

Supplemental Material

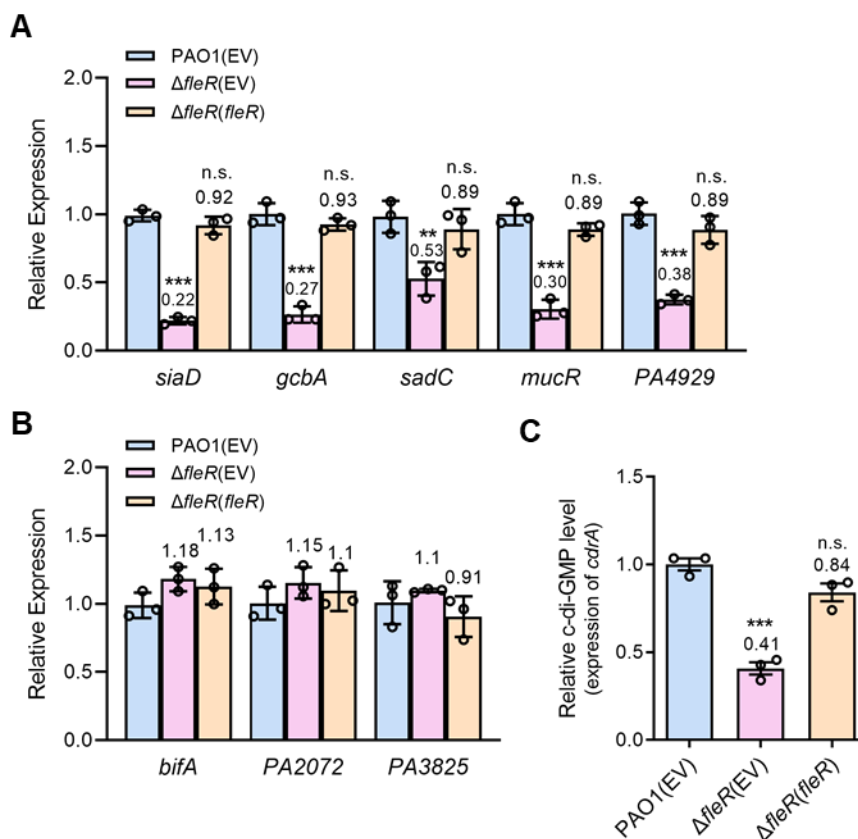


Figure S1. Intracellular c-di-GMP synthesis is inhibited in the absence of FleR.

(A) Relative expression of DGC genes measured by RT-qPCR in PAO1, $\Delta fleR$ and $\Delta fleR(fleR)$ strains. (B) Relative expression of PDE genes measured by RT-qPCR in PAO1, $\Delta fleR$ and $\Delta fleR(fleR)$ strains. (C) Relative intracellular c-di-GMP levels in PAO1, $\Delta fleR$ and $\Delta fleR(fleR)$ strains were determined by measuring the relative expression of *cdrA*. Data are represented as the mean \pm SD (n = 3). *** $p < 0.001$ versus PAO1(EV) based on paired Student's *t* test. n.s.: not significant. EV: Empty vector for the control.

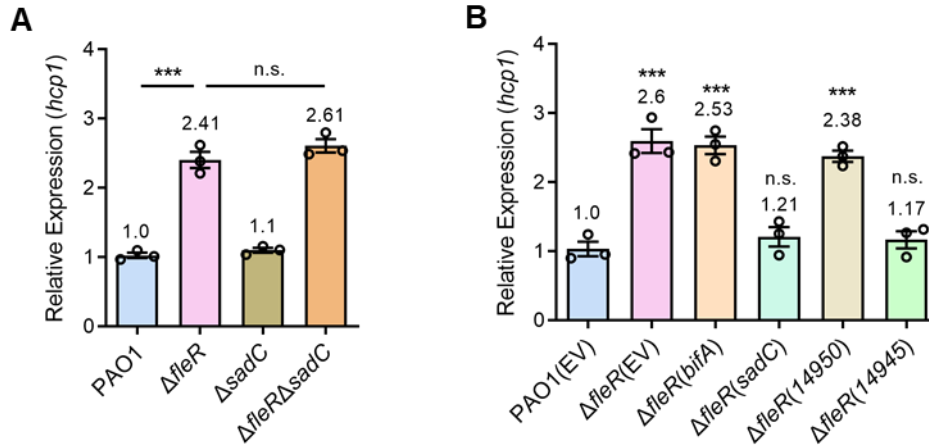


Figure S2. FleR regulates the expression of *hcp1* in a c-di-GMP-dependent manner. (A) Relative expression of *tse1* measured by RT-qPCR in the PAO1, $\Delta fleR$, $\Delta sadC$ and $\Delta fleR \Delta sadC$ strains. (B) Relative expression of *tse1* measured by RT-qPCR in the strains of PAO1, $\Delta fleR$, and $\Delta fleR$ with ectopic expression of DGCs and PDEs. Data are represented as the mean \pm SD (n = 3). *** $p < 0.001$ versus the indicated group based on paired Student's *t* test (A) or versus PAO1(EV) based on one-way ANOVA (B). n.s.: not significant. EV: Empty vector for the control.

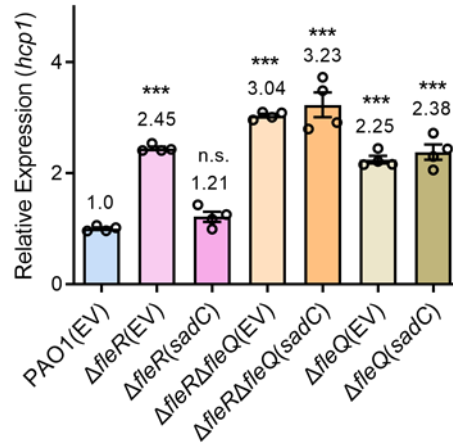


Figure S3. Relative expression of *hcp1* measured by RT-qPCR in the indicated PAO1 strains. Data are represented as the mean \pm SD (n = 3). *** p<0.001 versus PAO1(EV) based on one-way ANOVA. n.s.: not significant. EV: Empty vector for the control.

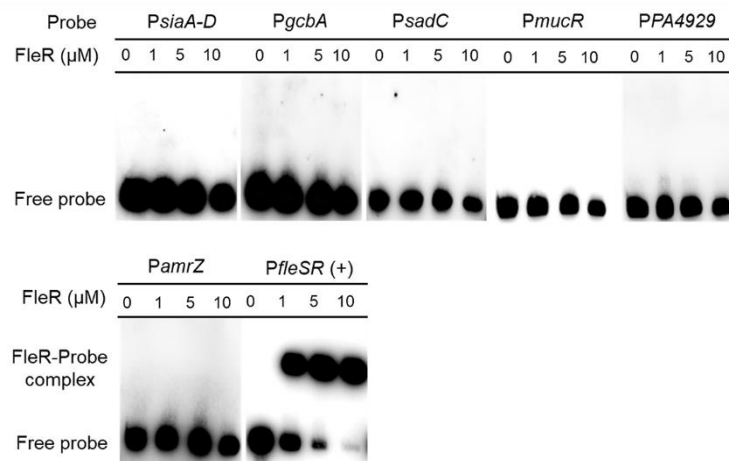


Figure S4. EMSA examination of the binding of FleR to the promoters of DGC genes and *amrZ*. Binding of FleR to its own promoter (*PfleSR*) serves as the positive control.

