

**Supplementary Table 1**

**Key terms**

ProtID - Protein ID  
 ProtLen - Protein length  
 SpCount - Spectral count  
 APEX - APEX score  
 FC - Fold change (*oprF* mutant / wt)  
 log2FC - log2(Fold change)  
 UpDown - Whether the protein is increased (Up) or decreased (Down) in the *oprF* mutant (>2 fold-change, FDR < 0.01)  
 Product - Protein product name (from PseudoCAP database)  
 PCAP Function - Protein function  
 Localization - Protein localization information (from PseudoCAP database)

ProtID	ProtLen	WT1 SpCount	WT2 SpCount	oprF1 SpCount	oprF2 SpCount	WT1 APEX	WT2 APEX	oprF1 APEX	oprF2 APEX	WT avg APEX	oprF avg APEX	FC (wt/oprF)	log2FC (wt/oprF)	UpDown	Product	PCAP Function	Localization
PA14_08110	36	2.0	3.0	0.0	0.0	32.54	12.38	0.00	0.00	22.46	0.00	1024.0	10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_08240	611	11.0	3.0	0.0	0.0	17.95	1.24	0.00	0.00	9.60	0.00	1024.0	10.0	Down	hypothetical protein	Related to phage, transposon, or plasmid	Periplasmic
PA14_08930 rpmC	63	9.0	42.0	0.0	0.0	52.55	62.19	0.00	0.00	57.37	0.00	1024.0	10.0	Down	50S ribosomal protein L29	Translation, post-translational modification, degradation	Cytoplasmic
PA14_15780	570	1.0	1.0	0.0	0.0	1.88	0.48	0.00	0.00	1.18	0.00	1024.0	10.0	NA	N-Acetyl-D-Glucosamine phosphotransferase system transporter	Transport of small molecules	CytoplasmicMembrane
PA14_41570 oprF	350	365.0	770.5	0.0	0.0	384.61	205.90	0.00	0.00	295.25	0.00	1024.0	10.0	Down	major porin and structural outer membrane porin OprF precursor	Membrane proteins	OuterMembrane
PA14_65170 rpsR	76	4.0	40.0	0.0	0.0	12.28	31.13	0.00	0.00	21.70	0.00	1024.0	10.0	Down	30S ribosomal protein S18	Translation, post-translational modification, degradation	Cytoplasmic
PA14_66960 tatA	82	2.0	1.0	0.0	0.0	9.99	1.27	0.00	0.00	5.63	0.00	1024.0	10.0	NA	twin arginine translocase protein A	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_67680 ntrC	476	1.0	1.0	0.0	0.0	1.36	0.35	0.00	0.00	0.86	0.00	1024.0	10.0	NA	two-component response regulator NtrC	Two-component regulatory systems	Cytoplasmic
PA14_71970 wbpW	479	1.0	2.0	0.0	0.0	2.41	1.22	0.00	0.00	1.82	0.00	1024.0	10.0	NA	GDP-mannose pyrophosphorylase	Cell wall / LPS / capsule	Cytoplasmic
PA14_62300	297	0.0	173.0	0.0	1.0	0.00	112.50	0.00	0.29	56.25	0.15	381.3	8.6	Down	hypothetical protein	Transport of small molecules	Unknown
PA14_07980	119	0.0	62.0	0.0	2.0	0.00	81.67	0.00	1.19	40.84	0.60	68.5	6.1	Down	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_64290	359	7.0	0.0	0.0	1.0	34.81	0.00	0.00	0.57	17.40	0.29	61.0	5.9	Down	putative permease of ABC transporter	Transport of small molecules	CytoplasmicMembrane
PA14_12760	449	2.0	1.0	0.0	0.5	2.00	0.25	0.00	0.06	1.12	0.03	39.5	5.3	NA	ATP-dependent RNA helicase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_51530 exoU	687	131.0	161.0	8.0	30.5	127.81	39.84	2.33	3.42	83.82	2.87	29.2	4.9	Down	ExoU	Secreted Factors (toxins, enzymes, alginate)	Extracellular
PA14_73290 atpF	156	0.0	110.0	0.0	8.5	0.00	56.32	0.00	1.97	28.16	0.99	28.6	4.8	Down	F0F1 ATP synthase subunit B	Energy metabolism	CytoplasmicMembrane
PA14_08020	108	0.0	6.0	0.0	0.5	0.00	8.38	0.00	0.32	4.19	0.16	26.5	4.7	NA	putative bacteriophage protein	Related to phage, transposon, or plasmid	Unknown
PA14_31620	464	9.0	4.0	1.0	1.0	13.36	1.50	0.44	0.17	7.43	0.31	24.2	4.6	Down	hypothetical protein	Transport of small molecules	CytoplasmicMembrane
PA14_32890	73	57.0	83.0	7.0	16.0	546.02	201.63	20.01	17.61	373.83	18.81	19.9	4.3	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_08740 rplJ	166	35.0	11.0	1.0	17.0	93.88	7.48	0.80	5.24	50.68	3.02	16.8	4.1	Down	50S ribosomal protein L10	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08280	200	3.0	5.0	1.0	0.0	9.69	4.10	0.96	0.00	6.89	0.48	14.3	3.8	NA	putative bacteriophage protein	Related to phage, transposon, or plasmid	CytoplasmicMembrane
PA14_57570	197	0.0	57.0	0.0	9.0	0.00	61.63	0.00	4.41	30.82	2.20	14.0	3.8	Down	putative cytochrome c reductase, iron-sulfur subun	Putative enzymes	CytoplasmicMembrane
PA14_08980 rpsN	101	2.0	62.0	0.0	11.0	6.00	47.21	0.00	3.79	26.61	1.90	14.0	3.8	Down	30S ribosomal protein S14	Translation, post-translational modification, degradation	Cytoplasmic
PA14_50270 fliD	474	269.0	1402.5	53.0	255.5	248.44	328.48	14.61	27.11	288.46	20.86	13.8	3.8	Down	flagellar capping protein FliD	Motility & Attachment	Extracellular
PA14_44020 sdhB	235	35.0	87.0	7.0	18.5	65.47	41.27	3.91	3.98	53.37	3.94	13.5	3.8	Down	succinate dehydrogenase iron-sulfur subunit	Energy metabolism	CytoplasmicMembrane
PA14_10090	303	0.0	6.0	0.0	1.0	0.00	3.87	0.00	0.29	1.93	0.15	13.2	3.7	NA	LysR family transcriptional regulator	Transcriptional regulators	Unknown
PA14_07170 epd	353	1.0	2.0	0.0	1.0	1.95	0.99	0.00	0.22	1.47	0.11	13.1	3.7	NA	D-erythrose 4-phosphate dehydrogenase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_40240	723	17.0	1.0	3.0	4.0	21.09	0.32	1.11	0.57	10.70	0.84	12.7	3.7	Down	putative ATP-binding/permease fusion ABC transporter	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_10360	99	0.0	162.0	0.0	35.0	0.00	927.65	0.00	90.78	463.83	45.39	10.2	3.4	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_48940 coaB	82	0.0	9.0	0.0	2.0	0.00	52.07	0.00	5.24	26.03	2.62	9.9	3.3	Down	coat protein B of bacteriophage P1)	Related to phage, transposon, or plasmid	Unknown

PA14_50360 figK	683	4.5	86.0	0.0	23.5	5.58	27.02	0.00	3.35	16.30	1.67	9.7	3.3	Down	flagellar hook-associated protein FigK	Motility & Attachment	OuterMembrane
PA14_44030 sdhA	590	20.0	26.0	1.0	23.0	24.44	8.06	0.36	3.23	16.25	1.80	9.0	3.2	Down	succinate dehydrogenase flavoprotein subunit	Energy metabolism	CytoplasmicMembrane
PA14_30490	360	0.0	4.0	0.0	1.0	0.00	2.31	0.00	0.26	1.15	0.13	8.8	3.1	NA	putative lavin-dependent oxidoreductase	Energy metabolism	Unknown
PA14_51810	248	1.0	0.0	0.0	1.0	7.82	0.00	0.00	0.90	3.91	0.45	8.7	3.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_59540	749	5.0	0.0	2.0	0.0	5.21	0.00	0.62	0.00	2.61	0.31	8.4	3.1	NA	hypothetical protein	Related to phage, transposon, or plasmid	Cytoplasmic
PA14_09010 rplR	116	28.5	56.0	9.0	24.0	74.81	37.28	7.05	7.24	56.04	7.14	7.8	3.0	Down	50S ribosomal protein L18	Translation, post-translational modification, degradation	Cytoplasmic
PA14_66760	231	18.0	74.0	11.0	14.0	62.14	64.78	11.33	5.55	63.46	8.44	7.5	2.9	Down	hypothetical protein	Cell division	CytoplasmicMembrane
PA14_23280 pheA	365	6.0	6.0	3.0	1.0	10.16	2.58	1.52	0.19	6.37	0.85	7.5	2.9	Down	chorismate mutase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_00300 picB	328	81.0	159.0	23.0	84.0	330.09	164.32	27.97	39.32	247.21	33.65	7.4	2.9	Down	phospholipase C, PicB	Hypothetical, unclassified, unknown	Unknown
PA14_08990 rpsH	130	10.0	16.0	1.0	14.0	24.61	9.99	0.73	3.96	17.30	2.35	7.4	2.9	Down	30S ribosomal protein S8	Translation, post-translational modification, degradation	Cytoplasmic
PA14_62810 secG	129	5.0	9.0	2.0	4.0	29.19	13.33	3.48	2.68	21.26	3.08	6.9	2.8	Down	preprotein translocase subunit SecG	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_55380	544	0.0	8.0	1.0	0.0	0.00	2.75	0.40	0.00	1.37	0.20	6.8	2.8	NA	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_64750	446	0.0	3.0	0.0	1.0	0.00	2.78	0.00	0.42	1.39	0.21	6.6	2.7	NA	putative MFS transporter	Transport of small molecules	CytoplasmicMembrane
PA14_08710 nusG	177	17.0	0.0	9.0	0.0	47.68	0.00	7.53	0.00	23.84	3.77	6.3	2.7	Down	transcription antitermination protein NusG	Transcription, RNA processing and degradation	Cytoplasmic
PA14_15960 fhh	457	7.0	0.0	3.0	2.0	13.04	0.00	1.67	0.43	6.52	1.05	6.2	2.6	NA	signal recognition particle protein Fhh	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_08880 rplB	273	11.0	40.0	0.0	30.0	13.35	12.31	0.00	4.18	12.83	2.09	6.1	2.6	Down	50S ribosomal protein L2	Translation, post-translational modification, degradation	Cytoplasmic
PA14_65030	231	37.0	33.0	22.0	9.0	87.94	19.89	15.61	2.46	53.92	9.03	6.0	2.6	Down	hypothetical protein	Membrane proteins	OuterMembrane
PA14_48140	414	16.0	60.0	0.0	48.0	80.10	76.18	0.00	27.61	78.14	13.80	5.7	2.5	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_25610	192	1.0	0.5	0.5	0.5	4.05	0.51	0.60	0.23	2.28	0.42	5.5	2.5	NA	Mar-like protein	Cell division	Cytoplasmic
PA14_52750 aotP	254	0.0	6.0	0.0	2.5	0.00	3.70	0.00	0.70	1.85	0.35	5.3	2.4	NA	arginine/ornithine transport protein AotP	Transport of small molecules	CytoplasmicMembrane
PA14_14630 secD	620	1.0	11.0	1.0	4.0	0.94	2.64	0.28	0.43	1.79	0.36	5.0	2.3	Down	preprotein translocase subunit SecD	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_53820	255	16.0	2.0	1.0	27.0	33.09	1.05	0.62	6.41	17.07	3.52	4.9	2.3	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_08920 rplP	137	74.0	30.0	39.5	52.0	128.03	13.16	20.40	10.34	70.60	15.37	4.6	2.2	Down	50S ribosomal protein L16	Translation, post-translational modification, degradation	Cytoplasmic
PA14_70940 betA	561	0.0	2.0	0.0	1.0	0.00	0.69	0.00	0.16	0.35	0.08	4.4	2.2	NA	choline dehydrogenase	Amino acid biosynthesis and metabolism	CytoplasmicMembrane
PA14_24380	543	0.0	14.0	0.0	7.0	0.00	5.92	0.00	1.34	2.96	0.67	4.4	2.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_12900	93	0.0	6.0	0.0	3.0	0.00	5.19	0.00	1.18	2.59	0.59	4.4	2.1	NA	putative DNA binding protein	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_07560 rpsU	71	0.0	4.0	0.0	2.0	0.00	3.21	0.00	0.73	1.60	0.36	4.4	2.1	NA	30S ribosomal protein S21	Translation, post-translational modification, degradation	Cytoplasmic
PA14_14610 yajC	112	0.0	2.0	0.0	1.0	0.00	3.02	0.00	0.69	1.51	0.34	4.4	2.1	NA	preprotein translocase subunit YajC	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_41590	274	0.0	1.0	0.0	0.5	0.00	0.84	0.00	0.19	0.42	0.10	4.4	2.1	NA	putative cytoplasmic membrane protein	Membrane proteins	CytoplasmicMembrane
PA14_54450 nadB	538	0.0	2.0	0.0	1.0	0.00	0.79	0.00	0.18	0.40	0.09	4.4	2.1	NA	L-aspartate oxidase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_70190 rpmB	78	2.0	2.0	0.0	5.0	11.38	2.88	0.00	3.27	7.13	1.63	4.4	2.1	NA	50S ribosomal protein L28	Translation, post-translational modification, degradation	Cytoplasmic
PA14_17180 pxD	353	1.0	0.0	0.0	2.0	3.38	0.00	0.00	0.78	1.69	0.39	4.4	2.1	NA	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Cell wall / LPS / capsule	Cytoplasmic
PA14_23830 fimV	924	2.0	1.0	0.0	5.0	2.45	0.31	0.00	0.70	1.38	0.35	3.9	2.0	NA	pilus assembly protein	Motility & Attachment	Periplasmic
PA14_50810	293	4.0	3.0	3.0	3.0	6.65	1.26	1.49	0.57	3.96	1.03	3.8	1.9	NA	hypothetical protein	Membrane proteins	OuterMembrane
PA14_23420	722	0.0	19.0	0.0	11.0	0.00	5.12	0.00	1.34	2.56	0.67	3.8	1.9	Down	putative zinc-binding dehydrogenase	Cell wall / LPS / capsule	Cytoplasmic
PA14_08030	295	16.0	15.0	0.0	46.0	51.02	12.13	0.00	16.85	31.57	8.42	3.8	1.9	NA	putative phage baseplate assembly protein	Related to phage, transposon, or plasmid	Cytoplasmic
PA14_08180	120	0.0	49.0	0.0	29.0	0.00	87.02	0.00	23.33	43.51	11.66	3.7	1.9	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_17470	297	1.0	54.0	0.0	36.0	2.70	37.00	0.00	11.17	19.85	5.59	3.6	1.8	Down	hypothetical protein	Cell wall / LPS / capsule	OuterMembrane
PA14_22440	610	0.0	4.0	1.0	0.0	0.00	1.38	0.41	0.00	0.69	0.20	3.4	1.8	NA	putative ATP-binding/permease fusion ABC transporter	Transport of small molecules	CytoplasmicMembrane
PA14_08210	164	20.0	26.0	19.0	20.0	165.75	54.65	47.00	19.04	110.20	33.02	3.3	1.7	Down	hypothetical protein	Related to phage, transposon, or plasmid	Unknown
PA14_42060	304	0.0	3.0	0.0	2.0	0.00	1.43	0.00	0.43	0.71	0.22	3.3	1.7	NA	putative transcriptional regulator	Transcriptional regulators	Cytoplasmic
PA14_09090 rpsK	129	28.0	37.5	26.0	37.5	52.64	17.88	14.59	8.10	35.26	11.34	3.1	1.6	Down	30S ribosomal protein S11	Translation, post-translational modification, degradation	Cytoplasmic

