TABLE S1 Complete list of genes dysregulated in *P. aeruginosa* H103 during growth in a phosphate-limiting (0.2 mM) medium compared to phosphate-sufficient (1 mM) conditions

Gene ID	Gene name	Fold change	p-value	Description
PA0006		-2.26	0.0188	conserved hypothetical protein
PA0007		2.02	0.0002	hypothetical protein
PA0008	*glyS*	-2.15	0.0031	glycyl-tRNA synthetase beta chain
PA0009	*glyQ*	-2.60	0.0005	glycyl-tRNA synthetase alpha chain
PA0024	*hemF*	-2.81	0.0001	coproporphyrinogen III oxidase, aerobic
PA0026	*plcB*	2.40	0.0001	phospholipase C
PA0027		2.21	0.0009	hypothetical protein
PA0028		2.63	0.0003	hypothetical protein
PA0035	*trpA*	-2.24	0.0015	tryptophan synthase alpha chain
PA0036	*trpB*	-2.40	0.0003	tryptophan synthase beta chain
PA0038		3.89	0.0001	hypothetical protein
PA0045		-2.49	0.0001	hypothetical protein
PA0047		-3.10	0.0004	hypothetical protein
PA0050		2.46	0.0022	hypothetical protein
PA0059	*osmC*	4.11	9.88E-05	osmotically inducible protein OsmC
PA0083	*tssB1*	4.00	4.11E-05	type VI secretion system protein
PA0084	*tssC1*	2.73	0.0001	type VI secretion system protein
PA0085	*htp1*	5.37	0.0004	type VI secretion system protein
PA0087	*tssE1*	2.10	0.0009	type VI secretion system protein
PA0088	*tssF1*	3.10	5.98E-05	type VI secretion system protein
PA0089	*tssG1*	3.85	0.0007	type VI secretion system protein
PA0090	*clpV1*	4.96	0.0001	type VI secretion system protein ATPase
PA0091	*vgrG1*	4.25	0.0001	type VI secretion system protein
PA0098		2.14	0.0018	hypothetical protein
PA0100		3.42	0.0022	hypothetical protein
PA0101		3.46	0.0022	hypothetical protein
PA0105	*coxB*	3.93	0.0126	cytochrome c oxidase, subunit II
PA0106	*coxA*	4.84	0.0129	cytochrome c oxidase, subunit I
PA0107		5.82	0.0003	conserved hypothetical protein
PA0108	*coIII*	3.72	0.0012	cytochrome c oxidase, subunit III
PA0109		2.15	0.0001	hypothetical protein
PA0110		2.73	0.001	hypothetical protein
PA0111		2.50	0.0006	hypothetical protein
PA0113		2.05	0.0018	probable cytochrome c oxidase assembly factor
PA0122		4.55	0.0141	conserved hypothetical protein
PA0165		-2.54	0.0012	hypothetical protein
PA0169		-2.11	0.0008	hypothetical protein
PA0170		-3.38	0.0003	hypothetical protein
PA0173		5.58	0.0001	probable chemotaxis-specific methylesterase
PA0174		5.59	0.0003	conserved hypothetical protein
PA0175		10.61	7.71E-05	probable chemotaxis protein methyltransferase

PA0176	*aer2*	15.43	0.0001	aerotaxis transducer
PA0177		9.10	6.68E-05	probable purine-binding chemotaxis protein
PA0178		4.89	0.0011	probable two-component sensor
PA0179		4.03	0.0001	probable two-component response regulator
PA0188		2.34	0.0224	hypothetical protein
PA0232	*pcaC*	2.44	0.0003	gamma-carboxymuconolactone decarboxylase
PA0259		2.07	0.0017	hypothetical protein
PA0260		2.31	0.0117	hypothetical protein
PA0265	*gabD*	2.93	0.0004	succinate-semialdehyde dehydrogenase
PA0266	*gabT*	2.37	2.79E-05	4-aminobutyrate aminotransferase
PA0280	*cysA*	-2.04	0.0005	sulfate transport protein CysA
PA0281	*cysW*	-4.07	0.0009	sulfate transport protein CysW
PA0282	*cysT*	-3.02	0.0001	sulfate transport protein CysT
PA0283	*sbp*	-3.63	3.05E-05	sulfate-binding protein precursor
PA0284		-3.05	0.0024	hypothetical protein
PA0291	*oprE*	-3.75	3.18E-06	Anaerobically-induced outer membrane porin OprE precursor
PA0315		2.63	0.0053	hypothetical protein
PA0316	*serA*	-2.88	0.0004	D-3-phosphoglycerate dehydrogenase
PA0329		3.74	2.33E-05	conserved hypothetical protein
PA0331	*ilvA1*	-2.48	5.63E-05	threonine dehydratase, biosynthetic
PA0347	*glpQ*	25.01	1.30E-07	glycerophosphoryl diester phosphodiesterase, periplasmic
PA0355	*pfpI*	2.00	0.0143	protease PfpI
PA0380		-2.40	3.52E-05	conserved hypothetical protein
PA0381	*thiG*	-3.13	0.001	thiamine biosynthesis protein, thiazole moiety
PA0390	*metX*	-2.22	0.0002	homoserine O-acetyltransferase
PA0426	*mexB*	2.59	3.20E-05	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB
PA0428		-2.19	0.0012	probable ATP-dependent RNA helicase
PA0447	*gcdH*	2.16	0.0006	glutaryl-CoA dehydrogenase
PA0450		4.13	0.0002	probable phosphate transporter
PA0459		5.51	3.60E-05	probable ClpA/B protease ATP binding subunit
PA0460		4.86	7.59E-07	hypothetical protein
PA0484		3.41	0.0009	conserved hypothetical protein
PA0500	*bioB*	-3.75	3.63E-05	biotin synthase
PA0501	*bioF*	-2.39	4.34E-05	8-amino-7-oxononanoate synthase
PA0504	*bioD*	-2.04	0.0001	dethiobiotin synthase
PA0508		5.35	0.0003	probable acyl-CoA dehydrogenase
PA0520	*nirQ*	2.03	0.0002	regulatory protein NirQ
PA0551	*epd*	-2.06	0.0004	D-erythrose 4-phosphate dehydrogenase
PA0565		2.70	0.0007	conserved hypothetical protein
PA0567		2.56	0.0001	conserved hypothetical protein
PA0572		6.18	0.0004	hypothetical protein
PA0575		3.65	0.0001	conserved hypothetical protein
PA0578		-4.92	9.54E-05	conserved hypothetical protein

