

MvfR and PqsE Controlled genes.

PA14 ID	PAO1 ortholog	Factor Name or Category	Gene name	pqsE ⁻	mvfR ⁻	mvfR ⁻ + PqsE	PA14 + PqsE	mvfR ⁻ + PqsE + PQS	PA14 + PqsE vs. mvfR ⁻ + PqsE	Description
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Known or putative virulence factors

Positively regulated genes

PA14_48600	PA1874	Adhesin		-2.73	-5.59	4.17	-21.65	-4.20	-2.76	surface adhesion protein, putative
PA14_18520	PA3543	Alginate	algK			17.83		-10.91	-8.75	alginate biosynthetic protein AlgK precursor
PA14_69390	PA5255	Alginate	algQ, algR2	-2.22	-2.85				2.16	Alginate regulatory protein AlgQ
PA14_08230	PA2274	Antibiotics		-39.36	-15.28	21.68				hypothetical protein, Putative monoxygenase SunT, ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms].
PA14_05590	PA1876	bacteriocin/lantibiotic		-3.07	-4.39		-16.23			FrvX, Cellulase M and related proteins [Carbohydrate transport and metabolism].
PA14_53290	PA2172	Cellulase		-5.38	-18.44	22.60	-4.98	-6.80	-3.43	FrvX, Cellulase M and related proteins [Carbohydrate transport and metabolism].
PA14_19350	PA3461	Cellulase	yhfE		-2.27	4.13	-7.25	-4.39	-3.31	Chitinase, 75% similar to chitinase of [Serratia marcescens]
PA14_61040	PA2300	Chitinase	chiC	-8.61	-3.95	43.78		-6.67		chitin-binding protein CbpD precursor
PA14_18800	PA0852	Chitin-binding protein	cbpD	-4.31	-4.29	13.75		-3.58		LasA protease precursor
PA14_48590	PA1871	Elastase	lasA	-3.53	-10.25	3.99	-6.71			LasD, zinc metalloprotease (elastase) [Amino acid COG2374; predicted extracellular nuclelease (general function); putative extracellular protein, homologous, AND-ribulose-5-phosphate isomerase, 58% similar to hsp gene product of conserved hypothetical protein, 58% similar to Asp hemolysin [Aspergillus fumigatus].]
PA14_08200	PA3724	Elastase	lasB	-2.02	-2.10	3.22	-7.09	-3.22		
PA14_47400	PA3909	Extracellular		-2.61	-2.23	3.31				
PA14_38270	PA1914	Halovibrin	hvn	-10.43	-3.97	26.47	-62.50	-4.88	-2.16	
PA14_66840	PA0122	Hemolysin		-3.13	-3.56	3.79			2.90	
PA14_48560	PA2367	Hemolysin		-2.97	-2.33		-6.67		3.08	
PA14_09220	PA2193	Hydrogen cyanide	hcnA	-5.82	-4.44	-4.52				hydrogen cyanide synthase HcnA
PA14_01490	PA2194	Hydrogen cyanide	hcnB	-4.33	-3.48	3.93		-3.07		hydrogen cyanide synthase HcnB
PA14_09300	PA2195	Hydrogen cyanide	hcnC	-5.34	-4.24					hydrogen cyanide synthase HcnC
PA14_55940	PA5481	Inhibitor of vertebrate lysozyme		-2.91	-2.10	3.39				hypothetical protein
PA14_36810	PA2570	Lectin	lecA, pa1L	-3.10	-9.99	7.29		-3.40		PA-I galactophilic lectin
PA14_20610	PA3361	Lectin	lecB	-5.02	-8.41					hypothetical protein
PA14_48540	PA1218	Mitomycin antibiotics/polyketide fumonisin like		-3.80	-2.44		-11.42			COG5285, Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_24180	PA0424	Multi-drug resistance	mexR	3.31	4.93		8.20			multidrug resistance operon repressor MexR
PA14_36330	PA1221	Peptide, actinomycin like		-4.41	-3.08		-6.62			EntF, Non-ribosomal peptide synthetase modules and related proteins, 49% similar to actinomycin synthetase II [Streptomyces chrysomallus], [Secondary metabolites biosynthesis, transport, and catabolism].

PA14_03490	PA1215	Peptide, Polyketide		-7.04	-2.00	4.04	-71.94			CaiC, Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II. 40% similar to a region of polyketide synthase [Amycolatopsis mediterraneii] [Lipid metabolism / Secondary metabolites biosynthesis, transport, and catabolism].
PA14_14780	PA4078	Peptide, saframycin Mx1 like		-2.17	-3.97	13.05	-3.08	-5.81	-2.49	probable nonribosomal peptide synthetase, 47% similar to saframycin Mx1 synthetase A [Myxococcus xanthus].
PA14_00640	PA0051	Phenazines	<i>phzH</i>	-2.77	-2.29	9.29				AsnB, Asparagine synthase (glutamine-hydrolyzing) [Amino acid transport and metabolism].
PA14_03520	PA4221	Pyochelin	<i>fptA</i>	-161.20	-2.99	4.79	-5.99	-3.56	-3.48	Fe(III)-pyochelin receptor precursor
PA14_34870	PA4222	Pyochelin	<i>pchl</i>	-111.70	-4.50		-9.43			MdlB, ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms].
PA14_21530	PA4223	Pyochelin	<i>pchH</i>	-40.02	-3.29		-6.13			MdlB, ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms].
PA14_35160	PA4224	Pyochelin	<i>pchG</i>	-1740.00	-2.82	-2.48	-13.70			PchG, Oxidoreductase (NAD-binding), involved in siderophore biosynthesis [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_58040	PA4225	Pyochelin	<i>pchF</i>	-277.10	-5.08		-12.44			pyochelin synthetase
PA14_61200	PA4226	Pyochelin	<i>pchE</i>	-122.10	-6.89	3.71	-14.10		-3.30	COG3626, Nonribosomal peptide synthetase modules and related systems for secondary metabolite biosynthesis transcriptional regulator PchR
PA14_60500	PA4227	Pyochelin	<i>pchR</i>	-2.73	-8.65	2.74	-4.02		-2.00	
PA14_68440	PA4228	Pyochelin	<i>pchD</i>	-2.72	-4.74	5.17	-20.24		-4.19	pyochelin biosynthesis protein PchD
PA14_64460	PA4229	Pyochelin	<i>pchC</i>	-2.08	-4.24		-13.74		-2.29	pyochelin biosynthetic protein PchC
PA14_53250	PA4230	Pyochelin	<i>pchB</i>	-90.32	-4.02		-8.93		-2.20	salicylate biosynthesis protein PchB
PA14_55780	PA4231	Pyochelin	<i>pchA</i>	-80.47	-5.59	3.05	-9.01			MenF, Isochorismate synthase [Coenzyme metabolism / Secondary metabolites biosynthesis, transport, and catabolism].
PA14_36730	PA0633	Pyocin F2			-3.11	3.54	-5.24		-2.37	hypothetical protein
PA14_37745	PA0635	Pyocin F2		-5.29	-14.76	10.15	-5.26	-6.13	-3.37	hypothetical protein
PA14_08050	PA0636	Pyocin F2		-2.41	-2.28	4.68	-4.50	-6.54	-3.45	COG5281, Phage-related minor tail protein [Function unknown].
PA14_37760	PA0637	Pyocin F2			-3.42	3.83	-5.05	-3.17	-2.48	COG4718, Phage-related protein [Function unknown].
PA14_16310	PA0638	Pyocin F2		-2.48	-3.67	3.12	-6.49	-3.62	-2.68	gp18, Phage-related protein [Function unknown].
PA14_56990	PA0639	Pyocin F2			-2.15	4.91	-3.60	-6.85	-2.57	COG1310, Predicted metal-dependent protease of the PAD1/JAB1 superfamily [General function prediction only].
PA14_08070	PA0616	Pyocin R2		-2.18	-2.26	2.86	-3.58			gpV, Phage P2 baseplate assembly protein gpV
PA14_09480	PA0617	Pyocin R2			-8.08	3.38	-3.86			COG3628, Phage baseplate assembly protein W
PA14_47210	PA0619	Pyocin R2			-2.99	3.02	-4.95			[General function prediction only].
PA14_31350	PA0620	Pyocin R2		-2.21	-2.75	4.24	-3.08	-3.52	-2.23	gpl, Bacteriophage P2-related tail formation protein
PA14_08060	PA0621	Pyocin R2			-2.53	4.12		-4.76	-2.85	[General function prediction only].
PA14_60190	PA0622	Pyocin R2			-6.33	2.12	-6.90	-5.21	-3.50	COG3497, Phage tail sheath protein FI [General function prediction only].
PA14_42950	PA0623	Pyocin R2			-2.04	2.77	-3.61	-3.39	-2.13	COG3498, Phage tail tube protein FII [General function prediction only].
PA14_09260	PA0625	Pyocin R2			-2.50	3.07		-4.48	-2.26	COG3941, Mu-like prophage protein [General function prediction only].
PA14_08270	PA0629	Pyocin R2			-2.11	5.30	-9.90	-3.60	-5.62	COG3179, Predicted chitinase [General function prediction only].
PA14_48550	PA0632	Pyocin R2			-2.38	2.92		-3.19		hypothetical protein

PA14_14770	PA1901	Pyocyanin	<i>phzC2</i>	-5.92	-14.11	5.45		phenazine biosynthesis, AroG, 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [Amino acid transport and metabolism].	
PA14_39925	PA1902	Pyocyanin	<i>phzD2</i>	-7.64	-20.76	4.87	-4.88	phenazine biosynthesis, EntB, Isochorismate hydrolase [Secondary metabolites biosynthesis, transport, and catabolism].	
PA14_39910	PA1903	Pyocyanin	<i>phzE2</i>	-6.32	-7.94	6.42	-3.60	phenazine biosynthesis protein PhzE	
PA14_39890	PA1904	Pyocyanin	<i>phzF2</i>	-5.81	-12.05		-4.42	phenazine biosynthesis protein PhzF	
PA14_72360	PA1905	Pyocyanin	<i>phzG2</i>	-5.46	-11.73	3.55	-3.48	phenazine biosynthesis protein PhzG	
PA14_36780	PA4209	Pyocyanin	<i>phzM</i>	-2.83	-2.70			phenazine biosynthesis protein PhzM	
PA14_39870	PA4210	Pyocyanin	<i>phzA1</i>	-28.09	-5.00	3.30		probable phenazine biosynthesis protein	
PA14_09470	PA4211	Pyocyanin	<i>phzB1</i>	-10.89	-10.12	5.95			
PA14_09400	PA4217	Pyocyanin	<i>phzS</i>	-3.17	-14.96			probable FAD-dependent monooxygenase	
PA14_33680	PA2398	Pyoverdine	<i>fpvA</i>		-27.10		-3.19	4.07	ferrypyoverdine receptor, fpvA (ferrypyoverdine receptor)
PA14_14710	PA3478	Rahmnolipids	<i>rhlB</i>	-4.07	-2.24	6.80	-5.65	-4.20	-2.20 rhamnosyltransferase chain B
PA14_09350	PA3479	Rahmnolipids	<i>rhlA</i>	-3.60	-3.14	5.77	-3.12	-3.22 rhamnosyltransferase chain A	
PA14_34110	PA3477	RhlR	<i>rhlR</i>	-2.10	-2.54			transcriptional regulator RhlR	
PA14_48060	PA1249	Secreted alkaline protease	<i>aprA</i>		-8.93		-10.85		alkaline metalloproteinase precursor
PA14_39945	PA2939	Secreted aminopeptidases	<i>pepB</i>	-2.45	-2.12	6.39	-14.60		lap, Predicted aminopeptidases [General function prediction only].
PA14_01600	PA4175	Secreted endoprotease	<i>piv, prpL</i>	-3.46	-4.98		-9.71		Endoproteinase Arg-C precursor; Pvds-regulated endoprotease, lysyl class
PA14_05510	PA0423	Secreted protease	<i>pasP, ycel</i>	-2.08	-7.42				conserved hypothetical protein
PA14_10340	PA4143	Toxin transporter	<i>cyaB, cvaB</i>	-2.02	-3.21				SunT, ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Defense mechanisms].
PA14_60400	PA1665	Type VI secretion system		-2.57	-11.38	2.00			COG3456, Uncharacterized conserved protein, contains FHA domain [Signal transduction mechanisms].

Negatively regulated genes

PA14_51360	PA1001	Anthranilic acid	<i>phnA</i>	2.67	-1075.00		-8.85	4.69	TrpE, Anthranilate/para-aminobenzoate synthases component I [Amino acid transport and metabolism / Coenzyme metabolism].
PA14_51350	PA1002	Anthranilic acid	<i>phnB</i>	2.41	-20.19		-8.55		Paba, Anthranilate/para-aminobenzoate synthases component II [Amino acid transport and metabolism / ACS, Acyl-coenzyme A synthetases/AMF-(fatty) acid linkers II lipid metabolism].
PA14_51430	PA0996	HAQs	<i>pqsA</i>	2.48	-21.05		-4.59	3.15	
PA14_51420	PA0997	HAQs	<i>pqsB</i>		-49.64		-13.28	11.05	FabH, 3-oxoacyl-[acyl-carrier-protein].
PA14_51410	PA0998	HAQs	<i>pqsC</i>		-262.60		-9.35	10.01	FabH, 3-oxoacyl-[acyl-carrier-protein].
PA14_51390	PA0999	HAQs	<i>pqsD, fabH1</i>	2.11	-137.20		-10.93	3.57	FabH, 3-oxoacyl-[acyl-carrier-protein].
<i>pqsE</i>	<i>pqsE</i>								
PA14_51380	PA1000	PqsE	<i>pqsE</i>	-12.58	-236.00	64.49		2.17	GloB, Zn-dependent hydrolases, including glyoxylases [General function prediction only].