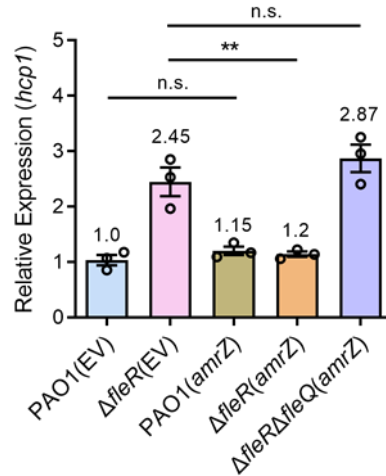


Figure S5. Relative expression of *hcp1* measured by RT-qPCR in the strains of PAO1 and $\Delta fleR$ with ectopic expression of *amrZ*. Data are represented as the mean \pm SD (n = 3). ** p<0.01 versus PAO1(EV) or $\Delta fleR$ (EV) based on paired Student's *t* test. n.s.: not significant. EV: Empty vector for the control.

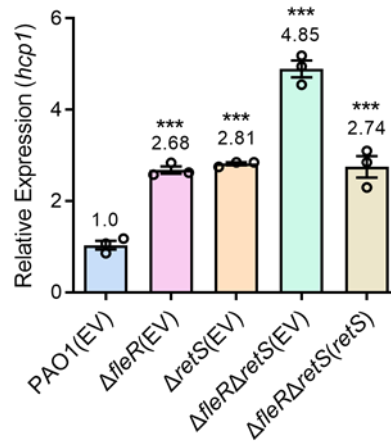


Figure S6. Relative expression of *hcp1* measured by RT-qPCR in the PAO1, $\Delta fleR$, $\Delta retS$ and $\Delta fleR \Delta retS$ strains. Data are represented as the mean \pm SD (n = 3). *** p<0.001 versus PAO1(EV) based on one-way ANOVA. EV: Empty vector for the control.

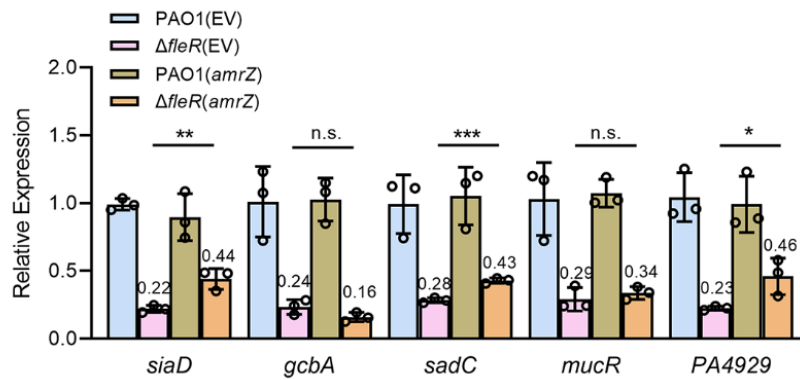


Figure S7. Relative expression of DGC genes in PAO1, $\Delta fleR$ strains with or without ectopic expression of *amrZ*. Data are represented as the mean \pm SD (n = 3).

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ versus $\Delta fleR(EV)$ based on paired Student's *t* test.

n.s.: not significant. EV: Empty vector for the control.

Table S1. Full list of differentially expressed genes (Log_2 fold change ≥ 1.2) in the *fleR* mutant compared to the wild-type strain. Significantly differentially expressed genes are determined by Cufflinks after Benjamini-Hochberg correction. The fold change is the ratio of the mutant FPKM to the wild-type FPKM.

Locus tag	Gene name	Fold chang	Gene function	Number of pathway // Name of pathway
PA0045	<i>PA0045</i>	-1.990	curli production assembly protein CsgG	-
PA0046	<i>PA0046</i>	-2.690	DUF4810 domain-containing protein	-
PA0047	<i>PA0047</i>	-1.234	lipoprotein	-
PA0075	<i>pppA</i>	1.541	serine/threonine phosphatase	ko03070//Bacterial secretion system
PA0083	<i>PA0083</i>	1.227	type VI secretion system-associated protein	-
PA0084	<i>PA0084</i>	1.305	EvpB/family type VI secretion protein	-
PA0085	<i>hcp1</i>	1.285	protein secretion apparatus assembly protein	ko03070//Bacterial secretion system
PA0087	<i>PA0087</i>	1.224	type VI secretion system lysozyme	-
PA0089	<i>PA0089</i>	1.350	type VI secretion protein	
PA0090	<i>clpVI</i>	1.822	secretion protein ClpV1	ko03070//Bacterial secretion system
PA0091	<i>vgrG1</i>	1.612	type VI secretion system protein VgrG	ko03070//Bacterial secretion system
PA0103	<i>PA0103</i>	2.038	sulfate transporter	-
PA0117	<i>PA0117</i>	-1.846	short-chain dehydrogenase	-
PA0119	<i>PA0119</i>	-1.876	C4-dicarboxylate transporter 1	ko02020//Two-component system
PA0122	<i>PA0122</i>	-1.296	hemolysin	-
PA0123	<i>PA0123</i>	-1.377	transcriptional regulator	-
PA0126	<i>PA0126</i>	-1.203	Uncharacterised protein	-
PA0128	<i>PA0128</i>	1.725	alkylphosphonate utilization protein	-
PA0137	<i>PA0137</i>	1.395	ABC transporter permease	-
PA0162	<i>opdC</i>	-1.464	histidine porin OpdC	-

PA0169	<i>PA0169</i>	-2.938	GGDEF domain-containing protein	-
PA0170	<i>PA0170</i>	-2.323	Fe-S oxidoreductase	-
PA0171	<i>PA0171</i>	-3.016	Uncharacterized protein PAE221_01065	-
PA0172	<i>PA0172</i>	-1.313	histidine kinase	-
PA0179	<i>PA0179</i>	-1.227	two-component response regulator	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA0195	<i>pntAA</i>	1.290	NAD(P) transhydrogenase subunit alpha	ko00760//Nicotinate and nicotinamide metabolism
PA0199	<i>exbD1</i>	-1.205	biopolymer transport protein ExbD	-
PA0200	<i>PA0200</i>	-1.284	DUF3079 domain-containing protein	-
PA0215	<i>PA0215</i>	1.533	malonate transporter MadL	-
PA0217	<i>PA0217</i>	1.247	transcriptional regulator	-
PA0222	<i>PA0222</i>	-1.435	ABC transporter, periplasmic spermidine putrescine-binding protein PotD	-
PA0238	<i>PA0238</i>	2.137	xylose isomerase	-
PA0251	<i>PA0251</i>	1.858	suppressor of fused family protein	-
PA0252	<i>PA0252</i>	-1.998	Uncharacterized protein PAE221_00084	-
PA0263	<i>hcpC</i>	-1.311	major exported protein, partial	ko03070//Bacterial secretion system
PA0280	<i>cysA</i>	-2.114	sulfate.thiosulfate ABC transporter ATP-binding protein CysA	ko02010//ABC transporters;ko00920//Sulfur metabolism
PA0281	<i>cysW</i>	-1.678	sulfate transporter CysW	ko02010//ABC transporters;ko00920//Sulfur metabolism
PA0282	<i>cysT</i>	-2.519	sulfate transporter CysT	ko02010//ABC transporters;ko00920//Sulfur metabolism
PA0320	<i>PA0320</i>	-1.614	TIGR00156 family protein	-
PA0323	<i>PA0323</i>	-1.629	Putrescine-binding periplasmic protein precursor	ko02010//ABC transporters