PA0579	*rpsU*	-5.03	0.0002	30S ribosomal protein S21
PA0580	*gcp*	-2.64	0.0002	O-sialoglycoprotein endopeptidase
PA0586		12.82	2.54E-05	conserved hypothetical protein
PA0587		16.56	0.0001	conserved hypothetical protein
PA0588		3.17	0.0005	conserved hypothetical protein
PA0595	*ostA*	-2.34	0.0245	organic solvent tolerance protein OstA precursor
PA0648		2.11	0.0004	hypothetical protein
PA0654	*speD*	2.22	0.0004	S-adenosylmethionine decarboxylase proenzyme
PA0656		3.08	2.73E-05	probable HIT family protein
PA0673		3.10	0.0003	hypothetical protein
PA0674		3.06	0.0001	hypothetical protein
PA0675		3.01	1.94E-05	probable sigma-70 factor, ECF subfamily
PA0676		4.19	1.73E-06	probable transmembrane sensor
PA0677	*hxcW*	4.59	3.68E-05	HxcW putative pseudopilin
PA0678	*hxcU*	8.23	7.24E-06	HxcU putative pseudopilin
PA0679	*hxcP*	7.27	1.88E-05	hypothetical protein
PA0680	*hxcV*	2.38	0.0004	HxcV putative pseudopilin
PA0681	*hxcT*	7.60	0.0001	HxcT pseudopilin
PA0682	*hxcX*	13.27	3.66E-05	HxcX atypical pseudopilin
PA0683	*hxcY*	8.82	1.79E-05	probable type II secretion system protein
PA0684	*hxcZ*	11.68	3.81E-06	probable type II secretion system protein
PA0685	*hxcQ*	12.31	1.07E-05	probable type II secretion system protein
PA0686	*hxcR*	13.14	8.43E-06	probable type II secretion system protein
PA0687	*hxcS*	3.60	5.62E-05	probable type II secretion system protein
PA0688		307.72	1.16E-06	probable binding protein component of ABC transporter
PA0689		8.04	0.0001	hypothetical protein
PA0690		7.82	2.23E-07	hypothetical protein
PA0691		4.90	0.0002	hypothetical protein
PA0692		4.49	3.99E-05	hypothetical protein
PA0693	*exbB2*	20.15	1.41E-07	transport protein ExbB2
PA0694	*exbD2*	29.57	8.62E-08	transport protein ExbD
PA0695		16.63	8.08E-08	hypothetical protein
PA0696		37.97	1.48E-06	hypothetical protein
PA0697		26.19	5.93E-07	hypothetical protein
PA0698		45.03	5.50E-08	hypothetical protein
PA0699		15.69	1.22E-06	probable peptidyl-prolyl cis-trans isomerase, PpiC-type
PA0700		22.81	8.25E-07	hypothetical protein
PA0701		5.00	5.34E-05	probable transcriptional regulator
PA0730		11.03	7.44E-08	probable transferase
PA0743		2.90	9.22E-05	probable 3-hydroxyisobutyrate dehydrogenase
PA0763	*mucA*	2.10	8.69E-05	anti-sigma factor MucA
PA0764	*mucB*	2.26	0.0074	negative regulator for alginate biosynthesis MucB
PA0778	*icp*	-3.20	0.0426	inhibitor of cysteine peptidase

PA0783	*putP*	-8.75	1.12E-05	sodium/proline symporter PutP
PA0788		2.18	0.0001	hypothetical protein
PA0792	*prpD*	5.13	7.41E-06	propionate catabolic protein PrpD
PA0793		4.00	1.48E-05	hypothetical protein
PA0794		3.59	4.31E-06	probable aconitate hydratase
PA0795	*prpC*	2.44	0.0001	citrate synthase 2
PA0796	*prpB*	3.44	6.52E-06	carboxyphosphonoenolpyruvate phosphonomutase
PA0797		2.95	2.41E-05	probable transcriptional regulator
PA0805		2.31	4.42E-05	hypothetical protein
PA0833		3.08	5.21E-05	hypothetical protein
PA0841		-2.08	0.0005	hypothetical protein
PA0842		33.54	8.31E-07	probable glycosyl transferase
PA0843	*plcR*	9.66	4.54E-05	phospholipase accessory protein PlcR precursor
PA0844	*plcH*	25.66	3.18E-05	hemolytic phospholipase C precursor
PA0848		6.92	0.0002	probable alkyl hydroperoxide reductase
PA0849	*trxB2*	4.62	3.48E-05	thioredoxin reductase 2
PA0854	*fumC2*	2.22	6.53E-05	fumarate hydratase
PA0867		2.05	6.79E-05	hypothetical protein
PA0898	*aruD*	2.22	0.0003	succinylglutamate 5-semialdehyde dehydrogenase
PA0899	*aruB*	3.50	1.95E-05	succinylarginine dihydrolase
PA0903	*alaS*	-2.51	0.0102	alanyl-tRNA synthetase
PA0945	*purM*	-2.47	0.0003	phosphoribosylaminoimidazole synthetase
PA0947		-2.22	0.0005	conserved hypothetical protein
PA0960		2.67	0.0005	hypothetical protein
PA0961		-2.17	0.0365	probable cold-shock protein
PA0963	*aspS*	-3.08	2.65E-05	aspartyl-tRNA synthetase
PA0964		-2.33	0.0015	conserved hypothetical protein
PA0978		4.74	2.98E-05	conserved hypothetical protein
PA0979		11.37	2.24E-06	conserved hypothetical protein
PA0981		4.17	0.0001	hypothetical protein
PA0982		2.05	0.0051	hypothetical protein
PA0983		2.67	0.0016	conserved hypothetical protein
PA0996	*pqsA*	4.16	0.019	probable coenzyme A ligase
PA0997	*pqsB*	4.98	0.0094	Homologous to beta-keto-acyl-acyl-carrier protein synthase
PA0998	*pqsC*	4.47	0.0031	Homologous to beta-keto-acyl-acyl-carrier protein synthase
PA0999	*pqsD*	3.20	0.0026	3-oxoacyl-[acyl-carrier-protein] synthase III
PA1000	*pqsE*	7.77	0.0031	Quinolone signal response protein
PA1001	*phnA*	6.61	0.0033	anthranilate synthase component I
PA1002	*phnB*	4.72	0.0047	anthranilate synthase component II
PA1003	*mvfR*	2.36	0.0003	Transcriptional regulator
PA1033		2.05	0.0007	probable glutathione S-transferase
PA1041		14.43	0.0002	probable outer membrane protein precursor

PA1066		4.56	0.0005	probable short-chain dehydrogenase
PA1070	*braG*	-2.80	0.003	branched-chain amino acid transport protein
PA1071	*braF*	-3.39	0.0009	branched-chain amino acid transport protein
PA1072	*braE*	-3.22	0.0001	branched-chain amino acid transport protein
PA1073	*braD*	-5.29	0.0001	branched-chain amino acid transport protein
PA1074	*braC*	-4.05	0.0023	branched-chain amino acid transport protein
PA1078	*flgC*	2.06	0.0005	flagellar basal-body rod protein FlgC
PA1082	*flgG*	2.00	0.0011	flagellar basal-body rod protein FlgG
PA1086	*flgK*	2.32	0.0003	flagellar hook-associated protein 1 FlgK
PA1087	*flgL*	2.04	4.93E-05	flagellar hook-associated protein type 3 FlgL
PA1088		2.93	2.35E-05	hypothetical protein
PA1090		3.53	0.0009	hypothetical protein
PA1092	*fliC*	2.28	0.0016	flagellin type B
PA1093		2.44	0.0003	hypothetical protein
PA1096		3.14	0.0009	hypothetical protein
PA1107		2.61	0.0002	conserved hypothetical protein
PA1112		2.14	0.0258	conserved hypothetical protein
PA1118		2.10	0.0084	hypothetical protein
PA1130	*rhlC*	2.64	0.0022	rhamnosyltransferase 2
PA1134		23.33	0.0002	hypothetical protein
PA1135		3.91	0.0001	conserved hypothetical protein
PA1147		2.20	0.0284	probable amino acid permease
PA1159		-2.52	0.007	probable cold-shock protein
PA1172	*napC*	5.50	0.0006	cytochrome c-type protein NapC
PA1173	*napB*	10.69	0.0003	cytochrome c-type protein NapB precursor
PA1174	*napA*	7.75	0.0003	periplasmic nitrate reductase protein NapA
PA1175	*napD*	7.43	0.0001	NapD protein of periplasmic nitrate reductase
PA1176	*napF*	4.67	0.0008	ferredoxin protein NapF
PA1177	*napE*	4.83	0.0005	periplasmic nitrate reductase protein NapE
PA1183	*dctA*	-4.73	0.0251	C4-dicarboxylate transport protein
PA1202		6.99	4.84E-05	probable hydrolase
PA1203		3.25	2.91E-05	hypothetical protein
PA1204		2.31	6.02E-05	conserved hypothetical protein
PA1205		2.38	8.72E-05	conserved hypothetical protein
PA1211		2.33	0.0227	hypothetical protein
PA1212		2.30	0.0015	probable major facilitator superfamily (MFS) transporter
PA1213		2.61	0.0035	hypothetical protein
PA1214		5.20	0.0134	hypothetical protein
PA1215		7.71	0.0008	hypothetical protein
PA1216		8.39	0.0022	hypothetical protein
PA1217		5.39	0.0004	probable 2-isopropylmalate synthase
PA1218		3.36	0.0003	hypothetical protein
PA1219		2.69	0.0086	hypothetical protein
PA1245		3.97	6.24E-05	hypothetical protein
PA1249	*aprA*	2.06	0.001	alkaline metalloproteinase precursor