Other genes

Positively regulated genes

PA14_03550	PA0273	Membrane proteins		3.36		-3.95	-4.06	CynX, Cyanate permease, MFS transporter [Inorganic ion transport and metabolism].
PA14_03670	PA0281	Membrane proteins	cysW	-7.09	-5.05	3.06		CysW, ABC-type sulfate transport system, permease component [Inorganic ion transport and metabolism].
PA14_29710	PA1048	Membrane proteins		-2.59	-2.74	-6.06		OmpA, Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cell envelope biogenesis, outer membrane].
PA14_48570	PA1212	Membrane proteins		-2.24	-35.46	3.84	-6.06	MelB, Na+/melibiose symporter and related transporters [Carbohydrate transport and metabolism].
PA14_46240	PA1408	Membrane proteins		-2.67	2.05			COG3264, Small-conductance mechanosensitive channel [Cell envelope biogenesis, outer membrane].
PA14_42900	PA1669	Membrane proteins		-2.52	-2.46			IcmF, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_40620	PA1848	Membrane proteins		9.14		-3.36	-3.57	AraJ, Arabinose efflux permease, MFS transporter [Carbohydrate transport and metabolism].
PA14_66880	PA2004	Membrane proteins		-2.13	-3.62	-6.25		GntT, H+/gluconate symporter and related permeases [Carbohydrate transport and metabolism / Amino acid transport and metabolism].
PA14_33570	PA2068	Membrane proteins		-5.71	-8.00	3.53	-3.03	hypothetical protein
PA14_05600	PA2148	Membrane proteins		-3.26	-2.27		-2.21	SapB, Uncharacterized membrane protein [Function unknown].
PA14_36080	PA2214	Membrane proteins			9.35	-12.15	-8.41	UhpC, Sugar phosphate permease [Carbohydrate transport and metabolism].
PA14_35020	PA2286	Membrane proteins		-2.30	5.07	3.06	-3.91	HtpX, Zn-dependent protease with chaperone function [Posttranslational modification, protein turnover, chaperones].
PA14_40310	PA2327	Membrane proteins		-3.19	-3.24			TauC, ABC-type nitrate/sulfonate/bicarbonate transport system, permease component [Inorganic ion transport and metabolism].
PA14_13130	PA2331	Membrane proteins		-2.01	-3.13	-2.26	-3.41	COG2128, Uncharacterized conserved protein [Function unknown].
PA14_32720	PA2467	Membrane proteins	foxR	-2.75	-5.35	11.59	-2.62	FecR, Fe2+-dicitrato sensor, membrane component [Inorganic ion transport and metabolism / Signal transduction mechanisms].
PA14_34510	PA2868	Membrane proteins		-3.28	-6.85	-2.35		XtnA, Phage terminase, small subunit [DNA replication, recombination, and repair].
PA14_26360	PA2914	Membrane proteins			4.44	-5.10	-3.44	FepD, ABC-type Fe3+-siderophore transport system, permease component [Inorganic ion transport and metabolism].
PA14_26300	PA2919	Membrane proteins		-2.56	5.21	-5.59	-4.59	hypothetical protein
PA14_24760	PA3041	Membrane proteins	yqjE	-14.19	2.09	-7.19		COG5393, Predicted membrane protein [Function unknown].

PA14_21190	PA3311	Membrane proteins	-2.10	-7.79	3.68		COG5001, Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Signal transduction mechanisms].	
PA14_20860	PA3340	Membrane proteins	-2.15	-2.07			FimV, Tfp pilus assembly protein FimV [Cell motility and secretion / Intracellular trafficking and secretion].	
PA14_30620	PA3370	Membrane proteins	-2.34	-2.14	4.78	-5.88	-2.99 hypothetical protein	
PA14_08160	PA3690	Membrane proteins	-2.12	-2.32	6.01	-3.64	-3.39 -2.17 ZntA, Cation transport ATPase [Inorganic ion transport and metabolism].	
PA14_13040	PA3718	Membrane proteins	-11.98	-2.05	2.78		AraJ, Arabinose efflux permease [Carbohydrate transport and metabolism].	
PA14_09520	PA4205	Membrane proteins	mexG	-87.50	-226.80	26.71		COG2259, Predicted membrane protein [Function unknown].
PA14_36570	PA4207	Membrane proteins	mexI	-33.35	-57.16	11.68		RND efflux transporter, AcrB, Cation/multidrug efflux pump [Defense mechanisms].
PA14_09470	PA4208	Membrane proteins	opmD	-18.74	-56.49	7.75	-5.32	TolC, Outer membrane protein [Cell envelope biogenesis, outer membrane / Intracellular trafficking and secretion].
PA14_39780	PA4218	Membrane proteins		-111.60	-11.46		-8.13	AraJ, Arabinose efflux permease [Carbohydrate transport and metabolism].
PA14_36740	PA4219	Membrane proteins	yfpB	-19.27	-18.84		-5.43 -2.29	PiuB, Uncharacterized iron-regulated membrane protein [Function unknown].
PA14_40230	PA4297	Membrane proteins	tadG	-2.05	-2.18	3.94		hypothetical protein
PA14_60960	PA4300	Membrane proteins	tadC	-2.16	-2.45		-3.33	hypothetical protein
PA14_40180	PA4614	Membrane proteins	mscL	-2.00	-2.07			MscL, Large-conductance mechanosensitive channel [Cell envelope biogenesis, outer membrane].
PA14_64240	PA4857	Membrane proteins		-2.22	-2.17			MarC, Multiple antibiotic transporter [Intracellular trafficking and secretion].
PA14_64680	PA4894	Membrane proteins			-6.24	89.57	-5.26 -12.80 -32.90	HupE, Hydrogenase/urease accessory protein [Posttranslational modification, protein turnover, chaperones].
PA14_64690	PA4895	Membrane proteins			-4.63	6.30		-5.08 -9.53 FecR, Fe2+-citrate sensor, membrane component [Inorganic ion transport and metabolism / Signal transduction mechanisms].
PA14_72180	PA5469	Membrane proteins			-6.52	11.75	41.72	-3.83 -6.16 TerC, Membrane protein TerC, possibly involved in tellurium resistance [Inorganic ion transport and metabolism].
PA14_16250	PA5482	Membrane proteins		-2.46	-6.82	3.32		hypothetical protein
PA14_00710	PA0059	Adaptation, Protection	osmC		-11.10	4.43		OsmC, Predicted redox protein, regulator of disulfide bond formation [Posttranslational modification, protein turnover, chaperones].
PA14_08040	PA0139	Adaptation, Protection	ahpC	-2.07	-2.23	3.26		AhpC, Peroxiredoxin [Posttranslational modification, protein turnover, chaperones].
PA14_24860	PA0140	Adaptation, Protection	ahpF	-2.89	-2.09	22.30	-6.76 -3.17	AhpF, Alkyl hydroperoxide reductase, large subunit [Posttranslational modification, protein turnover, chaperones].

PA14_02180	PA0173	Adaptation, Protection	-2.52	-8.96	-16.37		CheB, Chemotaxis response regulator containing a CheY-like receiver domain and a methylesterase domain [Cell motility and secretion / Signal transduction mechanisms].	
PA14_02250	PA0178	Adaptation, Protection	-2.08	-9.49	-6.85		CheA, Chemotaxis protein histidine kinase and related kinases [Cell motility and secretion / Signal transduction mechanisms].	
PA14_36520	PA0848	Adaptation, Protection	-12.59	-21.93	13.14	-9.43	AhpC, Peroxiredoxin [Posttranslational modification, protein turnover, chaperones].	
PA14_09240	PA2147	Adaptation, Protection	<i>katE</i>	-3.15	3.46	5.68	-8.70	KatE, Catalase [Inorganic ion transport and metabolism].
PA14_31810	PA2532	Adaptation, Protection	<i>tpx</i>	-2.61	-2.13	2.36		Tpx, Peroxiredoxin [Posttranslational modification, protein turnover, chaperones].
PA14_67350	PA2788	Adaptation, Protection		-2.11	-2.01			Tar, Methyl-accepting chemotaxis protein [Cell motility and secretion / Signal transduction mechanisms].
PA14_09150	PA4236	Adaptation, Protection	<i>katA, catA</i>	-2.15	-22.80	3.16	-3.51	catalase
PA14_55900	PA4612	Adaptation, Protection	<i>ankB</i>	-5.45	-2.80	7.80	-5.43	Arp, FOG: Ankyrin repeat [General function prediction only].
PA14_38260	PA4613	Adaptation, Protection	<i>katB</i>	-15.37	-7.41	11.73	-17.12	catalase
PA14_23000	PA0430	Amino acid biosynthesis	<i>metF</i>	-4.30	-5.24			MetF, 5,10-methylenetetrahydrofolate reductase [Amino acid transport and metabolism].
PA14_34050	PA0432	Amino acid biosynthesis	<i>sahH</i>	-2.86	-3.61			SAM1, S-adenosylhomocysteine hydrolase [Coenzyme metabolism].
PA14_36770	PA0546	Amino acid biosynthesis	<i>metK</i>	-2.32	-7.87		2.36	methionine adenosyltransferase
PA14_08020	PA1217	Amino acid biosynthesis		-10.59	-2.24	3.54	-26.25	LeuA, Isopropylmalate/homocitrate/citramalate synthases [Amino acid transport and metabolism].
PA14_03090	PA1927	Amino acid biosynthesis	<i>metE</i>	-11.36	-12.85	9.96	-4.95	5-methyltetrahydropteroylglutamate-homocysteine S-methyltransferase
PA14_19370	PA3459	Amino acid biosynthesis	<i>asnB</i>		-2.96	2.17		AsnB, Asparagine synthase (glutamine-hydrolyzing) [Amino acid transport and metabolism].
PA14_40290	PA3814	Amino acid biosynthesis	<i>iscS</i>	-10.67	-3.74	4.15		NifS, Cysteine sulfinate desulfurinase/cysteine desulfurase and related enzymes [Amino acid transport and metabolism].
PA14_22990	PA5100	Amino acid biosynthesis	<i>hutU</i>	-2.26	-4.45		-5.35	urocanase
PA14_31370	PA5373	Amino acid biosynthesis	<i>betB</i>		-2.75	5.32		PutA, NAD-dependent aldehyde dehydrogenases [Energy production and conversion].
PA14_38825	PA1985	Biosynthesis of cofactors	<i>pqqA</i>		-4.13	4.19	-2.20	pyrroloquinoline quinone biosynthesis protein A
PA14_07090	PA1987	Biosynthesis of cofactors	<i>pqqC</i>	-2.15	-3.33			COG5424, Pyrroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C [Coenzyme metabolism].
PA14_55820	PA3812	Biosynthesis of cofactors	<i>iscA</i>	-6.75	-4.24	4.09	-3.58	probable iron-binding protein IscA
PA14_08240	PA3813	Biosynthesis of cofactors	<i>iscU</i>	-6.85	-3.97	5.15	-5.38	IscU, NifU homolog involved in Fe-S cluster formation [Energy production and conversion].
PA14_64670	PA4893	Biosynthesis of cofactors	<i>ureG</i>		-2.75	7.72	-8.55	HypB, Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase [Posttranslational modification, protein turnover, chaperones / Transcription].

