

**Table 5. Results of *P. aeruginosa* whole cell ICAT analysis**

PA#	Protein name	Gene	Alt gene	Function	n	u-ICAT	Fold induction	SD	Alt ORF
1179	two-component response regulator PhoP	phoP		Transcriptional regulators	6	1	10.34	0.96	
4074	probable transcriptional regulator			Transcriptional regulators	1	1	7.79	na	
2735	probable restriction-modification system protein			Putative enzymes	1	1	7.27	na	
3554	conserved hypothetical protein			Putative enzymes	34	7	6.09	1.16	
4825	Mg(2+) transport ATPase, P-type 2	mgtA		Transport of small molecules	85	3	5.80	1.75	
1163	probable glucosyl transferase			Putative enzymes	1	1	5.06	na	
4635	conserved hypothetical protein	ndvB		Hypothetical, unclassified, unknown	13	1	3.99	0.56	
1563	conserved hypothetical protein	mgtC		Hypothetical, unclassified, unknown	2	1	3.55	0.39	
4774	hypothetical protein	ygdE		Hypothetical, unclassified, unknown	2	1	3.48	0.19	
2400	probable non-ribosomal peptide synthetase			Adaptation, protection	11	2	3.29	0.55	2402
1091	hypothetical protein			Hypothetical, unclassified, unknown	1	1	3.27	na	
3619	hypothetical protein			Hypothetical, unclassified, unknown	1	1	3.14	na	
1432	autoinducer synthesis protein LasI	lasI		Adaptation, protection	2	1	3.10	0.05	
3284	hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.99	0.96	
4284	exodeoxyribonuclease V beta chain	recB	rorA	DNA replication, recombination, modification	1	1	2.91	na	
3925	probable acyl-CoA thiolase			Putative enzymes	6	1	2.91	1.22	
3552	conserved hypothetical protein			Hypothetical, unclassified, unknown	7	1	2.84	0.25	
2127	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.79	na	
8	glycyl-tRNA synthetase beta chain	glyS		Amino acid biosynthesis and metabolism	11	1	2.74	0.36	
3735	threonine synthase	thrC		Amino acid biosynthesis and metabolism	1	1	2.71	na	
2040	probable glutamine synthetase			Putative enzymes	5	1	2.61	0.47	
2405	hypothetical protein			Hypothetical, unclassified, unknown	2	1	2.59	0.14	
3179	conserved hypothetical protein		yciL	Hypothetical, unclassified, unknown	2	1	2.54	0.20	
2343	xylulose kinase	mtlY		Carbon compound catabolism	1	1	2.44	na	
3553	probable glycosyl transferase		pmrF	Adaptation, protection; Putative enzymes	1	1	2.33	na	
4031	inorganic pyrophosphatase	ppa	ipyR	Central intermediary metabolism	6	1	2.24	0.46	
3578	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.21	na	
100	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.20	na	
3655	elongation factor Ts	tsf		Translation, post-translational modification	4	1	2.20	0.38	
5369	hypothetical protein			Hypothetical, unclassified, unknown	2	1	2.18	1.07	
865	4-hydroxyphenylpyruvate dioxygenase	hpd		Amino acid biosynthesis and metabolism	12	1	2.12	0.24	
1574	conserved hypothetical protein		yaiE	Hypothetical, unclassified, unknown	7	1	2.06	0.22	
998	hypothetical protein			Putative enzymes	6	2	2.04	0.24	
858	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.94	na	
4481	rod shape-determining protein MreB	mreB	envB rodY	Cell division; Cell wall / LPS / capsule	3	2	1.88	0.33	
3330	probable short chain dehydrogenase			Putative enzymes	5	1	1.86	0.08	
4457	conserved hypothetical protein		yrbH kpsF	Secreted Factors (toxins, enzymes, alginate)	3	1	1.82	0.15	
2968	malonyl-CoA-[acyl-carrier-protein] transacylase	fabD		Fatty acid and phospholipid metabolism	1	1	1.81	na	