PA0451	<i>PA0451</i>	1.312	peptidase	-
PA0471	<i>PA0471</i>	-1.628	transmembrane sensor	-
PA0472	<i>PA0472</i>	-1.899	RNA polymerase sigma factor	-
PA0493	<i>PA0493</i>	13.316	probable biotin-requiring enzyme	-
PA0513	<i>PA0513</i>	-1.387	heme d1 biosynthesis protein NirG	-
PA0517	<i>nirC</i>	-1.356	cytochrome c55X	-
PA0519	<i>nirS</i>	-1.273	nitrite reductase	ko00910//Nitrogen metabolism
PA0524	<i>norB</i>	-1.310	nitric oxide reductase subunit B	ko00910//Nitrogen metabolism
PA0534	<i>PA0534</i>	-1.867	Oxidoreductase	-
PA0579	<i>rpsU</i>	1.431	30S ribosomal protein S21	ko03010//Ribosome
PA0672	<i>hemO</i>	-1.450	heme oxygenase	-
PA0674	<i>vreA</i>	-4.254	VreA	-
PA0680	<i>PA0680</i>	3.410	HxcV pseudopilin	ko03070//Bacterial secretion system
PA0734	<i>PA0734</i>	1.949	cysteine-rich CWC family protein	-
PA0744	<i>PA0744</i>	-1.964	enoyl-CoA hydratase	-
PA0745	<i>PA0745</i>	-1.656	enoyl-CoA hydratase	-
PA0746	<i>PA0746</i>	-1.396	acyl-CoA dehydrogenase	ko00281//Geraniol degradation
PA0753	<i>PA0753</i>	-2.888	tripartite tricarboxylate transporter TctB family protein	ko02020//Two-component system
PA0754	<i>PA0754</i>	-1.291	C4-dicarboxylate ABC transporter substrate-binding protein	ko02020//Two-component system
PA0755	<i>opdH</i>	-1.437	cis-aconitate porin OpdH	-
PA0756	<i>PA0756</i>	1.810	two-component response regulator	ko02020//Two-component system
PA0793	<i>PA0793</i>	-1.726	3-methylitaconate isomerase	-
PA0794	<i>PA0794</i>	-2.059	aconitate hydratase	ko01230//Biosynthesis of amino acids;ko01200//Carbon

				metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko00020//Citrate cycle (TCA cycle);ko01210//2-Oxocarboxylic acid metabolism
PA0795	<i>prpC</i>	-2.380	methylcitrate synthase	ko00640//Propanoate metabolism
PA0796	<i>prpB</i>	-1.562	2-methylisocitrate lyase	ko00640//Propanoate metabolism
PA0837	<i>slyD</i>	1.240	peptidyl-prolyl cis-trans isomerase SlyD	-
PA0855	<i>PA0855</i>	-1.275	Protein of uncharacterised function (DUF2804)	-
				ko00350//Tyrosine metabolism;ko00360//Phenylalanine metabolism;ko00130//Ubiquinone and other terpenoid-quinone biosynthesis
PA0865	<i>hpd</i>	-1.350	4-hydroxyphenylpyruvate dioxygenase	-
PA0866	<i>aroP2</i>	-2.383	aromatic amino acid transporter AroP	ko01200//Carbon metabolism;ko00620//Pyruvate metabolism;ko00640//Propanoate metabolism;ko00010//Glycolysis / Gluconeogenesis;ko00680//Methane metabolism
PA0887	<i>acsA</i>	-3.339	acetyl-CoA synthetase	
PA0909	<i>PA0909</i>	2.979	putative membrane protein	-
PA0939	<i>PA0939</i>	-1.714	Rho-specific inhibitor of transcription termination YaeO	-
PA0960	<i>PA0960</i>	1.278	<i>slyX</i> protein	-
PA1058	<i>PA1058</i>	12.878	monovalent cation/H ⁺ antiporter subunit F	-
PA1070	<i>braG</i>	-1.288	branched-chain amino acid ABC transporter ATP-binding protein BraG	ko02010//ABC transporters
PA1071	<i>braF</i>	-1.259	branched-chain amino acid ABC transporter ATP-binding protein BraF	ko02010//ABC transporters

PA1077	<i>flgB</i>	-4.925	flagellar basal-body rod protein FlgB	ko02040//Flagellar assembly
PA1078	<i>flgC</i>	-4.174	flagellar basal body rod protein FlgC	ko02040//Flagellar assembly
PA1079	<i>flgD</i>	-4.029	flagellar basal body rod modification protein	ko02040//Flagellar assembly
PA1080	<i>flgE</i>	-4.774	flagellar hook protein FlgE	ko02040//Flagellar assembly
PA1081	<i>flgF</i>	-4.232	flagellar basal body rod protein FlgF	ko02040//Flagellar assembly
PA1092	<i>fliC</i>	-1.763	flagellin type B	ko02020//Two-component system;ko02040//Flagellar assembly
PA1099	<i>fleR</i>	-5.866	two-component response regulator	ko02020//Two-component system
PA1132	<i>PA1132</i>	-1.441	hypothetical protein	-
PA1137	<i>PA1137</i>	-1.860	oxidoreductase	-
PA1168	<i>PA1168</i>	-1.396	Uncharacterised protein	-
PA1196	<i>PA1196</i>	-2.201	transcriptional regulator	-
PA1197	<i>PA1197</i>	-1.565	NAD-dependent protein deacylase	-
PA1213	<i>PA1213</i>	-1.400	clavaminic acid synthetase	-
PA1240	<i>PA1240</i>	-1.955	enoyl-CoA hydratase	-
PA1254	<i>PA1254</i>	-1.709	dihydrodipicolinate synthetase	ko01230//Biosynthesis of amino acids;ko00300//Lysine biosynthesis;ko00261//Monobactam biosynthesis
PA1255	<i>PA1255</i>	-1.545	trans-3-hydroxy-L-proline dehydratase	-
PA1266	<i>PA1266</i>	-2.065	oxidoreductase	-
PA1267	<i>PA1267</i>	-1.839	FAD binding domain protein	-
PA1275	<i>cobD</i>	-1.843	cobalamin biosynthesis protein	ko00860//Porphyrin and chlorophyll metabolism
PA1276	<i>cobC</i>	-1.723	threonine-phosphate decarboxylase	ko00860//Porphyrin and chlorophyll metabolism
PA1277	<i>cobQ</i>	-1.716	cobyric acid synthase	ko00860//Porphyrin and chlorophyll metabolism
PA1279	<i>cobU</i>	-1.572	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	ko00860//Porphyrin and chlorophyll metabolism