PA14_65740	PA4973	Biosynthesis of cofactors	<i>thiC</i>		3.17		-4.29	-3.18	thiamin biosynthesis protein ThiC
PA14_02590	PA0212	Carbon compound catabolism	<i>mdcE</i>		-2.72	3.92	3.73	3.48	malonate decarboxylase gamma subunit
PA14_02760	PA0226	Carbon compound catabolism			4.77		-4.05	-3.15	AtoD, Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit [Lipid metabolism].
PA14_37530	PA2086	Carbon compound catabolism		-2.99	-2.42				MhpC, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [General function prediction only].
PA14_36530	PA2290	Carbon compound catabolism	<i>gcd</i>	-2.88	-2.04		-6.71		Gcd, Glucose dehydrogenase [Carbohydrate transport and metabolism].
PA14_39925	PA2414	Carbon compound catabolism		-2.26	-2.53	5.24	-3.15	-3.69	-3.44 COG2133, Glucose/sorbose dehydrogenases [Carbohydrate transport and metabolism].
PA14_33450	PA2416	Carbon compound catabolism	<i>treA</i>		-3.24	4.03		-2.42	periplasmic trehalase precursor
PA14_32240	PA2507	Carbon compound catabolism	<i>catA</i>		29.64		-33.33	-33.33	
PA14_32230	PA2508	Carbon compound catabolism	<i>catC</i>		3.43	11.90		-17.89	-17.37 CatC1, Muconolactone delta-isomerase [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_32220	PA2509	Carbon compound catabolism	<i>catB</i>			43.79		-9.09	-16.67
PA14_32160	PA2512	Carbon compound catabolism	<i>antA</i>		2.57	36.91		-48.31	-32.25 anthranilate dioxygenase large subunit
PA14_32150	PA2513	Carbon compound catabolism	<i>antB</i>		2.98	50.41		-56.18	-33.39 anthranilate dioxygenase small subunit
PA14_32140	PA2514	Carbon compound catabolism	<i>antC</i>		4.72	26.46		-86.96	-66.07 anthranilate dioxygenase reductase
PA14_49760	PA1130	Cell wall / LPS / capsule	<i>rhlC</i>		-3.04	6.05			COG1216, Predicted glycosyltransferases [General function prediction only].
PA14_46770	PA2717	Central intermediary metabolism	<i>cpo</i>	-2.79	-11.54		-7.94		MhpC, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [General function prediction only].
PA14_72370	PA5058	Central intermediary metabolism	<i>phaC</i>	-2.83	-2.39	3.41	-5.43		PhaC, Poly(3-hydroxyalcanoate) synthetase [Lipid metabolism].
PA14_68850	PA5213	Central intermediary metabolism	<i>gcvP1</i>	-2.06	-2.93		-4.59		GcvP, Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain [Amino acid transport and metabolism].
PA14_26020	PA3810	Chaperones and heat shock proteins	<i>hscA</i>	-4.96	-106.30	9.24		-6.10	-5.49 DnaK, Molecular chaperone, heat shock protein [Posttranslational modification, protein turnover, chaperones].
PA14_36660	PA3811	Chaperones and heat shock proteins	<i>hscB</i>	-6.03	-3.60	5.04	-3.45	-3.08	DjIA, DnaJ-domain-containing proteins 1, heat shock protein [Posttranslational modification, protein turnover, chaperones].

PA14_57020	PA4386	Chaperones and heat shock proteins	<i>groES, mopB</i>	-2.94	-4.65	-2.56	2.68	GroS, Co-chaperonin GroES (HSP10) [Posttranslational modification, protein turnover, chaperones].
PA14_09930	PA4172	DNA replication, recombination, modification and repair		-2.21		3.07		XthA, Exonuclease III [DNA replication, recombination, and repair].
PA14_06830	PA0524	Energy metabolism	<i>norB</i>	-2.28	-12.64	7.57	-3.01	NorB, Nitric oxide reductase large subunit [Inorganic ion transport and metabolism].
PA14_61010	PA1317	Energy metabolism	<i>cyoA</i>	-4.32	-8.77	2.21	-3.89	CyoA, Heme/copper-type cytochrome/quinol oxidases, subunit 2 [Energy production and conversion].
PA14_09290	PA1318	Energy metabolism	<i>cyoB</i>	-4.99	-4.67		-4.27	CyoB, Heme/copper-type cytochrome/quinol oxidases, subunit 1 [Energy production and conversion].
PA14_09540	PA1319	Energy metabolism	<i>cyoC</i>	-8.27	-15.58		-16.37	-2.86 CyoC, Heme/copper-type cytochrome/quinol oxidase, subunit 3 [Energy production and conversion].
PA14_09530	PA1320	Energy metabolism	<i>cyoD</i>	-7.19	-10.91		-10.95	CyoD, Heme/copper-type cytochrome/quinol oxidase, subunit 4 [Energy production and conversion].
PA14_47150	PA1321	Energy metabolism	<i>cyoE</i>	-15.17	-2.87		-4.12	CyoE, Polypropenyltransferase (cytochrome oxidase assembly factor) [Posttranslational modification, protein turnover, chaperones].
PA14_55200	PA1562	Energy metabolism	<i>acnA, can</i>	-2.19	-8.86		-3.85	-4.59 AcnA, Aconitase A [Energy production and conversion].
PA14_36310	PA2153	Energy metabolism	<i>glgB</i>	-4.10	-6.27		-7.46	-3.77 -3.46 1,4-alpha-glucan branching enzyme
PA14_16660	PA2165	Energy metabolism	<i>glgA</i>	-2.23	-9.68	8.92		-2.13 GlgA, Glycogen synthase [Carbohydrate transport and metabolism].
PA14_09500	PA3032	Energy metabolism	<i>snr1</i>	-5.08	-11.98	10.83	-5.59	-5.59 -4.31 MauG, Cytochrome c peroxidase [Inorganic ion transport and metabolism].
PA14_23070	PA3183	Energy metabolism	<i>zwf</i>	-2.11	-4.17			Zwf, Glucose-6-phosphate 1-dehydrogenase [Carbohydrate transport and metabolism].
PA14_20180	PA3394	Energy metabolism	<i>nosF</i>		-12.35	11.73	-5.18	-4.66 CcmA, ABC-type multidrug transport system, ATPase component [Defense mechanisms].
PA14_48200	PA3415	Energy metabolism		-2.44	-2.02		-5.92	AceF, Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component, and related enzymes [Energy production and conversion].
PA14_40630	PA3416	Energy metabolism		-3.03	-2.95	4.14	-26.95	-5.36 AcoB, Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit [Energy production and conversion].
PA14_19900	PA3417	Energy metabolism			-2.29	4.33	-10.40	-2.34 AcoA, Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Energy production and conversion].
PA14_09340	PA3809	Energy metabolism	<i>fdx2</i>	-4.53	-2.42	5.21		-2.31 Fdx, Ferredoxin, [2Fe-2S] [Energy production and conversion].
PA14_62960	PA3929	Energy metabolism	<i>cioB</i>	-3.29	-3.23	2.02		AppB, Cytochrome bd-type quinol oxidase, subunit 2 [Energy production and conversion].
PA14_39890	PA3930	Energy metabolism	<i>cioA</i>	-4.43	-4.31		-6.41	CydA, Cytochrome bd-type quinol oxidase, subunit 1 [Energy production and conversion].
PA14_58030	PA4470	Energy metabolism	<i>fumC1</i>		-54.64	6.80		-4.84 fumarate hydratase

PA14_48610	PA1869	Fatty acid and phospholipid metabolism	-4.46	-2.55		2.67	AcpP, Acyl carrier protein [Lipid metabolism / Secondary metabolites biosynthesis, transport, and catabolism].		
PA14_00650	PA0052	Hypothetical, unclassified, unknown		-2.64	3.30		COG1917, Uncharacterized conserved protein, contains double-stranded beta-helix domain [Function unknown].		
PA14_00700	PA0058	Hypothetical, unclassified, unknown	-2.61	-2.11			COG3531, Predicted protein-disulfide isomerase [Posttranslational modification, protein turnover, chaperones].		
PA14_19100	PA0250	Hypothetical, unclassified, unknown	-4.32	-3.76	7.35	-3.05	COG2905, Predicted signal-transduction protein containing cAMP-binding and CBS domains [Signal transduction mechanisms].		
PA14_09270	PA0269	Hypothetical, unclassified, unknown	-3.05	-2.31	3.93	-4.08	COG2128, Uncharacterized conserved protein [Function unknown].		
PA14_19910	PA0270	Hypothetical, unclassified, unknown	-2.66	-3.17	4.32	-3.03	COG1917, Uncharacterized conserved protein, contains double-stranded beta-helix domain [Function unknown].		
PA14_22980	PA0271	Hypothetical, unclassified, unknown	-3.25	-4.32	4.30	-3.73	COG1359, Uncharacterized conserved protein [Function unknown].		
PA14_48530	PA0315	Hypothetical, unclassified, unknown	-3.09	-8.06		-4.42	hypothetical protein		
PA14_52130	PA0429	Hypothetical, unclassified, unknown	-2.35	-2.65			hypothetical protein		
PA14_09320	PA0431	Hypothetical, unclassified, unknown	-4.51	-4.01			SpoT, Guanosine polyphosphate pyrophosphohydrolases/synthetases [Signal transduction mechanisms / Transcription].		
PA14_06120	PA0467	Hypothetical, unclassified, unknown	-2.23	-2.69		-4.85	Gst, Glutathione S-transferase [Posttranslational modification, protein turnover, chaperones].		
PA14_61190	PA0468	Hypothetical, unclassified, unknown	-2.11	-4.47		-3.13	Vgb, Streptogramin lyase [Defense mechanisms].		
PA14_07660	PA0587	Hypothetical, unclassified, unknown	yeaH	-2.17	4.95	-8.85	-7.09	-4.08	conserved hypothetical protein
PA14_07680	PA0588	Hypothetical, unclassified, unknown	yeaG	-21.01	4.42	-6.06	-3.97	-2.23	PrkA, Putative Ser protein kinase [Signal transduction mechanisms].
PA14_07980	PA0613	Hypothetical, unclassified, unknown	-4.11	2.57	6.45		2.47	hypothetical protein	
PA14_55570	PA0673	Hypothetical, unclassified, unknown	pigB		9.13		-14.79	-10.34	hypothetical protein
PA14_54080	PA0788	Hypothetical, unclassified, unknown	-2.23	-2.97			MrcB, Membrane carboxypeptidase (penicillin-binding protein) [Cell envelope biogenesis, outer membrane].		
PA14_53810	PA0808	Hypothetical, unclassified, unknown		-36.81	2.89			COG3832, Uncharacterized conserved protein [Function unknown].	
PA14_52940	PA0875	Hypothetical, unclassified, unknown			4.92	3.29	-3.41	-2.33	COG1289, Predicted membrane protein [Function unknown].

PA14_72540	PA0938	Hypothetical, unclassified, unknown	-2.76	-3.59		WzzB, Chain length determinant protein [Cell envelope biogenesis, outer membrane].	
PA14_59960	PA0982	Hypothetical, unclassified, unknown		-2.81	2.11	DsbG, Protein-disulfide isomerase [Posttranslational modification, protein turnover, chaperones].	
PA14_49330	PA1166	Hypothetical, unclassified, unknown	-2.09	-5.78	-4.59	COG0412, Dienelactone hydrolase and related enzymes [Secondary metabolites biosynthesis, transport, and catabolism].	
PA14_36500	PA1211	Hypothetical, unclassified, unknown	-9.80	-8.90	-11.39		
PA14_09370	PA1213	Hypothetical, unclassified, unknown	-5.07	-3.47	-8.26	hypothetical protein	
PA14_36620	PA1214	Hypothetical, unclassified, unknown	-6.27	3.86	-11.03	AsnB, Asparagine synthase (glutamine-hydrolyzing) [Amino acid transport and metabolism].	
PA14_09410	PA1216	Hypothetical, unclassified, unknown	-11.22	-2.16	3.84	COG4976, Predicted methyltransferase (contains TPR repeat) [General function prediction only].	
PA14_72510	PA1219	Hypothetical, unclassified, unknown	-3.34	-6.04	2.14	COG3319, Thioesterase domains of type I polyketide synthases or non-ribosomal peptide synthetases [Secondary metabolites biosynthesis, transport, and catabolism].	
PA14_09280	PA1220	Hypothetical, unclassified, unknown	-5.28	-3.12	-6.90		
PA14_38800	PA1289	Hypothetical, unclassified, unknown	-2.01	-3.24	-3.34		
PA14_47130	PA1323	Hypothetical, unclassified, unknown		-31.51	3.36	ElaB, Uncharacterized conserved protein [Function unknown].	
PA14_47120	PA1324	Hypothetical, unclassified, unknown		-11.26	2.32	-6.25	hypothetical protein
PA14_46840	PA1348	Hypothetical, unclassified, unknown		-3.21	4.46		
PA14_46820	PA1350	Hypothetical, unclassified, unknown	-2.10	-3.07		COG4312, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_11130	PA1353	Hypothetical, unclassified, unknown	-2.38	-2.36		PhnB, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_34500	PA1354	Hypothetical, unclassified, unknown	-3.21	-3.75	-3.52	COG3795, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_46750	PA1356	Hypothetical, unclassified, unknown	-2.05	-3.47	3.05		
PA14_43030	PA1658	Hypothetical, unclassified, unknown	-2.49	2.95		COG3517, Uncharacterized protein conserved in bacteria [Function unknown].	