85	conserved hypothetical protein			Hypothetical, unclassified, unknown	12	1	1.78	0.11	
704	probable amidase			Putative enzymes	1	1	1.77	na	
2036	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.71	na	
5036	glutamate synthase large chain precursor	gltB	aspB	Amino acid biosynthesis and metabolism	1	1	1.69	na	
1579	hypothetical protein			Hypothetical, unclassified, unknown	5	1	1.68	0.33	
3504	probable aldehyde dehydrogenase			Putative enzymes	3	1	1.68	0.02	
3736	homoserine dehydrogenase	hom		Amino acid biosynthesis and metabolism	1	1	1.66	na	
2953	electron transfer flavoprotein-ubiquinone oxidoreductase			Energy metabolism	9	4	1.66	0.13	
604	probable binding protein component of ABC transporter			Transport of small molecules	2	1	1.66	0.16	
3533	conserved hypothetical protein		ydH	Hypothetical, unclassified, unknown	10	1	1.65	0.15	
4742	tRNA pseudouridine 55 synthase	truB		Transcription, RNA processing and degradation	3	1	1.65	0.25	
3193	glucokinase	glk		Carbon compound catabolism	1	1	1.63	na	
999	3-oxoacyl-[acyl-carrier-protein] synthase III	fabH1		Fatty acid and phospholipid metabolism	4	1	1.63	0.13	
70	hypothetical protein			Hypothetical, unclassified, unknown	10	1	1.62	0.24	
5143	imidazoleglycerol-phosphate dehydratase	hisB		Amino acid biosynthesis and metabolism	3	1	1.61	0.11	
3531	bacterioferritin	bfrB		Transport of small molecules	3	1	1.59	0.14	
3819	conserved hypothetical protein		ycfJ	Hypothetical, unclassified, unknown	4	1	1.58	0.15	
5429	aspartate ammonia-lyase	aspA		Amino acid biosynthesis and metabolism	20	3	1.57	0.30	
996	probable coenzyme A ligase			Putative enzymes	1	1	1.57	na	
997	hypothetical protein			Hypothetical, unclassified, unknown	16	2	1.57	0.26	
3327	probable non-ribosomal peptide synthetase			Adaptation, protection	2	1	1.55	0.00	
2840	probable ATP-dependent RNA helicase	deaD		Transcription, RNA processing and degradation	2	1	1.54	0.23	
4054	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	ribB	ribA	Biosynthesis of cofactors, prosthetic groups	24	2	1.54	0.20	
2491	probable oxidoreductase			Putative enzymes	9	1	1.54	0.08	
4265	elongation factor Tu	tufA		Translation	250	8	1.53	0.24	4277
934	GTP pyrophosphokinase	relA		Adaptation, protection	2	1	1.53	0.00	
4669	isopentenyl monophosphate kinase	ipk	ychB	Biosynthesis of cofactors, prosthetic groups	2	1	1.52	0.17	
1520	probable transcriptional regulator			Transcriptional regulators	4	1	1.51	0.06	
4408	cell division protein FtsA	ftsA		Cell division	2	1	1.51	0.15	
5049	50S ribosomal protein L31	rpmE		Translation	6	2	1.51	0.12	
2641	NADH dehydrogenase I chain F	nuoF		Energy metabolism	2	1	1.50	0.01	
2014	probable acyl-CoA carboxyltransferase beta chain			Putative enzymes	16	2	1.50	0.23	
4410	D-alanine-D-alanine ligase	ddlB		Cell wall / LPS / capsule	2	1	1.48	0.08	
853	probable oxidoreductase			Putative enzymes	1	1	1.48	na	
4258	50S ribosomal protein L22	rplV		Translation	9	1	1.47	0.13	
3328	probable FAD-dependent monooxygenase			Putative enzymes	5	1	1.47	0.11	
5556	ATP synthase alpha chain	atpA	unca papA	Energy metabolism	45	1	1.47	0.12	
4246	30S ribosomal protein S5	rpsE		Translation	60	1	1.46	0.16	
3004	probable nucleoside phosphorylase			Nucleotide biosynthesis and metabolism	60	1	1.45	na	
3323	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.45	na	