PA1281	<i>cobV</i>	-3.316	adenosylcobinamide-GDP ribazoletransferase	ko00860//Porphyrin and chlorophyll metabolism
PA1282	<i>PA1282</i>	-1.803	MFS transporter	-
PA1286	<i>PA1286</i>	1.818	major facilitator superfamily transporter	-
PA1319	<i>cyoC</i>	-1.284	cytochrome o ubiquinol oxidase subunit III	ko00190//Oxidative phosphorylation
PA1343	<i>PA1343</i>	-1.235	sn-glycerol-3-phosphate transporter	-
PA1349	<i>PA1349</i>	1.297	dehydrogenase	-
PA1353	<i>PA1353</i>	1.736	VOC family protein	-
PA1380	<i>PA1380</i>	1.365	transcriptional regulator	-
PA1412	<i>PA1412</i>	1.651	major Facilitator Superfamily protein	-
				ko01230//Biosynthesis of amino acids;ko00650//Butanoate metabolism;ko01210//2-Oxocarboxylic acid metabolism;ko00770//Pantothenate and CoA biosynthesis;ko00290//Valine, leucine and isoleucine biosynthesis;ko00660//C5-Branched dibasic acid metabolism
PA1417	<i>PA1417</i>	-1.231	probable decarboxylase	
PA1420	<i>PA1420</i>	3.131	Undecaprenyl pyrophosphate synthase	-
PA1423	<i>bdlA</i>	-1.469	pili assembly chaperone	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA1428	<i>PA1428</i>	1.301	GNAT family N-acetyltransferase	-
PA1435	<i>PA1435</i>	-1.252	resistance-nodulation-cell division (RND) efflux membrane fusion protein	-
PA1441	<i>PA1441</i>	-2.471	flagellar hook-length control protein FliK	ko02040//Flagellar assembly
PA1442	<i>PA1442</i>	1.282	flagellar basal body protein FliL	-
PA1467	<i>PA1467</i>	-2.516	transcriptional regulator	-
PA1476	<i>ccmB</i>	1.304	heme exporter protein B	ko02010//ABC transporters

PA1487	<i>PA1487</i>	-1.280	carbohydrate kinase	ko00561//Glycerolipid metabolism ko01230//Biosynthesis of amino acids; ko01200//Carbon metabolism; ko00230//Purine metabolism; ko00620//Pyruvate metabolism; ko00010//Glycolysis / Gluconeogenesis
PA1498	<i>pykF</i>	1.853	pyruvate kinase	ko00630//Glyoxylate and dicarboxylate metabolism
PA1500	<i>PA1500</i>	-1.378	oxidoreductase	-
PA1545	<i>PA1545</i>	-1.612	Uncharacterised protein	-
PA1561	<i>aer</i>	-1.780	aerotaxis receptor Aer	ko02020//Two-component system; ko02030//Bacterial chemotaxis
PA1594	<i>PA1594</i>	1.231	thioesterase, partial	-
PA1596	<i>htpG</i>	-1.902	chaperone protein HtpG	-
PA1608	<i>PA1608</i>	-1.388	chemotaxis transducer	ko02020//Two-component system; ko02030//Bacterial chemotaxis
PA1635	<i>kdpC</i>	-2.520	potassium-transporting ATPase subunit C	ko02020//Two-component system ko00250//Alanine, aspartate and glutamate metabolism; ko00220//Arginine biosynthesis; ko00471//D-Glutamine and D-glutamate metabolism
PA1638	<i>PA1638</i>	1.235	glutaminase	-
PA1657	<i>PA1657</i>	-1.517	type VI secretion system-associated protein	-
PA1658	<i>PA1658</i>	-1.572	EvpB/family type VI secretion protein	-
PA1659	<i>PA1659</i>	-1.241	type VI secretion protein	-
PA1660	<i>PA1660</i>	-1.291	type VI secretion protein	-

PA1662	<i>PA1662</i>	-1.393	ClpA/B-type protease	ko03070//Bacterial secretion system
PA1663	<i>PA1663</i>	-1.560	transcriptional regulator	-
PA1665	<i>PA1665</i>	-1.299	signal peptide protein	-
PA1666	<i>PA1666</i>	-1.372	Type VI secretion lipoprotein/VasD	ko03070//Bacterial secretion system
PA1667	<i>PA1667</i>	-1.634	type VI secretion protein	-
PA1668	<i>PA1668</i>	-1.852	membrane protein	ko03070//Bacterial secretion system
PA1669	<i>PA1669</i>	-1.546	type VI secretion protein IcmF	ko03070//Bacterial secretion system
PA1671	<i>stkI</i>	-1.234	serine-threonine kinase Stk1	-
PA1679	<i>PA1679</i>	-2.013	Uncharacterized protein PAE221_02692	-
PA1698	<i>popN</i>	1.485	type III secretion outer membrane protein PopN	ko03070//Bacterial secretion system
PA1699	<i>PA1699</i>	1.227	Pcr1	-
PA1702	<i>PA1702</i>	3.059	chaperone protein yscY	-
PA1703	<i>pcrD</i>	1.205	type III secretory apparatus protein PcrD	ko03070//Bacterial secretion system
PA1705	<i>pcrG</i>	1.250	type III secretion regulator	-
PA1710	<i>exsC</i>	1.224	exoenzyme S synthesis protein ExsC	-
PA1715	<i>pscB</i>	1.291	type III export apparatus protein	-
PA1718	<i>pscE</i>	-1.382	type III export protein PscE	-
PA1727	<i>mucR</i>	-1.502	bifunctional diguanylate cyclase/phosphodiesterase	-
PA1747	<i>PA1747</i>	-1.327	putative secreted protein	-
PA1844	<i>PA1844</i>	2.029	Uncharacterized protein PAE221_01822	-
PA1845	<i>PA1845</i>	2.353	Uncharacterised protein	-
PA1852	<i>PA1852</i>	1.872	Uncharacterized protein PAE221_01813	-
PA1864	<i>PA1864</i>	-1.775	transcriptional regulator	-
PA1884	<i>PA1884</i>	1.270	transcriptional regulator	-
PA1888	<i>PA1888</i>	-1.264	Uncharacterised protein	-

PA1899	<i>phzA2</i>	1.337	phenazine biosynthesis protein	-
PA1902	<i>phzD2</i>	-1.698	phenazine biosynthesis protein PhzD	-
PA1903	<i>phzE2</i>	-1.324	phenazine biosynthesis protein PhzE	-
PA1904	<i>phzF2</i>	-1.369	2,3-dihydro-3-hydroxyanthranilate isomerase	-
PA1912	<i>femI</i>	-2.770	ECF sigma factor FemI	-
PA1913	<i>PA1913</i>	-5.281	Uncharacterized protein PAE221_00740	-
PA1920	<i>nrdD</i>	-1.281	anaerobic ribonucleoside triphosphate reductase	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism
PA1947	<i>rbsA</i>	-1.334	ribose transporter RbsA	ko02010//ABC transporters
PA1948	<i>rbsC</i>	-1.340	ABC transporter permease	ko02010//ABC transporters
PA1957	<i>PA1957</i>	1.270	N-acetylglucosamine-6-sulfatase	-
PA1967	<i>PA1967</i>	-2.970	Uncharacterised protein	-
PA1968	<i>PA1968</i>	1.207	Uncharacterised protein	-
PA1976	<i>ercS'</i>	-1.238	hybrid sensor histidine kinase/response regulator	-
PA1988	<i>pqqD</i>	-1.693	coenzyme PQQ synthesis protein D	-
PA1992	<i>ercS</i>	-1.635	sensor histidine kinase	-
PA2000	<i>dhcB</i>	-1.397	Succinyl-CoA:3-ketoacid coenzyme A transferase subunit B	ko00280//Valine, leucine and isoleucine degradation;ko00650//Butanoate metabolism;ko00072//Synthesis and degradation of ketone bodies
PA2001	<i>atoB</i>	-1.365	acetyl-CoA acetyltransferase	ko02020//Two-component system;ko01200//Carbon metabolism;ko00620//Pyruvate metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko01212//Fatty acid metabolism;ko00280//Valine, leucine and