PA14_42920	PA1667	Hypothetical, unclassified, unknown		-10.06	2.42		COG3522, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_42910	PA1668	Hypothetical, unclassified, unknown		-3.92	3.53		COG3455, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_42130	PA1733	Hypothetical, unclassified, unknown		-2.10	-2.40	-3.33	COG3484, Predicted proteasome-type protease [Posttranslational modification, protein turnover, chaperones].	
PA14_01580	PA1784	Hypothetical, unclassified, unknown		-2.63	-2.73	-3.56		
PA14_48630	PA1847	Hypothetical, unclassified, unknown	yhgI	-2.74	-2.01	3.96	COG0694, Thioredoxin-like proteins and domains [Posttranslational modification, protein turnover, chaperones].	
PA14_40110	PA1887	Hypothetical, unclassified, unknown		-14.85	3.13	-5.00	hypothetical protein	
PA14_55920	PA1888	Hypothetical, unclassified, unknown		-2.90	-2.39	-6.58	hypothetical protein	
PA14_08090	PA1906	Hypothetical, unclassified, unknown		-2.04	-9.76	3.07	Hit, Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases [Nucleotide transport and metabolism / Carbohydrate transport and metabolism / General function prediction only].	
PA14_09210	PA1907	Hypothetical, unclassified, unknown		-2.17	-36.28	3.28	-5.03	COG4188, Predicted dienelactone hydrolase [General function prediction only].
PA14_39270	PA1951	Hypothetical, unclassified, unknown		-4.63	7.72		hypothetical protein	
PA14_66850	PA2030	Hypothetical, unclassified, unknown		-3.59	-2.77	11.19	-6.25 -2.13	hypothetical protein
PA14_31360	PA2031	Hypothetical, unclassified, unknown		-4.85	-2.38	9.07	-6.90	hypothetical protein
PA14_38210	PA2034	Hypothetical, unclassified, unknown		-2.26	2.07		-4.25	CobL, Precorrin-6B methylase 2 [Coenzyme metabolism].
PA14_33900	PA2066	Hypothetical, unclassified, unknown		-2.92	-2.46			COG1434, Uncharacterized conserved protein [Function unknown].
PA14_36980	PA2134	Hypothetical, unclassified, unknown		-2.14	-3.92	-3.86		COG3652, Predicted outer membrane protein [Function unknown].
PA14_36880	PA2141	Hypothetical, unclassified, unknown		-2.54	7.70			CinA, Uncharacterized protein (competence- and mitomycin-induced) [General function prediction only].
PA14_36850	PA2143	Hypothetical, unclassified, unknown		-27.56	13.89			hypothetical protein
PA14_61520	PA2146	Hypothetical, unclassified, unknown	yciG	-2.33	-2.33	5.99	-5.52 -4.52	conserved hypothetical protein

PA14_04100	PA2149	Hypothetical, unclassified, unknown	-2.71	-2.03			-2.55	hypothetical protein
PA14_39590	PA2151	Hypothetical, unclassified, unknown	-2.55	-2.73	20.21	-5.15	-7.19	-8.89 AmyA, Glycosidases [Carbohydrate transport and metabolism].
PA14_14750	PA2159	Hypothetical, unclassified, unknown	-4.34	-5.26	4.25	-7.69		-2.10 COG0517, FOG: CBS domain [General function prediction only].
PA14_53300	PA2161	Hypothetical, unclassified, unknown	-2.66	-54.88	70.94	-6.71	-10.17	-7.38 hypothetical protein
PA14_08250	PA2163	Hypothetical, unclassified, unknown	-2.29	-2.58	3.95	-4.65		MalQ, 4-alpha-glucanotransferase [Carbohydrate transport and metabolism].
PA14_36300	PA2169	Hypothetical, unclassified, unknown	-3.52	-2.47		-4.50		hypothetical protein
PA14_39910	PA2171	Hypothetical, unclassified, unknown	-2.55	-4.07	9.61	-4.95	-8.40	-6.40 hypothetical protein
PA14_14800	PA2173	Hypothetical, unclassified, unknown	-2.87	-6.54	5.83	-6.06	-5.32	-3.62 hypothetical protein
PA14_36470	PA2174	Hypothetical, unclassified, unknown		-4.70	2.42			
PA14_36390	PA2179	Hypothetical, unclassified, unknown	-2.18	-2.49				HemK, Methylase of polypeptide chain release factors [Translation, ribosomal structure and biogenesis].
PA14_36375	PA2180	Hypothetical, unclassified, unknown	-2.18	-3.70	3.79		-3.08	-3.40 hypothetical protein
PA14_36350	PA2189	Hypothetical, unclassified, unknown	-2.70	-2.14				ClpP, Protease subunit of ATP-dependent Clp proteases [Posttranslational modification, protein turnover, chaperones / Intracellular trafficking and secretion].
PA14_47180	PA2328	Hypothetical, unclassified, unknown	-4.54	-5.47		-4.52		TauA, ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Inorganic ion transport and metabolism].
PA14_01720	PA2330	Hypothetical, unclassified, unknown	-11.90	-4.00		-6.80		CaiA, Acyl-CoA dehydrogenases [Lipid metabolism].
PA14_23030	PA2362	Hypothetical, unclassified, unknown	-2.24	-3.49		-6.80		COG3455, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_34490	PA2365	Hypothetical, unclassified, unknown	-4.81	-10.73		-5.46		COG3516, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_10350	PA2366	Hypothetical, unclassified, unknown	-3.52	-3.89		-6.29	-3.13	COG3517, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_26990	PA2368	Hypothetical, unclassified, unknown	-2.84	-2.44		-11.89	-3.69	COG3518, Uncharacterized protein conserved in bacteria [Function unknown].

PA14_29020	PA2381	Hypothetical, unclassified, unknown	-2.41	-2.18	-3.09			hypothetical protein
PA14_17480	PA2405	Hypothetical, unclassified, unknown	-2.08	-7.69	-12.61	3.54	-2.78	hypothetical protein
PA14_39860	PA2406	Hypothetical, unclassified, unknown	-2.06	-2.34	3.35	-3.06		
PA14_33250	PA2427	Hypothetical, unclassified, unknown	-9.59	5.91		-10.80		hypothetical protein
PA14_33160	PA2433	Hypothetical, unclassified, unknown	-4.60	2.22	-5.13			hypothetical protein
PA14_03510	PA2448	Hypothetical, unclassified, unknown	-3.21	-5.24	4.88	-3.45	-3.40	COG1574, Predicted metal-dependent hydrolase with the TIM-barrel fold [General function prediction only].
PA14_32280	PA2504	Hypothetical, unclassified, unknown	-4.44	3.82	-3.83	-3.08		COG4859, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_46780	PA2544	Hypothetical, unclassified, unknown	-2.17	-2.32				RimI, Acetyltransferases [General function prediction only].
PA14_70940	PA2564	Hypothetical, unclassified, unknown	<i>tam</i>	-3.94	-2.56	4.94		Tam, Trans-aconitate methyltransferase [General function prediction only].
PA14_70950	PA2565	Hypothetical, unclassified, unknown	-2.30	-2.32	6.14		-3.98	hypothetical protein
PA14_36320	PA2566	Hypothetical, unclassified, unknown	-2.64	-2.38	4.04	-4.00		HcaD, Uncharacterized NAD(FAD)-dependent dehydrogenases [General function prediction only].
PA14_15120	PA2658	Hypothetical, unclassified, unknown	-2.06	-2.31				COG3212, Predicted membrane protein [Function unknown].
PA14_40250	PA2659	Hypothetical, unclassified, unknown	-2.95	-2.00	-2.31			COG3212, Predicted membrane protein [Function unknown].
PA14_28600	PA2747	Hypothetical, unclassified, unknown	-2.22	-2.59				
PA14_05620	PA2927	Hypothetical, unclassified, unknown	-2.45	-2.59	-3.70			hypothetical protein
PA14_44290	PA3091	Hypothetical, unclassified, unknown	-2.07	-2.21				Smc, Chromosome segregation ATPases [Cell division and chromosome partitioning].
PA14_22320	PA3237	Hypothetical, unclassified, unknown	-92.82	-81.97	56.49	-14.81	-5.94	COG3205, Predicted membrane protein [Function unknown].
PA14_36630	PA3274	Hypothetical, unclassified, unknown	-3.13	-2.68	3.45			hypothetical protein
PA14_10360	PA3287	Hypothetical, unclassified, unknown	-6.46	-15.82	13.81	-19.31		Arp, FOG: Ankyrin repeat [General function prediction only].

PA14_20460	PA3371	Hypothetical, unclassified, unknown		-5.76	4.08	-4.65	-3.09	hypothetical protein
PA14_19110	PA3520	Hypothetical, unclassified, unknown		-10.12	-5.36	9.66	-2.41	CopZ, Copper chaperone [Inorganic ion transport and metabolism].
PA14_18680	PA3530	Hypothetical, unclassified, unknown	<i>bfd</i>	-3.17	-7.30	8.97		Bfd, Bacterioferritin-associated ferredoxin [Inorganic ion transport and metabolism].
PA14_16640	PA3691	Hypothetical, unclassified, unknown		-8.50	3.19	-3.04	-2.42	hypothetical protein
PA14_40240	PA3734	Hypothetical, unclassified, unknown		-2.70	-2.44			
PA14_50810	PA3784	Hypothetical, unclassified, unknown		-2.29	-4.79	-2.91	-7.58	-4.24
PA14_33870	PA3785	Hypothetical, unclassified, unknown		-2.19	-2.38	-2.28	-3.56	-6.21
PA14_14740	PA3815	Hypothetical, unclassified, unknown		-5.28	-3.46	5.68	4.35	COG1959, Predicted transcriptional regulator [Transcription].
PA14_14290	PA3844	Hypothetical, unclassified, unknown		-2.09	2.69			Gst, Glutathione S-transferase [Posttranslational modification, protein turnover, chaperones].
PA14_05580	PA3923	Hypothetical, unclassified, unknown		-2.16	-4.53	-5.49	-4.67	-3.92
PA14_13050	PA3928	Hypothetical, unclassified, unknown		-3.28	-2.71	4.68		hypothetical protein
PA14_10380	PA4139	Hypothetical, unclassified, unknown		-2.08	-7.09		-3.91	
PA14_31290	PA4141	Hypothetical, unclassified, unknown		-5.04	-2.21	9.94		hypothetical protein
PA14_20470	PA4220	Hypothetical, unclassified, unknown	<i>fptB</i>	-53.20	-7.75	5.18	-7.19	-5.35
PA14_55840	PA4298	Hypothetical, unclassified, unknown		-2.61	4.04	-6.21		hypothetical protein
PA14_14730	PA4384	Hypothetical, unclassified, unknown		-4.14	-3.28	4.46		COG4318, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_58010	PA4469	Hypothetical, unclassified, unknown		-110.25	4.28	-3.61	-3.60	hypothetical protein
PA14_09490	PA4573	Hypothetical, unclassified, unknown		-2.42	-3.38			hypothetical protein

PA14_61550	PA4607	Hypothetical, unclassified, unknown	-2.35	-23.67	-5.49	2.17	hypothetical protein	
PA14_65040	PA4624	Hypothetical, unclassified, unknown	-2.29	-37.78			FhaC, Hemolysin activation/secretion protein [Intracellular trafficking and secretion].	
PA14_13340	PA4625	Hypothetical, unclassified, unknown	-2.51	-3.42	3.39		hypothetical protein	
PA14_40100	PA4641	Hypothetical, unclassified, unknown	-2.49	-2.21			still frameshift hypothetical protein	
PA14_61430	PA4642	Hypothetical, unclassified, unknown	-4.13	5.38	5.83	3.02	hypothetical protein	
PA14_43050	PA4648	Hypothetical, unclassified, unknown	-2.09	-2.24	-3.52		COG5430, Uncharacterized secreted protein [Function unknown].	
PA14_32950	PA4650	Hypothetical, unclassified, unknown	-2.32	-5.10	5.26	-2.28	COG5430, Uncharacterized secreted protein [Function unknown].	
PA14_61540	PA4652	Hypothetical, unclassified, unknown		-9.23	6.55		FimD, P pilus assembly protein, porin PapC [Cell motility and secretion / Intracellular trafficking and secretion].	
PA14_09400	PA4653	Hypothetical, unclassified, unknown	-2.76	-4.79	-4.13		COG5430, Uncharacterized secreted protein [Function unknown].	
PA14_62680	PA4738	Hypothetical, unclassified, unknown	yjbJ	-4.98	9.47	-4.90	-3.40	COG3237, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_63330	PA4792	Hypothetical, unclassified, unknown		-2.79	2.20			UgpQ, Glycerophosphoryl diester phosphodiesterase [Energy production and conversion].
PA14_60520	PA4874	Hypothetical, unclassified, unknown	psiF	-2.20	-2.52	-4.69		conserved hypothetical protein
PA14_64930	PA4916	Hypothetical, unclassified, unknown		-2.05	-3.18			COG1051, ADP-ribose pyrophosphatase [Nucleotide transport and metabolism].
PA14_34030	PA4925	Hypothetical, unclassified, unknown		-2.60	-2.65	-3.22		MscS, Small-conductance mechanosensitive channel [Cell envelope biogenesis, outer membrane].
PA14_55850	PA5023	Hypothetical, unclassified, unknown	ydiU	-2.72	-37.36	3.96		COG0397, Uncharacterized conserved protein [Function unknown].
PA14_41500	PA5061	Hypothetical, unclassified, unknown	phal	-2.31	-2.87			conserved hypothetical protein
PA14_72520	PA5220	Hypothetical, unclassified, unknown		-2.13	-2.11			hypothetical protein
PA14_69640	PA5275	Hypothetical, unclassified, unknown	cyaY	-13.55	4.21	4.34	2.98	CyaY, Protein implicated in iron transport, frataxin homolog [Inorganic ion transport and metabolism].