PA14_28680 rpIT	118	28.0	33.0	24.0	41.0	133.25	39.83	34.09	22.41	86.54	28.25	3.1	1.6	Down	50S ribosomal protein L20	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08150	329	0.0	25.0	3.0	10.5	0.00	10.74	1.52	2.04	5.37	1.78	3.0	1.6	Down	putative phage late control gene D protein	Related to phage, transposon, or plasmid	Cytoplasmic
PA14_26020	536	309.0	1289.0	423.5	858.0	485.63	513.75	198.64	154.90	499.69	176.77	2.8	1.5	Down	putative aminopeptidase	Secreted Factors (toxins, enzymes, alginate)	Extracellular
PA14_14550	135	0.0	85.0	0.0	67.5	0.00	251.05	0.00	90.31	125.53	45.15	2.8	1.5	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_09130 rpIQ	129	44.0	4.0	51.0	9.0	114.55	2.64	39.62	2.69	58.59	21.16	2.8	1.5	NA	50S ribosomal protein L17	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08870 rpIW	99	19.0	23.0	22.0	21.0	52.42	16.09	18.12	6.66	34.26	12.39	2.8	1.5	Down	50S ribosomal protein L23	Translation, post-translational modification, degradation	Cytoplasmic
PA14_17060 rpsB	246	6.0	67.5	2.0	68.0	8.75	24.97	0.87	11.39	16.86	6.13	2.8	1.5	Down	30S ribosomal protein S2	Translation, post-translational modification, degradation	Cytoplasmic
PA14_44350	202	0.0	5.0	0.0	4.0	0.00	5.69	0.00	2.06	2.85	1.03	2.8	1.5	NA	putative cytochrome c oxidase subunit	Energy metabolism	Cytoplasmic
PA14_48060 aprA	479	154.0	791.0	81.5	941.5	503.36	655.67	79.50	353.51	579.52	216.51	2.7	1.4	Down	alkaline metalloproteinase precursor	Secreted Factors (toxins, enzymes, alginate)	Extracellular
PA14_66310 aceF	547	33.0	33.0	37.0	40.0	22.34	5.67	7.48	3.11	14.01	5.29	2.7	1.4	Down	dihydroipoamide acetyltransferase	Energy metabolism	Cytoplasmic
PA14_08900 rpIV	110	21.0	36.0	10.5	73.0	38.47	16.72	5.74	15.36	27.60	10.55	2.6	1.4	NA	50S ribosomal protein L22	Translation, post-translational modification, degradation	Cytoplasmic
PA14_57580 rpsI	130	17.0	76.5	34.0	35.0	51.74	59.05	30.89	12.24	55.40	21.56	2.6	1.4	Down	30S ribosomal protein S9	Translation, post-translational modification, degradation	Cytoplasmic
PA14_73230 atpC	141	9.0	10.0	8.5	17.0	29.42	8.29	8.29	6.38	18.85	7.34	2.6	1.4	NA	F0F1 ATP synthase subunit epsilon	Energy metabolism	Cytoplasmic
PA14_73300 atpE	85	0.0	8.0	0.0	7.0	0.00	128.27	0.00	50.84	64.13	25.42	2.5	1.3	NA	F0F1 ATP synthase subunit C	Energy metabolism	CytoplasmicMembrane
PA14_65370 amiB	475	11.0	24.0	17.0	15.0	16.09	8.90	7.42	2.52	12.50	4.97	2.5	1.3	Down	N-acetylmuramoyl-L-alanine amidase	Cell wall / LPS / capsule	OuterMembrane
PA14_08070	386	247.0	393.0	281.0	486.0	555.46	224.13	188.60	125.55	389.79	157.07	2.5	1.3	Down	putative phage tail sheath protein	Related to phage, transposon, or plasmid	Unknown
PA14_08810 rpsG	156	95.0	58.5	134.0	43.0	105.22	16.43	44.29	5.47	60.82	24.88	2.4	1.3	Down	30S ribosomal protein S7	Translation, post-translational modification, degradation	Cytoplasmic
PA14_09100 rpsD	206	34.0	136.0	61.0	91.5	35.24	35.75	18.87	10.89	35.49	14.88	2.4	1.3	Down	30S ribosomal protein S4	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08090	167	104.0	70.0	126.0	134.0	325.51	55.56	117.70	48.18	190.54	82.94	2.3	1.2	Down	putative phage tail tube protein	Related to phage, transposon, or plasmid	Unknown
PA14_05360 pilJ	682	0.0	11.0	0.0	11.0	0.00	5.33	0.00	2.41	2.66	1.21	2.2	1.1	NA	twitching motility protein PilJ	Chemotaxis	CytoplasmicMembrane
PA14_10300	203	0.0	1.0	0.0	1.0	0.00	4.04	0.00	1.83	2.02	0.91	2.2	1.1	NA	putative efflux protein	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_29030	411	0.0	4.0	0.0	4.0	0.00	2.01	0.00	0.91	1.00	0.45	2.2	1.1	NA	putative FMN oxidoreductase	Energy metabolism	Cytoplasmic
PA14_14900	214	0.0	3.0	0.0	3.0	0.00	1.59	0.00	0.72	0.80	0.36	2.2	1.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_18340	295	0.0	2.0	0.0	2.0	0.00	1.02	0.00	0.46	0.51	0.23	2.2	1.1	NA	hypothetical protein	Carbon compound catabolism	Cytoplasmic
PA14_25090 fadA	391	0.0	1.0	0.0	1.0	0.00	1.01	0.00	0.46	0.51	0.23	2.2	1.1	NA	3-ketoacyl-CoA thiolase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_07730 ksgA	268	0.0	1.0	0.0	1.0	0.00	0.68	0.00	0.31	0.34	0.15	2.2	1.1	NA	dimethyladenosine transferase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_55530	213	0.0	1.0	0.0	1.0	0.00	0.54	0.00	0.24	0.27	0.12	2.2	1.1	NA	putative type II secretion system protein	Protein secretion/export apparatus	Cytoplasmic
PA14_58840	209	0.0	1.0	0.0	1.0	0.00	0.51	0.00	0.23	0.25	0.12	2.2	1.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_44420	471	0.0	1.0	0.0	1.0	0.00	0.51	0.00	0.23	0.25	0.11	2.2	1.1	NA	putative ferredoxin	Energy metabolism	CytoplasmicMembrane
PA14_05540 mexB	1046	0.0	1.0	0.0	1.0	0.00	0.44	0.00	0.20	0.22	0.10	2.2	1.1	NA	RND multidrug efflux transporter MexB	Transport of small molecules	CytoplasmicMembrane
PA14_71820	464	0.0	1.0	0.0	1.0	0.00	0.39	0.00	0.18	0.20	0.09	2.2	1.1	NA	putative peptidase	Putative enzymes	Cytoplasmic
PA14_68850 gcvP1	958	0.0	1.0	0.0	1.0	0.00	0.32	0.00	0.15	0.16	0.07	2.2	1.1	NA	glycine dehydrogenase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_54940	994	0.0	1.0	0.0	1.0	0.00	0.18	0.00	0.08	0.09	0.04	2.2	1.1	NA	putative siderophore biosynthesis enzyme	Putative enzymes	Cytoplasmic
PA14_65200 mrn	907	0.0	1.0	0.0	1.0	0.00	0.18	0.00	0.08	0.09	0.04	2.2	1.1	NA	exoribonuclease RNase R	Transcription, RNA processing and degradation	Cytoplasmic
PA14_16100	406	15.0	138.5	31.0	120.0	40.73	95.36	25.12	37.43	68.05	31.27	2.2	1.1	Down	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_73280 atpH	178	3.0	4.0	0.0	17.0	8.64	2.92	0.00	5.63	5.78	2.81	2.1	1.0	NA	F0F1 ATP synthase subunit delta	Energy metabolism	Cytoplasmic
PA14_59220	498	13.0	36.0	16.0	53.5	14.38	10.10	5.28	6.80	12.24	6.04	2.0	1.0	NA	pyocin S5	Secreted Factors (toxins, enzymes, alginate)	Extracellular
PA14_62190	259	0.0	63.0	0.0	69.0	0.00	144.30	0.00	71.59	72.15	35.80	2.0	1.0	Down	hypothetical protein	Hypothetical, unclassified, unknown	Extracellular
PA14_73260 atpA	514	15.0	97.0	37.0	89.5	9.43	15.47	6.94	6.46	12.45	6.70	1.9	0.9	Down	F0F1 ATP synthase subunit alpha	Energy metabolism	Cytoplasmic
PA14_08050	691	31.0	13.0	49.0	36.0	45.58	4.85	21.50	6.08	25.21	13.79	1.8	0.9	NA	putative tail fiber protein	Related to phage, transposon, or plasmid	Extracellular
PA14_08130	290	8.0	15.0	14.5	19.0	16.48	7.84	8.92	4.50	12.16	6.71	1.8	0.9	NA	hypothetical protein	Related to phage, transposon, or plasmid	Unknown

PA14_57010 groEL	547	413.0	935.0	854.5	942.5	211.94	121.68	130.87	55.56	166.81	93.22	1.8	0.8	Down	chaperonin GroEL	Chaperones & heat shock proteins	Cytoplasmic
PA14_51750 tolQ	231	4.0	9.0	0.0	31.0	16.04	9.15	0.00	14.28	12.59	7.14	1.8	0.8	NA	TolQ protein	Transport of small molecules	CytoplasmicMembrane
PA14_73410	578	0.0	4.0	0.0	5.0	0.00	2.05	0.00	1.16	1.02	0.58	1.8	0.8	NA	putative inner membrane protein translocase component YidC	Membrane proteins	CytoplasmicMembrane
PA14_50290 flhC	488	550.5	2743.5	1256.5	2916.0	718.26	907.77	489.28	437.05	813.02	463.16	1.8	0.8	Down	flagellin type B	Motility & Attachment	Extracellular
PA14_49900	168	17.0	0.0	21.0	32.5	57.78	0.00	21.30	12.69	28.89	17.00	1.7	0.8	Down	hypothetical protein	Membrane proteins	OuterMembrane
PA14_11170	278	0.0	2.0	1.0	0.0	0.00	1.67	0.98	0.00	0.83	0.49	1.7	0.8	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_69090	357	0.0	5.0	0.0	6.5	0.00	1.46	0.00	0.86	0.73	0.43	1.7	0.8	NA	hypothetical protein	Membrane proteins	CytoplasmicMembrane
PA14_42290 pscH	143	1.0	0.0	2.0	0.0	4.11	0.00	2.46	0.00	2.06	1.23	1.7	0.7	NA	type III export protein PscH	Protein secretion/export apparatus	Cytoplasmic
PA14_08790 rpsL	123	0.0	6.0	0.0	8.0	0.00	9.82	0.00	5.93	4.91	2.96	1.7	0.7	NA	30S ribosomal protein S12	Translation, post-translational modification, degradation	Cytoplasmic
PA14_33280 pvdL	4342	0.0	3.0	1.0	1.5	0.00	0.13	0.05	0.03	0.06	0.04	1.6	0.7	NA	peptide synthase	Adaptation, Protection	Unknown
PA14_69660 ppL	46	9.0	4.0	16.0	12.0	234.30	26.41	124.31	35.89	130.35	80.10	1.6	0.7	NA	Lipopeptide LppL precursor	Fatty acid and phospholipid metabolism; Cell wall / LPS / capsule	Unknown
PA14_08730 rplA	231	23.0	12.5	46.0	26.5	30.73	4.24	18.34	4.07	17.48	11.21	1.6	0.6	NA	50S ribosomal protein L1	Translation, post-translational modification, degradation	Cytoplasmic
PA14_17600	136	0.0	76.0	0.0	108.5	0.00	95.20	0.00	61.56	47.60	30.78	1.6	0.6	NA	hypothetical protein	Protein secretion/export apparatus	Unknown
PA14_58730 pilA	179	2.0	108.0	35.0	76.5	7.71	105.59	40.27	33.88	56.65	37.07	1.5	0.6	Down	type IV pilin structural subunit	Motility & Attachment	Extracellular
PA14_41170 fabI	265	0.0	9.0	0.0	13.0	0.00	6.22	0.00	4.07	3.11	2.04	1.5	0.6	NA	NADH-dependent enoyl-ACP reductase	Fatty acid and phospholipid metabolism	CytoplasmicMembrane
PA14_57510	192	3.0	121.0	6.0	179.0	9.68	98.98	5.78	66.33	54.33	36.05	1.5	0.6	NA	putative secreted lipoprotein	Fatty acid and phospholipid metabolism	Periplasmic
PA14_17530 recA	346	22.0	19.5	30.0	77.5	28.84	6.48	11.74	11.67	17.66	11.70	1.5	0.6	NA	recombinase A	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_09000 rplF	177	14.0	19.0	26.0	42.0	25.35	8.72	14.05	8.74	17.04	11.39	1.5	0.6	NA	50S ribosomal protein L6	Translation, post-translational modification, degradation	Cytoplasmic
PA14_05480	496	4.0	1.0	0.0	25.0	4.33	0.28	0.00	3.11	2.30	1.56	1.5	0.6	NA	hypothetical protein	Amino acid biosynthesis and metabolism	Unknown
PA14_62720 rpsO	89	9.0	4.0	12.0	28.0	31.97	3.60	12.72	11.43	17.79	12.07	1.5	0.6	NA	30S ribosomal protein S15	Translation, post-translational modification, degradation	Cytoplasmic
PA14_69430	376	0.0	14.0	5.0	8.0	0.00	7.34	3.09	1.90	3.67	2.49	1.5	0.6	NA	hypothetical protein	Biosynthesis of cofactors, prosthetic groups and carriers	CytoplasmicMembrane
PA14_32950	580	0.0	1.0	0.0	1.5	0.00	0.32	0.00	0.21	0.16	0.11	1.5	0.6	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_33050	291	0.0	3.0	1.0	2.0	0.00	1.97	0.77	0.60	0.99	0.69	1.4	0.5	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_57590 rplM	142	0.0	44.0	16.0	26.0	0.00	27.37	11.71	7.33	13.69	9.52	1.4	0.5	Down	50S ribosomal protein L13	Translation, post-translational modification, degradation	Cytoplasmic
PA14_12090	341	30.0	28.0	72.5	39.5	59.11	13.99	42.64	8.94	36.55	25.79	1.4	0.5	NA	RlpA family lipoprotein	Hypothetical, unclassified, unknown	Periplasmic
PA14_08220	115	0.0	22.0	0.0	35.0	0.00	27.25	0.00	19.64	13.63	9.82	1.4	0.5	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_09040 rplO	144	0.0	12.0	2.0	14.0	0.00	6.23	1.22	3.29	3.12	2.26	1.4	0.5	NA	50S ribosomal protein L15	Translation, post-translational modification, degradation	Cytoplasmic
PA14_02060	278	24.5	25.0	43.0	89.0	82.27	21.29	43.09	34.33	51.78	38.71	1.3	0.4	NA	hypothetical protein	Membrane proteins	OuterMembrane
PA14_08970 rplE	179	49.0	26.0	118.0	59.0	61.36	8.26	44.10	8.49	34.81	26.30	1.3	0.4	NA	50S ribosomal protein L5	Translation, post-translational modification, degradation	Cytoplasmic
PA14_41500	231	0.0	7.0	0.0	12.0	0.00	6.46	0.00	5.02	3.23	2.51	1.3	0.4	NA	putative lyase	Putative enzymes	Unknown
PA14_44620	108	0.0	4.0	0.0	7.0	0.00	8.80	0.00	6.98	4.40	3.49	1.3	0.3	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_25280 nqrA	445	0.0	4.0	0.0	7.0	0.00	1.63	0.00	1.29	0.81	0.65	1.3	0.3	NA	Na(+)-translocating NADH-quinone reductase subunit A	Energy metabolism	Cytoplasmic
PA14_09080 rpsM	118	39.0	97.0	65.5	278.0	84.44	53.26	42.33	69.14	68.85	55.74	1.2	0.3	NA	30S ribosomal protein S13	Translation, post-translational modification, degradation	Cytoplasmic
PA14_16000 rplS	116	36.0	75.5	108.0	116.0	69.94	37.20	62.62	25.89	53.57	44.25	1.2	0.3	NA	50S ribosomal protein L19	Transcription, RNA processing and degradation	Cytoplasmic
PA14_40290 lasA	418	8.0	148.0	29.0	253.5	17.07	80.09	18.47	62.14	48.58	40.30	1.2	0.3	NA	LasA protease precursor	Translation, post-translational modification, degradation	OuterMembrane
PA14_04710	143	18.0	16.0	35.0	70.5	108.53	24.46	62.98	48.83	66.50	55.91	1.2	0.3	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_14650 secF	306	2.0	1.0	1.0	14.0	7.99	1.01	1.19	6.42	4.50	3.81	1.2	0.2	NA	preprotein translocase subunit SecF	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_35380 ptxR	312	0.0	3.0	1.0	3.0	0.00	1.57	0.62	0.71	0.79	0.66	1.2	0.2	NA	transcriptional regulator PtxR	Transcriptional regulators	Cytoplasmic
PA14_73240 atpD	458	34.0	54.0	85.0	150.0	34.40	13.86	25.67	17.43	24.13	21.55	1.1	0.2	NA	F0F1 ATP synthase subunit beta	Energy metabolism	Cytoplasmic
PA14_18060	176	0.0	2.0	0.0	4.0	0.00	3.29	0.00	2.98	1.65	1.49	1.1	0.1	NA	hypothetical protein	Energy metabolism	CytoplasmicMembrane
PA14_54350 lepB	284	0.0	4.0	0.0	8.0	0.00	2.21	0.00	2.00	1.11	1.00	1.1	0.1	NA	signal peptidase I	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_29470	250	0.0	2.0	0.0	4.0	0.00	1.34	0.00	1.21	0.67	0.61	1.1	0.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_07310	224	0.0	1.0	0.0	2.0	0.00	0.82	0.00	0.74	0.41	0.37	1.1	0.1	NA	putative hydrolase	Putative enzymes	Cytoplasmic
PA14_24220 ppnK	295	0.0	1.0	0.0	2.0	0.00	0.81	0.00	0.73	0.41	0.37	1.1	0.1	NA	inorganic polyphosphate/ATP-NAD kinase	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_11260	309	0.0	1.0	0.0	2.0	0.00	0.70	0.00	0.64	0.35	0.32	1.1	0.1	NA	putative epimerase	Central intermediary metabolism	Cytoplasmic
PA14_69670 lysA	415	0.0	2.5	0.0	5.0	0.00	0.65	0.00	0.59	0.32	0.29	1.1	0.1	NA	diaminopimelate decarboxylase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_68810	454	0.0	1.0	0.0	2.0	0.00	0.33	0.00	0.30	0.16	0.15	1.1	0.1	NA	hypothetical protein	Putative enzymes	Unknown