3918	molybdopterin biosynthetic protein C	moaC		Biosynthesis of cofactors, prosthetic groups	1	1	1.45	na	
1580	citrate synthase	gltA	cisY	Energy metabolism	45	4	1.44	0.14	
1787	aconitate hydratase 2	acnB		Energy metabolism	5	1	1.44	0.09	
1266	probable oxidoreductase			Putative enzymes	1	1	1.43	na	
4101	probable two-component response regulator			Transcriptional regulators	1	1	1.43	na	
5300	cytochrome c5	cycB		Energy metabolism	5	1	1.43	0.11	
4239	30S ribosomal protein S4	rpsD		Translation	70	6	1.43	0.28	
5312	probable aldehyde dehydrogenase		kaueB	Putative enzymes	11	1	1.43	0.11	
2827	conserved hypothetical protein		yeaA	Hypothetical, unclassified, unknown	1	1	1.42	na	
3167	3-phosphoserine aminotransferase	serC		Amino acid biosynthesis and metabolism	1	1	1.42	na	
609	anthranilate synthetase component I	trpE		Amino acid biosynthesis and metabolism	2	1	1.42	0.11	
301	polyamine transport protein	potF3		Transport of small molecules	7	1	1.41	0.27	
4935	30S ribosomal protein S6	rpsF		Translation	32	1	1.41	0.14	
4260	50S ribosomal protein L2	rplB		Translation	26	3	1.41	0.29	
547	probable transcriptional regulator			Transcriptional regulators	4	1	1.39	0.23	
2023	UTP-glucose-1-phosphate uridylyltransferase	galU	hasC gtaB	Central intermediary metabolism	43	2	1.39	0.27	
266	4-aminobutyrate aminotransferase	gabT		Amino acid biosynthesis and metabolism	13	2	1.39	0.07	
920	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.38	na	
834	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.38	0.09	
5051	arginyl-tRNA synthetase	argS		Translation	2	1	1.38	0.09	
4254	30S ribosomal protein S17	rpsQ		Translation	17	1	1.38	0.14	
872	phenylalanine-4-hydroxylase	phhA		Amino acid biosynthesis and metabolism	10	1	1.38	0.17	
4406	UDP-3-O-acetyl-N-acetylglucosamine deacetylase	lpxC	envA asmB	Cell wall / LPS / capsule	2	1	1.37	0.00	
1583	succinate dehydrogenase (A subunit)	sdhA		Energy metabolism	25	4	1.36	0.22	
265	succinate-semialdehyde dehydrogenase	gabD		Amino acid biosynthesis and metabolism	20	2	1.36	0.12	
4769	probable transcriptional regulator		lldR	Transcriptional regulators	2	1	1.36	0.08	
1748	probable enoyl-CoA hydratase/isomerase			Putative enzymes	2	1	1.35	0.19	

892	arginine/ornithine transport protein AotP	aotP	Transport of small molecules	1	1	1.35	na	
2620	ATP-binding protease component ClpA	clpA	Translation	1	1	1.35	na	
3831	leucine aminopeptidase	pepA	Translation	14	1	1.35	0.15	
1674	GTP cyclohydrolase I precursor	folE2	Biosynthesis of cofactors, prosthetic groups	7	1	1.35	0.14	3438
782	proline dehydrogenase PutA	putA	Amino acid biosynthesis and metabolism	42	5	1.34	0.22	
3134	glutamyl-tRNA synthetase	gltX	Translation	7	2	1.34	0.10	
2247	2-oxoisovalerate dehydrogenase (alpha subunit)	bkdA1	Amino acid biosynthesis and metabolism	3	1	1.34	0.17	
2889	probable acyl-CoA dehydrogenase		Putative enzymes	1	1	1.34	na	
4447	histidinol-phosphate aminotransferase	hisC1	Amino acid biosynthesis and metabolism	2	1	1.33	0.10	
4450	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA	Cell wall / LPS / capsule	9	3	1.33	0.10	
2386	L-ornithine N5-oxygenase	pvdA	Adaptation, protection	65	2	1.33	0.17	
5046	malic enzyme		Central intermediary metabolism	15	2	1.33	0.16	
506	probable acyl-CoA dehydrogenase		Putative enzymes	37	2	1.33	0.28	
5555	ATP synthase gamma chain	atpG	Energy metabolism	11	1	1.33	0.08	