PA1273	*cobB*	-2.62	0.0001	cobyrinic acid a,c-diamide synthase
PA1274		-2.01	0.001	conserved hypothetical protein
PA1275	*cobD*	-2.53	0.0048	cobalamin biosynthetic protein CobD
PA1276	*cobC*	-2.07	0.0081	cobalamin biosynthetic protein CobC
PA1278	*cobP*	-2.46	0.0014	cobinamide kinase
PA1323		2.76	3.89E-05	hypothetical protein
PA1327		8.94	1.09E-06	probable protease
PA1330		2.16	0.0001	probable short-chain dehydrogenase
PA1331		-2.01	0.0282	conserved hypothetical protein
PA1338	*ggt*	-2.53	0.0017	gamma-glutamyltranspeptidase precursor
PA1341		-2.24	0.03	probable permease of ABC transporter
PA1344		2.51	0.0054	probable short-chain dehydrogenase
PA1366		2.61	0.0132	hypothetical protein
PA1389		2.26	0.003	probable glycosyl transferase
PA1423		2.67	0.0036	probable chemotaxis transducer
PA1456	*cheY*	2.58	0.0038	two-component response regulator CheY
PA1471		2.88	0.0001	hypothetical protein
PA1473		2.49	0.0004	hypothetical protein
PA1478		-2.29	0.0015	hypothetical protein
PA1479	*ccmE*	-2.51	0.0002	cytochrome C-type biogenesis protein CcmE
PA1482	*ccmH*	-2.50	0.0001	cytochrome C-type biogenesis protein CcmH
PA1483	*cycH*	-2.28	0.0002	cytochrome c-type biogenesis protein
PA1493	*cysP*	-2.14	0.0158	sulfate-binding protein of ABC transporter
PA1524	*xdhA*	-2.15	0.0009	xanthine dehydrogenase
PA1545		3.24	0.0002	hypothetical protein
PA1546	*hemN*	2.25	0.0128	oxygen-independent coproporphyrinogen III oxidase
PA1552		-4.87	2.14E-05	probable cytochrome c
PA1553		-3.62	9.97E-05	probable cytochrome c oxidase subunit
PA1561	*aer*	2.23	4.73E-05	aerotaxis receptor Aer
PA1562	*acnA*	6.70	5.17E-06	aconitate hydratase 1
PA1571		24.96	2.28E-08	hypothetical protein
PA1587	*lpdG*	-2.30	0.0019	lipoamide dehydrogenase-glc
PA1592		2.07	0.0015	hypothetical protein
PA1604		2.59	0.0166	hypothetical protein
PA1606		34.82	1.32E-08	hypothetical protein
PA1609	*fabB*	-2.67	0.0004	beta-ketoacyl-ACP synthase I
PA1610	*fabA*	-2.41	0.0001	beta-hydroxydecanoyl-ACP dehydrase
PA1665		2.04	0.0047	hypothetical protein
PA1689		-4.93	0.0069	conserved hypothetical protein
PA1712	*exsB*	-2.13	0.0098	exoenzyme S synthesis protein B
PA1731		2.43	0.0011	conserved hypothetical protein
PA1732		2.11	0.0003	conserved hypothetical protein
PA1733		2.99	0.0004	conserved hypothetical protein
PA1745		3.76	0.0007	hypothetical protein
PA1750		-2.90	0.0028	phospho-2-dehydro-3-deoxyheptonate aldolase

PA1753		2.51	0.0002	conserved hypothetical protein
PA1784		2.13	0.0017	hypothetical protein
PA1787	*acnB*	-2.63	0.0017	aconitate hydratase 2
PA1790		-2.83	0.0112	hypothetical protein
PA1794	*glnS*	-2.26	0.014	glutaminyl-tRNA synthetase
PA1800	*tig*	-3.51	0.0022	trigger factor
PA1806	*fabI*	2.18	0.0011	NADH-dependent enoyl-ACP reductase
PA1838	*cysI*	-3.30	0.0001	sulfite reductase
PA1842		-2.01	0.0013	hypothetical protein
PA1860		2.82	0.0033	hypothetical protein
PA1864		2.38	0.0211	probable transcriptional regulator
PA1871	*lasA*	5.45	0.0281	LasA protease precursor
PA1873		2.98	0.0002	hypothetical protein
PA1880		3.04	0.002	probable oxidoreductase
PA1881		3.47	0.0005	probable oxidoreductase
PA1887		2.36	0.0004	hypothetical protein
PA1888		5.71	5.32E-05	hypothetical protein
PA1900	*phzB2*	11.73	0.0252	probable phenazine biosynthesis protein
PA1901	*phzC2*	6.75	0.0106	phenazine biosynthesis protein PhzC
PA1902	*phzD2*	11.46	0.0025	phenazine biosynthesis protein PhzD
PA1903	*phzE2*	2.97	0.0305	phenazine biosynthesis protein PhzE
PA1904	*phzF2*	9.00	0.0064	probable phenazine biosynthesis protein
PA1905	*phzG2*	7.17	0.0055	probable pyridoxamine 5'-phosphate oxidase
PA1914		4.66	0.0027	conserved hypothetical protein
PA1926		-2.04	0.0064	conserved hypothetical protein
PA1930		2.95	0.0006	probable chemotaxis transducer
PA1945		2.61	0.002	probable transcriptional regulator
PA1972		-2.61	0.0231	conserved hypothetical protein
PA1985	*pqqA*	3.17	0.001	pyrroloquinoline quinone biosynthesis protein A
PA1987	*pqqC*	2.22	0.0005	pyrroloquinoline quinone biosynthesis protein C
PA2015	*gnyD*	-2.04	0.0006	Citronelloyl-CoA dehydrogenase, GnyD
PA2022		52.40	8.10E-07	probable nucleotide sugar dehydrogenase
PA2023	*galU*	5.77	6.38E-06	UTP--glucose-1-phosphate uridylyltransferase
PA2030		2.64	0.0025	hypothetical protein
PA2031		2.39	0.0002	hypothetical protein
PA2046		2.07	0.0122	hypothetical protein
PA2048		5.73	3.53E-06	hypothetical protein
PA2067		3.79	0.014	probable hydrolase
PA2068		4.59	0.0248	probable major facilitator superfamily (MFS) transporter
PA2069		19.26	0.0002	probable carbamoyl transferase
PA2071	*fusA2*	2.49	0.0003	elongation factor G
PA2104		2.05	0.0046	probable cysteine synthase
PA2106		2.03	0.0007	hypothetical protein
PA2119		3.33	7.48E-05	alcohol dehydrogenase (Zn-dependent)
PA2171		2.12	0.001	hypothetical protein