PA14_71100	PA5383	Hypothetical, unclassified, unknown	<i>yelH</i>		7.82	-6.54	-3.66	COG2855, Predicted membrane protein [Function unknown].	
PA14_71200	PA5392	Hypothetical, unclassified, unknown		-3.35	-3.81			TdcF, Putative translation initiation inhibitor, yigF family [Translation, ribosomal structure and biogenesis].	
PA14_10330	PA5395	Hypothetical, unclassified, unknown		-2.11	-3.62		2.74	COG3558, Uncharacterized protein conserved in bacteria [Function unknown].	
PA14_08210	PA4299	Motility and Attachment	<i>tadD</i>	-2.57	-2.34	3.84	-4.31	hypothetical protein	
PA14_33480	PA4303	Motility and Attachment	<i>tadZ</i>	-2.95	-11.11	5.97	-3.83	hypothetical protein	
PA14_55930	PA4305	Motility and Attachment	<i>rcpC</i>		-2.26	2.73		hypothetical protein	
PA14_08260	PA4306	Motility and Attachment	<i>fip</i>	-4.09	-15.54	3.31	2.08	Flp, Flp pilus assembly protein, pilin Flp [Intracellular trafficking and secretion].	
PA14_34880	PA4651	Motility and Attachment		-2.62	-14.19		-14.81	FimC, P pilus assembly protein, chaperone PapD [Cell motility and secretion / Intracellular trafficking and secretion].	
PA14_61020	PA0849	Nucleotide biosynthesis	<i>trxB2</i>	-4.62	-6.49	10.97	-8.13	-3.39	TrxB, Thioredoxin reductase [Posttranslational modification, protein turnover, chaperones].
PA14_61530	PA5496	Nucleotide biosynthesis	<i>nrdJb</i>	-2.31	-10.67				hypothetical protein
PA14_13030	PA5497	Nucleotide biosynthesis	<i>nrdJa</i>	-3.13	-8.74				hypothetical protein
PA14_48620	PA1875	Protein secretion/export apparatus	<i>opmL</i>	-3.73	-5.08		-12.55	-2.19	TolC, Outer membrane protein [Cell envelope biogenesis, outer membrane / Intracellular trafficking and secretion].
PA14_21670	PA1877	Protein secretion/export apparatus		-2.59	-3.56	3.83	-14.43		EmrA, Multidrug resistance efflux pump [Defense mechanisms].
PA14_09380	PA4142	Protein secretion/export apparatus		-4.62	-5.11				EmrA, Multidrug resistance efflux pump [Defense mechanisms].
PA14_61410	PA4144	Protein secretion/export apparatus	<i>opmK</i>	-2.25	-539.10				TolC, Outer membrane protein [Cell envelope biogenesis, outer membrane / Intracellular trafficking and secretion].
PA14_08120	PA4302	Protein secretion/export apparatus	<i>tadA, hvbA</i>	-2.20	-2.43	3.28	-22.42	-5.12	probable type II secretion system protein, CpaF, Flp pilus assembly protein, ATPase CpaF [Intracellular trafficking and secretion].
PA14_34070	PA4304	Protein secretion/export apparatus	<i>rcpA, xqhC</i>	-3.64	-6.78		-3.16		probable type II secretion system protein
PA14_15130	PA0249	Putative enzymes		-2.11	-2.71				RimI, Acetyltransferases [General function prediction only].
PA14_34020	PA0704	Putative enzymes		-2.44	-12.00		-10.08		GatA, Asp-tRNAAasn/Glu-tRNAGln amidotransferase A subunit and related amidases [Translation, ribosomal structure and biogenesis].
PA14_53110	PA0863	Putative enzymes			-2.21	3.82	-3.89	-2.24	Qor, NADPH:quinone reductase and related Zn-dependent oxidoreductases [Energy production and conversion / General function prediction only].
PA14_51050	PA1027	Putative enzymes	<i>pcd</i>		-2.79	3.06			PutA, NAD-dependent aldehyde dehydrogenases [Energy production and conversion].

PA14_09900	PA1240	Putative enzymes	-2.85	-6.54				CaiD, Enoyl-CoA hydratase/carnithine racemase [Lipid metabolism].	
PA14_47550	PA1287	Putative enzymes	-2.55	-2.34				BtuE, Glutathione peroxidase [Posttranslational modification, protein turnover, chaperones].	
PA14_66160	PA1391	Putative enzymes			23.82	-7.19	-3.48	RfaG, Glycosyltransferase [Cell envelope biogenesis, outer membrane].	
PA14_42980	PA1662	Putative enzymes	-2.15	-4.25				ClpA, ATPases with chaperone activity, ATP-binding subunit [Posttranslational modification, protein turnover, chaperones].	
PA14_40430	PA1860	Putative enzymes		-2.12	2.34			COG3315, O-Methyltransferase involved in polyketide biosynthesis [Secondary metabolites biosynthesis, transport, and catabolism].	
PA14_19920	PA1880	Putative enzymes	-2.20	-11.64		-4.50		CoxL, Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs [Energy production and conversion].	
PA14_27730	PA1881	Putative enzymes	-2.13	-5.49		-5.29		CoxS, Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs [Energy production and conversion].	
PA14_40200	PA2067	Putative enzymes	-2.08	-7.21		-4.63		COG0637, Predicted phosphatase/phosphohexomutase [General function prediction only].	
PA14_36490	PA2069	Putative enzymes	-3.41	-2.53	7.44	-3.83		COG2192, Predicted carbamoyl transferase, NodU family [Posttranslational modification, protein turnover, chaperones].	
PA14_37340	PA2108	Putative enzymes			3.53	-3.03	-3.27	IlvB, Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphopyruvate decarboxylase] [Amino acid transport and metabolism / Coenzyme metabolism].	
PA14_55890	PA2152	Putative enzymes	-2.92	-5.45	3.37	-4.81	-2.50	Ble, Uncharacterized protein, probably involved in trehalose biosynthesis [Carbohydrate transport and metabolism].	
PA14_40260	PA2158	Putative enzymes	-7.91	-3.41	4.58	-13.76	-3.14	Tdh, Threonine dehydrogenase and related Zn-dependent dehydrogenases [Amino acid transport and metabolism / General function prediction only].	
PA14_01710	PA2160	Putative enzymes	glgX	-10.06	-5.83	3.33	-11.72	PulA, Type II secretory pathway, pullulanase PulA and related glycosidases [Carbohydrate transport and metabolism].	
PA14_36590	PA2162	Putative enzymes		-2.27	-6.80	4.10	-5.10	TreY, Maltooligosyl trehalose synthase [Carbohydrate transport and metabolism].	
PA14_36580	PA2164	Putative enzymes			-8.33	4.98	-3.55	GlgB, 1,4-alpha-glucan branching enzyme [Carbohydrate transport and metabolism].	
PA14_35150	PA2275	Putative enzymes	yahK		12.10	5.88	-5.65	-3.77	AdhP, Zn-dependent alcohol dehydrogenases [General function prediction only].
PA14_31660	PA2298	Putative enzymes		-2.05	-43.31			SdhA, Succinate dehydrogenase/fumarate reductase, flavoprotein subunit [Energy production and conversion].	
PA14_47190	PA2378	Putative enzymes		-3.65	-2.26		-3.83	CoxL, Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs [Energy production and conversion].	
PA14_16100	PA2815	Putative enzymes	yafH	-2.31	-10.38		-5.21	CaiA, Acyl-CoA dehydrogenases [Lipid metabolism].	
PA14_19360	PA3460	Putative enzymes		-2.32	-9.03	7.14	-6.17	-7.58	-6.30 DdIA, D-alanine-D-alanine ligase and related ATP-grasp enzymes [Cell envelope biogenesis, outer membrane].

PA14_16930	PA3667	Putative enzymes		-2.76	-2.17		CsdB, Selenocysteine lyase [Amino acid transport and metabolism].	
PA14_12680	PA3957	Putative enzymes		-2.10	-9.65	3.42	2.78 DltE, Short-chain dehydrogenases of various substrate specificities [General function prediction only].	
PA14_34520	PA4079	Putative enzymes		-2.77	-4.53		DltE, Short-chain dehydrogenases of various substrate specificities [General function prediction only].	
PA14_09630	PA4199	Putative enzymes		-2.09	-2.28		CaiA, Acyl-CoA dehydrogenases [Lipid metabolism].	
PA14_62330	PA4709	Putative enzymes	<i>phuS</i>	-2.14	-5.46	5.36	-2.83 HemS, Putative heme degradation protein [Inorganic ion transport and metabolism].	
PA14_62400	PA4715	Putative enzymes	<i>yfdZ</i>	-2.20	-4.69		-2.02 COG0436, Aspartate/tyrosine/aromatic aminotransferase [Amino acid transport and metabolism].	
PA14_68040	PA5150	Putative enzymes		-2.51	4.38		FabG, Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Secondary metabolites biosynthesis, transport, and catabolism / General function prediction only].	
PA14_36650	PA5181	Putative enzymes		-2.50	-12.82	4.76	BisC, Anaerobic dehydrogenases, typically selenocysteine-containing [Energy production and conversion].	
PA14_70160	PA5313	Putative enzymes	<i>paaT</i>	-2.39	4.89		-3.10 BioA, Adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Coenzyme metabolism].	
PA14_71110	PA5384	Putative enzymes		-2.23	5.21		Aes, Esterase/lipase [Lipid metabolism].	
PA14_73140	PA5546	Putative enzymes		-11.81	9.44		Cfa, Cyclopropane fatty acid synthase and related methyltransferases [Cell envelope biogenesis, outer membrane].	
PA14_48980	PA0719	Related to phage, transposon, or plasmid		-22.17	2.53		hypothetical protein of bacteriophage P11	
PA14_03010	PA0243	Transcriptional regulators		-2.85	-2.26		AcrR, Transcriptional regulator [Transcription].	
PA14_06180	PA0472	Transcriptional regulators	<i>fiul</i>	-4.42	7.00		probable sigma-70 factor, ECF subfamily	
PA14_55550	PA0675	Transcriptional regulators		-3.24	6.46		RpoE, DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Transcription].	
PA14_08010	PA1300	Transcriptional regulators		-2.21	-4.24	3.13	4.45	-2.79 RpoE, DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Transcription].
PA14_48640	PA2196	Transcriptional regulators		-4.78	-2.27		3.92	2.88 AcrR, Transcriptional regulator [Transcription].
PA14_35540	PA2246	Transcriptional regulators	<i>bkdR</i>	-2.14	-2.24	2.03		Lrp, Transcriptional regulators [Transcription].
PA14_36710	PA2299	Transcriptional regulators		-2.96	-5.48			PhnF, Transcriptional regulators [Transcription].
PA14_33260	PA2426	Transcriptional regulators	<i>pvdS</i>	-33.33	48.69	-3.85		sigma factor PvdS
PA14_32710	PA2468	Transcriptional regulators	<i>foxl</i>	-11.04	4.75		-4.98	-3.40 probable sigma-70 factor, ECF subfamily
PA14_36605	PA2588	Transcriptional regulators		-2.36	-2.90	4.29		AraC, AraC-type DNA-binding domain-containing proteins, probable transcriptional regulator [Transcription].
PA14_26190	PA3622	Transcriptional regulators	<i>rpoS</i>	-2.23	-9.31		-5.35	RpoD, DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32) [Transcription].

PA14_36820	PA5059	Transcriptional regulators	<i>phaD</i>	-3.25	-2.84	8.29	-6.13			AcrR, Transcriptional regulator [Transcription].
	Pae_tR	Translation, post-translational modification, degradation		-5.36	-3.10	5.22	-6.13	-11.15	-12.12	tRNA_Cysteine, 2918603-2918676 (-) strand
PA14_49130	PA1183	Transport of small molecules	<i>dctA</i>	-2.35	-10.03					GltP, Na+/H+-dicarboxylate symporters [Energy production and conversion].
PA14_47160	PA2329	Transport of small molecules		-4.51	-4.07		-5.99			TauB, ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component [Inorganic ion transport and metabolism].
PA14_34970	PA3186	Transport of small molecules	<i>oprB</i>	-2.48	-2.34			2.68		OprB, Carbohydrate-selective porin [Cell envelope biogenesis, outer membrane].
PA14_55860	PA3187	Transport of small molecules	<i>gltK</i>	-2.04	-2.52		-3.30			MalK, ABC-type sugar transport systems, ATPase components [Carbohydrate transport and metabolism].
PA14_37780	PA3189	Transport of small molecules	<i>gltF</i>	-2.52	-2.85					UgpA, ABC-type sugar transport systems, permease components [Carbohydrate transport and metabolism].
PA14_66410	PA3190	Transport of small molecules	<i>gltB</i>	-2.41	-2.49	4.11				UgpB, ABC-type sugar transport system, periplasmic component [Carbohydrate transport and metabolism].
PA14_20450	PA3372	Transport of small molecules	<i>phnP</i>			8.05		-4.10	-3.43	PhnP, Metal-dependent hydrolases of the beta-lactamase superfamily I [General function prediction only].
PA14_20010	PA3408	Transport of small molecules	<i>hasR</i>		-2.27	3.35			-2.05	heme acquisition protein HasR
PA14_15070	PA3790	Transport of small molecules	<i>oprC</i>	-2.04	-4.22					CirA, Outer membrane receptor proteins, mostly Fe transport [Inorganic ion transport and metabolism].
PA14_11140	PA4206	Transport of small molecules	<i>mexH</i>	-71.64	-151.80	47.32	-3.14			RND efflux, AcrA, Membrane-fusion protein [Cell envelope biogenesis, outer membrane].
PA14_06170	PA0471	Two-component regulatory systems	<i>fiuR</i>	-2.88	-5.29	4.76				FecR, Fe2+-dicitrate sensor, membrane component [Inorganic ion transport and metabolism / Signal transduction mechanisms].
PA14_29360	PA2687	Two-component regulatory systems	<i>pfeS</i>		-3.62	4.69		-3.27	-3.75	BaeS, Signal transduction histidine kinase [Signal transduction mechanisms].
PA14_30240	PA4293	Two-component regulatory systems	<i>pprA</i>	-2.00	-2.62	2.26	-6.67			COG4191, Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Signal transduction mechanisms].