2624	isocitrate dehydrogenase	idh	Energy metabolism	1	1	1.33	na	
4241	30S ribosomal protein S13	rpsM	Translation	74	3	1.32	0.23	
5263	argininosuccinate lyase	argH	Amino acid biosynthesis and metabolism	3	1	1.31	0.01	
4670	ribose-phosphate pyrophosphokinase	prs	Carbon compound catabolism	10	2	1.31	0.12	
3244	cell division inhibitor MinD	minD	Cell division	5	2	1.31	0.38	
5005	probable carbamoyl transferase		Putative enzymes	2	1	1.30	0.08	
4314	formyltetrahydrofolate deformylase	purU1	Nucleotide biosynthesis and metabolism	9	1	1.30	0.25	
2744	threonyl-tRNA synthetase	thrS	Amino acid biosynthesis and metabolism	6	2	1.29	0.07	
4483	Glu-tRNA(Gln) amidotransferase subunit A	gatA	Translation, post-translational modification	1	1	1.29	na	
2071	elongation factor G	fusA2	Translation, post-translational modification	11	1	1.29	0.12	4266
659	hypothetical protein		Hypothetical, unclassified, unknown	2	1	1.29	0.04	
794	probable aconitase hydratase		Energy metabolism	5	2	1.28	0.14	
136	probable ATP-binding component of ABC transporter		Transport of small molecules	1	1	1.28	na	
1532	DNA polymerase subunits gamma and tau	dnaX	DNA replication, recombination, modification	1	1	1.28	na	
4270	DNA-directed RNA polymerase beta chain	rpoB	Transcription, RNA processing and degradation	15	3	1.27	0.16	
3656	30S ribosomal protein S2	rpsB	Translation, post-translational modification	15	1	1.27	0.05	
3798	probable aminotransferase	ybdL	Putative enzymes	2	2	1.27	0.16	
935	conserved hypothetical protein	mazG	Hypothetical, unclassified, unknown	2	1	1.26	0.23	
4673	conserved hypothetical protein	ychF	Hypothetical, unclassified, unknown	2	1	1.26	0.07	
4448	histidinol dehydrogenase	hisD	Amino acid biosynthesis and metabolism	2	1	1.26	0.13	
84	conserved hypothetical protein		Hypothetical, unclassified, unknown	7	1	1.26	0.09	
4236	catalase	katA	Adaptation, protection	5	1	1.25	0.04	
3001	probable glyceraldehyde-3-phosphate dehydrogenase		Putative enzymes	41	3	1.25	0.12	
3834	valyl-tRNA synthetase	valS	Amino acid biosynthesis and metabolism	2	1	1.24	0.01	
3482	methionyl-tRNA synthetase	metG	Amino acid biosynthesis and metabolism	2	2	1.24	0.24	
4395	conserved hypothetical protein		Hypothetical, unclassified, unknown	7	2	1.24	0.18	
2976	ribonuclease E	rne	Transcription, RNA processing and degradation	12	1	1.24	0.07	
130	probable aldehyde dehydrogenase		Putative enzymes	2	1	1.24	0.00	
1760	probable transcriptional regulator		Transcriptional regulators	1	1	1.24	na	
4730	pantoate-beta-alanine ligase	panC	Biosynthesis of cofactors, prosthetic groups	3	1	1.23	0.14	
3664	conserved hypothetical protein	yffB	Hypothetical, unclassified, unknown	2	2	1.23	0.08	
867	hypothetical protein		Hypothetical, unclassified, unknown	30	1	1.23	0.20	
774	conserved hypothetical protein	yecP	Hypothetical, unclassified, unknown	1	1	1.22	na	
1984	probable aldehyde dehydrogenase	exaC1	Putative enzymes	37	4	1.22	0.26	4022
4500	probable binding protein component of ABC transporter		Transport of small molecules	5	1	1.21	0.22	
3770	inosine-5'-monophosphate dehydrogenase	guaB	Nucleotide biosynthesis and metabolism	4	1	1.21	0.13	
945	phosphoribosylaminoimidazole synthetase	purM	Nucleotide biosynthesis and metabolism	3	1	1.21	0.09	
1339	probable ATP-binding component of ABC transporter		Transport of small molecules	8	1	1.21	0.20	