PA2174		4.43	0.004	hypothetical protein
PA2190		2.51	0.0025	conserved hypothetical protein
PA2197		2.15	0.0163	conserved hypothetical protein
PA2204		-3.90	0.0004	probable binding protein component of ABC transporter
PA2264		2.90	0.0076	conserved hypothetical protein
PA2265		2.04	0.0002	gluconate dehydrogenase
PA2266		3.29	4.39E-05	probable cytochrome c precursor
PA2302		8.91	6.27E-05	probable non-ribosomal peptide synthetase
PA2303		4.53	9.61E-05	hypothetical protein
PA2304		2.25	0.0009	hypothetical protein
PA2323		4.99	0.0003	probable glyceraldehyde-3-phosphate dehydrogenase
PA2352		5.83	2.37E-05	probable glycerophosphoryl diester phosphodiesterase
PA2360		3.22	0.003	hypothetical protein
PA2365		8.73	0.0002	conserved hypothetical protein
PA2366		7.08	0.0055	conserved hypothetical protein
PA2367		2.94	0.0025	hypothetical protein
PA2368		4.49	0.0036	hypothetical protein
PA2369		3.35	0.0017	hypothetical protein
PA2370		3.46	0.0016	hypothetical protein
PA2371		3.04	0.003	probable ClpA/B-type protease
PA2372		3.15	0.0088	hypothetical protein
PA2373		3.65	0.0054	conserved hypothetical protein
PA2374		2.24	0.0089	hypothetical protein
PA2375		2.47	0.001	hypothetical protein
PA2381		9.18	3.53E-07	hypothetical protein
PA2396	*pvdF*	2.07	0.0449	pyoverdine synthetase F
PA2426	*pvdS*	4.29	0.0095	sigma factor PvdS
PA2427		3.33	9.18E-05	hypothetical protein
PA2428		17.82	8.88E-08	hypothetical protein
PA2433		4.37	0.0005	hypothetical protein
PA2444	*glyA2*	-2.05	0.0003	serine hydroxymethyltransferase
PA2445	*gcvP2*	-3.27	3.02E-05	glycine cleavage system protein P2
PA2453		-2.40	9.01E-05	hypothetical protein
PA2475		2.66	0.0005	probable cytochrome P450
PA2485		2.06	0.0052	hypothetical protein
PA2505		-6.71	9.54E-05	probable porin
PA2519	*xylS*	-2.40	0.0116	transcriptional regulator XylS
PA2520	*czcA*	-2.92	0.0014	Resistance-Nodulation-Cell Division (RND) divalent metal cation efflux transporter CzcA
PA2521	*czcB*	-4.80	0.0015	Resistance-Nodulation-Cell Division (RND) divalent metal cation efflux membrane fusion protein CzcB precursor
PA2522	*czcC*	-3.59	0.001	outer membrane protein precursor CzcC

PA2525		2.19	0.0006	probable outer membrane protein precursor
PA2533		-2.26	0.0052	probable sodium:alanine symporter
PA2544		2.35	0.0036	hypothetical protein
PA2548		4.21	0.0003	hypothetical protein
PA2561		2.80	0.0011	probable chemotaxis transducer
PA2562		8.51	4.00E-06	hypothetical protein
PA2565		2.16	0.0049	hypothetical protein
PA2566		2.59	0.0155	conserved hypothetical protein
PA2571		4.19	0.0015	probable two-component sensor
PA2572		2.22	0.0008	probable two-component response regulator
PA2573		4.95	0.0022	probable chemotaxis transducer
PA2592		4.40	0.0023	probable periplasmic spermidine/putrescine-binding protein
PA2618		2.52	0.0028	hypothetical protein
PA2619	*infA*	-3.00	1.92E-05	initiation factor
PA2620	*clpA*	2.15	0.0015	ATP-binding protease component ClpA
PA2621		2.37	0.0007	conserved hypothetical protein
PA2624	*idh*	-2.58	0.0002	isocitrate dehydrogenase
PA2625		-2.03	0.0024	conserved hypothetical protein
PA2635		87.04	3.60E-09	hypothetical protein
PA2700		2.82	0.0006	probable porin
PA2701		2.29	0.0032	probable major facilitator superfamily (MFS) transporter
PA2717	*cpo*	4.19	0.0016	chloroperoxidase precursor
PA2731		2.58	0.0003	hypothetical protein
PA2739	*pheT*	-2.10	0.0023	phenylalanyl-tRNA synthetase, beta subunit
PA2740	*pheS*	-2.70	0.001	phenylalanyl-tRNA synthetase, alpha-subunit
PA2741	*rplT*	-2.18	6.32E-05	50S ribosomal protein L20
PA2764		2.30	0.001	hypothetical protein
PA2770		-2.90	0.0004	hypothetical protein
PA2771		3.55	0.0013	conserved hypothetical protein
PA2781		2.07	0.0011	hypothetical protein
PA2787	*cpg2*	2.26	0.0053	carboxypeptidase G2 precursor
PA2788		2.16	0.0019	probable chemotaxis transducer
PA2795		-2.11	0.003	conserved hypothetical protein
PA2803		8.84	6.07E-05	hypothetical protein
PA2804		14.90	2.86E-06	hypothetical protein
PA2815		5.27	0.0003	probable acyl-CoA dehydrogenase
PA2840		-3.27	0.0007	probable ATP-dependent RNA helicase
PA2851	*efp*	-3.50	0.0001	translation elongation factor P
PA2879		2.67	0.0001	probable transcriptional regulator
PA2881		18.90	2.32E-06	probable two-component response regulator
PA2882		13.32	0.0002	probable two-component sensor
PA2904	*cobI*	-2.60	0.0002	precorrin-2 methyltransferase CobI
PA2918		3.11	0.0052	probable short-chain dehydrogenase
PA2920		2.23	0.0018	probable chemotaxis transducer

PA2937		4.39	0.0011	hypothetical protein
PA2939		25.19	0.0441	probable aminopeptidase
PA2943		-2.86	0.0002	phospho-2-dehydro-3-deoxyheptonate aldolase
PA2945		-2.17	0.0274	conserved hypothetical protein
PA2963		-2.03	0.0212	conserved hypothetical protein
PA2965	*fabF1*	-2.13	0.0018	beta-ketoacyl-acyl carrier protein synthase II
PA2968	*fabD*	-2.35	0.0002	malonyl-CoA-[acyl-carrier-protein] transacylase
PA2969	*plsX*	-2.27	0.0025	fatty acid biosynthesis protein PlsX
PA2970	*rpmF*	-5.76	1.45E-05	50S ribosomal protein L32
PA2971		-5.89	6.07E-06	conserved hypothetical protein
PA2985		3.37	0.0018	hypothetical protein
PA2994	*nqrF*	-2.33	0.0002	Na+-translocating NADH:quinone oxidoreductase, subunit Nqr6
PA2995	*nqrE*	-2.88	0.0013	Na+-translocating NADH:quinone oxidoreductase subunit Nqr5
PA2996	*nqrD*	-2.83	6.35E-05	Na+-translocating NADH:uniquinone oxidoreductase subunit Nqr4
PA2997	*nqrC*	-3.51	0.0003	Na+-translocating NADH:ubiquinone oxidoreductase subunit Nrq3
PA2998	*nqrB*	-4.39	0.0002	Na+-translocating NADH:ubiquinone oxidoreductase subunit Nrq2
PA2999	*nqrA*	-2.04	0.0009	Na+-translocating NADH:ubiquinone oxidoreductase subunit Nrq1
PA3013	*foaB*	2.90	8.11E-06	fatty-acid oxidation complex beta-subunit
PA3014	*faoA*	2.76	5.59E-05	fatty-acid oxidation complex alpha-subunit
PA3018		-2.47	0.0005	hypothetical protein
PA3019		-2.36	0.0007	probable ATP-binding component of ABC transporter
PA3021		2.02	0.0027	hypothetical protein
PA3028	*moeA2*	-2.43	0.0195	molybdenum cofactor biosynthesis protein A2
PA3040		3.01	9.86E-05	conserved hypothetical protein
PA3041		2.34	0.0002	hypothetical protein
PA3049	*rmf*	7.08	0.0071	ribosome modulation factor
PA3095	*xcpZ*	2.60	7.96E-05	general secretion pathway protein M
PA3096	*xcpY*	2.78	0.0001	general secretion pathway protein L
PA3097	*xcpX*	2.94	0.0008	general secretion pathway protein K
PA3098	*xcpW*	2.79	9.25E-05	general secretion pathway protein J
PA3099	*xcpV*	2.21	8.24E-05	general secretion pathway protein I
PA3100	*xcpU*	2.85	8.71E-05	General secretion pathway outer membrane protein H precursor
PA3101	*xcpT*	4.89	2.13E-06	general secretion pathway protein G
PA3102	*xcpS*	3.00	5.12E-05	general secretion pathway protein F
PA3103	*xcpR*	2.70	5.09E-05	general secretion pathway protein E
PA3104	*xcpP*	3.90	3.49E-05	secretion protein XcpP
PA3105	*xcpQ*	4.58	2.37E-05	general secretion pathway protein D
PA3108	*purF*	-2.06	0.0219	amidophosphoribosyltransferase

