	58577	66212	209178	65619	0.31	
TonB-depen receptor KT2440	FYGIEAQDR	2/y8	549.8 / 951.5	25.50	4357.12	25.50	22790.29	24.85	38729.81	24.72	1944.18	24.90	4139.69	25.17	4707.40	24.76	6424	18117	23446	2065	3482	4707	15996	3418	0.21	
TonB-depen receptor KT2440	NYIGLIGTGNTR	2/y8	639.8 / 831.5	27.36	23965.21	27.36	50177.70	26.52	64846.12	26.38	12464.58	26.53	21153.08	26.99	14213.50	26.40	35331	39889	39256	13241	17793	14214	38159	15082	0.40	
TonB-depen receptor KT2440	NYIGLIGTGNTR	2/y9	639.8 / 888.5	27.36	142340.20	27.36	372938.94	26.52	432678.11	26.38	88034.21	26.53	132552.65	27.00	64526.40	26.39	209847	296466	261932	93520	111495	64526	256082	89847	0.35	
TonB-depen receptor KT2440	NYIGLIGTGNTR	2/y7	639.8 / 718.4	27.36	86830.58	27.36	212114.49	26.52	247031.07	26.38	52683.36	26.52	70036.90	27.00	44272.45	26.40	128011	168619	149546	55966	58910	44272	148726	53050	0.36	
UDP-glucos 4-epimeras KT2440	QITALDAQR	2/y6	508.3 / 673.4	22.29	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
UDP-glucos 4-epimeras KT2440	QITALDAQR	2/y7	508.3 / 774.4	22.92	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
UDP-glucos 4-epimeras KT2440	LVADASK	2/y5	352.2 / 491.3	23.45	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										
UDP-glucos 4-epimeras KT2440	LVADASK	2/y6	352.2 / 590.3	23.46	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A										??? (Infinity Van)
UDP-glucos 4-epimeras KT2440	EAVTVFGR	2/y5	439.7 / 579.3	25.27	N/A	N/A	N/A	N/A	N/A	N/A	9232.63	24.70	11393.97	25.02	10139.77	24.61				9808	9584	10140		9844	infinity	
UDP-glucos 4-epimeras KT2440	EAVTVFGR	2/y6	439.7 / 678.4	24.81	N/A	N/A	N/A	N/A	N/A	N/A	2567.37	24.68	3885.86	25.01	2529.82	24.60				2727	3269	2530		2842	infinity	