PA2004	<i>PA2004</i>	-1.326	citrate transporter family protein	-
PA2013	<i>liuC</i>	-1.311	gamma-carboxygeranoyl-CoA hydratase	isoleucine degradation;ko00640//Propanoate metabolism;ko00650//Butanoate metabolism;ko00362//Benzoate degradation;ko00071//Fatty acid degradation;ko00380//Tryptophan metabolism;ko00310//Lysine degradation;ko00900//Terpenoid backbone biosynthesis;ko00072//Synthesis and degradation of ketone bodies
PA2027	<i>PA2027</i>	2.036	Uncharacterized protein PAE221_00397	-
PA2029	<i>PA2029</i>	1.285	winged helix-turn helix family protein	-
PA2036	<i>PA2036</i>	-1.579	methyltransferase domain protein	-
PA2040	<i>PA2040</i>	-1.249	glutamine synthetase	ko02020//Two-component system;ko01230//Biosynthesis of amino acids;ko00630//Glyoxylate and dicarboxylate metabolism;ko00910//Nitrogen metabolism;ko00250//Alanine, aspartate and glutamate metabolism;ko00220//Arginine biosynthesis
PA2048	<i>PA2048</i>	-12.152	antibiotic biosynthesis monooxygenase	-
PA2056	<i>PA2056</i>	-1.745	LysR family transcriptional regulator	-
PA2061	<i>PA2061</i>	1.617	ABC transporter ATP-binding protein	ko02010//ABC transporters
PA2096	<i>PA2096</i>	-1.316	transcriptional regulator	-

PA2099	<i>PA2099</i>	-2.643	short-chain dehydrogenase	-
PA2110	<i>PA2110</i>	-2.114	allophanate hydrolase subunit 2 family protein	-
PA2112	<i>PA2112</i>	-1.807	LamB/YcsF family protein	-
PA2113	<i>opdO</i>	-1.439	pyroglutamate porin	-
PA2134	<i>PA2134</i>	1.335	membrane protein	-
PA2136	<i>PA2136</i>	-1.688	Uncharacterized protein PAE221_01703	-
PA2137	<i>PA2137</i>	2.860	histidine kinase	-
PA2138	<i>PA2138</i>	3.330	multifunctional non-homologous end joining protein LigD	ko03450//Non-homologous end-joining
PA2147	<i>katE</i>	1.410	catalase HPII	ko01200//Carbon metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko00380//Tryptophan metabolism
PA2148	<i>PA2148</i>	1.813	methyltransferase	-
PA2154	<i>PA2154</i>	1.309	membrane protein	-
PA2160	<i>PA2160</i>	1.920	glycosyl hydrolase	ko00500//Starch and sucrose metabolism
PA2161	<i>PA2161</i>	2.983	Protein of uncharacterised function (DUF2934)	-
PA2162	<i>PA2162</i>	1.438	malto-oligosyltrehalose synthase	ko00500//Starch and sucrose metabolism
PA2164	<i>PA2164</i>	1.268	glycosyl hydrolase	ko00500//Starch and sucrose metabolism
PA2166	<i>PA2166</i>	2.361	Protein of uncharacterised function (DUF3509)	-
PA2173a	<i>PA2173a</i>	2.226	Uncharacterised protein	-
PA2174	<i>PA2174</i>	1.656	Uncharacterised protein	-
PA2203	<i>PA2203</i>	-2.285	amino acid permease	-
PA2204	<i>PA2204</i>	-2.799	ABC transporter	-
PA2213	<i>PA2213</i>	1.463	porin	-
PA2217	<i>PA2217</i>	-1.644	aldehyde dehydrogenase	ko01220//Degradation of aromatic

				compounds;ko00930//Caprolactam degradation
PA2225	<i>PA2225</i>	1.565	Uncharacterised protein	-
PA2259	<i>ptxS</i>	-1.244	transcriptional regulator PtxS	-
PA2274	<i>PA2274</i>	-1.440	antibiotic biosynthesis monooxygenase family protein	-
PA2279	<i>arsC</i>	-2.050	low molecular weight phosphatase	-
PA2287	<i>PA2287</i>	-1.249	Uncharacterised protein	-
PA2312a	<i>PA2312a</i>	2.133	Uncharacterised protein	-
PA2314	<i>PA2314</i>	-2.174	MFS transporter	-
				ko01200//Carbon
PA2323	<i>PA2323</i>	-1.301	glyceraldehyde-3-phosphate dehydrogenase	metabolism;ko00010//Glycolysis / Gluconeogenesis;ko00030//Pentose phosphate pathway
PA2334	<i>PA2334</i>	2.738	transcriptional regulator	-
PA2350	<i>PA2350</i>	1.458	methionine import ATP-binding protein MetN 1	ko02010//ABC transporters
PA2374	<i>PA2374</i>	1.304	MORN repeat variant family protein	-
PA2384	<i>PA2384</i>	-3.519	ferric uptake regulator, Fur family	-
PA2386	<i>pvdA</i>	-1.765	L-ornithine N5-oxygenase	-
PA2391	<i>opmQ</i>	-1.477	probable outer membrane protein precursor	-
PA2395	<i>pvdO</i>	-1.553	pyoverdine biosynthesis protein PvdO	-
PA2398	<i>fjpvA</i>	-1.342	ferripyoverdine receptor	-
PA2404	<i>PA2404</i>	-1.225	PA2404	-
PA2407	<i>PA2407</i>	-1.676	adhesion protein	ko02010//ABC transporters
PA2408	<i>PA2408</i>	-2.442	ABC transporter ATP-binding protein	ko02010//ABC transporters
PA2409	<i>PA2409</i>	-3.708	ABC transporter permease	ko02010//ABC transporters
PA2462	<i>PA2462</i>	-2.249	hemagglutinin	-

PA2463	<i>PA2463</i>	-3.458	hemolysin secretion/activation ShlB/FhaC/HecB family protein	-
PA2466	<i>foxA</i>	-1.274	ferrioxamine receptor FoxA	-
PA2470	<i>gtdA</i>	-1.488	gentsitate 1,2-dioxygenase	ko00350//Tyrosine metabolism ko00362//Benzoate degradation;ko01220//Degradation of aromatic compounds;ko00364//Fluorobenzoate degradation;ko00361//Chlorocyclohexane and chlorobenzene degradation;ko00623//Toluene degradation ko00362//Benzoate degradation;ko01220//Degradation of aromatic compounds;ko00364//Fluorobenzoate degradation;ko00622//Xylene degradation
PA2507	<i>catA</i>	-1.461	catechol 1,2-dioxygenase	
PA2518	<i>xytX</i>	1.822	toluate 1,2-dioxygenase subunit alpha	
PA2538	<i>PA2538</i>	1.354	Uncharacterised protein	-
PA2552	<i>PA2552</i>	-1.585	acyl-CoA dehydrogenase	ko00281//Geraniol degradation ko02020//Two-component system;ko01200//Carbon metabolism;ko00620//Pyruvate metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko01212//Fatty acid metabolism;ko00280//Valine, leucine and isoleucine degradation;ko00640//Propanoate metabolism;ko00650//Butanoate metabolism;ko00362//Benzoate degradation;ko00071//Fatty acid
PA2553	<i>PA2553</i>	-1.413	acyl-CoA thiolase	