Negatively regulated genes

PA14_43220	PA1646	Adaptation, Protection		2.23	-6.33		4.09	2.62		Tar, Methyl-accepting chemotaxis protein [Cell motility and secretion / Signal transduction mechanisms].
PA14_21020	PA3327	Adaptation, Protection		5.62	-3.50					EntF, Non-ribosomal peptide synthetase modules and related proteins [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_20950	PA3331	Adaptation, Protection		2.55	4.30	-3.52				CypX, Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_18360	PA3553	Adaptation, Protection	<i>armC, pmrF</i>	2.52	2.18	-6.90	-8.93			WcaA, Glycosyltransferases involved in cell wall biogenesis [Cell envelope biogenesis, outer membrane].

PA14_61780	PA4671	Adaptation, Protection	<i>rplY</i>	2.05	3.52			RplY, Ribosomal protein L25 (general stress protein Ctc) [Translation, ribosomal structure and biogenesis].
PA14_06750	PA0132	Amino acid biosynthesis	<i>oapT</i>	3.00	3.41	-5.41	3.98	3.11 beta-alanine--pyruvate transaminase
PA14_51330	PA1004	Amino acid biosynthesis	<i>nadA</i>	2.03	-3.28			NadA, Quinolinate synthase [Coenzyme metabolism].
PA14_44010	PA1585	Amino acid biosynthesis	<i>sucA</i>	-2.56	-2.83	-3.98	-4.24	-2.21 SucA, 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Energy production and conversion].
PA14_35530	PA2247	Amino acid biosynthesis	<i>bkdA1</i>	-4.83	-3.56	-7.09	-4.41	-2.51 2-oxoisovalerate dehydrogenase (alpha subunit)
PA14_62600	PA4731	Amino acid biosynthesis	<i>panD</i>	2.11	-3.08			PanD, Aspartate 1-decarboxylase [Coenzyme metabolism].
PA14_12440	PA4759	Amino acid biosynthesis	<i>dapB</i>	4.93	3.02	-4.57		DapB, Dihydrodipicolinate reductase [Amino acid transport and metabolism].
PA14_65110	PA4930	Amino acid biosynthesis	<i>alr</i>	7.13	-3.03	3.93	4.33	2.49 Alr, Alanine racemase [Cell envelope biogenesis, outer membrane].
PA14_65795	PA4977	Amino acid biosynthesis	<i>arul</i>	2.00	4.58			IlvB, Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboxylase, phosphonopyruvate decarboxylase] [Amino acid transport and metabolism / Coenzyme metabolism].
PA14_11690	PA5495	Amino acid biosynthesis	<i>thrB</i>	6.25	2.15	-2.55		COG2334, Putative homoserine kinase type II (protein kinase fold) [General function prediction only].
PA14_38580	PA0509	Biosynthesis of cofactors	<i>nirN</i>	2.06	6.83			CccA, Cytochrome c, mono- and diheme variants [Energy production and conversion].
PA14_34900	PA0510	Biosynthesis of cofactors	<i>nirE</i>	5.26	18.31			CysG, Uroporphyrinogen-III methylase [Coenzyme metabolism].
PA14_37770	PA0511	Biosynthesis of cofactors	<i>nirJ</i>	2.99	2.63			COG0535, Predicted Fe-S oxidoreductases [General function prediction only].
PA14_09230	PA0513	Biosynthesis of cofactors	<i>nirG</i>	3.36	8.65			Lrp, Transcriptional regulators [Transcription].
PA14_29720	PA0515	Biosynthesis of cofactors	<i>nirD</i>	3.36	2.38			Lrp, Transcriptional regulators [Transcription].
PA14_60700	PA0517	Biosynthesis of cofactors	<i>nirC</i>	5.21	28.40	-6.17		CccA, Cytochrome c, mono- and diheme variants [Energy production and conversion].
PA14_72260	PA0518	Biosynthesis of cofactors	<i>nirM</i>	5.65	13.90	-4.03	2.08	cytochrome c-551 precursor
PA14_44470	PA1546	Biosynthesis of cofactors	<i>hemN</i>	2.19	8.48	-4.05		HemN, Coproporphyrinogen III oxidase and related Fe-S oxidoreductases [Coenzyme metabolism].
PA14_13260	PA3915	Biosynthesis of cofactors	<i>moaB1</i>	23.26	45.13	-3.36		MoaB, Molybdopterin biosynthesis enzymes [Coenzyme metabolism].
PA14_12020	PA4006	Biosynthesis of cofactors	<i>nadD, ybeN</i>		3.05	-3.21		NadD, Nicotinic acid mononucleotide adenyltransferase [Coenzyme metabolism].
PA14_28050	PA4919	Biosynthesis of cofactors	<i>pncB1</i>	2.34	2.15		4.93	PncB, Nicotinic acid phosphoribosyltransferase [Coenzyme metabolism].
PA14_02550	PA0208	Carbon compound catabolism	<i>mdcA</i>	2.56		-4.55	5.62	7.01 4.81 malonate decarboxylase alpha subunit
PA14_02610	PA0213	Carbon compound catabolism	<i>mdcG</i>	3.19	2.08		5.61	hypothetical protein

PA14_54000	PA0792	Carbon compound catabolism	<i>prpD</i>	-4.01	-2.53	-6.90				PrpD, Uncharacterized protein involved in propionate catabolism [General function prediction only].
PA14_70390	PA5332	Carbon compound catabolism	<i>crc</i>	2.26	-4.02	3.95	3.96	3.76		catabolite repression control protein
PA14_64950	PA3337	Cell wall / LPS / capsule	<i>rfaD</i>	7.19	9.58	-5.03	4.44	6.06		ADP-L-glycero-D-mannoheptose 6-epimerase
PA14_72500	PA3584	Central intermediary metabolism	<i>glpD</i>	2.00	-4.07	-5.65				GlpA, Glycerol-3-phosphate dehydrogenase [Energy production and conversion].
PA14_43770	PA4563	Central intermediary metabolism	<i>rpsT</i>	2.35	2.44	-2.99	30.05	2.01		RpsT, Ribosomal protein S20 [Translation, ribosomal structure and biogenesis].
PA14_62830	PA4748	Central intermediary metabolism	<i>tpiA</i>		5.78	-3.11	5.05	5.17	2.50	TpiA, Triosephosphate isomerase [Carbohydrate transport and metabolism].
PA14_71740	PA5436	Central intermediary metabolism		3.42	5.03	-7.52				AccC, Biotin carboxylase [Lipid metabolism].
PA14_23680	PA3126	Chaperones and heat shock proteins	<i>ibpA, hslT</i>	4.78	2.65	-6.85		2.22		IbpA, Molecular chaperone, heat shock protein (small heat shock protein) [Posttranslational modification, protein turnover, chaperones].
PA14_61000	PA5053	Chaperones and heat shock proteins	<i>hslV</i>	3.97	3.97	-3.50				HslV, ATP-dependent protease HslVU (ClpYQ), peptidase subunit [Posttranslational modification, protein turnover, chaperones].
PA14_07530	PA0577	DNA replication, recombination, modification and DNA repair	<i>dnaG</i>		4.98	-3.17				DnaG, DNA primase (bacterial type) [DNA replication, recombination, and repair].
PA14_15970	PA3745	DNA replication, recombination, modification and repair	<i>rpsP</i>		8.62	-3.03	3.50	3.16	2.29	RpsP, Ribosomal protein S16 [Translation, ribosomal structure and biogenesis].
PA14_04750	PA0362	Energy metabolism	<i>fdx1</i>		3.00	-3.19				ferredoxin [4Fe-4S]
PA14_66770	PA0516	Energy metabolism	<i>nirF</i>	2.79	5.96	-3.42				heme d1 biosynthesis protein NirF
PA14_21010	PA0519	Energy metabolism	<i>nirS</i>	4.69	53.09	-5.56				nitrite reductase precursor
PA14_06810	PA0523	Energy metabolism	<i>norC</i>	5.41	24.76					nitric-oxide reductase subunit C
PA14_44360	PA1555	Energy metabolism	<i>ccoP, fixP</i>	2.96	6.44	-9.52		3.44		CccA, Cytochrome c, mono- and diheme variants [Energy production and conversion].
PA14_44350	PA1556	Energy metabolism	<i>ccoO, fixO</i>	2.77	9.35	-8.47		3.13		CcoO, Cbb3-type cytochrome oxidase, cytochrome c subunit [Energy production and conversion].
PA14_44340	PA1557	Energy metabolism	<i>ccoN, fixN, cytN</i>	2.83	27.46	-12.21		2.79		CcoN, Cbb3-type cytochrome oxidase, subunit 1 [Posttranslational modification, protein turnover, chaperones].
PA14_34640	PA2321	Energy metabolism	<i>gntV, gntK, gnuK</i>		3.62	-3.91	3.13	8.87	5.41	gluconokinase
PA14_32530	PA2482	Energy metabolism		2.04	2.18					COG2863, Cytochrome c553 [Energy production and conversion].
PA14_01620	PA3621	Energy metabolism	<i>fdxA</i>	3.86	13.28	-5.26	5.79	2.08		COG1146, Ferredoxin [Energy production and conversion].
PA14_13830	PA3872	Energy metabolism	<i>narl</i>	2.28	2.50					Narl, Nitrate reductase gamma subunit [Energy production and conversion].

PA14_13810	PA3873	Energy metabolism	<i>narJ</i>	2.58	2.03			NarJ, Nitrate reductase delta subunit [Energy production and conversion].		
PA14_13740	PA3878	Energy metabolism	<i>narX</i>		5.03	-6.58		NarQ, Signal transduction histidine kinase, nitrate/nitrite-specific [Signal transduction mechanisms].		
PA14_13730	PA3879	Energy metabolism	<i>narL</i>	5.41	4.67	-8.06	3.16	two-component response regulator , CitB, Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Signal transduction mechanisms / Transcription].		
PA14_09030	PA4571	Energy metabolism		2.15	9.25	-3.38		COG3258, Cytochrome c [Energy production and conversion].		
PA14_30100	PA5427	Energy metabolism	<i>adhA</i>	3.29	2.56	-3.82	3.08	AdhP, Zn-dependent alcohol dehydrogenases [General function prediction only].		
PA14_20980	PA3333	Fatty acid and phospholipid metabolism	<i>fabH2</i>	2.56	6.69	-3.76	-4.81	FabH, 3-oxoacyl-[acyl-carrier-protein].		
PA14_20890	PA334	Fatty acid and phospholipid metabolism		3.75	3.97	-4.44		hypothetical protein		
PA14_17675	PA3603	Fatty acid and phospholipid metabolism	<i>dgkA</i>		2.83	-3.98	3.72	2.25	DgkA, Diacylglycerol kinase [Cell envelope biogenesis, outer membrane].	
PA14_66080	PA4997	Fatty acid and phospholipid metabolism	<i>msbA</i>		5.46	-3.14			MdlB, ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms].	
PA14_01730	PA0141	Hypothetical, unclassified, unknown		2.19	4.58	-6.85			COG2326, Uncharacterized conserved protein [Function unknown].	
PA14_02060	PA0165	Hypothetical, unclassified, unknown		2.03	2.88		3.18		Tsx, Nucleoside-binding outer membrane protein [Cell envelope biogenesis, outer membrane].	
PA14_02530	PA0201	Hypothetical, unclassified, unknown		3.46	21.46	-9.35	53.47	8.21	12.12	COG3545, Predicted esterase of the alpha/beta hydrolase fold [General function prediction only].
PA14_03160	PA0256	Hypothetical, unclassified, unknown				-5.38		4.59	2.20	hypothetical protein
PA14_06860	PA0526	Hypothetical, unclassified, unknown		4.07	14.62					hypothetical protein
PA14_06890	PA0529	Hypothetical, unclassified, unknown			5.59	2.37	-3.36			COG2258, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_07040	PA0542	Hypothetical, unclassified, unknown	<i>yqjC</i>	2.34	2.53					conserved hypothetical protein
PA14_07330	PA0563	Hypothetical, unclassified, unknown		2.21	3.62		8.94	2.04		COG3152, Predicted membrane protein [Function unknown].
PA14_54820	PA0731	Hypothetical, unclassified, unknown		2.25	3.42					hypothetical protein
PA14_51850	PA0960	Hypothetical, unclassified, unknown				-3.02		3.27	2.80	SlyX, Uncharacterized protein conserved in bacteria [Function unknown].