2835	probable MFS transporter		Membrane proteins	1	1	1.21	na	
3013	fatty-acid oxidation complex beta-subunit	foaB	Amino acid biosynthesis and metabolism	17	1	1.21	0.24	
4266	elongation factor G	fusA1	Translation	21	2	1.21	0.11	
382	DNA mismatch repair protein MicA	micA	DNA replication, recombination, modification	2	1	1.20	0.08	
300	polyamine transport protein	potF2	Transport of small molecules	18	1	1.20	0.09	
3299	long-chain-fatty-acid-CoA ligase	fadD1	Fatty acid and phospholipid metabolism	14	1	1.20	0.11	
2195	hydrogen cyanide synthase HcnC	hcnC	Central intermediary metabolism	1	1	1.20	na	
2874	hypothetical protein		Hypothetical, unclassified, unknown	1	1	1.20	na	
4688	iron (III)-transport system permease HiiB	hiiB	Membrane proteins	1	1	1.20	na	
4726	probable two-component response regulator		Transcriptional regulators	6	2	1.19	0.12	
4542	ClpB protein	clpB	Translation	5	1	1.19	0.16	
4760	DnaJ protein	dnaJ	Adaptation, protection; Chaperones	13	1	1.19	0.08	
3440	conserved hypothetical protein		Hypothetical, unclassified, unknown	5	1	1.19	0.13	
2345	conserved hypothetical protein		Hypothetical, unclassified, unknown	1	1	1.19	na	
4758	carbamoyl-phosphate synthase small chain	carA	Nucleotide biosynthesis and metabolism	2	1	1.18	0.07	
936	hypothetical protein		Hypothetical, unclassified, unknown	5	1	1.18	0.06	
534	conserved hypothetical protein		Putative enzymes	6	1	1.18	0.15	
3813	probable iron-binding protein IscU	iscU	Biosynthesis of cofactors	14	2	1.18	0.11	
4756	carbamoylphosphate synthetase large subunit	carB	Nucleotide biosynthesis and metabolism	3	2	1.17	0.12	
5025	homocysteine synthase	metY	Amino acid biosynthesis and metabolism	11	1	1.17	0.18	
5557	ATP synthase delta chain	atpH	Energy metabolism	5	1	1.17	0.17	
4633	probable chemotaxis transducer		Adaptation, protection; Chemotaxis	2	1	1.15	0.06	
401	noncatalytic dihydroorotase-like protein	pyrX, pyrC'	Nucleotide biosynthesis and metabolism	1	1	1.15	na	
3166	chorismate mutase	pheA	Amino acid biosynthesis and metabolism	1	1	1.15	na	
3760	probable phosphotransferase protein	nagF	Transport of small molecules	1	1	1.15	na	
3139	probable amino acid aminotransferase	aspC; tyrB	Amino acid biosynthesis and metabolism	28	1	1.15	0.13	
3814	L-cysteine desulfurase (pyridoxal phosphate-dependent)	iscS	Amino acid biosynthesis and metabolism	7	1	1.14	0.19	
5152	probable ATP-binding component of ABC transporter		Transport of small molecules	1	1	1.14	na	
546	methionine adenosyltransferase	metK	Amino acid biosynthesis and metabolism	50	6	1.14	0.13	
5554	ATP synthase beta chain	atpD	Energy metabolism	45	1	1.14	0.13	
4751	cell division protein FtsH	ftsH	Cell division	8	2	1.13	0.13	
222	probable dihydrodipicolinate synthetase		Amino acid biosynthesis and metabolism	1	1	1.13	na	
1589	succinyl-CoA synthetase alpha chain	sucD	Energy metabolism	76	4	1.13	0.20	
3529	probable peroxidase		Adaptation, protection; Putative enzymes	13	1	1.12	0.16	
5106	conserved hypothetical protein	tsaA	Hypothetical, unclassified, unknown	6	2	1.12	0.13	
4269	DNA-directed RNA polymerase beta* chain	rpoC	Transcription, RNA processing and degradation	24	3	1.12	0.20	
1770	phosphoenolpyruvate synthase	ppsA	Carbon compound catabolism	40	3	1.12	0.23	
4015	conserved hypothetical protein		Hypothetical, unclassified, unknown	5	1	1.12	0.06	