				degradation;ko00380//Tryptophan metabolism;ko00310//Lysine degradation;ko00900//Terpenoid backbone biosynthesis;ko00072//Synthesis and degradation of ketone bodies
PA2557	<i>PA2557</i>	-1.407	AMP-binding protein	-
PA2567	<i>PA2567</i>	-1.534	sensor domain-containing phosphodiesterase	-
PA2607	<i>PA2607</i>	1.226	DsrH family protein	ko04122//Sulfur relay system
PA2652	<i>PA2652</i>	-2.108	methyl-accepting chemotaxis protein	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA2675	<i>PA2675</i>	1.909	type II secretion system protein	ko03070//Bacterial secretion system
PA2701	<i>PA2701</i>	1.302	major facilitator superfamily transporter	-
PA2714	<i>PA2714</i>	-1.419	molybdopterin oxidoreductase	-
PA2746a	<i>PA2746a</i>	1.600	predicted protein	-
PA2752	<i>PA2752</i>	2.230	Inner membrane protein YqaA	-
PA2754a	<i>PA2754a</i>	-2.690	filamentous hemagglutinin	-
PA2766	<i>PA2766</i>	1.394	transcriptional regulator	-
PA2773	<i>PA2773</i>	1.970	membrane protein	-
PA2788	<i>PA2788</i>	-2.143	chemotaxis transducer	-
PA2862	<i>lipA</i>	-1.686	lactonizing lipase	ko00561//Glycerolipid metabolism
PA2867	<i>PA2867</i>	-3.315	chemotaxis transducer	-
PA2879	<i>PA2879</i>	-1.544	transcriptional regulator	-
PA2887	<i>atuB</i>	-2.299	citronellol catabolism dehydrogenase	ko00281//Geraniol degradation
PA2890	<i>atuE</i>	-4.298	isohexenylglutaconyl-CoA hydratase	ko00281//Geraniol degradation
PA2928	<i>PA2928</i>	1.633	Uncharacterised protein	-
PA3009	<i>PA3009</i>	1.390	ABC transporter ATP-binding protein	-

PA3038	<i>PA3038</i>	-2.391	porin	-
PA3039	<i>PA3039</i>	1.993	transporter	-
PA3067	<i>PA3067</i>	1.814	transcriptional regulator	-
PA3079	<i>PA3079</i>	-1.889	patched family protein	-
PA3126	<i>ibpA</i>	-1.849	heat-shock protein IbpA	-
PA3136	<i>PA3136</i>	1.398	secretion protein	-
PA3181	<i>PA3181</i>	-1.330	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	ko01200//Carbon metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko00030//Pentose phosphate pathway
PA3182	<i>pgl</i>	-2.220	6-phosphogluconolactonase	ko01200//Carbon metabolism;ko00030//Pentose phosphate pathway
PA3183	<i>zwf</i>	-2.022	glucose-6-phosphate 1-dehydrogenase	ko01200//Carbon metabolism;ko00030//Pentose phosphate pathway;ko00480//Glutathione metabolism
PA3186	<i>oprB</i>	-3.460	porin B	-
PA3187	<i>PA3187</i>	-2.904	ABC transporter ATP-binding protein	ko02010//ABC transporters
PA3189	<i>PA3189</i>	-1.454	sugar ABC transporter permease	ko02010//ABC transporters
PA3190	<i>PA3190</i>	-1.862	sugar ABC transporter substrate-binding protein	ko02010//ABC transporters
PA3192	<i>gltR</i>	-1.969	two-component response regulator GltR	-
PA3194	<i>edd</i>	-1.813	phosphogluconate dehydratase	ko01200//Carbon metabolism;ko00030//Pentose phosphate pathway
PA3195	<i>gapA</i>	-1.919	glyceraldehyde 3-phosphate dehydrogenase	ko01230//Biosynthesis of amino acids;ko01200//Carbon metabolism;ko00010//Glycolysis / Gluconeogenesis

PA3209	<i>PA3209</i>	12.001	zinc/iron-chelating domain-containing protein	-	ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko03440//Homologous recombination;ko03430//Mismatch repair;ko03030//DNA replication
PA3232	<i>PA3232</i>	-1.374	DNA polymerase III subunit epsilon	-	
PA3233	<i>PA3233</i>	-1.808	cyclic nucleotide-binding domain protein	-	
PA3234	<i>PA3234</i>	-3.020	acetate permease	-	
PA3235	<i>PA3235</i>	-2.130	membrane protein	-	
PA3236	<i>PA3236</i>	-1.907	glycine betaine-binding protein	-	ko02010//ABC transporters
PA3282	<i>PA3282</i>	-2.139		-	
PA3291	<i>PA3291</i>	-1.644	DUF3304 domain-containing protein	-	
PA3292	<i>PA3292</i>	-1.312	DUF3304 domain-containing protein	-	
PA3329	<i>PA3329</i>	-1.329	Malonyl CoA-acyl carrier protein transacylase	-	
PA3330	<i>PA3330</i>	-1.262	short-chain dehydrogenase	-	
PA3353	<i>PA3353</i>	-1.538	pilus assembly protein PilZ	-	
PA3358	<i>PA3358</i>	-11.948	EamA family transporter	-	
PA3376	<i>PA3376</i>	-2.276	phosphonate C-P lyase system protein PhnK	-	
PA3385	<i>amrZ</i>	-1.372	alginate and motility regulator Z	-	
PA3425	<i>PA3425</i>	1.219	cupin	-	
PA3442	<i>PA3442</i>	-1.243	aliphatic sulfonates ABC transporter ATP-binding subunit	-	ko02010//ABC transporters;ko00920//Sulfur metabolism
PA3444	<i>PA3444</i>	-1.421	alkanesulfonate monooxygenase	-	ko00920//Sulfur metabolism
PA3484	<i>PA3484(Tse3)</i>	-1.459	Uncharacterized protein PAE221_01533	-	
PA3487	<i>pldA</i>	-1.255	phospholipase D	-	
PA3502	<i>PA3502</i>	-2.117	Uncharacterised protein	-	

PA3506	<i>PA3506</i>	-1.850	probable decarboxylase	ko01230//Biosynthesis of amino acids;ko00650//Butanoate metabolism;ko01210//2-Oxocarboxylic acid metabolism;ko00770//Pantothenate and CoA biosynthesis;ko00290//Valine, leucine and isoleucine biosynthesis;ko00660//C5-Branched dibasic acid metabolism
PA3507	<i>PA3507</i>	-2.411	short-chain dehydrogenase	-
PA3508	<i>PA3508</i>	-2.018	transcriptional regulator	-
PA3510	<i>PA3510</i>	-1.481	cupin domain protein	-
PA3519	<i>PA3519</i>	-1.509	Pyrrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C	-
PA3523	<i>PA3523</i>	-1.438	resistance-nodulation-cell division (RND) efflux membrane fusion protein	-
PA3526	<i>PA3526</i>	-2.106	probable outer membrane protein precursor	-
PA3568	<i>PA3568</i>	-3.847	propionyl-CoA synthetase	ko00640//Propanoate metabolism
PA3569	<i>mmsB</i>	-2.780	3-hydroxyisobutyrate dehydrogenase	ko00280//Valine, leucine and isoleucine degradation ko01200//Carbon metabolism;ko00280//Valine, leucine and isoleucine
PA3570	<i>mmsA</i>	-2.312	methylmalonate-semialdehyde dehydrogenase	degradation;ko00640//Propanoate metabolism;ko00410//beta-Alanine metabolism;ko00562//Inositol phosphate
PA3593	<i>PA3593</i>	1.591	acyl-CoA dehydrogenase	-
PA3601	<i>PA3601</i>	-2.114	50S ribosomal protein L31	ko03010//Ribosome
Continued				