PA14_00030 recF	369	0.0	0.5	0.0	1.0	0.00	0.23	0.00	0.21	0.11	0.10	1.1	0.1	NA	recombination protein F	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_19020	408	0.0	3.5	1.0	4.5	0.00	1.45	0.49	0.84	0.72	0.67	1.1	0.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	CytoplasmicMembrane
PA14_60400 rpsT	91	27.0	16.0	87.0	30.5	171.69	25.80	165.10	22.28	98.74	93.69	1.1	0.1	NA	30S ribosomal protein S20	Translation, post-translational modification, degradation	Cytoplasmic
PA14_21820	253	6.0	14.0	26.0	12.0	13.52	8.00	17.49	3.11	10.76	10.30	1.1	0.1	NA	putative peptidyl-prolyl cis-trans isomerase, FkpP-type	Translation, post-translational modification, degradation	OuterMembrane
PA14_08940 rpsQ	88	1.0	5.0	0.0	19.0	3.70	4.69	0.00	8.08	4.20	4.04	1.0	0.1	NA	30S ribosomal protein S17	Translation, post-translational modification, degradation	Cytoplasmic
PA14_65280 hflK	400	0.0	13.0	2.0	23.0	0.00	4.96	0.90	3.97	2.48	2.43	1.0	0.0	NA	protease subunit HflK	Translation, post-translational modification, degradation	Unknown
PA14_47540	424	138.0	323.0	435.0	759.5	203.58	120.84	191.52	128.71	162.21	160.12	1.0	0.0	Up	putative outer membrane protein precursor	Membrane proteins	OuterMembrane
PA14_10540	573	0.0	8.0	0.0	18.0	0.00	2.53	0.00	2.58	1.26	1.29	1.0	0.0	NA	putative iron-sulfur cluster-binding protein	Energy metabolism	CytoplasmicMembrane
PA14_51710 oprL	168	0.0	71.0	17.0	118.0	0.00	95.32	26.86	71.76	47.66	49.31	1.0	-0.1	NA	Peptidoglycan associated lipoprotein OprL precursor	Transport of small molecules	OuterMembrane
PA14_61850	742	27.0	29.0	41.0	211.5	24.06	6.55	10.90	21.65	15.31	16.28	0.9	-0.1	Up	putative TonB-dependent receptor	Transport of small molecules	OuterMembrane
PA14_44000 sucB	409	1.0	2.0	0.0	14.0	1.09	0.55	0.00	1.75	0.82	0.87	0.9	-0.1	NA	dihydroipoamide succinyltransferase	Energy metabolism	Cytoplasmic
PA14_10380	99	0.0	5.0	0.0	12.0	0.00	11.31	0.00	12.30	5.66	6.15	0.9	-0.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_09280 pchF	1809	2.0	1.0	4.0	11.0	0.97	0.12	0.58	0.61	0.55	0.59	0.9	-0.1	NA	pyochelin synthetase	Transport of small molecules	Cytoplasmic
PA14_49200 oprH	200	251.5	625.5	963.5	1451.5	625.31	394.40	714.96	414.57	509.86	564.76	0.9	-0.2	Up	PhoP/Q and low Mg2+ inducible outer membrane prote	Membrane proteins	OuterMembrane
PA14_61390	195	33.0	25.5	125.0	57.0	101.85	19.96	115.14	20.21	60.90	67.67	0.9	-0.2	NA	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_25600	326	0.0	1.0	0.0	2.5	0.00	0.65	0.00	0.73	0.32	0.37	0.9	-0.2	NA	putative peptidase	Translation, post-translational modification, degradation	CytoplasmicMembrane
PA14_66875 phaF	309	0.0	1.0	0.0	2.5	0.00	0.52	0.00	0.59	0.26	0.30	0.9	-0.2	NA	polyhydroxyalkanoate synthesis protein PhaF	Central intermediary metabolism	CytoplasmicMembrane
PA14_19065	364	1.0	0.0	0.0	10.0	2.94	0.00	0.00	3.38	1.47	1.69	0.9	-0.2	NA	hypothetical protein	Cell division	CytoplasmicMembrane
PA14_06990	202	0.0	20.0	8.0	31.0	0.00	9.72	4.57	6.82	4.86	5.70	0.9	-0.2	NA	hypothetical protein	Protein secretion/export apparatus	Unknown
PA14_66290 aceE	882	8.5	16.0	28.5	54.5	4.32	2.06	4.32	3.18	3.19	3.75	0.9	-0.2	NA	pyruvate dehydrogenase subunit E1	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_08040	177	0.0	5.0	0.0	13.0	0.00	2.95	0.00	3.48	1.48	1.74	0.9	-0.2	NA	putative phage tail protein	Related to phage, transposon, or plasmid	Cytoplasmic
PA14_22020 minD	271	0.0	4.0	0.0	10.5	0.00	2.29	0.00	2.72	1.15	1.36	0.8	-0.3	NA	cell division inhibitor MinD	Cell division	Cytoplasmic
PA14_24770	109	0.0	10.0	0.0	27.0	0.00	23.78	0.00	29.08	11.89	14.54	0.8	-0.3	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_11430 ribH	158	9.0	10.0	36.0	30.0	33.36	9.40	39.82	12.77	21.38	26.30	0.8	-0.3	NA	6,7-dimethyl-8-ribityllumazine synthase	Biosynthesis of cofactors, prosthetic groups and carriers	CytoplasmicMembrane
PA14_06160	797	7.0	1.0	15.5	37.5	5.78	0.21	3.82	3.56	3.00	3.69	0.8	-0.3	NA	putative hydroxamate-type ferrisiderophore receptor	Transport of small molecules	OuterMembrane
PA14_51690	274	14.0	56.5	23.0	245.5	26.41	27.03	12.95	53.20	26.72	33.08	0.8	-0.3	Up	hypothetical protein	Hypothetical, unclassified, unknown	Periplasmic
PA14_02680	496	0.0	2.0	0.0	5.5	0.00	0.66	0.00	0.83	0.33	0.41	0.8	-0.3	NA	putative aldehyde dehydrogenase	Energy metabolism	Cytoplasmic
PA14_08120	745	5.0	14.0	12.0	63.0	4.95	3.52	3.55	7.17	4.24	5.36	0.8	-0.3	NA	putative tail length determinant protein	Related to phage, transposon, or plasmid	OuterMembrane
PA14_44380	203	1.0	16.0	12.0	25.0	3.04	12.33	10.89	8.73	7.69	9.81	0.8	-0.4	NA	putative cytochrome c oxidase, cbb3-type, subunit II	Energy metabolism	Cytoplasmic
PA14_09400 phzS	402	0.0	2.0	0.0	6.0	0.00	1.52	0.00	2.06	0.76	1.03	0.7	-0.4	NA	hypothetical protein	Putative enzymes	Cytoplasmic
PA14_08000	171	0.0	1.0	0.0	3.0	0.00	1.11	0.00	1.51	0.55	0.75	0.7	-0.4	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_11270 oprG	232	53.0	322.5	134.5	1304.0	241.81	373.15	183.15	683.45	307.48	433.30	0.7	-0.5	Up	outer membrane protein OprG precursor	Membrane proteins	OuterMembrane
PA14_09020 rpsE	166	12.0	51.0	72.0	119.5	25.29	27.26	45.29	28.93	26.27	37.11	0.7	-0.5	NA	30S ribosomal protein S5	Translation, post-translational modification, degradation	Cytoplasmic
PA14_50450 figE	462	0.0	19.0	7.0	42.0	0.00	17.62	7.64	17.65	8.81	12.64	0.7	-0.5	NA	flagellar hook protein FigE	Motility & Attachment	Extracellular
PA14_05530 mexA	383	0.0	7.0	0.0	22.5	0.00	2.81	0.00	4.10	1.41	2.05	0.7	-0.5	NA	RND multidrug efflux membrane fusion protein MexA precursor	Transport of small molecules	CytoplasmicMembrane
PA14_09270 pchE	1438	0.0	5.0	0.0	16.0	0.00	0.72	0.00	1.05	0.36	0.53	0.7	-0.5	NA	dihydroaeruginic acid synthetase	Transport of small molecules	Unknown
PA14_51880 oprD	443	20.0	290.5	125.5	870.0	42.31	155.85	79.24	211.43	99.08	145.33	0.7	-0.6	Up	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	Transport of small molecules	OuterMembrane
PA14_59250 pilN2	545	0.0	2.0	2.5	0.0	0.00	0.76	1.12	0.00	0.38	0.56	0.7	-0.6	NA	Type IV B pilus protein	Motility & Attachment	OuterMembrane
PA14_03800 oprE	463	33.5	123.0	159.5	429.0	39.52	36.79	56.15	58.13	38.15	57.14	0.7	-0.6	Up	anaerobically-induced outer membrane porin OprE precursor	Membrane proteins	OuterMembrane