PA3112	*accD*	-2.42	0.0025	acetyl-CoA carboxylase beta subunit
PA3118	*leuB*	-2.49	8.48E-05	3-isopropylmalate dehydrogenase
PA3119		-3.30	0.0006	conserved hypothetical protein
PA3120	*leuD*	-2.32	0.0016	3-isopropylmalate dehydratase small subunit
PA3121	*leuC*	-3.36	0.0001	3-isopropylmalate dehydratase large subunit
PA3149	*wbpH*	2.25	0.0001	probable glycosyltransferase WbpH
PA3162	*rpsA*	-3.82	1.68E-05	30S ribosomal protein S1
PA3167	*serC*	-2.52	0.0023	3-phosphoserine aminotransferase
PA3181		2.14	0.0118	2-keto-3-deoxy-6-phosphogluconate aldolase
PA3182	*pgl*	3.07	0.0229	6-phosphogluconolactonase
PA3219		18.20	2.83E-06	hypothetical protein
PA3221	*csaA*	2.13	0.0137	CsaA protein
PA3249		6.55	0.0002	probable transcriptional regulator
PA3250		6.04	3.94E-06	hypothetical protein
PA3251		5.42	0.0001	hypothetical protein
PA3252		2.01	0.0003	probable permease of ABC transporter
PA3253		5.70	0.0002	probable permease of ABC transporter
PA3254		2.49	0.0003	probable ATP-binding component of ABC transporter
PA3255		2.51	0.0024	hypothetical protein
PA3279	*oprP*	249.93	7.79E-08	Phosphate-specific outer membrane porin OprP precursor
PA3280	*oprO*	16.59	3.31E-06	Pyrophosphate-specific outer membrane porin OprO precursor
PA3289		2.00	0.0011	hypothetical protein
PA3296	*phoA*	69.06	2.30E-09	alkaline phosphatase
PA3308	*hepA*	-2.05	0.0023	RNA helicase HepA
PA3319	*plcN*	16.36	1.12E-07	non-hemolytic phospholipase C precursor
PA3326		3.11	0.0024	probable Clp-family ATP-dependent protease
PA3327		4.00	3.83E-05	probable non-ribosomal peptide synthetase
PA3328		8.62	0.0003	probable FAD-dependent monooxygenase
PA3329		18.35	0.0002	hypothetical protein
PA3330		28.49	0.0002	probable short chain dehydrogenase
PA3331		22.44	0.0004	cytochrome P450
PA3332		17.85	0.0001	conserved hypothetical protein
PA3333	*fabH2*	15.12	0.0006	3-oxoacyl-[acyl-carrier-protein] synthase III
PA3334		7.86	0.0005	probable acyl carrier protein
PA3335		6.66	0.0013	hypothetical protein
PA3344	*recQ*	-3.18	2.16E-05	ATP-dependent DNA helicase RecQ
PA3347		2.96	0.0002	hypothetical protein
PA3369		40.29	1.78E-08	hypothetical protein
PA3370		21.81	2.59E-07	hypothetical protein
PA3371		22.52	2.20E-07	hypothetical protein
PA3372	*phnP*	5.30	1.78E-05	conserved hypothetical protein
PA3373	*phnN*	6.32	7.97E-07	conserved hypothetical protein
PA3374	*phnM*	25.35	1.32E-07	conserved hypothetical protein

PA3375	*phnL*	17.98	6.48E-06	probable ATP-binding component of ABC transporter
PA3376	*phnK*	18.56	1.31E-06	probable ATP-binding component of ABC transporter
PA3377	*phnJ*	25.55	4.71E-07	conserved hypothetical protein
PA3378	*phnI*	20.34	1.42E-06	conserved hypothetical protein
PA3379	*phnH*	13.82	2.36E-06	conserved hypothetical protein
PA3380	*phnG*	19.86	5.29E-07	conserved hypothetical protein
PA3381	*phnF*	6.64	4.69E-06	probable transcriptional regulator
PA3382	*phnE*	52.55	8.96E-08	phosphonate transport protein PhnE
PA3383	*phnD*	90.96	2.00E-09	binding protein component of ABC phosphonate transporter
PA3384	*phnC*	27.21	2.47E-07	ATP-binding component of ABC phosphonate transporter
PA3397	*fpr*	-7.24	2.72E-05	ferredoxin--NADP+ reductase
PA3416		3.23	0.0021	probable pyruvate dehydrogenase E1 component, beta chain
PA3417		2.40	0.0084	probable pyruvate dehydrogenase E1 component, alpha subunit
PA3418	*ldh*	5.39	5.04E-05	leucine dehydrogenase
PA3431		2.84	0.0128	conserved hypothetical protein
PA3432		5.16	0.0009	hypothetical protein
PA3441		-2.10	0.0063	probable molybdopterin-binding protein
PA3442		-2.68	0.0041	probable ATP-binding component of ABC transporter
PA3445		-2.93	0.0004	conserved hypothetical protein
PA3450		-3.06	0.0028	probable antioxidant protein
PA3451		4.36	6.24E-05	hypothetical protein
PA3459		7.86	3.27E-07	probable glutamine amidotransferase
PA3460		23.03	1.05E-07	probable acetyltransferase
PA3461		24.38	5.29E-07	conserved hypothetical protein
PA3462		2.17	0.0007	probable sensor/response regulator hybrid
PA3476	*rhlI*	2.96	0.0002	autoinducer synthesis protein RhlI
PA3477	*rhlR*	4.65	0.0002	transcriptional regulator RhlR
PA3478	*rhlB*	8.97	0.001	rhamnosyltransferase chain B
PA3479	*rhlA*	11.46	0.0005	rhamnosyltransferase chain A
PA3515		-3.81	0.0025	hypothetical protein
PA3516		-5.13	0.0012	probable lyase
PA3517		-9.93	1.39E-06	probable lyase
PA3518		-10.94	1.18E-06	hypothetical protein
PA3519		-8.29	5.36E-06	hypothetical protein
PA3520		2.36	0.0012	hypothetical protein
PA3522		-3.08	0.0026	probable Resistance-Nodulation-Cell Division (RND) efflux transporter
PA3523		-3.31	0.0049	probable Resistance-Nodulation-Cell Division (RND) efflux membrane fusion protein

				precursor
PA3537	*argF*	-2.12	0.0003	ornithine carbamoyltransferase, anabolic
PA3540	*algD*	2.31	0.0006	GDP-mannose 6-dehydrogenase AlgD
PA3550	*algF*	2.22	0.0099	alginate o-acetyltransferase AlgF
PA3551	*algA*	5.08	0.0002	phosphomannose isomerase / guanosine 5'-diphospho-D-mannose pyrophosphorylase
PA3558		2.69	0.0006	hypothetical protein
PA3559		5.02	2.58E-05	probable nucleotide sugar dehydrogenase
PA3586		3.14	0.027	probable hydrolase
PA3603	*dgkA*	-2.02	0.0013	diacylglycerol kinase
PA3615		2.41	0.0023	hypothetical protein
PA3622	*rpoS*	3.12	0.0005	sigma factor RpoS
PA3632		-2.73	4.27E-05	conserved hypothetical protein
PA3639	*accA*	-2.04	0.0001	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit)
PA3656	*rpsB*	-13.85	2.82E-07	30S ribosomal protein S2
PA3666	*dapD*	-2.10	0.0013	tetrahydrodipicolinate succinylase
PA3674		2.17	0.0053	hypothetical protein
PA3691		3.34	4.78E-05	hypothetical protein
PA3692		4.34	3.49E-05	probable outer membrane protein precursor
PA3700	*lysS*	-3.02	0.0006	lysyl-tRNA synthetase
PA3702	*wspR*	2.41	0.0007	probable two-component response regulator
PA3723		7.33	0.0006	probable FMN oxidoreductase
PA3742	*rplS*	-10.96	3.50E-06	50S ribosomal protein L19
PA3743	*trmD*	-5.80	4.86E-06	tRNA (guanine-N1)-methyltransferase
PA3744	*rimM*	-5.16	0.0002	16S rRNA processing protein
PA3745	*rpsP*	-5.53	1.06E-05	30S ribosomal protein S16
PA3746	*ffh*	-2.78	0.0034	signal recognition particle protein Ffh
PA3762		3.78	0.0012	hypothetical protein
PA3768		-2.01	0.0027	probable metallo-oxidoreductase
PA3769	*guaA*	-4.21	0.0004	GMP synthase
PA3770	*guaB*	-3.21	0.0002	inosine-5'-monophosphate dehydrogenase
PA3792	*leuA*	-2.30	4.40E-05	2-isopropylmalate synthase
PA3795		2.25	0.0015	probable oxidoreductase
PA3806		-2.08	0.0053	conserved hypothetical protein
PA3807	*ndk*	-2.14	0.0001	nucleoside diphosphate kinase
PA3809	*fdx2*	-2.22	0.0002	ferredoxin [2Fe-2S]
PA3810	*hscA*	-2.98	5.28E-05	heat shock protein HscA
PA3811	*hscB*	-2.33	9.39E-05	heat shock protein HscB
PA3812	*iscA*	-2.29	0.0003	probable iron-binding protein IscA
PA3815		-2.13	0.0016	conserved hypothetical protein
PA3818		-3.39	1.20E-05	extragenic suppressor protein SuhB
PA3819		6.15	6.79E-06	conserved hypothetical protein
PA3820	*secF*	-4.36	0.0002	secretion protein SecF
PA3821	*secD*	-2.88	2.01E-05	secretion protein SecD
PA3822		-2.90	0.0002	conserved hypothetical protein