Protein ID	Protein ID	Gene Name	Start	End	Length	Score	Signal Peptide	Description				
PA14_51690	PA0974	Hypothetical, unclassified, unknown				2.22	-5.03	COG1729, Uncharacterized protein conserved in bacteria [Function unknown].				
PA14_48870	PA1192	Hypothetical, unclassified, unknown	ydaO			7.25	-3.34	3.19	MesJ, Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cell division and chromosome partitioning].			
PA14_20940	PA1343	Hypothetical, unclassified, unknown				6.80	2.01	-4.29		-5.88	-4.12	hypothetical protein
PA14_44270	PA1564	Hypothetical, unclassified, unknown				3.38	2.46					SirA, Predicted redox protein, regulator of disulfide bond formation [Posttranslational modification, protein turnover, chaperones].
PA14_44140	PA1574	Hypothetical, unclassified, unknown	yaiE			3.75	4.48	-3.53				COG3123, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_23010	PA1604	Hypothetical, unclassified, unknown				5.52	2.27					HisJ, ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Amino acid transport and metabolism / Signal transduction mechanisms].
PA14_43720	PA1607	Hypothetical, unclassified, unknown				2.07	-4.85			3.22	3.51	COG1733, Predicted transcriptional regulators [Transcription].
PA14_42860	PA1673	Hypothetical, unclassified, unknown				4.27	10.49	-39.06	6.45	12.71	17.79	COG2703, Hemerythrin [Inorganic ion transport and metabolism].
PA14_60490	PA1746	Hypothetical, unclassified, unknown				4.18	4.16	-3.31		4.31	6.58	COG2110, Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1 [General function prediction only].
PA14_41440	PA1789	Hypothetical, unclassified, unknown				2.33	-3.11	-7.58	-3.73		2.50	UspA, Universal stress protein UspA and related nucleotide-binding proteins [Signal transduction mechanisms].
PA14_41030	PA1817	Hypothetical, unclassified, unknown				2.42	-6.09	-5.46		3.24	4.10	COG3631, Ketosteroid isomerase-related protein [General function prediction only].
PA14_37080	PA2126	Hypothetical, unclassified, unknown				2.47	3.04					Spo0J, Predicted transcriptional regulators [Transcription].
PA14_37070	PA2127	Hypothetical, unclassified, unknown				8.40	4.85	-9.17	6.20			COG3969, Predicted phosphoadenosine phosphosulfate sulfotransferase [General function prediction only].
PA14_36450	PA2176	Hypothetical, unclassified, unknown				2.10	-4.36	2.99				COG2910, Putative NADH-flavin reductase [General function prediction only].
PA14_34740	PA2311	Hypothetical, unclassified, unknown				8.85	-3.04	6.03	3.53	2.96		hypothetical protein
PA14_32890	PA2453	Hypothetical, unclassified, unknown				2.79	4.42					hypothetical protein
PA14_06720	PA2485	Hypothetical, unclassified, unknown				2.31	2.67	-3.37				hypothetical protein
PA14_30550	PA2594	Hypothetical, unclassified, unknown				2.34	-4.22	7.14	4.57	3.80		TauA, ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Inorganic ion transport and metabolism].

PA14_46900	PA2630	Hypothetical, unclassified, unknown	<i>ycfD</i>	3.62	2.89	-4.00		2.63	COG2850, Uncharacterized conserved protein [Function unknown].
PA14_29590	PA2667	Hypothetical, unclassified, unknown		2.44	6.90	-3.19	7.18		conserved hypothetical protein
PA14_28500	PA2753	Hypothetical, unclassified, unknown		10.13	4.72	-14.22	3.34	4.12	8.93
PA14_28490	PA2754	Hypothetical, unclassified, unknown		4.12					ElaB, Uncharacterized conserved protein [Function unknown].
PA14_27870	PA2805	Hypothetical, unclassified, unknown		2.93	2.10		3.16		hypothetical protein
PA14_25620	PA2971	Hypothetical, unclassified, unknown	<i>yceD</i>	22.94	-3.27	8.27			COG1399, Predicted metal-binding, possibly nucleic acid-binding protein [General function prediction only].
PA14_25140	PA3009	Hypothetical, unclassified, unknown		6.29	-4.02	5.25	4.67	3.13	hypothetical protein
PA14_24880	PA3031	Hypothetical, unclassified, unknown			-3.22		3.23	2.21	hypothetical protein
PA14_24300	PA3081	Hypothetical, unclassified, unknown		2.15	2.21				conserved hypothetical protein
PA14_21650	PA3276	Hypothetical, unclassified, unknown			-3.86	3.62	5.87	2.13	hypothetical protein
PA14_21220	PA3309	Hypothetical, unclassified, unknown	<i>uspK</i>	4.20	-3.12	-6.71		5.40	10.89
PA14_21000	PA3329	Hypothetical, unclassified, unknown		2.15	6.39	-12.21	-3.51	5.04	5.13
PA14_01610	PA3332	Hypothetical, unclassified, unknown		2.67	5.04	-5.26	-3.55		COG3631, Ketosteroid isomerase-related protein [General function prediction only].
PA14_19120	PA3335	Hypothetical, unclassified, unknown		2.37	3.51			2.79	hypothetical protein
PA14_20800	PA3345	Hypothetical, unclassified, unknown		2.39	-3.86		3.96	2.19	ArcB, FOG: HPt domain [Signal transduction mechanisms].
PA14_19500	PA3449	Hypothetical, unclassified, unknown			-6.90	19.03	10.69	6.10	TauA, ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Inorganic ion transport and metabolism].
PA14_19205	PA3470	Hypothetical, unclassified, unknown		2.49	-7.35				MutT, NTP pyrophosphohydrolases including oxidative damage repair enzymes [DNA replication, recombination, and repair / General function prediction only].
PA14_19170	PA3472	Hypothetical, unclassified, unknown		3.04	-2.76				Spr, Cell wall-associated hydrolases (invasion-associated proteins) [Cell envelope biogenesis, outer membrane].

PA14_19020	PA3484	Hypothetical, unclassified, unknown		2.15	2.84					hypothetical protein
PA14_68940	PA3496	Hypothetical, unclassified, unknown		2.09	3.69	3.52				hypothetical protein
PA14_18370	PA3552	Hypothetical, unclassified, unknown	<i>armB, pmrH</i>	2.85	3.13	-13.97	-11.09		-3.09	WeeE, Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis [Cell envelope biogenesis, outer membrane].
PA14_18100	PA3572	Hypothetical, unclassified, unknown		4.00	3.15	-15.67	8.88	6.06	12.53	hypothetical protein
PA14_17580	PA3613	Hypothetical, unclassified, unknown		2.40	2.61	-2.74				COG3957, Phosphoketolase [Carbohydrate transport and metabolism].
PA14_34460	PA3662	Hypothetical, unclassified, unknown		6.29	4.14		6.42		2.95	hypothetical protein
PA14_16830	PA3675	Hypothetical, unclassified, unknown			2.42	-3.28				
PA14_16720	PA3684	Hypothetical, unclassified, unknown		3.10	2.75					hypothetical protein
PA14_16180	PA3729	Hypothetical, unclassified, unknown		2.15	2.95					COG2268, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_14610	PA3822	Hypothetical, unclassified, unknown	<i>yajC</i>	2.59	9.26					YajC, Preprotein translocase subunit YajC [Intracellular trafficking and secretion].
PA14_13720	PA3880	Hypothetical, unclassified, unknown		2.83	4.20	-14.35		3.11	5.71	COG4273, Uncharacterized conserved protein [Function unknown].
PA14_12370	PA3978	Hypothetical, unclassified, unknown		2.36	2.18					COG0790, FOG: TPR repeat, SEL1 subfamily [General function prediction only].
PA14_12360	PA3979	Hypothetical, unclassified, unknown			6.13	-3.75	4.91	4.97	3.29	COG4517, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_11250	PA4069	Hypothetical, unclassified, unknown			3.51	-3.83		3.22	2.48	RfbD, dTDP-4-dehydrorhamnose reductase [Cell envelope biogenesis, outer membrane].
PA14_56540	PA4348	Hypothetical, unclassified, unknown		2.25	5.03	-9.26			3.24	FpaA, Uncharacterized flavoproteins [Energy production and conversion].
PA14_56930	PA4379	Hypothetical, unclassified, unknown		2.19	7.75	-6.10	3.27	7.66	3.03	UbiE, Methylase involved in ubiquinone/menaquinone biosynthesis [Coenzyme metabolism].
PA14_57460	PA4421	Hypothetical, unclassified, unknown	<i>yabB</i>		2.15	-3.92	5.00	3.12	2.56	COG2001, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_57690	PA4441	Hypothetical, unclassified, unknown		2.06	2.60					COG3105, Uncharacterized protein conserved in bacteria [Function unknown].

PA14_57850	PA4454	Hypothetical, unclassified, unknown	<i>yrbD</i>	2.63	-2.34			Ttg2C, ABC-type transport system involved in resistance to organic solvents, periplasmic component [Secondary metabolites biosynthesis, transport, and catabolism].
PA14_60560	PA4577	Hypothetical, unclassified, unknown		3.41	-25.84	5.01	9.80	DksA, DnaK suppressor protein [Signal transduction mechanisms].
PA14_71630	PA4610	Hypothetical, unclassified, unknown		7.46	3.09	-3.55		hypothetical protein
PA14_61390	PA4639	Hypothetical, unclassified, unknown			-4.90	3.07	2.30	hypothetical protein
PA14_61840	PA4674	Hypothetical, unclassified, unknown	<i>vapl</i>	2.73	2.07	5.04	4.37	Vapl, Plasmid maintenance system antidote protein [General function prediction only].
PA14_62170	PA4697	Hypothetical, unclassified, unknown		2.42	2.10	-5.18	3.05	2.45
PA14_62880	PA4753	Hypothetical, unclassified, unknown	<i>yhbY</i>	2.11	6.37	5.99		COG1534, Predicted RNA-binding protein containing KH domain, possibly ribosomal protein [Translation, ribosomal structure and biogenesis].
PA14_63110	PA4773	Hypothetical, unclassified, unknown		2.11	2.56	-17.18	-4.59	3.19
PA14_63940	PA4836	Hypothetical, unclassified, unknown			-6.06	5.24	3.38	hypothetical protein, Hypothetical protein
PA14_20960	PA4918	Hypothetical, unclassified, unknown		2.54	9.01	-5.24	3.51	20.86
PA14_68800	PA5208	Hypothetical, unclassified, unknown		2.56	4.24	-7.94		4.24
PA14_69090	PA5232	Hypothetical, unclassified, unknown	<i>yhil</i>	3.77	2.58	-6.99		3.66
PA14_62940	PA5475	Hypothetical, unclassified, unknown		3.66	3.06	-4.33	4.16	7.46
PA14_61500	PA5492	Hypothetical, unclassified, unknown	<i>ysxC, yihA</i>	2.70	2.29			COG0218, Predicted GTPase [General function prediction only].
PA14_06730	PA5494	Hypothetical, unclassified, unknown		6.37	6.03	-5.92		4.03
PA14_48790	PA1199	Membrane proteins			-3.95	4.80	3.47	Spr, Cell wall-associated hydrolases (invasion-associated proteins) [Cell envelope biogenesis, outer membrane].
PA14_48140	PA1245	Membrane proteins	<i>aprX</i>	-2.74	-3.62		2.25	hypothetical protein
PA14_45970	PA1429	Membrane proteins		6.37	2.26	-7.25	2.29	MgtA, Cation transport ATPase [Inorganic ion transport and metabolism].
PA14_42100	PA1735	Membrane proteins		2.15	4.15	-3.50		COG0679, Predicted permeases [General function prediction only].

PA14_32310	PA2501	Membrane proteins		3.85	-2.27	-16.45	4.33	4.68	9.80	hypothetical protein
PA14_25470	PA2985	Membrane proteins			5.49	-3.21				COG3216, Uncharacterized protein conserved in bacteria [Function unknown].
PA14_21630	PA3278	Membrane proteins		9.62	3.47	-15.04	7.93	3.07	7.87	hypothetical protein
PA14_20900	PA3336	Membrane proteins		2.38	2.62	-3.79		3.39	2.68	AraJ, Arabinose efflux permease, MFS transporter [Carbohydrate transport and metabolism].
PA14_18060	PA3575	Membrane proteins		2.56	4.65	-9.09				CybB, Cytochrome B561 [Energy production and conversion].
PA14_17920	PA3585	Membrane proteins	glpM		2.02	-3.08				GlpM, Uncharacterized membrane protein required for alginate biosynthesis [General function prediction only].
PA14_14360	PA3839	Membrane proteins	yfbS	3.40	2.34					CitT, Di- and tricarboxylate transporters [Inorganic ion transport and metabolism].
PA14_47530	PA3877	Membrane proteins	narK1	27.32	2.35					NarK, Nitrate/nitrite transporter [Inorganic ion transport and metabolism].
PA14_12560	PA3966	Membrane proteins		2.17	11.35	-2.15	5.19			hypothetical protein
PA14_11270	PA4067	Membrane proteins	oprG, yciD, ompW	2.79	4.03	-8.85		3.16		OmpW, Outer membrane protein W [Cell envelope biogenesis, outer membrane].
PA14_09050	PA4243	Membrane proteins	secY, prlA		2.70	-2.02				SecY, Preprotein translocase subunit SecY [Intracellular trafficking and secretion].
PA14_57030	PA4387	Membrane proteins	fxsA	3.25		-3.09				FxsA, Protein affecting phage T7 exclusion by the F plasmid [General function prediction only].
PA14_06130	PA4747	Membrane proteins	secG	2.09	2.02					SecG, Preprotein translocase subunit SecG [Intracellular trafficking and secretion].
PA14_72630	PA5504	Membrane proteins			6.13	-3.57	3.65	3.02		AbcD, ABC-type metal ion transport system, permease component [Inorganic ion transport and metabolism].
PA14_73320	PA5561	Membrane proteins	atpl, uncI		4.39	-3.36	5.53	4.49	2.43	Atpl, F0F1-type ATP synthase, subunit I [Energy production and conversion].
PA14_05340	PA0410	Motility and Attachment	pilI		2.09	-3.04				CheW, Chemotaxis signal transduction protein [Cell motility and secretion / Signal transduction mechanisms].
PA14_05360	PA0411	Motility and Attachment	pilJ		3.26	-3.97				Tar, Methyl-accepting chemotaxis protein [Cell motility and secretion / Signal transduction mechanisms].
PA14_37060	PA2128	Motility and Attachment	cupA1	2.53	2.04	-16.29	7.42	4.11	7.35	FimA, P pilus assembly protein, pilin FimA [Cell motility and secretion / Intracellular trafficking and secretion].
PA14_69940	PA5298	Nucleotide biosynthesis	xpt		4.13	-4.72				Apt, Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins [Nucleotide transport and metabolism].
PA14_06360	PA0489	Putative enzymes				-6.06	6.33	6.68	5.65	ComFC, Predicted amidophosphoribosyltransferases [General function prediction only].
PA14_07070	PA0545	Putative enzymes		11.11	2.89	-8.20		3.10	3.69	COG4097, Predicted ferric reductase [Inorganic ion transport and metabolism].
PA14_53470	PA0836	Putative enzymes	ackA, tdcD	7.75	2.58	-12.87		2.24		ackA, Acetate kinase [Energy production and conversion].