PA14_60460 rplU	103	4.0	20.0	26.5	49.5	9.01	11.43	17.82	12.81	10.22	15.32	0.7	-0.6	NA	50S ribosomal protein L21	Translation, post-translational modification, degradation	Cytoplasmic
PA14_17250	471	0.0	3.0	0.0	10.0	0.00	2.88	0.00	4.35	1.44	2.18	0.7	-0.6	NA	putative amino acid permease	Transport of small molecules	CytoplasmicMembrane
PA14_02020	444	50.0	115.5	240.0	439.0	87.33	51.16	125.10	88.08	69.24	106.59	0.7	-0.6	Up	putative outer membrane porin cytochrome c5	Membrane proteins Energy metabolism	OuterMembrane Unknown
PA14_69970 cycB	136	0.0	11.0	10.0	11.5	0.00	9.78	10.47	4.63	4.89	7.55	0.7	-0.6	NA	5,10-methylenetetrahydrofolate reductase	Central intermediary metabolism	Cytoplasmic
PA14_05590 metF	290	0.0	2.0	0.0	7.0	0.00	1.03	0.00	1.64	0.52	0.82	0.6	-0.7	NA	ATP-dependent protease ATP-binding subunit HslU	Chaperones & heat shock proteins	Cytoplasmic
PA14_66790 hslU	447	2.0	7.0	0.0	52.5	2.31	2.06	0.00	6.98	2.19	3.49	0.6	-0.7	Up	50S ribosomal protein L4	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08860 rplD	200	19.0	21.0	99.0	95.0	35.36	9.91	54.99	20.31	22.64	37.65	0.6	-0.7	Up	50S ribosomal protein L14	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08950 rplN	122	11.0	27.0	66.0	88.5	23.29	14.50	41.71	21.53	18.90	31.62	0.6	-0.7	Up	outer membrane OprD family porin	Membrane proteins	OuterMembrane
PA14_28400	425	70.0	56.0	402.0	190.5	96.81	19.64	165.93	30.27	58.23	98.10	0.6	-0.8	Up	hypothetical protein	Membrane proteins	CytoplasmicMembrane
PA14_00550	469	0.0	1.0	0.0	4.0	0.00	0.60	0.00	1.08	0.30	0.54	0.6	-0.9	NA	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	Cell wall / LPS / capsule	Cytoplasmic
PA14_57370 murD	448	0.0	0.5	0.0	2.0	0.00	0.18	0.00	0.32	0.09	0.16	0.6	-0.9	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_57920	175	0.0	6.0	0.0	24.5	0.00	4.18	0.00	7.74	2.09	3.87	0.5	-0.9	NA	RNA-binding protein Hfq	Related to phage, transposon, or plasmid	Cytoplasmic
PA14_65310 hfq	82	0.0	4.0	4.0	6.0	0.00	3.04	3.58	2.06	1.52	2.82	0.5	-0.9	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_46900	152	8.0	2.0	48.5	15.0	30.95	1.96	56.00	6.67	16.46	31.33	0.5	-0.9	Up	putative cytochrome c1 precursor	Energy metabolism	Unknown
PA14_57540	260	0.0	16.0	0.0	69.0	0.00	7.14	0.00	13.94	3.57	6.97	0.5	-1.0	NA	putative lytic enzyme	Putative enzymes	Unknown
PA14_08160	209	0.0	6.0	1.0	25.0	0.00	3.03	0.59	5.72	1.52	3.16	0.5	-1.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_21220	151	4.0	7.0	34.0	18.5	10.23	4.54	25.96	5.44	7.39	15.70	0.5	-1.1	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_06040	234	1.0	0.0	5.0	5.5	2.50	0.00	3.73	1.58	1.25	2.65	0.5	-1.1	NA	30S ribosomal protein S16	Translation, post-translational modification, degradation	Cytoplasmic
PA14_15970 rpsP	83	11.0	19.5	88.0	72.5	49.37	22.20	117.88	37.38	35.79	77.63	0.5	-1.1	Up	30S ribosomal protein S3	Translation, post-translational modification, degradation	Cytoplasmic
PA14_08910 rpsC	228	4.0	25.0	52.5	62.5	6.25	9.90	24.47	11.21	8.07	17.84	0.5	-1.1	NA	L-lactate dehydrogenase	Energy metabolism	Cytoplasmic
PA14_63090 lldD	381	0.0	2.0	0.0	10.0	0.00	0.76	0.00	1.72	0.38	0.86	0.4	-1.2	NA	putative glutathione S-transferase	Central intermediary metabolism	Cytoplasmic
PA14_40070	207	0.0	1.0	0.0	5.0	0.00	0.75	0.00	1.70	0.37	0.85	0.4	-1.2	NA	hypothetical protein	Energy metabolism	Unknown
PA14_30800	200	0.0	1.0	0.0	5.0	0.00	0.73	0.00	1.66	0.37	0.83	0.4	-1.2	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_33120	144	0.0	1.0	0.0	5.0	0.00	0.72	0.00	1.64	0.36	0.82	0.4	-1.2	NA	hypothetical protein	Transport of small molecules	CytoplasmicMembrane
PA14_57110	278	0.0	1.0	0.0	5.0	0.00	0.65	0.00	1.47	0.32	0.73	0.4	-1.2	NA	hypothetical protein	Membrane proteins	CytoplasmicMembrane
PA14_14500	372	0.0	1.0	0.0	5.0	0.00	0.64	0.00	1.45	0.32	0.72	0.4	-1.2	NA	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_50740	154	24.0	32.0	187.0	168.0	120.43	40.72	280.04	96.84	80.57	188.44	0.4	-1.2	Up	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_50630	221	0.0	9.0	0.0	46.5	0.00	8.35	0.00	19.54	4.17	9.77	0.4	-1.2	NA	putative AcrB/AcrD/AcrF family protein	Antibiotic resistance and susceptibility	CytoplasmicMembrane
PA14_57060	335	19.0	17.0	118.0	179.0	29.75	6.75	55.15	32.20	18.25	43.68	0.4	-1.3	Up	hypothetical protein	Hypothetical, unclassified, unknown ; Motility & Attachment	CytoplasmicMembrane
PA14_46590	1029	0.0	7.0	0.0	37.0	0.00	1.74	0.00	4.16	0.87	2.08	0.4	-1.3	NA	translocation protein TolB	Transport of small molecules	Periplasmic
PA14_65540	691	1.0	0.0	4.0	10.5	1.10	0.00	1.31	1.32	0.55	1.31	0.4	-1.3	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_51720 tolB	432	20.0	45.0	90.0	444.5	32.14	18.34	43.16	82.06	25.24	62.61	0.4	-1.3	Up	ApaG	Hypothetical, unclassified, unknown	Unknown
PA14_64030	356	0.0	5.0	8.0	6.5	0.00	2.46	4.64	1.45	1.23	3.04	0.4	-1.3	NA	hypothetical protein	Translation, post-translational modification, degradation	Unknown
PA14_07710 apaG	126	0.0	1.0	0.0	5.5	0.00	2.78	0.00	6.92	1.39	3.46	0.4	-1.3	NA	hypothetical protein	Transport of small molecules	Cytoplasmic
PA14_18650	108	0.0	5.0	0.0	28.0	0.00	9.23	0.00	23.41	4.62	11.71	0.4	-1.3	NA	putative outer membrane lipoprotein	Membrane proteins	Unknown
PA14_07430	923	0.0	3.0	0.0	17.0	0.00	0.66	0.00	1.69	0.33	0.84	0.4	-1.4	NA	bacterioferritin	Transport of small molecules	Cytoplasmic
PA14_09340 fptA	720	39.0	83.0	310.5	546.0	30.33	16.37	72.08	48.78	23.35	60.43	0.4	-1.4	Up	Fe(III)-pyochelin outer membrane receptor precursor	Translation, post-translational modification, degradation	Cytoplasmic
PA14_29270	367	0.0	12.0	18.0	23.0	0.00	4.71	8.31	4.09	2.35	6.20	0.4	-1.4	NA	50S ribosomal protein L11	Translation, post-translational modification, degradation	Cytoplasmic
PA14_09160 bfrA	154	12.0	1.0	97.5	30.5	97.62	2.06	236.73	28.50	49.84	132.62	0.4	-1.4	Up	Lipid A 3-O-deacylase	Hypothetical, unclassified, unknown ; Cell wall / LPS / capsule	Unknown
PA14_08720 rplK	143	2.0	15.0	30.0	68.0	4.37	8.30	19.54	17.05	6.33	18.29	0.4	-1.5	Up	elongation factor Tu	Translation, post-translational modification, degradation	Cytoplasmic
PA14_61650 pagL	173	37.0	60.0	295.0	584.5	109.61	45.07	260.81	198.90	77.34	229.85	0.3	-1.6	Up	D-ala-D-ala-carboxypeptidase	Cell wall / LPS / capsule	CytoplasmicMembrane
PA14_08830 tufA	397	0.0	21.0	34.0	54.0	0.00	3.78	7.21	4.41	1.89	5.81	0.3	-1.6	NA	3-ketoacyl-(acyl-carrier-protein) reductase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_12100 dacC	386	0.0	3.5	8.0	3.5	0.00	1.72	4.62	0.78	0.86	2.70	0.3	-1.7	NA	aspartyl-tRNA synthetase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_25660 fabG	247	0.0	15.0	16.0	66.0	0.00	10.78	13.53	21.48	5.39	17.51	0.3	-1.7	NA			
PA14_51820 aspS	591	5.0	8.5	48.0	83.5	4.51	1.94	12.92	8.65	3.23	10.78	0.3	-1.7	Up			

PA14_17270 accA	316	0.0	2.0	0.0	15.0	0.00	1.12	0.00	3.81	0.56	1.90	0.3	-1.8	NA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	Fatty acid and phospholipid metabolism	CytoplasmicMembrane
PA14_30110 purB	456	0.0	1.0	3.0	0.0	0.00	0.37	1.31	0.00	0.19	0.66	0.3	-1.8	NA	adenylosuccinate lyase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_19050 metG	678	0.0	1.0	0.0	8.0	0.00	0.21	0.00	0.75	0.10	0.37	0.3	-1.9	NA	methionyl-tRNA synthetase	Translation, post-translational modification, degradation	Cytoplasmic
PA14_39070	130	9.0	18.0	75.0	239.5	45.16	22.91	112.32	138.05	34.03	125.18	0.3	-1.9	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_65180 rpsF	139	0.0	3.0	4.0	14.0	0.00	1.73	2.72	3.66	0.87	3.19	0.3	-1.9	NA	30S ribosomal protein S6	Translation, post-translational modification, degradation	Cytoplasmic
PA14_67510 estA	646	4.0	34.0	76.5	213.5	6.36	13.72	36.32	39.02	10.04	37.67	0.3	-1.9	Up	esterase EstA	Fatty acid and phospholipid metabolism	OuterMembrane
PA14_51380 pqsE	301	0.0	1.5	0.0	12.5	0.00	0.75	0.00	2.82	0.37	1.41	0.3	-1.9	NA	Quinolone signal response protein		Cytoplasmic
PA14_16630	261	2.0	102.0	118.0	617.5	5.05	65.34	88.96	179.19	35.20	134.07	0.3	-1.9	Up	putative outer membrane protein, OmpA	Membrane proteins	OuterMembrane
PA14_73250 atpG	286	0.0	3.0	5.5	13.0	0.00	1.35	2.91	2.64	0.67	2.78	0.2	-2.0	NA	F0F1 ATP synthase subunit gamma	Energy metabolism	Cytoplasmic
PA14_61290	273	0.0	8.0	5.0	60.0	0.00	6.13	4.51	20.84	3.07	12.67	0.2	-2.1	NA	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_19470 mqoA	523	0.0	1.0	2.0	4.0	0.00	0.54	1.28	0.98	0.27	1.13	0.2	-2.1	NA	malate:quinone oxidoreductase	Central intermediary metabolism	Unknown
PA14_15310 guaB	489	0.0	7.0	8.5	43.0	0.00	2.54	3.62	7.06	1.27	5.34	0.2	-2.1	NA	inosine 5'-monophosphate dehydrogenase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_24290 glt	654	0.0	7.0	2.0	63.5	0.00	3.11	1.05	12.79	1.56	6.92	0.2	-2.2	Up	glycine betaine transmethylase	Amino acid biosynthesis and metabolism	OuterMembrane
PA14_61780	204	0.0	5.0	11.0	23.0	0.00	1.72	4.44	3.57	0.86	4.01	0.2	-2.2	NA	50S ribosomal protein L25/general stress protein Ctc	Translation, post-translational modification, degradation	Cytoplasmic
PA14_53500	237	0.0	30.0	66.0	152.0	0.00	24.22	62.72	55.59	12.11	59.16	0.2	-2.3	Up	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_05550 oprM	485	2.0	15.0	43.0	147.5	3.09	5.87	19.80	26.15	4.48	22.97	0.2	-2.4	Up	major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	Membrane proteins	OuterMembrane
PA14_00910	1102	1.0	0.0	7.0	27.0	0.58	0.00	1.21	1.79	0.29	1.50	0.2	-2.4	NA	hypothetical protein	Hypothetical, unclassified, unknown	CytoplasmicMembrane
PA14_08680 tufB	397	0.0	21.0	44.0	128.0	0.00	3.78	9.33	10.45	1.89	9.89	0.2	-2.4	Up	elongation factor Tu	Translation, post-translational modification, degradation	Cytoplasmic
PA14_33070	666	0.0	5.0	0.0	61.0	0.00	1.61	0.00	8.88	0.80	4.44	0.2	-2.5	Up	hypothetical protein	Hypothetical, unclassified, unknown	CytoplasmicMembrane
PA14_62990 grpE	186	0.0	1.0	1.0	10.0	0.00	1.05	1.24	4.78	0.53	3.01	0.2	-2.5	NA	heat shock protein GrpE	Chaperones & heat shock proteins	Cytoplasmic
PA14_50340 flgL	439	0.0	3.0	12.0	6.5	0.00	0.84	3.95	0.82	0.42	2.38	0.2	-2.5	NA	flagellar hook-associated protein FlgL	Motility & Attachment	Extracellular
PA14_57480	604	8.0	6.0	109.0	235.5	11.87	2.26	48.25	40.12	7.06	44.19	0.2	-2.7	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	CytoplasmicMembrane
PA14_23030 oprB	454	0.0	29.5	77.5	207.0	0.00	13.77	42.58	43.78	6.89	43.18	0.2	-2.7	Up	glucose/carbohydrate outer membrane porin OprB precursor	Transport of small molecules	OuterMembrane
PA14_15070 oprC	723	7.0	11.0	135.5	189.0	5.39	2.15	31.11	16.70	3.77	23.91	0.2	-2.7	Up	outer membrane copper receptor OprC	Transport of small molecules	OuterMembrane
PA14_54520	427	0.0	1.0	0.0	14.0	0.00	0.39	0.00	2.48	0.20	1.24	0.2	-2.7	NA	porin	Membrane proteins	OuterMembrane
PA14_30230 cipA	758	0.0	0.5	0.0	7.0	0.00	0.13	0.00	0.80	0.06	0.40	0.2	-2.7	NA	ATP-dependent ctp protease, ATP-binding subunit CtpA	Translation, post-translational modification, degradation	Cytoplasmic
PA14_34960	452	0.0	24.5	64.5	179.0	0.00	11.54	35.77	38.20	5.77	36.98	0.2	-2.7	Up	glucose-sensitive porin	Transport of small molecules	OuterMembrane
PA14_16640	134	0.0	24.5	0.0	353.0	0.00	76.81	0.00	501.29	38.40	250.65	0.2	-2.7	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_33680 fpvA	815	0.0	1.0	2.0	9.5	0.00	0.23	0.54	0.99	0.11	0.76	0.2	-2.7	NA	ferripyoverdine receptor	Transport of small molecules	OuterMembrane
PA14_00820	304	0.0	27.0	32.0	325.0	0.00	14.31	19.96	78.01	7.15	48.98	0.2	-2.8	Up	hypothetical protein	Hypothetical, unclassified, unknown	CytoplasmicMembrane
PA14_41690	179	1.0	0.0	15.0	23.0	3.01	0.00	13.46	7.94	1.50	10.70	0.1	-2.8	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_60230 comL	341	0.0	3.0	5.0	35.0	0.00	1.21	2.37	6.38	0.60	4.38	0.1	-2.9	NA	competence protein ComL	Cell wall / LPS / capsule	OuterMembrane
PA14_63030 omlA	176	0.0	4.0	21.0	11.0	0.00	7.04	43.48	8.77	3.52	26.12	0.1	-2.9	NA	outer membrane lipoprotein OmlA precursor	Cell wall / LPS / capsule	OuterMembrane
PA14_14470 pepA	495	0.0	4.0	21.0	11.0	0.00	1.05	6.47	1.30	0.52	3.89	0.1	-2.9	NA	leucyl aminopeptidase	Translation, post-translational modification, degradation	Cytoplasmic
PA14_23380 orfH	422	0.0	1.0	0.0	16.5	0.00	0.38	0.00	2.81	0.19	1.40	0.1	-2.9	NA	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	Cell wall / LPS / capsule	Cytoplasmic
PA14_64480 osmE	114	0.0	23.0	122.0	70.0	0.00	29.33	183.12	40.44	14.67	111.78	0.1	-2.9	Up	DNA-binding transcriptional activator OsmE	Membrane proteins	Unknown
PA14_16250 lasB	498	0.0	7.0	4.0	115.0	0.00	2.67	1.80	19.87	1.33	10.83	0.1	-3.0	Up	elastase LasB	Amino acid biosynthesis and metabolism	Extracellular
PA14_25560 rne	1057	0.0	3.0	17.0	10.0	0.00	0.52	3.49	0.79	0.26	2.14	0.1	-3.0	NA	ribonuclease E	Transcription, RNA processing and degradation	Cytoplasmic
PA14_08850 rplC	211	0.0	6.0	33.0	24.0	0.00	3.53	22.87	6.40	1.77	14.64	0.1	-3.1	NA	50S ribosomal protein L3	Translation, post-translational modification, degradation	Cytoplasmic
PA14_43850 htpG	634	0.0	30.0	144.5	176.0	0.00	3.74	21.20	9.94	1.87	15.57	0.1	-3.1	Up	heat shock protein 90	Chaperones & heat shock proteins	Cytoplasmic