PA3612	<i>PA3612</i>	1.463	Putative cytoplasmic protein	-
PA3662	<i>PA3662</i>	-3.114	Uncharacterised protein	-
PA3714	<i>PA3714</i>	-1.513	LuxR family transcriptional regulator	ko02020//Two-component system
PA3720	<i>PA3720</i>	-1.775	Uncharacterised protein	-
PA3721	<i>nalC</i>	-1.702	transcriptional regulator	-
PA3722	<i>PA3722</i>	-2.087	Uncharacterised protein	-
PA3727	<i>PA3727</i>	-1.526	nuclease	-
PA3728	<i>PA3728</i>	-1.759	AAA domain family protein	-
PA3729	<i>PA3729</i>	-1.637	Inner membrane protein YqiK	-
PA3731	<i>PA3731</i>	-1.209	phage shock protein A	-
PA3740	<i>PA3740</i>	-1.216	Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB	-
PA3745	<i>rpsP</i>	1.231	30S ribosomal protein S16	ko03010//Ribosome
PA3758	<i>PA3758</i>	-1.434	N-acetylglucosamine-6-phosphate deacetylase	ko00520//Amino sugar and nucleotide sugar metabolism
PA3759	<i>PA3759</i>	-1.294	aminotransferase	ko00250//Alanine, aspartate and glutamate metabolism;ko00520//Amino sugar and nucleotide sugar metabolism
PA3760	<i>PA3760</i>	-1.408	phosphoenolpyruvate--protein phosphotransferase	-
PA3761	<i>PA3761</i>	-1.296	N-acetyl-D-glucosamine phosphotransferase system transporter	ko00520//Amino sugar and nucleotide sugar metabolism;ko02060//Phosphotransferase system (PTS)
PA3838	<i>PA3838</i>	-1.475	ABC transporter ATP-binding protein	-
PA3842	<i>PA3842</i>	1.216	chaperone	-
PA3856	<i>PA3856</i>	1.254	ketosteroid isomerase	-
PA3867	<i>PA3867</i>	1.511	DNA invertase	-

PA3870	<i>moaA1</i>	1.329	molybdenum cofactor biosynthesis protein A	ko00790//Folate biosynthesis;ko04122//Sulfur relay system
PA3871	<i>PA3871</i>	1.444	peptidyl-prolyl cis-trans isomerase	-
PA3873	<i>narJ</i>	1.417	respiratory nitrate reductase subunit delta	ko02020//Two-component system;ko00910//Nitrogen metabolism
PA3874	<i>narH</i>	1.383	respiratory nitrate reductase subunit beta	ko02020//Two-component system;ko00910//Nitrogen metabolism
PA3875	<i>narG</i>	1.476	respiratory nitrate reductase subunit alpha	ko02020//Two-component system;ko00910//Nitrogen metabolism
PA3876	<i>narK2</i>	1.645	nitrite extrusion protein 2	ko00910//Nitrogen metabolism
PA3884	<i>PA3884</i>	12.097	putative membrane protein	-
PA3923	<i>PA3923</i>	-1.339	adhesin	-
PA3935	<i>tauD</i>	-1.871	taurine dioxygenase	ko00920//Sulfur metabolism;ko00430//Taurine and hypotaurine metabolism
PA3937	<i>PA3937</i>	-1.929	taurine ABC transporter ATP-binding protein	ko02010//ABC transporters;ko00920//Sulfur metabolism
PA4022	<i>PA4022</i>	-1.474	aldehyde dehydrogenase	ko00620//Pyruvate metabolism;ko00010//Glycolysis / Gluconeogenesis
PA4023	<i>PA4023</i>	-2.337	transporter	-
PA4038	<i>PA4038</i>	1.567	possible ABC transporter permease component	-
PA4072	<i>PA4072</i>	-1.542	amino acid permease	-
PA4073	<i>PA4073</i>	-1.489	Phenylacetaldehyde dehydrogenase	ko00360//Phenylalanine metabolism;ko00643//Styrene degradation
PA4089	<i>PA4089</i>	2.707	3-ketoacyl-ACP reductase	ko01212//Fatty acid metabolism;ko00061//Fatty acid biosynthesis;ko00780//Biotin

				metabolism;ko01040//Biosynthesis of unsaturated fatty acids
PA4093	<i>PA4093</i>	-2.515	thioesterase	-
PA4107	<i>PA4107</i>	-2.520	EF-hand domain pair family protein	-
PA4124	<i>hpcB</i>	-1.495	3,4-dihydroxyphenylacetate 2,3-dioxygenase	ko01220//Degradation of aromatic compounds;ko00350//Tyrosine metabolism
PA4139	<i>PA4139</i>	-1.531	Uncharacterized protein PAE221_02180	-
PA4140	<i>PA4140</i>	-1.620	FAD-linked oxidase	-
PA4151	<i>acoB</i>	1.356	acetoin catabolism protein AcoB	ko01200//Carbon metabolism;ko00620//Pyruvate metabolism;ko00010//Glycolysis / Gluconeogenesis;ko00020//Citrate cycle (TCA cycle)
PA4171	<i>PA4171</i>	1.501	glutamine amidotransferase	-
PA4188	<i>PA4188</i>	-1.842	dihydrodipicolinate synthase family protein	ko01230//Biosynthesis of amino acids;ko00300//Lysine biosynthesis;ko00261//Monobactam biosynthesis
PA4189	<i>PA4189</i>	-2.000	aldehyde dehydrogenase	ko00330//Arginine and proline metabolism
PA4191	<i>PA4191</i>	-1.353	iron oxidase	-
PA4192	<i>PA4192</i>	-2.193	ABC transporter ATP-binding protein	-
PA4198	<i>PA4198</i>	-1.273	acyl-CoA synthetase	-
PA4204	<i>ppgL</i>	-1.214	gluconolactonase PpgL	-
PA4211	<i>phzB1</i>	-1.678	phenazine biosynthesis protein PhzB1	-
PA4213	<i>phzD1</i>	-1.698	phenazine biosynthesis protein PhzD	-
Continued				
PA4214	<i>phzE1</i>	-1.324	phenazine biosynthesis protein PhzE	-
PA4215	<i>phzF1</i>	-1.369	2,3-dihydro-3-hydroxyanthranilate isomerase	-

PA4221	<i>fptA</i>	-1.568	Fe(III)-pyochelin outer membrane receptor	-
PA4222	<i>PA4222</i>	-1.774	ABC transporter ATP-binding protein	-
PA4223	<i>PA4223</i>	-2.059	ABC transporter ATP-binding protein	ko02010//ABC transporters
PA4224	<i>pchG</i>	-1.551	pyochelin biosynthetic protein PchG	ko01053//Biosynthesis of siderophore group nonribosomal peptides
PA4225	<i>pchF</i>	-2.527	pyochelin synthetase	ko01053//Biosynthesis of siderophore group nonribosomal peptides
PA4226	<i>pchE</i>	-2.000	dihydroaeruginosic acid synthetase	ko01053//Biosynthesis of siderophore group nonribosomal peptides
PA4231	<i>pchA</i>	-1.843	salicylate biosynthesis isochorismate synthase	ko00130//Ubiquinone and other terpenoid-quinone biosynthesis;ko01053//Biosynthesis of siderophore group nonribosomal peptides
PA4290	<i>PA4290</i>	-1.329	chemotaxis transducer	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA4291	<i>PA4291</i>	1.270	hypothetical protein	-
PA4298	<i>PA4298</i>	-1.629	Protein of uncharacterised function (DUF3613)	-
PA4306	<i>flp</i>	-1.410	type IVb pilin Flp	-
PA4309	<i>pctA</i>	-1.419	methyl-accepting chemotaxis protein PctA	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA4310	<i>pctB</i>	-1.687	methyl-accepting chemotaxis protein PctB	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA4324	<i>PA4324</i>	-2.674	pilus assembly protein PilZ	-
PA4326	<i>PA4326</i>	-2.200	lipoprotein	-
PA4332	<i>PA4332</i>	-1.419	FOG: GGDEF domain	-
PA4500	<i>PA4500</i>	-1.586	ABC transporter	ko02010//ABC transporters;ko02030//Bacterial