PA14_48440	PA1225	Putative enzymes		-3.52	3.37	2.59	MdaB, Putative NADPH-quinone reductase (modulator of drug activity B) [General function prediction only].		
PA14_47340	PA1306	Putative enzymes		4.09	-4.65		Hit, Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases [Nucleotide transport and metabolism / Carbohydrate transport and metabolism / General function prediction only].		
PA14_46890	PA1344	Putative enzymes	yvaG	-2.24	-3.16	-4.88	FabG, Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Secondary metabolites biosynthesis, transport, and catabolism / General function prediction only].		
PA14_34750	PA2310	Putative enzymes		-7.30	6.98	12.46	8.06	TauD, Probable taurine catabolism dioxygenase [Secondary metabolites biosynthesis, transport, and catabolism].	
PA14_21640	PA3277	Putative enzymes		2.04	5.08	-9.62	2.38	DltE, Short-chain dehydrogenases of various substrate specificities [General function prediction only].	
PA14_17930	PA3328	Putative enzymes		2.93	2.49	-5.62	2.76	UbiH, 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases [Coenzyme metabolism / Energy production and conversion].	
PA14_06740	PA3330	Putative enzymes		3.25	14.29	-3.85	-4.52	COG4221, Short-chain alcohol dehydrogenase of unknown specificity [General function prediction only].	
PA14_19560	PA3444	Putative enzymes	ssuD	2.67	3.13	17.69	4.53	3.13	COG2141, Coenzyme F420-dependent N5,N10-methylene tetrahydromenopterin reductase and related flavin-dependent oxidoreductases [Energy production and conversion].
PA14_51820	PA0963	Transcription, RNA processing and degradation	aspS, syd		2.53	-2.72		AspS, Aspartyl-tRNA synthetase [Translation, ribosomal structure and biogenesis].	
PA14_08710	PA4275	Transcription, RNA processing and degradation	nusG	2.43	5.95	3.11		NusG, Transcription antiterminator [Transcription].	
PA14_33580	PA4944	Transcription, RNA processing and degradation	hfq	2.56	2.23			conserved hypothetical protein	
PA14_06870	PA0527	Transcriptional regulators	dnr		4.76	-6.71	3.64	transcriptional regulator Dnr	
PA14_54430	PA0762	Transcriptional regulators	algU, algT	4.85	-3.22	5.82	3.96	2.75	RpoE, DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Transcription]. positive regulator for alginate biosynthesis MucC, regulator of sigma E activity [Signal transduction mechanisms].
PA14_54400	PA0765	Transcriptional regulators	mucC		-5.35	3.36	2.16		
PA14_49180	PA1179	Transcriptional regulators	phoP	2.21		-5.29	-5.85	-4.68	two-component response regulator, OmpR, Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Signal transduction mechanisms / Transcription].
PA14_32490	PA1603	Transcriptional regulators		2.85	2.04	-3.15		MarR, Transcriptional regulators [Transcription].	

PA14_41260	PA1799	Transcriptional regulators		2.09	-3.22	6.18	2.13	OmpR, Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Signal transduction mechanisms / Transcription].		
PA14_35210	PA2270	Transcriptional regulators		3.26	-3.53	3.06	2.23	AcrR, Transcriptional regulator [Transcription].		
PA14_26760	PA2885	Transcriptional regulators	<i>atuR</i>	2.35	4.81	-5.56	2.06	AcrR, Transcriptional regulator [Transcription].		
PA14_25180	PA3006	Transcriptional regulators	<i>psrA</i>	2.32	2.07	-5.10	4.30	3.04	2.28	AcrR, Transcriptional regulator [Transcription].
PA14_20730	PA3351	Transcriptional regulators	<i>flgM</i>		2.18	-5.24	3.40	2.93	hypothetical protein	
PA14_19380	PA3458	Transcriptional regulators		7.09	2.88		2.82	MarR, Transcriptional regulators [Transcription].		
PA14_18080	PA3574	Transcriptional regulators			3.15	-6.25	3.72	3.66	AcrR, Transcriptional regulator [Transcription].	
PA14_16280	PA3721	Transcriptional regulators		3.66	-8.22		3.47		AcrR, Transcriptional regulator [Transcription].	
PA14_12780	PA3948	Transcriptional regulators	<i>rocA1</i>	2.68	2.23	-3.19			CitB, Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Signal transduction mechanisms / Transcription].	
PA14_17490	PA3973	Transcriptional regulators		4.37	2.13	-5.03			AcrR, Transcriptional regulator [Transcription].	
PA14_60810	PA4596	Transcriptional regulators		3.28	3.31	-7.75	2.33	probable transcriptional regulator		
PA14_64050	PA4843	Transcriptional regulators		2.29	2.39	-4.20	2.36	PleD, Response regulator containing a CheY-like receiver domain and a GGDEF domain [Signal transduction mechanisms].		
PA14_00200	PA0019	Translation, post-translational modification, degradation	<i>def</i>	2.02	3.15	-3.72	2.02	Def, N-formylmethionyl-tRNA deformylase [Translation, ribosomal structure and biogenesis].		
PA14_07560	PA0579	Translation, post-translational modification, degradation	<i>rpsU</i>	2.21	6.94		7.56		RpsU, Ribosomal protein S21 [Translation, ribosomal structure and biogenesis].	
PA14_41190	PA1805	Translation, post-translational modification, degradation	<i>ppiD</i>			-4.93	4.04	2.20	peptidyl-prolyl cis-trans isomerase D	
PA14_66750	PA2619	Translation, post-translational modification, degradation	<i>infA</i>	2.23	2.90	-2.29	3.76	2.27	InfA, Translation initiation factor 1 (IF-1) [Translation, ribosomal structure and biogenesis].	
PA14_28720	PA2738	Translation, post-translational modification, degradation	<i>himA</i>	2.87	2.15	-2.27			HimA, Bacterial nucleoid DNA-binding protein [DNA replication, recombination, and repair].	
PA14_27210	PA2851	Translation, post-translational modification, degradation	<i>efp</i>	2.80	2.58	-2.46			Efp, Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A) [Translation, ribosomal structure and biogenesis].	
PA14_25630	PA2970	Translation, post-translational modification, degradation	<i>rpmF</i>	2.13	2.98		7.95		RpmF, Ribosomal protein L32 [Translation, ribosomal structure and biogenesis].	

PA14_21820	PA3262	Translation, post-translational modification, degradation		-3.19	3.84	2.82	FkpA, FKBP-type peptidyl-prolyl cis-trans isomerases 1 [Posttranslational modification, protein turnover, chaperones].	
PA14_17070	PA3655	Translation, post-translational modification, degradation	<i>tsf</i>	2.25	3.64		Tsf, Translation elongation factor Ts [Translation, ribosomal structure and biogenesis].	
PA14_17060	PA3656	Translation, post-translational modification, degradation	<i>rpsB</i>	2.24	-2.33	3.07	RpsB, Ribosomal protein S2 [Translation, ribosomal structure and biogenesis].	
PA14_16000	PA3742	Translation, post-translational modification, degradation	<i>rplS</i>	2.80	3.17	5.04	RplS, Ribosomal protein L19 [Translation, ribosomal structure and biogenesis].	
PA14_09130	PA4237	Translation, post-translational modification, degradation	<i>rplQ</i>	2.55	2.54		RplQ, Ribosomal protein L17 [Translation, ribosomal structure and biogenesis].	
PA14_20970	PA4245	Translation, post-translational modification, degradation	<i>rpmD</i>	2.05	4.59	-3.45	RpmD, Ribosomal protein L30/L7E [Translation, ribosomal structure and biogenesis].	
PA14_08960	PA4252	Translation, post-translational modification, degradation	<i>rplX</i>		4.28	-3.23	RplX, Ribosomal protein L24 [Translation, ribosomal structure and biogenesis].	
PA14_08750	PA4271	Translation, post-translational modification, degradation	<i>rplL</i>	2.30	3.20	6.94	RplL, Ribosomal protein L7/L12 [Translation, ribosomal structure and biogenesis].	
PA14_58170	PA4482	Translation, post-translational modification, degradation	<i>gatC</i>	2.04	5.62		Glu-tRNA(Gln) amidotransferase subunit C	
PA14_60450	PA4567	Translation, post-translational modification, degradation	<i>rpmA</i>		11.47	-2.49	7.27	RpmA, Ribosomal protein L27 [Translation, ribosomal structure and biogenesis].
PA14_71230	PA4934	Translation, post-translational modification, degradation	<i>rpsR</i>	2.34	11.04		12.22	RpsR, Ribosomal protein S18 [Translation, ribosomal structure and biogenesis].
PA14_66710	PA5049	Translation, post-translational modification, degradation	<i>rpmE</i>	2.12	12.85	-2.55	16.38	RpmE, Ribosomal protein L31 [Translation, ribosomal structure and biogenesis].
PA14_41970	PA5051	Translation, post-translational modification, degradation	<i>argS</i>	2.02	2.93	-3.03		ArgS, Arginyl-tRNA synthetase [Translation, ribosomal structure and biogenesis].
PA14_70190	PA5316	Translation, post-translational modification, degradation	<i>rpmB</i>		17.30	-2.75	13.54	RpmB, Ribosomal protein L28 [Translation, ribosomal structure and biogenesis].

PA14_73420	PA5569	Translation, post-translational modification, degradation	<i>rnpA</i>	2.72	-3.65				RnpA, RNase P protein component [Translation, ribosomal structure and biogenesis].
	Pae_tR	Translation, post-translational modification, degradation		2.49	2.03	5.50	6.39	4.41	tRNA_Isoleucine, 723696-723772 (+) strand
PA14_45110	PA1493	Transport of small molecules	<i>cysP</i>		-7.30		4.90	4.12	Sbp, ABC-type sulfate transport system, periplasmic component [Inorganic ion transport and metabolism].
PA14_34410	PA2339	Transport of small molecules	<i>mtfF</i>	2.21	9.88			-2.07	UgpA, ABC-type sugar transport systems, permease components [Carbohydrate transport and metabolism].
PA14_03080	PA2505	Transport of small molecules	<i>opdT, oprD3</i>	2.11	2.56				hypothetical protein
PA14_24790	PA3038	Transport of small molecules	<i>opdQ</i>	2.51	5.99	-3.26			hypothetical protein
PA14_18670	PA3531	Transport of small molecules	<i>bfrB</i>	7.81	10.59	-14.04	8.58	4.78	bacterioferritin, bfrB (bacterioferritin)
PA14_12920	PA3938	Transport of small molecules	<i>tauA</i>		11.56	-5.43	8.18	11.54	TauA, ABC-type taurine transport system, periplasmic component [Inorganic ion transport and metabolism].
PA14_09160	PA4235	Transport of small molecules	<i>bfrA</i>	2.02	2.21	-5.68		2.49	bacterioferritin
PA14_57960	PA4464	Transport of small molecules	<i>ptsN</i>	2.90	2.08				PtsN, Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type) [Carbohydrate transport and metabolism / Signal transduction mechanisms].
PA14_58570	PA4514	Transport of small molecules	<i>piuA</i>	2.22	2.22	2.01	-3.58	-2.38	probable outer membrane receptor for iron transport, piuA.
PA14_05320	PA0408	Two-component regulatory systems	<i>pilG</i>	2.90	6.99	-8.93	3.78	3.70	twitching motility protein PilG
PA14_05330	PA0409	Two-component regulatory systems	<i>pilH</i>	2.71	3.00	-5.71		2.13	twitching motility protein PilH
PA14_58320	PA4494	Two-component regulatory systems		2.74	-3.34				BaeS, Signal transduction histidine kinase [Signal transduction mechanisms].