PA3823	*tgt*	-2.21	0.0003	queuine tRNA-ribosyltransferase
PA3824	*queA*	-2.15	0.0038	S-adenosylmethionine:trna ribosyltransferase-isomerase
PA3836		-3.38	5.36E-05	hypothetical protein
PA3837		-2.51	0.0006	probable permease of ABC transporter
PA3851		2.55	0.0001	hypothetical protein
PA3852		3.32	4.86E-05	hypothetical protein
PA3891		2.05	0.0006	probable ATP-binding component of ABC transporter
PA3903	*prfC*	-2.28	0.0003	peptide chain release factor 3
PA3909		143.98	2.89E-08	hypothetical protein
PA3910		34.61	3.25E-07	hypothetical protein
PA3916	*moaE*	3.18	0.0011	molybdopterin converting factor, large subunit
PA3917	*moaD*	2.77	0.0106	molybdopterin converting factor, small subunit
PA3918	*moaC*	2.09	0.0043	molybdopterin biosynthetic protein C
PA3919		8.47	0.0002	conserved hypothetical protein
PA3924		2.03	0.0004	probable medium-chain acyl-CoA ligase
PA3928		3.38	0.0004	hypothetical protein
PA3929	*cioB*	2.11	0.0004	cyanide insensitive terminal oxidase
PA3931		-2.61	3.46E-05	conserved hypothetical protein
PA3936		-3.29	0.003	probable permease of ABC taurine transporter
PA3937		-2.52	0.0002	probable ATP-binding component of ABC taurine transporter
PA3938		-3.14	0.0002	probable periplasmic taurine-binding protein precursor
PA3943		2.63	0.003	conserved hypothetical protein
PA3944		2.03	0.0006	conserved hypothetical protein
PA3945		5.72	0.0003	conserved hypothetical protein
PA3962		2.03	0.0082	hypothetical protein
PA3980		-2.77	3.88E-05	conserved hypothetical protein
PA3986		5.69	0.0005	hypothetical protein
PA3989	*holA*	-2.03	0.0003	DNA polymerase III, delta subunit
PA4006	*nadD*	-3.10	0.0043	nicotinic acid mononucleotide adenylyltransferase
PA4021		-2.08	0.0098	probable transcriptional regulator
PA4026		2.33	0.0003	probable acetyltransferase
PA4027		2.07	0.0007	hypothetical protein
PA4029		-3.25	0.001	conserved hypothetical protein
PA4042	*xseB*	-2.82	0.0439	exodeoxyribonuclease VII small subunit
PA4051	*thiL*	-2.47	1.34E-05	thiamine monophosphate kinase
PA4052	*nusB*	-2.19	0.0001	NusB protein
PA4053	*ribE*	-2.12	0.0002	6,7-dimethyl-8-ribityllumazine synthase
PA4055	*ribC*	-2.27	0.003	riboflavin synthase alpha chain
PA4104		2.08	0.005	conserved hypothetical protein
PA4108		2.08	0.0039	hypothetical protein
PA4112		2.67	0.0015	probable sensor/response regulator hybrid

PA4139		3.83	0.0414	hypothetical protein
PA4140		2.00	0.0422	hypothetical protein
PA4141		2.35	0.0044	hypothetical protein
PA4142		2.06	0.0401	probable secretion protein
PA4164		-2.17	0.0101	hypothetical protein
PA4190	*pqsL*	2.60	3.82E-05	probable FAD-dependent monooxygenase
PA4191		-2.06	0.0059	probable iron/ascorbate oxidoreductase
PA4209	*phzM*	7.15	0.0235	probable phenazine-specific methyltransferase
PA4210	*phzA1*	2.46	0.0069	probable phenazine biosynthesis protein
PA4211	*phzB1*	55.07	0.0016	probable phenazine biosynthesis protein
PA4217	*phzS*	29.57	0.0012	flavin-containing monooxygenase
PA4237	*rplQ*	-5.44	0.0005	50S ribosomal protein L17
PA4238	*rpoA*	-9.60	1.28E-05	DNA-directed RNA polymerase alpha chain
PA4239	*rpsD*	-9.74	1.04E-05	30S ribosomal protein S4
PA4240	*rpsK*	-4.41	0.0003	30S ribosomal protein S11
PA4241	*rpsM*	-13.04	7.78E-07	30S ribosomal protein S13
PA4242	*rpmJ*	-2.35	0.0004	50S ribosomal protein L36
PA4243	*secY*	-11.17	1.02E-05	secretion protein SecY
PA4244	*rplO*	-4.22	9.56E-05	50S ribosomal protein L15
PA4245	*rpmD*	-4.12	1.44E-05	50S ribosomal protein L30
PA4246	*rpsE*	-4.74	8.38E-05	30S ribosomal protein S5
PA4247	*rplR*	-12.49	1.36E-05	50S ribosomal protein L18
PA4248	*rplF*	-7.77	9.55E-05	50S ribosomal protein L6
PA4249	*rpsH*	-5.66	3.04E-05	30S ribosomal protein S8
PA4250	*rpsN*	-17.29	7.98E-06	30S ribosomal protein S14
PA4251	*rplE*	-9.91	0.0093	50S ribosomal protein L5
PA4252	*rplX*	-10.99	5.03E-07	50S ribosomal protein L24
PA4253	*rplN*	-14.28	1.65E-08	50S ribosomal protein L14
PA4254	*rpsQ*	-11.34	2.35E-07	30S ribosomal protein S17
PA4255	*rpmC*	-7.26	2.06E-07	50S ribosomal protein L29
PA4256	*rplP*	-21.72	4.22E-08	50S ribosomal protein L16
PA4257	*rpsC*	-16.99	1.69E-05	30S ribosomal protein S3
PA4258	*rplV*	-12.59	1.31E-05	50S ribosomal protein L22
PA4259	*rpsS*	-8.06	7.18E-05	30S ribosomal protein S19
PA4260	*rplB*	-14.39	1.32E-05	50S ribosomal protein L2
PA4261	*rplW*	-15.06	0.0048	50S ribosomal protein L23
PA4262	*rplD*	-11.66	1.85E-05	50S ribosomal protein L4
PA4263	*rplC*	-8.92	6.39E-07	50S ribosomal protein L3
PA4264	*rpsJ*	-9.32	8.10E-07	30S ribosomal protein S10
PA4269	*rpoC*	-7.91	8.10E-05	DNA-directed RNA polymerase beta* chain
PA4270	*rpoB*	-4.29	7.76E-05	DNA-directed RNA polymerase beta chain
PA4271	*rplL*	-7.53	2.08E-07	50S ribosomal protein L7 / L12
PA4272	*rplJ*	-15.08	7.90E-06	50S ribosomal protein L10
PA4273	*rplA*	-12.12	2.40E-06	50S ribosomal protein L1
PA4274	*rplK*	-9.49	9.35E-05	50S ribosomal protein L11
PA4275	*nusG*	-3.30	7.22E-05	transcription antitermination protein NusG