PA14_08760 rpoB	1357	0.0	16.0	59.0	150.5	0.00	1.30	5.64	5.54	0.65	5.59	0.1	-3.1	Up	DNA-directed RNA polymerase subunit beta	Translation, post-translational modification, degradation	Cytoplasmic
PA14_46520	379	0.0	2.0	0.0	39.0	0.00	0.67	0.00	5.91	0.33	2.95	0.1	-3.1	Up	hypothetical protein	Hypothetical, unclassified, unknown	Periplasmic
PA14_51240 purC	236	0.0	9.0	55.0	36.5	0.00	4.53	32.55	8.31	2.26	20.43	0.1	-3.2	Up	phosphoribosylaminoimidazole-succinocarboxamide synthase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_70040 dadA	432	0.0	8.0	48.0	44.5	0.00	4.07	28.71	10.25	2.03	19.48	0.1	-3.3	Up	D-amino acid dehydrogenase small subunit	Amino acid biosynthesis and metabolism	CytoplasmicMembrane
PA14_25250	461	0.0	7.0	37.0	56.0	0.00	2.01	12.49	7.28	1.00	9.89	0.1	-3.3	Up	glyceraldehyde-3-phosphate dehydrogenase	Carbon compound catabolism	Cytoplasmic
PA14_58570	753	0.0	7.0	40.5	48.0	0.00	1.43	9.70	4.43	0.71	7.06	0.1	-3.3	Up	putative outer membrane ferric siderophore receptor	Transport of small molecules	OuterMembrane
PA14_08840 rpsJ	103	0.0	6.5	41.0	44.0	0.00	3.19	23.71	9.79	1.60	16.75	0.1	-3.4	Up	30S ribosomal protein S10	Translation, post-translational modification, degradation	Cytoplasmic
PA14_26550	119	0.0	4.0	18.0	46.5	0.00	4.91	26.01	25.86	2.46	25.94	0.1	-3.4	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_25390 sth	464	0.0	1.0	0.0	24.0	0.00	0.35	0.00	3.85	0.18	1.93	0.1	-3.4	Up	soluble pyridine nucleotide transhydrogenase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_05510	191	0.0	12.0	10.0	273.0	0.00	5.52	5.41	56.88	2.76	31.15	0.1	-3.5	Up	hypothetical protein	Membrane proteins	Unknown
PA14_41230 clpX	426	0.0	1.0	6.5	8.0	0.00	0.33	2.54	1.20	0.17	1.87	0.1	-3.5	NA	ATP-dependent protease ATP-binding subunit ClpX	Chaperones & heat shock proteins	Cytoplasmic
PA14_24445 gdhB	1620	0.0	3.0	22.0	25.5	0.00	0.29	2.50	1.11	0.14	1.81	0.1	-3.6	Up	NAD-dependent glutamate dehydrogenase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_25860 lefB	249	0.0	2.0	0.0	55.5	0.00	1.21	0.00	15.19	0.60	7.59	0.1	-3.7	Up	electron transfer flavoprotein beta-subunit	Energy metabolism	Unknown
PA14_20750	310	0.0	1.0	8.0	7.0	0.00	0.51	4.81	1.62	0.26	3.22	0.1	-3.7	NA	putative chemotaxis protein	Chemotaxis	Cytoplasmic
PA14_65720	248	0.0	2.5	19.0	21.0	0.00	1.73	15.51	6.60	0.87	11.05	0.1	-3.7	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_08780 rpoC	1399	0.0	7.0	38.0	101.5	0.00	0.55	3.53	3.63	0.28	3.58	0.1	-3.7	Up	DNA-directed RNA polymerase subunit beta'	Transcription, RNA processing and degradation	Cytoplasmic
PA14_62710 pnp	701	0.0	1.0	8.5	8.0	0.00	0.17	1.65	0.60	0.08	1.12	0.1	-3.8	NA	polynucleotide phosphorylase/polyadenylase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_69240 hemB	337	0.0	3.0	28.0	19.5	0.00	2.59	28.41	7.61	1.29	18.01	0.1	-3.8	Up	delta-aminolevulinic acid dehydratase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_66900 ubiE	256	0.0	1.0	9.0	8.0	0.00	0.59	6.23	2.13	0.29	4.18	0.1	-3.8	NA	ubiquinone/menaquinone biosynthesis methyltransferase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_62000 hltA	335	0.0	2.0	12.0	37.0	0.00	1.30	9.21	10.94	0.65	10.08	0.1	-4.0	Up	ferric iron-binding periplasmic protein HltA	Transport of small molecules	Periplasmic
PA14_47800	616	0.0	5.0	45.0	55.5	0.00	1.45	15.30	7.26	0.72	11.28	0.1	-4.0	Up	putative tonB-dependent receptor	Transport of small molecules	OuterMembrane
PA14_70490	243	0.0	4.0	18.0	98.0	0.00	2.35	12.42	26.03	1.17	19.23	0.1	-4.0	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_67600 glnA	469	0.0	5.0	43.0	69.5	0.00	1.59	16.05	9.99	0.79	13.02	0.1	-4.0	Up	glutamine synthetase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_54170 putA	1060	0.0	6.5	45.5	120.0	0.00	0.64	5.28	5.36	0.32	5.32	0.1	-4.1	Up	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_07770 ostA	924	0.0	21.0	194.5	277.0	0.00	3.97	43.23	23.70	1.98	33.47	0.1	-4.1	Up	organic solvent tolerance protein OstA precursor	Adaptation, Protection	OuterMembrane
PA14_05560	639	0.0	2.0	20.0	27.5	0.00	0.46	5.35	2.83	0.23	4.09	0.1	-4.2	Up	ATP-dependent RNA helicase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_67490 fbp	336	0.0	1.0	10.5	14.0	0.00	0.80	9.85	5.05	0.40	7.45	0.1	-4.2	NA	fructose-1,6-bisphosphatase	Central intermediary metabolism	Cytoplasmic
PA14_47120	170	0.0	11.0	140.5	100.0	0.00	13.51	203.04	55.62	6.75	129.33	0.1	-4.3	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_21730	721	0.0	6.0	67.0	82.0	0.00	1.71	22.41	10.56	0.85	16.49	0.1	-4.3	Up	putative TonB-dependent receptor	Transport of small molecules	OuterMembrane
PA14_62690	114	0.0	5.0	39.0	114.0	0.00	5.09	46.74	52.59	2.55	49.67	0.1	-4.3	Up	hypothetical protein	Hypothetical, unclassified, unknown	Periplasmic
PA14_17070 tsf	289	0.0	5.0	34.5	129.0	0.00	1.01	8.19	11.78	0.50	9.98	0.1	-4.3	Up	elongation factor Ts	Translation, post-translational modification, degradation	Cytoplasmic
PA14_60580	618	0.0	1.0	8.0	24.5	0.00	0.30	2.81	3.31	0.15	3.06	0.1	-4.4	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_21790 rdgC	306	0.0	1.0	11.0	17.0	0.00	0.35	4.51	2.69	0.17	3.60	0.1	-4.4	NA	recombination associated protein	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_29990 nuoD	593	0.0	1.0	13.0	13.0	0.00	0.31	4.74	1.82	0.15	3.28	0.1	-4.4	NA	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	Energy metabolism	Cytoplasmic
PA14_09200 ssb	165	0.0	1.0	11.0	18.5	0.00	1.20	15.49	10.03	0.60	12.76	0.1	-4.4	NA	single-stranded DNA-binding protein	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_68330 arcA	418	0.0	2.0	20.5	44.5	0.00	0.67	8.14	6.80	0.34	7.47	0.1	-4.5	Up	arginine deiminase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_44010 sucA	943	0.0	0.5	1.0	25.0	0.00	0.11	0.26	2.48	0.06	1.37	0.0	-4.6	NA	2-oxoglutarate dehydrogenase E1 component	Energy metabolism	Cytoplasmic
PA14_56590	286	0.0	1.0	14.0	27.0	0.00	0.45	7.47	5.54	0.23	6.51	0.0	-4.8	Up	hypothetical protein	Adaptation, Protection	Cytoplasmic
PA14_52020	345	0.0	1.0	8.0	43.0	0.00	0.77	7.26	15.01	0.39	11.14	0.0	-4.9	Up	hypothetical protein	Hypothetical, unclassified, unknown	Periplasmic
PA14_14730 iscS	404	0.0	1.0	1.0	62.0	0.00	0.42	0.50	11.95	0.21	6.22	0.0	-4.9	Up	cysteine desulfurase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_53250 cpbD	389	0.0	4.0	67.0	89.0	0.00	2.17	42.88	21.92	1.09	32.40	0.0	-4.9	Up	chitin-binding protein CbpD precursor	Secreted Factors (toxins, enzymes, alginate)	Extracellular
PA14_41220 lon	798	0.0	1.0	18.0	24.5	0.00	0.16	3.36	1.76	0.08	2.56	0.0	-5.0	Up	Lon protease	Translation, post-translational modification, degradation	Cytoplasmic



PA14_41470 acnB	869	0.0	2.0	33.0	59.0	0.00	0.25	4.93	3.39	0.13	4.16	0.0	-5.0	Up	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	Energy metabolism	Cytoplasmic
PA14_36310 hcnC	417	0.0	1.0	21.0	20.0	0.00	0.49	12.09	4.43	0.24	8.26	0.0	-5.1	Up	hydrogen cyanide synthase HcnC	Central intermediary metabolism	Cytoplasmic
PA14_53200	182	0.0	1.0	14.0	42.0	0.00	0.80	13.15	15.19	0.40	14.17	0.0	-5.2	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_14850 pilF	252	1.0	7.5	310.5	169.5	2.03	3.87	188.47	39.60	2.95	114.04	0.0	-5.3	Up	type 4 fimbrial biogenesis protein PilF	Motility & Attachment	Unknown
PA14_32790	5212	1.0	6.0	185.0	409.0	0.12	0.18	6.58	5.59	0.15	6.08	0.0	-5.3	Up	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_72400	259	0.0	1.0	33.0	8.0	0.00	0.58	22.38	2.09	0.29	12.23	0.0	-5.4	Up	putative N-acetylmuramoyl-L- alanine amidase family protein	Putative enzymes	Cytoplasmic
PA14_14910	380	0.0	3.0	74.5	93.0	0.00	1.84	53.71	25.81	0.92	39.76	0.0	-5.4	Up	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_72600	262	0.0	1.0	31.5	18.0	0.00	0.77	28.46	6.26	0.38	17.36	0.0	-5.5	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_62840 gimM	445	0.0	2.0	18.0	164.0	0.00	1.06	11.19	39.25	0.53	25.22	0.0	-5.6	Up	phosphoglucosamine mutase	Cell wall / LPS / capsule	Cytoplasmic
PA14_00570	228	0.0	1.0	22.5	52.5	0.00	0.77	20.38	18.31	0.39	19.34	0.0	-5.7	Up	putative lipoprotein	Cell wall / LPS / capsule	Unknown
PA14_65590	236	0.0	1.0	25.5	46.5	0.00	0.78	23.45	16.46	0.39	19.96	0.0	-5.7	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_52600 alaS	874	0.0	0.5	7.0	38.5	0.00	0.09	1.55	3.28	0.05	2.41	0.0	-5.7	NA	alanyl-tRNA synthetase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_44290 acnA	910	0.0	1.0	18.5	70.0	0.00	0.23	5.07	7.39	0.12	6.23	0.0	-5.7	Up	aconitate hydratase	Energy metabolism	Cytoplasmic
PA14_25080 fadB	715	0.0	1.0	53.0	36.5	0.00	0.22	13.46	3.57	0.11	8.52	0.0	-6.3	Up	multifunctional fatty acid oxidation complex subunit alpha	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_12210	207	0.0	2.0	112.0	68.5	0.00	1.32	86.82	20.44	0.66	53.63	0.0	-6.4	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_17150	794	0.0	1.0	37.0	96.5	0.00	0.30	13.24	13.29	0.15	13.26	0.0	-6.5	Up	putative outer membrane antigen	Cell wall / LPS / capsule	OuterMembrane
PA14_67810	436	0.0	1.0	64.0	95.0	0.00	0.39	29.01	16.57	0.19	22.79	0.0	-6.9	Up	putative carboxyl-terminal protease	Related to phage, transposon, or plasmid	CytoplasmicMembrane
PA14_58410	484	0.0	1.0	35.0	265.5	0.00	0.47	19.17	55.96	0.23	37.56	0.0	-7.3	Up	putative porin	Transport of small molecules	OuterMembrane
PA14_00510	3443	0.0	1.0	66.5	195.0	0.00	0.04	3.42	3.86	0.02	3.64	0.0	-7.4	Up	putative hemagglutinin	Membrane proteins	OuterMembrane
PA14_07200	66	0.0	0.0	25.0	27.0	0.00	0.00	111.56	46.37	0.00	78.97	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_52960	88	0.0	0.0	18.0	29.0	0.00	0.00	61.91	38.39	0.00	50.15	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_20600	224	0.0	0.0	22.0	119.0	0.00	0.00	30.14	62.76	0.00	46.45	0.0	-10.0	Up	hypothetical protein	Hypothetical, unclassified, unknown	CytoplasmicMembrane
PA14_11370	156	0.0	0.0	48.0	43.5	0.00	0.00	58.81	20.52	0.00	39.66	0.0	-10.0	Up	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_72450 dsbA	211	0.0	0.0	67.0	37.0	0.00	0.00	60.70	12.90	0.00	36.80	0.0	-10.0	Up	thiol:disulfide interchange protein DsbA	Biosynthesis of cofactors, prosthetic groups and carriers	Periplasmic
PA14_09150 katA	482	0.0	0.0	81.0	86.0	0.00	0.00	41.18	16.83	0.00	29.00	0.0	-10.0	Up	catalase	Adaptation, Protection	Cytoplasmic
PA14_07760 surA	430	0.0	0.0	84.0	129.0	0.00	0.00	35.74	21.13	0.00	28.44	0.0	-10.0	Up	peptidyl-prolyl cis-trans isomerase SurA	Adaptation, Protection	Periplasmic
PA14_22010 minE	84	0.0	0.0	17.0	9.0	0.00	0.00	43.52	8.87	0.00	26.19	0.0	-10.0	NA	cell division topological specificity factor MinE	Cell division	Cytoplasmic
PA14_33310	342	0.0	0.0	60.0	66.5	0.00	0.00	35.28	15.05	0.00	25.17	0.0	-10.0	Up	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_06010	192	0.0	0.0	21.5	31.0	0.00	0.00	31.34	17.39	0.00	24.37	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_72500	96	0.0	0.0	11.0	47.5	0.00	0.00	17.59	29.24	0.00	23.41	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_57840	215	0.0	0.0	36.0	44.0	0.00	0.00	31.83	14.97	0.00	23.40	0.0	-10.0	NA	hypothetical protein	Adaptation, Protection	Unknown
PA14_00490	562	0.0	0.0	96.0	119.5	0.00	0.00	31.06	14.88	0.00	22.97	0.0	-10.0	Up	putative hemolysin activation/secretion protein	Protein secretion/export apparatus	OuterMembrane
PA14_28450 eco	156	0.0	0.0	41.0	20.0	0.00	0.00	38.24	7.18	0.00	22.71	0.0	-10.0	NA	ecotin	Translation, post-translational modification, degradation	Periplasmic
PA14_63220	81	0.0	0.0	16.0	23.0	0.00	0.00	28.79	15.93	0.00	22.36	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_16840	132	0.0	0.0	6.0	38.0	0.00	0.00	12.70	30.96	0.00	21.83	0.0	-10.0	NA	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_65750	482	0.0	0.0	83.0	139.5	0.00	0.00	26.11	16.89	0.00	21.50	0.0	-10.0	Up	putative outer membrane efflux protein precursor	Protein secretion/export apparatus	OuterMembrane
PA14_62430	158	0.0	0.0	23.0	11.0	0.00	0.00	36.25	6.67	0.00	21.46	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_03610	252	0.0	0.0	38.0	27.0	0.00	0.00	33.28	9.10	0.00	21.19	0.0	-10.0	NA	putative putative Zn-dependent protease with chaperone function	Chaperones & heat shock proteins	Unknown
PA14_03920 spuD	367	0.0	0.0	42.0	48.0	0.00	0.00	28.48	12.53	0.00	20.50	0.0	-10.0	Up	polyamine transport protein	Transport of small molecules	Periplasmic
PA14_58300	186	0.0	0.0	9.0	12.0	0.00	0.00	26.77	13.74	0.00	20.26	0.0	-10.0	NA	putative two-component response regulator	Two-component regulatory systems	Cytoplasmic
PA14_67720 secB	163	0.0	0.0	28.5	7.5	0.00	0.00	34.86	3.53	0.00	19.19	0.0	-10.0	NA	preprotein translocase subunit SecB	Protein secretion/export apparatus	Cytoplasmic
PA14_30310 lolA	208	0.0	0.0	26.0	53.0	0.00	0.00	20.97	16.45	0.00	18.71	0.0	-10.0	NA	outer-membrane lipoprotein carrier protein	Chaperones & heat shock proteins	Periplasmic
PA14_32780	565	0.0	0.0	85.0	75.0	0.00	0.00	26.68	9.06	0.00	17.87	0.0	-10.0	Up	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_49660	282	0.0	0.0	9.0	46.5	0.00	0.00	11.94	23.73	0.00	17.84	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Periplasmic
PA14_62580 panB	266	0.0	0.0	19.0	6.0	0.00	0.00	31.14	3.79	0.00	17.46	0.0	-10.0	NA	3-methyl-2-oxobutanoate hydroxymethyltransferase	Biosynthesis of cofactors, prosthetic groups and carriers	Unknown
PA14_38510 hmgA	432	0.0	0.0	29.0	48.0	0.00	0.00	21.00	13.38	0.00	17.19	0.0	-10.0	NA	homogentisate 1,2-dioxygenase	Carbon compound catabolism	Unknown
PA14_04090	256	0.0	0.0	34.0	69.5	0.00	0.00	19.19	15.10	0.00	17.15	0.0	-10.0	Up	putative binding protein component of ABC transporter	Transport of small molecules	Periplasmic