PA4501	<i>opdP</i>	-2.560	porin	chemotaxis
PA4502	<i>PA4502</i>	-2.093	ABC transporter	-
PA4504	<i>PA4504</i>	-1.624	ABC transporter permease	ko02010//ABC transporters;ko02030//Bacterial chemotaxis
PA4505	<i>PA4505</i>	-1.528	ABC transporter ATP-binding protein	ko02010//ABC transporters
PA4506	<i>PA4506</i>	-1.516	peptide ABC transporter ATP-binding protein	ko02010//ABC transporters
PA4520	<i>PA4520</i>	-1.391	chemotaxis transducer	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA4563	<i>rpsT</i>	1.423	30S ribosomal protein S20	ko03010//Ribosome
PA4571	<i>PA4571</i>	-2.853	cytochrome c	-
PA4573	<i>PA4573</i>	1.360	cation transporter	-
PA4582	<i>PA4582</i>	-1.434	SPFH domain / Band 7 family protein	-
PA4590	<i>pra</i>	-1.482	protein activator	-
PA4592	<i>PA4592</i>	-1.258	probable outer membrane protein precursor	-
PA4596	<i>PA4596</i>	-3.429	transcriptional regulator	-
PA4625	<i>PA4625</i>	-1.401	hemagglutination protein	-
PA4633	<i>PA4633</i>	-2.364	chemotaxis protein	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA4644	<i>PA4644</i>	1.251	Tryptophan synthase beta chain like	-
PA4675	<i>PA4675</i>	-1.497	TonB-dependent receptor	-
PA4683	<i>PA4683</i>	-2.179	Uncharacterized protein PAE221_00037	-
PA4709	<i>PA4709</i>	1.355	hemin degrading factor	-
PA4746	<i>PA4746</i>	1.260	ribosome maturation factor RimP	-
PA4764	<i>fur</i>	1.299	ferric uptake regulation protein	-
PA4766	<i>PA4766</i>	2.354	protein RnfH	-

PA4768	<i>smpB</i>	1.411	SsrA-binding protein	-
PA4780	<i>PA4780</i>	1.611	serine protein kinase RIO	-
PA4789	<i>PA4789</i>	1.534	pyrophosphatase	-
PA4817	<i>PA4817</i>	2.426	zinc/iron-chelating domain-containing protein	-
PA4843	<i>PA4843</i>	-4.397	diguanylate cyclase response regulator	-
PA4844	<i>PA4844</i>	-2.290	chemotaxis transducer	-
PA4889	<i>PA4889</i>	1.261	oxidoreductase	-
PA4901	<i>mdlC</i>	-1.512	benzoylformate decarboxylase	ko00627//Aminobenzoate degradation
PA4911	<i>PA4911</i>	-1.297	branched-chain amino acid ABC transporter permease	ko02010//ABC transporters
PA4919	<i>pncB1</i>	-1.621	nicotinate phosphoribosyltransferase	ko00760//Nicotinate and nicotinamide metabolism
PA4929	<i>PA4929</i>	-1.840	sensor domain-containing diguanylate cyclase	-
PA4989	<i>PA4989</i>	-1.234	transcriptional regulator	-
PA5054	<i>hslU</i>	-1.298	ATP-dependent protease ATP-binding subunit HslU	-
PA5072	<i>PA5072</i>	-1.354	chemotaxis transducer	ko02020//Two-component system;ko02030//Bacterial chemotaxis
PA5098	<i>hutH</i>	-1.932	histidine ammonia-lyase	ko00340//Histidine metabolism
PA5099	<i>PA5099</i>	-1.373	transporter	-
PA5100	<i>hutU</i>	-1.668	urocanate hydratase	ko00340//Histidine metabolism
PA5153	<i>PA5153</i>	-1.940	amino acid ABC transporter substrate-binding protein	-
PA5154	<i>PA5154</i>	-1.853	ABC transporter permease	-
PA5155	<i>PA5155</i>	-1.606	amino acid ABC transporter permease	-
PA5167	<i>PA5167</i>	-1.207	C4-dicarboxylate-binding protein	ko02020//Two-component system
PA5181	<i>PA5181</i>	-1.343	oxidoreductase	-
PA5285	<i>PA5285</i>	1.320	Uncharacterised protein	-

PA5289	<i>PA5289</i>	1.518	membrane fusogenic activity family protein	-
PA5383	<i>PA5383</i>	-1.707	membrane protein	-
PA5387	<i>cdhC</i>	2.967	carnitine dehydrogenase	-
PA5396	<i>PA5396</i>	-1.535	membrane dipeptidase family protein	-
PA5397	<i>PA5397</i>	-2.565	hydrocarbon binding protein	-
PA5398	<i>dgcA</i>	-2.146	dimethylglycine catabolism protein DgcA	-
PA5399	<i>dgcB</i>	-1.630	(Fe-S)-binding protein	-
PA5410	<i>gbcA</i>	-1.560	Rieske (2Fe-2S) protein	-
				ko01230//Biosynthesis of amino acids;ko01200//Carbon metabolism;ko00630//Glyoxylate and dicarboxylate metabolism;ko00260//Glycine, serine and threonine metabolism;ko00680//Methane metabolism;ko00670//One carbon pool by folate;ko00460//Cyanoamino acid metabolism
PA5415	<i>glyA1</i>	-2.044	serine hydroxymethyltransferase	ko00260//Glycine, serine and threonine metabolism
PA5416	<i>soxB</i>	-2.042	sarcosine oxidase subunit beta	ko00260//Glycine, serine and threonine metabolism
PA5417	<i>soxD</i>	-2.744	sarcosine oxidase subunit delta	ko00260//Glycine, serine and threonine metabolism
PA5418	<i>soxA</i>	-2.625	sarcosine oxidase subunit alpha	ko00260//Glycine, serine and threonine metabolism
PA5419	<i>soxG</i>	-1.468	sarcosine oxidase subunit gamma	ko00260//Glycine, serine and threonine metabolism
PA5420	<i>purU2</i>	-1.969	formyltetrahydrofolate deformylase	ko00630//Glyoxylate and dicarboxylate metabolism;ko00670//One carbon pool by folate

PA5421	<i>fdhA</i>	-1.876	glutathione-independent formaldehyde dehydrogenase	ko01200//Carbon metabolism;ko00680//Methane metabolism;ko00625//Chloroalkane and chloroalkene degradation
PA5444	<i>PA5444</i>	1.566	transporter	-
PA5445	<i>PA5445</i>	-1.549	coenzyme A transferase	ko01200//Carbon metabolism;ko00620//Pyruvate metabolism;ko00650//Butanoate metabolism;ko00020//Citrate cycle (TCA cycle)
PA5462	<i>PA5462</i>	1.895	Holliday junction resolvase	-
PA5491	<i>PA5491</i>	1.240	cytochrome	-
PA5515	<i>PA5515</i>	1.324	Protein of uncharacterised function (DUF3301)	-
PA5536	<i>PA5536</i>	2.970	DksA/TraR family C4-type zinc finger protein	-
PA5550	<i>glmR</i>	1.377	GlmR transcriptional regulator	-
PA5566	<i>PA5566</i>	-1.603	hypothetical protein	-