PA4276	*secE*	-3.89	9.15E-06	secretion protein SecE
PA4289		2.06	0.0018	probable transporter
PA4290		3.00	0.0094	probable chemotaxis transducer
PA4292		-3.61	9.72E-05	probable phosphate transporter
PA4296		3.30	0.003	probable two-component response regulator
PA4298		3.32	0.0002	hypothetical protein
PA4299		4.07	1.42E-05	hypothetical protein
PA4300		2.96	0.0002	hypothetical protein
PA4302		2.66	0.0002	probable type II secretion system protein
PA4303		2.19	0.0013	hypothetical protein
PA4305		2.57	0.003	hypothetical protein
PA4306		3.27	0.0318	hypothetical protein
PA4311		2.96	9.43E-05	conserved hypothetical protein
PA4312		4.31	0.0003	conserved hypothetical protein
PA4314	*purU1*	-2.53	0.0003	formyltetrahydrofolate deformylase
PA4350	*olsB*	28.97	2.20E-07	conserved hypothetical protein
PA4351	*olsA*	18.72	2.24E-08	probable acyltransferase
PA4357		-2.09	0.0032	conserved hypothetical protein
PA4358		-2.46	0.0005	probable ferrous iron transport protein
PA4359		-2.17	0.0147	conserved hypothetical protein
PA4370	*icmP*	-4.21	0.0005	Insulin-cleaving metalloproteinase outer membrane protein precursor
PA4373		-2.16	0.0016	hypothetical protein
PA4377		2.62	0.0005	hypothetical protein
PA4378	*inaA*	2.35	0.0004	InaA protein
PA4428	*sspA*	-2.01	0.0016	stringent starvation protein A
PA4429		-3.76	0.0001	probable cytochrome c1 precursor
PA4431		-3.42	0.0001	probable iron-sulfur protein
PA4432	*rpsI*	-5.96	1.86E-05	30S ribosomal protein S9
PA4433	*rplM*	-4.99	4.35E-05	50S ribosomal protein L13
PA4442	*cysN*	-3.89	0.0002	ATP sulfurylase GTP-binding subunit/APS kinase
PA4443	*cysD*	-4.87	7.28E-05	ATP sulfurylase small subunit
PA4448	*hisD*	-2.12	0.0054	histidinol dehydrogenase
PA4449	*hisG*	-2.31	0.0173	ATP-phosphoribosyltransferase
PA4472	*pmbA*	2.04	0.0319	PmbA protein
PA4480	*mreC*	-2.64	0.001	rod shape-determining protein MreC
PA4481	*mreB*	-3.71	3.61E-05	rod shape-determining protein MreB
PA4482	*gatC*	-2.82	7.05E-05	Glu-tRNA(Gln) amidotransferase subunit C
PA4483	*gatA*	-3.97	0.0019	Glu-tRNA(Gln) amidotransferase subunit A
PA4488		3.11	0.0139	conserved hypothetical protein
PA4495		2.36	0.0014	hypothetical protein
PA4498		-2.01	0.042	probable metallopeptidase
PA4500		-4.58	0.001	probable binding protein component of ABC transporter
PA4517		-2.09	0.0004	conserved hypothetical protein

PA4531		-2.14	0.0412	hypothetical protein
PA4551	*pilV*	2.41	0.009	type 4 fimbrial biogenesis protein PilV
PA4555	*pilY2*	2.03	0.0126	type 4 fimbrial biogenesis protein PilY2
PA4563	*rpsT*	-5.94	8.90E-06	30S ribosomal protein S20
PA4567	*rpmA*	-4.56	1.96E-05	50S ribosomal protein L27
PA4568	*rplU*	-9.15	4.74E-06	50S ribosomal protein L21
PA4572	*fklB*	-2.40	0.0001	peptidyl-prolyl cis-trans isomerase FklB
PA4577		2.13	0.0018	hypothetical protein
PA4578		-2.38	0.0002	hypothetical protein
PA4588	*gdhA*	-2.95	0.0004	glutamate dehydrogenase
PA4602	*glyA3*	-2.76	0.0009	serine hydroxymethyltransferase
PA4607		9.30	6.04E-05	hypothetical protein
PA4608		2.82	1.43E-05	hypothetical protein
PA4614	*mscL*	4.14	0.0001	conductance mechanosensitive channel
PA4669	*ipk*	-3.05	0.0001	isopentenyl monophosphate kinase
PA4670	*prs*	-4.30	6.81E-06	ribose-phosphate pyrophosphokinase
PA4671		-11.84	1.48E-06	probable ribosomal protein L25
PA4672		-2.86	0.001	peptidyl-tRNA hydrolase
PA4675		-4.26	4.81E-05	probable TonB-dependent receptor
PA4684		-2.22	0.0001	hypothetical protein
PA4688	*hitB*	-2.10	0.0004	iron (III)-transport system permease HitB
PA4694	*ilvC*	-2.14	0.0009	ketol-acid reductoisomerase
PA4696	*ilvI*	-3.44	0.0013	acetolactate synthase large subunit
PA4702		2.21	0.0002	hypothetical protein
PA4703		3.69	0.0044	hypothetical protein
PA4717		2.89	2.90E-05	conserved hypothetical protein
PA4723	*dksA*	-3.45	2.53E-05	suppressor protein DksA
PA4731	*panD*	-2.06	0.0001	aspartate 1-decarboxylase precursor
PA4738		2.19	0.0014	conserved hypothetical protein
PA4739		2.59	0.007	conserved hypothetical protein
PA4740	*pnp*	-7.56	1.26E-06	polyribonucleotide nucleotidyltransferase
PA4741	*rpsO*	-6.22	1.53E-05	30S ribosomal protein S15
PA4742	*truB*	-3.38	4.46E-05	tRNA pseudouridine 55 synthase
PA4743	*rbfA*	-3.51	3.82E-05	ribosome-binding factor A
PA4744	*infB*	-2.99	0.0007	translation initiation factor IF-2
PA4745	*nusA*	-3.50	0.0001	N utilization substance protein A
PA4746		-2.42	0.0002	conserved hypothetical protein
PA4747	*secG*	-3.29	7.90E-05	secretion protein SecG
PA4748	*tpiA*	-3.39	6.78E-05	triosephosphate isomerase
PA4754		-2.26	0.0004	hypothetical protein
PA4755	*greA*	-2.46	5.70E-05	transcription elongation factor GreA
PA4756	*carB*	-2.08	0.0006	carbamoylphosphate synthetase large subunit
PA4768	*smpB*	-2.24	0.0006	SmpB protein
PA4781		3.69	0.0016	probable two-component response regulator
PA4785		2.01	0.0005	probable acyl-CoA thiolase
PA4839	*speA*	3.12	3.14E-05	biosynthetic arginine decarboxylase