PA14_09420 phzF1	278	0.0	0.0	20.0	33.0	0.00	0.00	20.57	13.07	0.00	16.82	0.0	-10.0	NA	phenazine biosynthesis protein	Secreted Factors (toxins, enzymes, alginate)	Cytoplasmic
PA14_47550	184	0.0	0.0	34.0	15.0	0.00	0.00	28.71	4.88	0.00	16.79	0.0	-10.0	NA	putative glutathione peroxidase	Adaptation, Protection	Periplasmic
PA14_54390 mucD	474	0.0	0.0	30.5	63.0	0.00	0.00	18.46	14.68	0.00	16.57	0.0	-10.0	Up	serine protease MucD precursor	Secreted Factors (toxins, enzymes, alginate)	Periplasmic
PA14_04100	145	0.0	0.0	8.0	51.0	0.00	0.00	8.59	21.08	0.00	14.84	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_65000 azu	148	0.0	0.0	15.0	14.0	0.00	0.00	21.40	7.69	0.00	14.54	0.0	-10.0	NA	azurin precursor	Energy metabolism	Periplasmic
PA14_43950 sucC	388	0.0	0.0	41.0	208.0	0.00	0.00	9.76	19.06	0.00	14.41	0.0	-10.0	Up	succinyl-CoA synthetase subunit beta	Energy metabolism	Cytoplasmic
PA14_62130 ilvC	338	0.0	0.0	31.0	57.0	0.00	0.00	16.51	11.69	0.00	14.10	0.0	-10.0	Up	ketol-acid reductoisomerase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_21130	242	0.0	0.0	33.5	10.0	0.00	0.00	24.05	2.76	0.00	13.41	0.0	-10.0	NA	putative outer membrane lipoprotein	Membrane proteins	Unknown
PA14_46960 ggt	557	0.0	0.0	58.0	33.5	0.00	0.00	21.27	4.73	0.00	13.00	0.0	-10.0	Up	gamma-glutamyltranspeptidase precursor	Central intermediary metabolism	Periplasmic
PA14_51830	156	0.0	0.0	9.0	47.0	0.00	0.00	8.64	17.36	0.00	13.00	0.0	-10.0	NA	DNA-binding stress protein	Adaptation, Protection	Cytoplasmic
PA14_38350 galU	279	0.0	0.0	6.5	71.0	0.00	0.00	4.99	20.96	0.00	12.97	0.0	-10.0	NA	UTP-glucose-1-phosphate uridylyltransferase	Central intermediary metabolism	Cytoplasmic
PA14_52790 aotJ	259	0.0	0.0	27.0	80.0	0.00	0.00	12.06	13.76	0.00	12.91	0.0	-10.0	Up	arginine/ornithine binding protein AotJ	Transport of small molecules	Periplasmic
PA14_51410 pgsC	348	0.0	0.0	10.5	40.5	0.00	0.00	10.29	15.27	0.00	12.78	0.0	-10.0	NA	PgsC	Energy metabolism	Cytoplasmic
PA14_40830	330	0.0	0.0	19.0	53.0	0.00	0.00	12.27	13.17	0.00	12.72	0.0	-10.0	NA	putative oxidoreductase	Energy metabolism	Cytoplasmic
PA14_67620	134	0.0	0.0	1.0	39.0	0.00	0.00	1.58	23.77	0.00	12.68	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_43940 sucD	295	0.0	0.0	46.0	46.5	0.00	0.00	17.78	6.92	0.00	12.35	0.0	-10.0	Up	succinyl-CoA synthetase subunit alpha	Energy metabolism	Cytoplasmic
PA14_21175	335	0.0	0.0	48.0	55.5	0.00	0.00	16.86	7.50	0.00	12.18	0.0	-10.0	Up	hypothetical protein	Transport of small molecules	Periplasmic
PA14_47010	68	0.0	0.0	8.0	6.5	0.00	0.00	18.54	5.80	0.00	12.17	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_48800	205	0.0	0.0	25.0	0.5	0.00	0.00	24.00	0.18	0.00	12.09	0.0	-10.0	Up	hypothetical protein	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_39890 phzF2	278	0.0	0.0	20.0	9.0	0.00	0.00	20.57	3.56	0.00	12.07	0.0	-10.0	NA	phenazine biosynthesis protein	Secreted Factors (toxins, enzymes, alginate)	Cytoplasmic
PA14_09500 opmD	487	0.0	0.0	47.0	56.0	0.00	0.00	15.56	7.13	0.00	11.35	0.0	-10.0	Up	outer membrane protein	Membrane proteins	Outer/Membrane
PA14_12160	448	0.0	0.0	37.0	43.0	0.00	0.00	15.64	7.00	0.00	11.32	0.0	-10.0	NA	putative murein transglycosylase	Putative enzymes	Cytoplasmic/Membrane
PA14_18630	995	0.0	0.0	30.0	175.0	0.00	0.00	6.96	15.62	0.00	11.29	0.0	-10.0	Up	putative serine protease	Putative enzymes	Outer/Membrane
PA14_58330	236	0.0	0.0	13.0	34.0	0.00	0.00	11.19	11.27	0.00	11.23	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_66880	138	0.0	0.0	19.5	35.0	0.00	0.00	13.17	9.10	0.00	11.13	0.0	-10.0	NA	hypothetical protein	Transcriptional regulators	Unknown
PA14_14660	182	0.0	0.0	18.0	14.0	0.00	0.00	16.93	5.07	0.00	11.00	0.0	-10.0	NA	hypothetical protein	Protein secretion/export apparatus	Outer/Membrane
PA14_38440 gnyD	387	0.0	0.0	27.0	18.0	0.00	0.00	16.93	4.34	0.00	10.64	0.0	-10.0	NA	Citronellol-CoA dehydrogenase, GnyD	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_46910	302	0.0	0.0	6.0	84.0	0.00	0.00	3.21	17.29	0.00	10.25	0.0	-10.0	Up	putative binding protein component of ABC transporter	Transport of small molecules	Periplasmic
PA14_09450 phzD1	207	0.0	0.0	4.0	19.0	0.00	0.00	6.99	12.78	0.00	9.88	0.0	-10.0	NA	phenazine biosynthesis protein PhzD	Secreted Factors (toxins, enzymes, alginate)	Cytoplasmic
PA14_45580	368	0.0	0.0	21.0	13.0	0.00	0.00	15.60	3.72	0.00	9.66	0.0	-10.0	NA	chemotaxis-specific methyltransferase	Chemotaxis	Cytoplasmic
PA14_17400 adhC	370	0.0	0.0	17.0	12.0	0.00	0.00	14.66	3.98	0.00	9.32	0.0	-10.0	NA	alcohol dehydrogenase class III	Central intermediary metabolism	Cytoplasmic
PA14_03930 spuE	365	0.0	0.0	26.0	6.5	0.00	0.00	16.98	1.63	0.00	9.31	0.0	-10.0	NA	polyamine transport protein	Transport of small molecules	Periplasmic
PA14_60700 ccpR	346	0.0	0.0	19.0	4.0	0.00	0.00	16.98	1.38	0.00	9.18	0.0	-10.0	NA	cytochrome c551 peroxidase precursor	Energy metabolism	Periplasmic
PA14_01020	498	0.0	0.0	22.0	34.0	0.00	0.00	11.49	6.84	0.00	9.17	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_50520 braC	373	0.0	0.0	23.0	55.5	0.00	0.00	9.34	8.68	0.00	9.01	0.0	-10.0	NA	branched-chain amino acid transport protein BraC	Transport of small molecules	Periplasmic
PA14_56160	335	0.0	0.0	22.0	16.0	0.00	0.00	14.02	3.93	0.00	8.97	0.0	-10.0	NA	hypothetical protein	Putative enzymes	Cytoplasmic
PA14_66250 waaF	345	0.0	0.0	11.0	44.5	0.00	0.00	6.97	10.86	0.00	8.91	0.0	-10.0	NA	heptosyltransferase II	Cell wall / LPS / capsule	Cytoplasmic
PA14_05620 sahH	469	0.0	0.0	23.0	29.5	0.00	0.00	11.57	5.71	0.00	8.64	0.0	-10.0	NA	S-adenosyl-L-homocysteine hydrolase	Central intermediary metabolism	Cytoplasmic
PA14_60470 jipB	322	0.0	0.0	19.0	20.0	0.00	0.00	12.15	4.92	0.00	8.53	0.0	-10.0	NA	octaprenyl-diphosphate synthase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_32610 dsbG	256	0.0	0.0	11.0	9.0	0.00	0.00	12.81	4.04	0.00	8.42	0.0	-10.0	NA	disulfide isomerase/thiol-disulfide oxidase	Translation, post-translational modification, degradation	Periplasmic
PA14_16950 dapD	344	0.0	0.0	16.0	31.0	0.00	0.00	9.05	6.75	0.00	7.90	0.0	-10.0	NA	tetrahydrodipicolinate succinylase	Amino acid biosynthesis and metabolism	Unknown
PA14_58390	533	0.0	0.0	10.0	51.0	0.00	0.00	5.33	10.47	0.00	7.90	0.0	-10.0	NA	putative binding protein component of ABC transporter	Transport of small molecules	Periplasmic
PA14_49460 nrdA	963	0.0	0.0	37.0	108.5	0.00	0.00	7.39	8.34	0.00	7.86	0.0	-10.0	Up	ribonucleotide-diphosphate reductase subunit alpha	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_44780	259	0.0	0.0	13.0	24.0	0.00	0.00	9.16	6.51	0.00	7.84	0.0	-10.0	NA	putative transcriptional regulator	Transcriptional regulators	Cytoplasmic
PA14_05250 pyrC	423	0.0	0.0	19.0	2.0	0.00	0.00	14.68	0.59	0.00	7.64	0.0	-10.0	NA	dihydroorotase	Nucleotide biosynthesis and metabolism	Unknown
PA14_07680	640	0.0	0.0	22.0	94.5	0.00	0.00	5.68	9.39	0.00	7.53	0.0	-10.0	Up	hypothetical protein	Two-component regulatory systems	Cytoplasmic

PA14_57260 pxc	303	0.0	0.0	18.0	20.0	0.00	0.00	10.50	4.49	0.00	7.50	0.0	-10.0	NA	UDP-3-O-[3-hydroxymristoyl] N-acetylglucosamine deacetylase	Cell wall / LPS / capsule	Cytoplasmic
PA14_36320 hcnB	464	0.0	0.0	15.0	34.0	0.00	0.00	7.92	6.91	0.00	7.41	0.0	-10.0	NA	hydrogen cyanide synthase HcnB	Central intermediary metabolism	Cytoplasmic
PA14_14880 ispG	371	0.0	0.0	23.0	23.5	0.00	0.00	10.51	4.13	0.00	7.32	0.0	-10.0	NA	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_59610	224	0.0	0.0	16.5	8.0	0.00	0.00	12.26	2.29	0.00	7.27	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_14390	325	0.0	0.0	9.0	43.0	0.00	0.00	4.99	9.17	0.00	7.08	0.0	-10.0	NA	putative ABC-type transport protein, periplasmic c	Transport of small molecules	Unknown
PA14_71440 ltaA	346	0.0	0.0	4.0	41.5	0.00	0.00	2.81	11.22	0.00	7.02	0.0	-10.0	NA	low specificity L-threonine aldolase	Amino acid biosynthesis and metabolism	Unknown
PA14_68260	331	0.0	0.0	20.0	16.0	0.00	0.00	10.63	3.27	0.00	6.96	0.0	-10.0	NA	c4-dicarboxylate-binding protein	Membrane proteins	Periplasmic
PA14_43530	220	0.0	0.0	7.0	7.0	0.00	0.00	9.86	3.79	0.00	6.83	0.0	-10.0	NA	hypothetical protein	Central intermediary metabolism	Cytoplasmic
PA14_07040	139	0.0	0.0	4.0	16.0	0.00	0.00	5.36	8.25	0.00	6.80	0.0	-10.0	NA	hypothetical protein	Protein secretion/export apparatus	Unknown
PA14_07260	255	0.0	0.0	9.0	25.0	0.00	0.00	6.57	7.02	0.00	6.79	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_66230 waaG	373	0.0	0.0	11.0	13.0	0.00	0.00	9.16	4.17	0.00	6.66	0.0	-10.0	NA	UDP-glucose:(heptosyl) LPS alpha 1,3-glucosyltransferase WaaG	Cell wall / LPS / capsule	Cytoplasmic
PA14_21880 lsp	698	0.0	0.0	17.0	56.0	0.00	0.00	5.86	7.43	0.00	6.64	0.0	-10.0	NA	periplasmic tail-specific protease	Translation, post-translational modification, degradation	CytoplasmicMembrane
PA14_68340 arcB	336	0.0	0.0	12.0	16.0	0.00	0.00	8.55	4.39	0.00	6.47	0.0	-10.0	NA	ornithine carbamoyltransferase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_53230	207	0.0	0.0	9.5	18.0	0.00	0.00	7.39	5.39	0.00	6.39	0.0	-10.0	NA	oxidoreductase	Putative enzymes	Cytoplasmic
PA14_04290	647	0.0	0.0	10.5	50.0	0.00	0.00	4.46	8.18	0.00	6.32	0.0	-10.0	NA	hypothetical protein	Membrane proteins	OuterMembrane
PA14_52800 lacsA	651	0.0	0.0	14.0	42.0	0.00	0.00	5.85	6.76	0.00	6.30	0.0	-10.0	NA	acetyl-CoA synthetase	Central intermediary metabolism	Cytoplasmic
PA14_04110 serA	409	0.0	0.0	7.5	57.5	0.00	0.00	3.18	9.38	0.00	6.28	0.0	-10.0	NA	D-3-phosphoglycerate dehydrogenase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_23370 orfK	378	0.0	0.0	14.0	26.0	0.00	0.00	7.30	5.22	0.00	6.26	0.0	-10.0	NA	putative UDP-N-acetylglucosamine 2-epimerase	Cell wall / LPS / capsule	Cytoplasmic
PA14_16830	226	0.0	0.0	13.5	7.0	0.00	0.00	9.87	1.97	0.00	5.92	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_66580	551	0.0	0.0	5.0	32.0	0.00	0.00	3.40	8.38	0.00	5.89	0.0	-10.0	NA	hypothetical protein	Protein secretion/export apparatus	CytoplasmicMembrane
PA14_61720	590	0.0	0.0	18.0	34.0	0.00	0.00	6.78	4.93	0.00	5.85	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_63250	425	0.0	0.0	22.0	4.0	0.00	0.00	10.88	0.76	0.00	5.82	0.0	-10.0	NA	acetyl-CoA acetyltransferase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_69470 algR	248	0.0	0.0	8.0	14.0	0.00	0.00	6.92	4.66	0.00	5.79	0.0	-10.0	NA	alginate biosynthesis regulatory protein AlgR	Two-component regulatory systems	Cytoplasmic
PA14_24990	128	0.0	0.0	2.0	24.5	0.00	0.00	1.97	9.29	0.00	5.63	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_13430 fecA	784	0.0	0.0	19.0	57.0	0.00	0.00	5.16	5.96	0.00	5.56	0.0	-10.0	NA	Fe(III) dicitrate transport protein FecA	Transport of small molecules	OuterMembrane
PA14_09900 prpL	462	0.0	0.0	5.0	35.0	0.00	0.00	2.86	7.70	0.00	5.28	0.0	-10.0	NA	Pvds-regulated endoprotease, lysyl class	Putative enzymes	Extracellular
PA14_67050	266	0.0	0.0	11.0	9.0	0.00	0.00	7.97	2.51	0.00	5.24	0.0	-10.0	NA	putative binding protein component of ABC transporter	Transport of small molecules	Periplasmic
PA14_72540	734	0.0	0.0	14.0	58.0	0.00	0.00	3.90	6.22	0.00	5.06	0.0	-10.0	NA	putative ribonucleotide reductase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_14040 rhl	507	0.0	0.0	14.0	10.0	0.00	0.00	7.90	2.17	0.00	5.04	0.0	-10.0	NA	ATP-dependent RNA helicase RhlB	Transcription, RNA processing and degradation	Cytoplasmic
PA14_72550	307	0.0	0.0	5.0	4.5	0.00	0.00	7.45	2.58	0.00	5.02	0.0	-10.0	NA	putative adhesin	Transport of small molecules	Periplasmic
PA14_15340 guaA	525	0.0	0.0	16.0	46.0	0.00	0.00	4.74	5.25	0.00	5.00	0.0	-10.0	NA	GMP synthase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_27560	296	0.0	0.0	9.0	22.0	0.00	0.00	5.12	4.82	0.00	4.97	0.0	-10.0	NA	hypothetical protein	Putative enzymes	Cytoplasmic
PA14_22980	420	0.0	0.0	9.0	35.5	0.00	0.00	3.89	5.90	0.00	4.89	0.0	-10.0	NA	putative binding protein component of ABC sugar transporter	Transport of small molecules	Periplasmic
PA14_61740 lolB	205	0.0	0.0	1.0	40.0	0.00	0.00	0.59	9.14	0.00	4.87	0.0	-10.0	NA	outer membrane lipoprotein LolB	Cell wall / LPS / capsule	Unknown
PA14_65660 parE	629	0.0	0.0	19.0	32.5	0.00	0.00	5.85	3.85	0.00	4.85	0.0	-10.0	NA	DNA topoisomerase IV subunit B	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_17940 glpR	251	0.0	0.0	12.0	3.0	0.00	0.00	8.81	0.85	0.00	4.83	0.0	-10.0	NA	glycerol-3-phosphate regulon repressor	Transcriptional regulators	Cytoplasmic
PA14_25840	551	0.0	0.0	17.5	35.0	0.00	0.00	5.41	4.16	0.00	4.79	0.0	-10.0	NA	electron transfer flavoprotein-ubiquinone oxidoreductase	Energy metabolism	Cytoplasmic
PA14_27960 tal	307	0.0	0.0	1.5	47.0	0.00	0.00	0.73	8.79	0.00	4.76	0.0	-10.0	NA	transaldolase B	Energy metabolism	Cytoplasmic
PA14_51910	318	0.0	0.0	6.0	14.0	0.00	0.00	4.82	4.32	0.00	4.57	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_17930 glpD	512	0.0	0.0	18.0	16.0	0.00	0.00	6.79	2.32	0.00	4.55	0.0	-10.0	NA	glycerol-3-phosphate dehydrogenase	Energy metabolism	Cytoplasmic
PA14_35500 bkdB	428	0.0	0.0	10.0	17.0	0.00	0.00	5.46	3.57	0.00	4.51	0.0	-10.0	NA	branched-chain alpha-keto acid dehydrogenase subunit E2	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_13140	455	0.0	0.0	10.0	29.0	0.00	0.00	4.24	4.74	0.00	4.49	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown

PA14_24690	476	0.0	0.0	9.5	18.0	0.00	0.00	5.18	3.78	0.00	4.48	0.0	-10.0	NA	putative D-alanyl-D-alanine carboxypeptidase	Cell wall / LPS / capsule	Periplasmic
PA14_05840 gcdH	393	0.0	0.0	2.0	24.0	0.00	0.00	1.59	7.32	0.00	4.46	0.0	-10.0	NA	glutaryl-CoA dehydrogenase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_46640	813	0.0	0.0	21.0	42.0	0.00	0.00	5.03	3.87	0.00	4.45	0.0	-10.0	NA	siderophore receptor	Transport of small molecules	OuterMembrane
PA14_61190	568	0.0	0.0	21.0	30.5	0.00	0.00	5.57	3.12	0.00	4.34	0.0	-10.0	NA	hypothetical protein	Protein secretion/export apparatus	OuterMembrane
PA14_57050 fabG	252	0.0	0.0	1.5	20.5	0.00	0.00	1.38	7.24	0.00	4.31	0.0	-10.0	NA	3-ketoacyl-(acyl-carrier-protein) reductase	Putative enzymes	Cytoplasmic
PA14_54210	799	0.0	0.0	11.5	46.0	0.00	0.00	3.35	5.17	0.00	4.26	0.0	-10.0	NA	putative ATP-dependent protease	Putative enzymes	Cytoplasmic
PA14_21370 fadD1	562	0.0	0.0	15.0	15.5	0.00	0.00	5.97	2.38	0.00	4.18	0.0	-10.0	NA	acyl-CoA synthetase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_17960 glpK	505	0.0	0.0	10.5	27.0	0.00	0.00	4.18	4.14	0.00	4.16	0.0	-10.0	NA	glycerol kinase	Central intermediary metabolism	Cytoplasmic
PA14_69230 ppk	736	0.0	0.0	7.0	51.0	0.00	0.00	2.17	6.09	0.00	4.13	0.0	-10.0	NA	polyphosphate kinase	Nucleotide biosynthesis and metabolism	CytoplasmicMembrane
PA14_26560	269	0.0	0.0	2.0	34.5	0.00	0.00	1.08	7.16	0.00	4.12	0.0	-10.0	NA	putative outer membrane protein precursor	Membrane proteins	OuterMembrane
PA14_51390 ppsD	337	0.0	0.0	4.0	9.0	0.00	0.00	4.37	3.79	0.00	4.08	0.0	-10.0	NA	3-oxoacyl-(acyl carrier protein) synthase III		Cytoplasmic
PA14_21340 fadD2	562	0.0	0.0	24.5	6.0	0.00	0.00	7.42	0.70	0.00	4.06	0.0	-10.0	NA	acyl-CoA synthetase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_41670 ppsA	791	0.0	0.0	23.0	45.0	0.00	0.00	4.63	3.48	0.00	4.06	0.0	-10.0	NA	phosphoenolpyruvate synthase	Central intermediary metabolism	Cytoplasmic
PA14_49800	329	0.0	0.0	10.0	4.0	0.00	0.00	7.02	1.08	0.00	4.05	0.0	-10.0	NA	oxidoreductase	Putative enzymes	Cytoplasmic
PA14_11650	333	0.0	0.0	3.5	38.0	0.00	0.00	1.54	6.43	0.00	3.99	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_00050 gyrB	806	0.0	0.0	20.5	17.5	0.00	0.00	5.99	1.97	0.00	3.98	0.0	-10.0	NA	DNA gyrase subunit B	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_01150	144	0.0	0.0	1.5	8.5	0.00	0.00	2.45	5.33	0.00	3.89	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_51900 proS	571	0.0	0.0	16.0	21.0	0.00	0.00	5.17	2.61	0.00	3.89	0.0	-10.0	NA	prolyl-tRNA synthetase	Translation, post-translational modification, degradation	Cytoplasmic
PA14_30570	367	0.0	0.0	7.0	11.0	0.00	0.00	4.69	2.84	0.00	3.77	0.0	-10.0	NA	putative periplasmic spermidine/putrescine-binding protein	Transport of small molecules	Periplasmic
PA14_13130	641	0.0	0.0	0.5	25.5	0.00	0.00	0.36	7.16	0.00	3.76	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_05000 trmB	223	0.0	0.0	3.0	14.0	0.00	0.00	2.69	4.82	0.00	3.75	0.0	-10.0	NA	tRNA (guanine-N(7)-)-methyltransferase	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_30150 mmmA	375	0.0	0.0	1.5	32.0	0.00	0.00	0.81	6.65	0.00	3.73	0.0	-10.0	NA	tRNA-specific 2-thiouridylase MmmA	Transcription, RNA processing and degradation	Cytoplasmic
PA14_71840	733	0.0	0.0	19.0	13.5	0.00	0.00	5.86	1.60	0.00	3.73	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_26420	718	0.0	0.0	7.0	38.0	0.00	0.00	2.29	4.78	0.00	3.53	0.0	-10.0	NA	putative TonB-dependent receptor	Membrane proteins	OuterMembrane
PA14_60445 obgE	406	0.0	0.0	8.0	4.5	0.00	0.00	5.80	1.26	0.00	3.53	0.0	-10.0	NA	GTPase ObgE		Cytoplasmic
PA14_72110	652	0.0	0.0	19.0	23.5	0.00	0.00	4.74	2.26	0.00	3.50	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_65230 purA	430	0.0	0.0	15.0	24.0	0.00	0.00	4.20	2.58	0.00	3.39	0.0	-10.0	NA	adenylosuccinate synthetase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_41360 cysS	460	0.0	0.0	9.0	17.5	0.00	0.00	3.76	2.81	0.00	3.29	0.0	-10.0	NA	cysteinyI-tRNA synthetase	Translation, post-translational modification, degradation	Cytoplasmic
PA14_01710 ahpC	187	0.0	0.0	8.0	15.0	0.00	0.00	3.79	2.73	0.00	3.26	0.0	-10.0	NA	alkyl hydroperoxide reductase subunit C	Adaptation, Protection	Cytoplasmic
PA14_30010 nuoB	225	0.0	0.0	1.0	14.0	0.00	0.00	1.01	5.47	0.00	3.24	0.0	-10.0	NA	NADH dehydrogenase subunit B	Energy metabolism	CytoplasmicMembrane
PA14_49280	398	0.0	0.0	3.0	35.0	0.00	0.00	1.17	5.27	0.00	3.22	0.0	-10.0	NA	transglycolase	Putative enzymes	CytoplasmicMembrane
PA14_04760 coaD	159	0.0	0.0	4.0	10.0	0.00	0.00	3.24	3.12	0.00	3.18	0.0	-10.0	NA	phosphopantetheine adenylyltransferase	Central intermediary metabolism	Cytoplasmic
PA14_22830	209	0.0	0.0	1.0	14.0	0.00	0.00	0.99	5.34	0.00	3.17	0.0	-10.0	NA	SUA5/YciO/YrdC/YwIC family protein	Translation, post-translational modification, degradation	Cytoplasmic
PA14_00210	341	0.0	0.0	4.0	23.0	0.00	0.00	1.96	4.33	0.00	3.15	0.0	-10.0	NA	lysine domain-containing protein	Putative enzymes	Unknown
PA14_07230 lda	354	0.0	0.0	6.0	21.5	0.00	0.00	2.60	3.59	0.00	3.10	0.0	-10.0	NA	fructose-1,6-bisphosphate aldolase	Carbon compound catabolism	Cytoplasmic
PA14_01550	166	0.0	0.0	2.0	12.0	0.00	0.00	1.83	4.24	0.00	3.04	0.0	-10.0	NA	putative lipoprotein	Fatty acid and phospholipid metabolism	Unknown
PA14_32420	339	0.0	0.0	7.5	4.0	0.00	0.00	4.99	1.02	0.00	3.01	0.0	-10.0	NA	putative oxidoreductase	Energy metabolism	Cytoplasmic
PA14_60190 cipB	854	0.0	0.0	24.0	39.5	0.00	0.00	3.63	2.30	0.00	2.96	0.0	-10.0	NA	cipB protein	Chaperones & heat shock proteins	Cytoplasmic
PA14_43690 fabB	405	0.0	0.0	4.0	10.0	0.00	0.00	2.98	2.86	0.00	2.92	0.0	-10.0	NA	3-oxoacyl-(acyl carrier protein) synthase I	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_09115 rpoA	333	0.0	0.0	12.0	14.5	0.00	0.00	3.84	1.79	0.00	2.81	0.0	-10.0	NA	DNA-directed RNA polymerase subunit alpha	Transcription, RNA processing and degradation	Cytoplasmic
PA14_67450 blc	189	0.0	0.0	5.0	8.0	0.00	0.00	3.44	2.12	0.00	2.78	0.0	-10.0	NA	outer membrane lipoprotein Blc	Cell wall / LPS / capsule	OuterMembrane
PA14_54640	272	0.0	0.0	4.0	12.0	0.00	0.00	2.56	2.96	0.00	2.76	0.0	-10.0	NA	enoyl-CoA hydratase	Putative enzymes	CytoplasmicMembrane
PA14_56240 pykA	483	0.0	0.0	4.0	27.5	0.00	0.00	1.51	4.00	0.00	2.76	0.0	-10.0	NA	pyruvate kinase	Energy metabolism	Cytoplasmic
PA14_50220 fleQ	490	0.0	0.0	5.0	10.5	0.00	0.00	3.04	2.46	0.00	2.75	0.0	-10.0	NA	transcriptional regulator FleQ	Transcriptional regulators	Cytoplasmic
PA14_35530 bkdA1	410	0.0	0.0	1.0	15.0	0.00	0.00	0.80	4.61	0.00	2.71	0.0	-10.0	NA	2-oxoisovalerate dehydrogenase (alpha subunit)	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_54480	314	0.0	0.0	1.0	17.5	0.00	0.00	0.70	4.72	0.00	2.71	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown

PA14_70860	323	0.0	0.0	6.0	5.5	0.00	0.00	4.00	1.41	0.00	2.71	0.0	-10.0	NA	hypothetical protein	Transport of small molecules	CytoplasmicMembrane
PA14_64110 jaccC	449	0.0	0.0	13.0	9.5	0.00	0.00	4.19	1.18	0.00	2.68	0.0	-10.0	NA	acetyl-CoA carboxylase biotin carboxylase subunit	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_61590	305	0.0	0.0	2.0	9.0	0.00	0.00	1.92	3.33	0.00	2.62	0.0	-10.0	NA	hypothetical protein	Putative enzymes	Cytoplasmic
PA14_27160 tesA	201	0.0	0.0	3.0	4.0	0.00	0.00	3.40	1.74	0.00	2.57	0.0	-10.0	NA	acyl-CoA thioesterase I precursor	Fatty acid and phospholipid metabolism	Periplasmic
PA14_62230	520	0.0	0.0	6.0	22.0	0.00	0.00	2.10	2.97	0.00	2.53	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_63990 speA	636	0.0	0.0	10.0	7.0	0.00	0.00	3.97	1.07	0.00	2.52	0.0	-10.0	NA	arginine decarboxylase	Amino acid biosynthesis and metabolism	Unknown
PA14_24360	974	0.0	0.0	5.0	57.0	0.00	0.00	0.92	4.05	0.00	2.49	0.0	-10.0	NA	hypothetical protein	Putative enzymes	OuterMembrane
PA14_26540	282	0.0	0.0	1.0	17.0	0.00	0.00	0.65	4.26	0.00	2.45	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_67090 mdoG	525	0.0	0.0	3.0	24.5	0.00	0.00	1.16	3.64	0.00	2.40	0.0	-10.0	NA	glucan biosynthesis protein G	Putative enzymes	Periplasmic
PA14_16530 lysS	501	0.0	0.0	10.0	15.0	0.00	0.00	3.00	1.73	0.00	2.37	0.0	-10.0	NA	lysyl-tRNA synthetase	Translation, post-translational modification, degradation	Cytoplasmic
PA14_38080	624	0.0	0.0	10.0	9.0	0.00	0.00	3.46	1.20	0.00	2.33	0.0	-10.0	NA	hypothetical protein	Transport of small molecules	OuterMembrane
PA14_70140	497	0.0	0.0	5.0	11.5	0.00	0.00	2.48	2.19	0.00	2.33	0.0	-10.0	NA	putative aldehyde dehydrogenase	Putative enzymes	Cytoplasmic
PA14_67560 typA	605	0.0	0.0	6.0	10.0	0.00	0.00	2.83	1.82	0.00	2.32	0.0	-10.0	NA	GTP-binding protein TypA/BipA	Adaptation, Protection	CytoplasmicMembrane
PA14_61820	366	0.0	0.0	7.0	8.0	0.00	0.00	3.12	1.37	0.00	2.25	0.0	-10.0	NA	GTP-dependent nucleic acid-binding protein EngD	Translation, post-translational modification, degradation	Cytoplasmic
PA14_17190 fabZ	146	0.0	0.0	2.0	3.0	0.00	0.00	2.77	1.60	0.00	2.19	0.0	-10.0	NA	(3R)-hydroxymyristoyl-ACP dehydratase	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_57410 murE	487	0.0	0.0	10.0	2.0	0.00	0.00	4.00	0.31	0.00	2.16	0.0	-10.0	NA	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	Cell wall / LPS / capsule	Cytoplasmic
PA14_66170	585	0.0	0.0	8.0	9.0	0.00	0.00	3.01	1.30	0.00	2.16	0.0	-10.0	NA	putative carbamoyl transferase	Central intermediary metabolism	Cytoplasmic
PA14_22460	275	0.0	0.0	4.0	7.0	0.00	0.00	2.56	1.72	0.00	2.14	0.0	-10.0	NA	alpha/beta family hydrolase	Putative enzymes	Cytoplasmic
PA14_30240 infA	72	0.0	0.0	1.0	2.0	0.00	0.00	2.38	1.83	0.00	2.10	0.0	-10.0	NA	translation initiation factor IF-1	Translation, post-translational modification, degradation	Cytoplasmic
PA14_21990	429	0.0	0.0	3.0	12.0	0.00	0.00	1.65	2.54	0.00	2.09	0.0	-10.0	NA	putative aminopeptidase 2	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_38480 gnyA	655	0.0	0.0	8.0	8.0	0.00	0.00	3.00	1.16	0.00	2.08	0.0	-10.0	NA	alpha subunit of geranyl-CoA carboxylase, GnyA	Carbon compound catabolism	Cytoplasmic
PA14_24300	455	0.0	0.0	3.0	13.0	0.00	0.00	1.46	2.44	0.00	1.95	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_23330 rpsA	559	0.0	0.0	12.5	27.0	0.00	0.00	2.12	1.76	0.00	1.94	0.0	-10.0	NA	30S ribosomal protein S1	Translation, post-translational modification, degradation	Cytoplasmic
PA14_58150  mreB	345	0.0	0.0	5.0	11.5	0.00	0.00	2.04	1.81	0.00	1.92	0.0	-10.0	NA	rod shape-determining protein MreB	Cell wall / LPS / capsule	Cytoplasmic
PA14_65270  hflC	289	0.0	0.0	5.0	7.0	0.00	0.00	2.50	1.34	0.00	1.92	0.0	-10.0	NA	protease subunit HflC	Translation, post-translational modification, degradation	Cytoplasmic
PA14_27230	151	0.0	0.0	1.5	2.0	0.00	0.00	2.52	1.29	0.00	1.91	0.0	-10.0	NA	MarR family transcriptional regulator	Transcriptional regulators	Cytoplasmic
PA14_18670 bfrB	158	0.0	0.0	1.0	3.0	0.00	0.00	1.77	2.04	0.00	1.90	0.0	-10.0	NA	bacterioferritin	Transport of small molecules	Cytoplasmic
PA14_33000 gcvP2	959	0.0	0.0	7.0	6.0	0.00	0.00	2.85	0.94	0.00	1.90	0.0	-10.0	NA	glycine dehydrogenase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_06870 dnr	227	0.0	0.0	1.0	12.0	0.00	0.00	0.67	3.10	0.00	1.88	0.0	-10.0	NA	transcriptional regulator Dnr	Transcriptional regulators	Cytoplasmic
PA14_70560	310	0.0	0.0	5.5	2.0	0.00	0.00	3.28	0.46	0.00	1.87	0.0	-10.0	NA	LysR family transcriptional regulator	Transcriptional regulators	Cytoplasmic
PA14_62770 nusA	493	0.0	0.0	7.0	2.0	0.00	0.00	3.29	0.36	0.00	1.83	0.0	-10.0	NA	transcription elongation factor NusA	Transcription, RNA processing and degradation	Cytoplasmic
PA14_62350	764	0.0	0.0	8.0	22.5	0.00	0.00	1.71	1.85	0.00	1.78	0.0	-10.0	NA	putative haem/haemoglobin uptake outer membrane receptor PhuR precursor	Transport of small molecules	OuterMembrane
PA14_33040 gcvT2	373	0.0	0.0	2.0	9.0	0.00	0.00	1.30	2.25	0.00	1.77	0.0	-10.0	NA	glycine cleavage system protein T2	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_00670	168	0.0	0.0	2.0	3.0	0.00	0.00	2.18	1.26	0.00	1.72	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_45640 fleN	280	0.0	0.0	1.0	9.5	0.00	0.00	0.71	2.61	0.00	1.66	0.0	-10.0	NA	flagellar synthesis regulator FleN	Motility & Attachment	CytoplasmicMembrane
PA14_43650	705	0.0	0.0	2.0	22.5	0.00	0.00	0.62	2.68	0.00	1.65	0.0	-10.0	NA	hypothetical protein	Membrane proteins	OuterMembrane
PA14_04660	274	0.0	0.0	2.0	4.0	0.00	0.00	1.79	1.38	0.00	1.58	0.0	-10.0	NA	hypothetical protein	Two-component regulatory systems	Unknown
PA14_09550	388	0.0	0.0	1.0	15.5	0.00	0.00	0.45	2.71	0.00	1.58	0.0	-10.0	NA	hypothetical protein	Carbon compound catabolism	Unknown
PA14_50860	269	0.0	0.0	4.0	5.0	0.00	0.00	2.02	0.97	0.00	1.49	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_04510	459	0.0	0.0	6.0	4.0	0.00	0.00	2.34	0.60	0.00	1.47	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_58630	387	0.0	0.0	2.0	12.0	0.00	0.00	0.85	1.96	0.00	1.41	0.0	-10.0	NA	ornithine decarboxylase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_51930	154	0.0	0.0	1.0	6.0	0.00	0.00	0.84	1.93	0.00	1.39	0.0	-10.0	NA	thioredoxin	Putative enzymes	Periplasmic
PA14_68190 rmlD	302	0.0	0.0	2.0	6.0	0.00	0.00	1.28	1.48	0.00	1.38	0.0	-10.0	NA	dTDP-4-dehydrohamnose reductase	Cell wall / LPS / capsule	Cytoplasmic
PA14_06600	601	0.0	0.0	0.5	14.0	0.00	0.00	0.23	2.46	0.00	1.35	0.0	-10.0	NA	putative acyl-CoA dehydrogenase	Fatty acid and phospholipid metabolism	Cytoplasmic

PA14_03430 gabD	483	0.0	0.0	5.0	3.5	0.00	0.00	2.10	0.57	0.00	1.34	0.0	-10.0	NA	succinate-semialdehyde dehydrogenase I	Central intermediary metabolism	Cytoplasmic
PA14_19370	589	0.0	0.0	7.0	5.5	0.00	0.00	2.02	0.61	0.00	1.32	0.0	-10.0	NA	putative asparagine synthetase, glutamine-hydrolyzing	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_62270	295	0.0	0.0	2.0	2.0	0.00	0.00	1.86	0.72	0.00	1.29	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_60410	154	0.0	0.0	1.0	5.0	0.00	0.00	0.87	1.67	0.00	1.27	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_27755	206	0.0	0.0	1.0	5.0	0.00	0.00	0.84	1.62	0.00	1.23	0.0	-10.0	NA	glutathione S-transferase	Central intermediary metabolism	Cytoplasmic
PA14_15740 purL	1298	0.0	0.0	4.5	21.0	0.00	0.00	0.87	1.56	0.00	1.22	0.0	-10.0	NA	phosphoribosylformylglycinamide synthase	Nucleotide biosynthesis and metabolism	Cytoplasmic
PA14_68070	250	0.0	0.0	1.0	7.0	0.00	0.00	0.63	1.70	0.00	1.17	0.0	-10.0	NA	amino acid (lysine/arginine/ornithine/histidine/octopine) ABC transporter periplasmic binding protein	Transport of small molecules	Periplasmic
PA14_23110	386	0.0	0.0	2.0	3.0	0.00	0.00	1.43	0.82	0.00	1.13	0.0	-10.0	NA	hypothetical protein	Translation, post-translational modification, degradation	Cytoplasmic
PA14_06450	458	0.0	0.0	2.0	9.0	0.00	0.00	0.80	1.38	0.00	1.09	0.0	-10.0	NA	acetyl-CoA carboxylase biotin carboxylase subunit	Fatty acid and phospholipid metabolism	Cytoplasmic
PA14_20870	728	0.0	0.0	3.0	11.0	0.00	0.00	0.88	1.24	0.00	1.06	0.0	-10.0	NA	hypothetical protein	Cell wall / LPS / capsule	OuterMembrane
PA14_14700 cysE	258	0.0	0.0	2.0	1.5	0.00	0.00	1.62	0.47	0.00	1.04	0.0	-10.0	NA	serine O-acetyltransferase	Amino acid biosynthesis and metabolism	Cytoplasmic
PA14_27370	567	0.0	0.0	2.5	12.5	0.00	0.00	0.70	1.35	0.00	1.03	0.0	-10.0	NA	ATP-dependent RNA helicase	Transcription, RNA processing and degradation	Cytoplasmic
PA14_43970 lpdG	478	0.0	0.0	1.5	11.0	0.00	0.00	0.52	1.48	0.00	1.00	0.0	-10.0	NA	dihydroilpoamide dehydrogenase	Energy metabolism	Cytoplasmic
PA14_52180 reiA	747	0.0	0.0	4.0	16.0	0.00	0.00	0.79	1.21	0.00	1.00	0.0	-10.0	NA	GTP pyrophosphokinase	Adaptation, Protection	Cytoplasmic
PA14_38460 gnyB	535	0.0	0.0	1.0	10.0	0.00	0.00	0.40	1.54	0.00	0.97	0.0	-10.0	NA	acyl-CoA carboxyltransferase beta chain	Carbon compound catabolism	CytoplasmicMembrane
PA14_21890	320	0.0	0.0	2.0	5.0	0.00	0.00	0.98	0.94	0.00	0.96	0.0	-10.0	NA	putative oxidoreductase	Energy metabolism	CytoplasmicMembrane
PA14_25900	398	0.0	0.0	3.0	10.0	0.00	0.00	0.84	1.08	0.00	0.96	0.0	-10.0	NA	trans-2-enoyl-CoA reductase	Putative enzymes	Cytoplasmic
PA14_23970 xcpQ	658	0.0	0.0	2.0	6.0	0.00	0.00	0.83	0.96	0.00	0.89	0.0	-10.0	NA	general secretion pathway protein D	Protein secretion/export apparatus	OuterMembrane
PA14_66910	208	0.0	0.0	1.0	2.0	0.00	0.00	0.91	0.70	0.00	0.80	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_50570	764	0.0	0.0	1.0	12.0	0.00	0.00	0.28	1.29	0.00	0.78	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_07870	348	0.0	0.0	2.0	1.0	0.00	0.00	1.18	0.23	0.00	0.70	0.0	-10.0	NA	putative binding protein component of ABC transporter	Transport of small molecules	Periplasmic
PA14_11350	220	0.0	0.0	1.0	1.0	0.00	0.00	1.01	0.39	0.00	0.70	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_72380 algB	449	0.0	0.0	2.0	3.0	0.00	0.00	0.88	0.51	0.00	0.70	0.0	-10.0	NA	two-component response regulator AlgB	Two-component regulatory systems	Cytoplasmic
PA14_11320	196	0.0	0.0	1.0	1.0	0.00	0.00	0.99	0.38	0.00	0.69	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Unknown
PA14_44630 dnaX	701	0.0	0.0	3.0	1.0	0.00	0.00	1.19	0.15	0.00	0.67	0.0	-10.0	NA	DNA polymerase III subunits gamma and tau	DNA replication, recombination, modification and repair	CytoplasmicMembrane
PA14_54180	687	0.0	0.0	4.0	1.0	0.00	0.00	1.22	0.12	0.00	0.67	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	OuterMembrane
PA14_17260 dnaE	1173	0.0	0.0	2.0	12.0	0.00	0.00	0.38	0.88	0.00	0.63	0.0	-10.0	NA	DNA polymerase III subunit alpha	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_30630 pqsH	382	0.0	0.0	1.0	3.5	0.00	0.00	0.54	0.73	0.00	0.63	0.0	-10.0	NA	putative FAD-dependent monooxygenase	Biosynthesis of cofactors, prosthetic groups and carriers	Cytoplasmic
PA14_11890	213	0.0	0.0	1.0	2.0	0.00	0.00	0.70	0.54	0.00	0.62	0.0	-10.0	NA	hypothetical protein	Hypothetical, unclassified, unknown	Cytoplasmic
PA14_05390 chpA	2476	0.0	0.0	3.5	10.0	0.00	0.00	0.48	0.53	0.00	0.51	0.0	-10.0	NA	ChpA	Chemotaxis	Cytoplasmic
PA14_25400	240	0.0	0.0	0.5	2.0	0.00	0.00	0.38	0.58	0.00	0.48	0.0	-10.0	NA	putative phosphodiesterase	Central intermediary metabolism	Cytoplasmic
PA14_72490 polA	913	0.0	0.0	2.0	5.0	0.00	0.00	0.47	0.46	0.00	0.46	0.0	-10.0	NA	DNA polymerase I	DNA replication, recombination, modification and repair	Cytoplasmic
PA14_08820 fusA1	706	0.0	0.0	1.0	12.0	0.00	0.00	0.15	0.69	0.00	0.42	0.0	-10.0	NA	elongation factor G	Transcription, RNA processing and degradation	Cytoplasmic
PA14_02220	679	0.0	0.0	2.5	1.0	0.00	0.00	0.72	0.11	0.00	0.41	0.0	-10.0	NA	putative chemotaxis transducer	Chemotaxis	CytoplasmicMembrane
PA14_52230	742	0.0	0.0	1.0	5.0	0.00	0.00	0.27	0.52	0.00	0.39	0.0	-10.0	NA	outer membrane receptor FepA	Transport of small molecules	OuterMembrane
PA14_66620 pilQ	710	0.0	0.0	1.5	5.0	0.00	0.00	0.34	0.44	0.00	0.39	0.0	-10.0	NA	type 4 fimbrial biogenesis outer membrane protein PilQ precursor	Motility & Attachment	OuterMembrane
PA14_18260 fruK	314	0.0	0.0	1.0	1.0	0.00	0.00	0.51	0.20	0.00	0.36	0.0	-10.0	NA	1-phosphofructokinase	Transport of small molecules	Cytoplasmic
PA14_09460 phzC1	405	0.0	0.0	0.5	2.0	0.00	0.00	0.25	0.38	0.00	0.31	0.0	-10.0	NA	phenazine biosynthesis protein PhzC	Secreted Factors (toxins, enzymes, alginate)	Cytoplasmic
PA14_39945 phzC2	405	0.0	0.0	0.5	2.0	0.00	0.00	0.25	0.38	0.00	0.31	0.0	-10.0	NA	phenazine biosynthesis protein PhzC	Secreted Factors (toxins, enzymes, alginate)	Cytoplasmic
PA14_00120	295	0.0	0.0	1.0	0.5	0.00	0.00	0.50	0.10	0.00	0.30	0.0	-10.0	NA	lipid A biosynthesis lauroyl acyltransferase	Cell wall / LPS / capsule	CytoplasmicMembrane
PA14_23500 tyrB	398	0.0	0.0	1.0	1.0	0.00	0.00	0.37	0.14	0.00	0.25	0.0	-10.0	NA	aromatic amino acid aminotransferase	Amino acid biosynthesis and metabolism	Cytoplasmic
		4954.5	15900.0	16288.0	34456.0	9924.6	9339.2	9920.0	8891.4	9631.9	9405.7						