PA4844		7.05	0.0001	probable chemotaxis transducer
PA4846	*aroQ1*	-2.48	0.0007	3-dehydroquinate dehydratase
PA4850	*prmA*	-2.06	0.0001	ribosomal protein L11 methyltransferase
PA4852		-3.15	0.0001	conserved hypothetical protein
PA4853	*fis*	-3.83	9.85E-05	DNA-binding protein Fis
PA4854	*purH*	-2.56	1.98E-05	phosphoribosylaminoimidazolecarboxamide formyltransferase
PA4855	*purD*	-4.36	1.88E-06	phosphoribosylamine--glycine ligase
PA4870		2.72	0.0009	conserved hypothetical protein
PA4874		2.48	0.0003	conserved hypothetical protein
PA4875		3.15	1.23E-05	hypothetical protein
PA4876	*osmE*	5.78	8.40E-06	osmotically inducible lipoprotein OsmE
PA4880		3.45	5.47E-05	probable bacterioferritin
PA4882		2.62	0.0044	hypothetical protein
PA4884		9.51	0.0009	hypothetical protein
PA4888		-3.13	9.79E-05	conserved hypothetical protein
PA4889		-2.66	0.0003	probable oxidoreductase
PA4915		2.06	0.0016	probable chemotaxis transducer
PA4918		-2.51	9.70E-05	hypothetical protein
PA4919	*pncB1*	-3.12	0.0008	nicotinate phosphoribosyltransferase
PA4925		2.02	0.0005	conserved hypothetical protein
PA4932	*rplI*	-8.62	1.44E-05	50S ribosomal protein L9
PA4933		-10.99	1.38E-05	hypothetical protein
PA4934	*rpsR*	-9.97	1.70E-06	30S ribosomal protein S18
PA4935	*rpsF*	-16.89	7.60E-06	30S ribosomal protein S6
PA4957	*psd*	-2.49	0.005	phosphatidylserine decarboxylase
PA5020		-2.06	0.0177	probable acyl-CoA dehydrogenase
PA5030		2.40	0.0464	probable major facilitator superfamily (MFS) transporter
PA5034	*hemE*	-2.11	0.0002	uroporphyrinogen decarboxylase
PA5035	*gltD*	-5.15	2.48E-05	glutamate synthase small chain
PA5036	*gltB*	-2.29	0.0008	glutamate synthase large chain precursor
PA5046		-6.99	1.73E-06	malic enzyme
PA5049	*rpmE*	-5.39	1.92E-06	50S ribosomal protein L31
PA5056	*phaC1*	3.12	0.0001	poly(3-hydroxyalkanoic acid) synthase 1
PA5057	*phaD*	3.77	5.75E-05	poly(3-hydroxyalkanoic acid) depolymerase
PA5058	*phaC2*	4.79	1.15E-05	poly(3-hydroxyalkanoic acid) synthase 2
PA5059		2.50	0.0003	probable transcriptional regulator
PA5061		4.27	7.45E-05	conserved hypothetical protein
PA5073		2.15	0.0017	hypothetical protein
PA5074		-2.01	0.0003	probable ATP-binding component of ABC transporter
PA5092	*hutI*	2.26	0.0003	imidazolone-5-propionate hydrolase HutI
PA5112	*estA*	-2.53	0.0046	esterase EstA
PA5118	*thiI*	-3.58	5.61E-06	thiazole biosynthesis protein ThiI
PA5125	*ntrC*	-2.33	0.0011	two-component response regulator NtrC

PA5137		-3.35	0.0002	hypothetical protein
PA5138		-2.69	0.0004	hypothetical protein
PA5142	*hisH1*	-2.38	0.0008	glutamine amidotransferase
PA5143	*hisB*	-2.40	8.49E-05	imidazoleglycerol-phosphate dehydratase
PA5152		-2.24	6.61E-05	probable ATP-binding component of ABC transporter
PA5153		-3.36	0.0022	probable periplasmic binding protein
PA5154		-2.76	0.0174	probable permease of ABC transporter
PA5155		-2.42	0.0009	probable permease of ABC transporter
PA5167		-3.48	0.0022	probable c4-dicarboxylate-binding protein
PA5168		-4.17	0.0016	probable dicarboxylate transporter
PA5169		-8.52	0.0014	probable C4-dicarboxylate transporter
PA5174		-3.27	4.49E-05	probable beta-ketoacyl synthase
PA5178		12.66	4.43E-08	conserved hypothetical protein
PA5182		2.22	0.0002	hypothetical protein
PA5201		-2.87	1.94E-05	conserved hypothetical protein
PA5202		-2.06	0.0011	hypothetical protein
PA5212		3.98	3.87E-06	hypothetical protein
PA5213	*gcvP1*	2.30	0.0072	glycine cleavage system protein P1
PA5244		-2.26	0.0049	conserved hypothetical protein
PA5252		-2.05	0.0004	probable ATP-binding component of ABC transporter
PA5261	*algR*	2.37	7.92E-05	alginate biosynthesis regulatory protein AlgR
PA5271		3.08	3.42E-05	hypothetical protein
PA5285		2.53	0.0012	hypothetical protein
PA5296	*rep*	-2.10	0.0001	ATP-dependent DNA helicase Rep
PA5297	*poxB*	6.39	2.78E-05	pyruvate dehydrogenase (cytochrome)
PA5305		3.23	8.55E-05	conserved hypothetical protein
PA5306		4.26	1.96E-06	conserved hypothetical protein
PA5315	*rpmG*	-2.72	0.0004	50S ribosomal protein L33
PA5316	*rpmB*	-3.40	0.0002	50S ribosomal protein L28
PA5335		-2.14	0.0007	conserved hypothetical protein
PA5340		-2.17	0.0196	hypothetical protein
PA5351	*rubA1*	-3.16	7.10E-05	Rubredoxin 1
PA5357		-2.05	0.0038	hypothetical protein
PA5360	*phoB*	16.05	5.40E-07	two-component response regulator PhoB
PA5361	*phoR*	9.27	5.35E-05	two-component sensor PhoR
PA5365	*phoU*	18.66	9.50E-09	phosphate uptake regulatory protein PhoU
PA5366	*pstB*	19.02	2.21E-08	ATP-binding component of ABC phosphate transporter
PA5367	*pstA*	25.70	7.40E-09	membrane protein component of ABC phosphate transporter
PA5368	*pstC*	27.67	3.90E-09	membrane protein component of ABC phosphate transporter
PA5369		223.30	2.60E-09	hypothetical protein
PA5380		-4.58	0.0037	probable transcriptional regulator

PA5419	*soxG*	2.06	0.0374	sarcosine oxidase gamma subunit
PA5424		3.30	0.0001	conserved hypothetical protein
PA5425	*purK*	-2.39	3.87E-05	phosphoribosylaminoimidazole carboxylase
PA5426	*purE*	-2.56	2.19E-05	phosphoribosylaminoimidazole carboxylase, catalytic subunit
PA5429	*aspA*	-2.08	0.0009	aspartate ammonia-lyase
PA5439		2.03	0.0005	probable glucose-6-phosphate dehydrogenase
PA5440		-2.97	5.29E-06	probable peptidase
PA5446		2.25	0.0103	hypothetical protein
PA5460		2.33	0.0003	hypothetical protein
PA5470		-2.38	0.0004	probable peptide chain release factor
PA5474		2.09	0.0043	probable metalloprotease
PA5475		2.67	4.79E-05	hypothetical protein
PA5479	*gltP*	-2.41	0.0002	proton-glutamate symporter
PA5497		-2.03	0.001	hypothetical protein
PA5504		-2.85	0.0004	probable permease of ABC transporter
PA5521		4.68	0.0001	probable short-chain dehydrogenase
PA5522		2.88	0.0001	probable glutamine synthetase
PA5523		2.91	0.0056	probable aminotransferase
PA5527		2.04	0.0001	hypothetical protein
PA5530		-5.72	1.49E-05	probable MFS dicarboxylate transporter
PA5546		5.74	2.52E-06	conserved hypothetical protein
PA5553	*atpC*	-2.78	0.0006	ATP synthase epsilon chain
PA5554	*atpD*	-10.62	7.81E-06	ATP synthase beta chain
PA5555	*atpG*	-8.91	0.0002	ATP synthase gamma chain
PA5556	*atpA*	-2.50	0.0037	ATP synthase alpha chain
PA5557	*atpH*	-4.17	0.0002	ATP synthase delta chain
PA5558	*atpF*	-6.83	1.85E-05	ATP synthase B chain
PA5559	*atpE*	-4.35	0.0029	atp synthase C chain
PA5560	*atpB*	-2.95	2.83E-05	ATP synthase A chain
PA5561	*atpI*	-2.11	0.0001	ATP synthase protein I
PA5568		-2.28	0.0028	conserved hypothetical protein
PA5569	*rnpA*	-5.87	9.53E-05	ribonuclease P protein component
PA5570	*rpmH*	-4.55	0.0003	50S ribosomal protein L34