4234	excinuclease ABC subunit A	uvrA	DNA replication, recombination, modification	3	1	1.12	0.02	
4749	phosphoglucosamine mutase	glmM	Cell wall / LPS / capsule	5	2	1.12	0.11	
4307	chemotactic transducer PctC	pctC	Adaptation, protection; Chemotaxis	30	2	1.11	0.14	4309, 4310
1742	probable amidotransferase		Putative enzymes	6	1	1.11	0.15	
1301	probable transmembrane sensor		Membrane proteins; Transcriptional regulators	4	1	1.11	0.11	
1609	beta-ketoacyl-ACP synthase I	fabB	Fatty acid and phospholipid metabolism	39	4	1.11	0.15	
4217	probable FAD-dependent monooxygenase		Putative enzymes	1	1	1.10	na	
5274	nucleoside diphosphate kinase regulator	rnk	Transcriptional regulators	2	1	1.10	0.00	
3790	outer membrane protein OprC	oprC	Transport of small molecules	2	2	1.10	0.18	
1588	succinyl-CoA synthetase beta chain	sucC	Energy metabolism	110	5	1.10	0.15	
4525	type 4 fibrillar precursor PilA	pilA	Motility & Attachment	25	2	1.10	0.23	
2445	glycine cleavage system protein P2	gcvP2	Amino acid biosynthesis and metabolism	85	5	1.10	0.27	
2197	conserved hypothetical protein	ycnB	Putative enzymes	3	1	1.10	0.03	
3762	hypothetical protein		Hypothetical, unclassified, unknown	4	1	1.10	0.05	
1013	phosphoribosylaminoimidazole-succinocarboxamide synthase	purC	Nucleotide biosynthesis and metabolism	12	2	1.09	0.15	
91	conserved hypothetical protein		Hypothetical, unclassified, unknown	1	1	1.09	na	
4578	hypothetical protein		Hypothetical, unclassified, unknown	2	1	1.09	na	
4052	NusB protein	nusB	Transcription, RNA processing and degradation	3	1	1.09	0.14	
964	conserved hypothetical protein	ssyB	Hypothetical, unclassified, unknown	6	1	1.09	0.11	
2385	probable acylase	yebC	Putative enzymes	23	3	1.09	0.16	
3397	ferredoxin--NADP+ reductase	fpr	Biosynthesis of cofactors, prosthetic groups	3	1	1.09	0.09	
3021	hypothetical protein		Hypothetical, unclassified, unknown	8	1	1.08	0.10	

548	transketolase	tktA	Energy metabolism	5	1	1.08	0.09	
2950	hypothetical protein		Hypothetical, unclassified, unknown	10	1	1.07	0.04	
4240	30S ribosomal protein S11	rpsK	Translation	12	2	1.07	0.10	
2621	conserved hypothetical protein		Hypothetical, unclassified, unknown	2	1	1.07	0.14	
4423	conserved hypothetical protein	yraM	Hypothetical, unclassified, unknown	1	1	1.07	na	
3329	hypothetical protein		Hypothetical, unclassified, unknown	30	2	1.07	0.08	
854	fumarate hydratase	fumC2	Carbon compound catabolism	3	1	1.07	0.09	
3645	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase	fabZ	Cell wall / LPS / capsule	2	1	1.06	0.01	
4938	adenylosuccinate synthetase	purA	Nucleotide biosynthesis and metabolism	10	1	1.06	0.10	
3263	conserved hypothetical protein		Hypothetical, unclassified, unknown	1	1	1.06	na	
3999	D-ala-D-ala-carboxypeptidase	yaiD	Cell wall / LPS / capsule	12	1	1.05	0.11	
4701	conserved hypothetical protein	dacC	dacD	12	2	1.05	0.11	
2770	hypothetical protein		Hypothetical, unclassified, unknown	1	1	1.05	na	
4431	probable iron-sulfur protein		Putative enzymes	2	1	1.05	0.00	
1585	2-oxoglutarate dehydrogenase (E1 subunit)	sucA	Energy metabolism	9	1	1.04	0.03	
3347	hypothetical protein		Hypothetical, unclassified, unknown	2	1	1.04	0.01	
5164	dTDP-4-dehydrohamnose 3,5-epimerase	rmlC	Cell wall / LPS / capsule	2	1	1.04	0.09	
4560	isoleucyl-tRNA synthetase	ileS	Translation	10	2	1.04	0.06	
4694	ketol-acid reductoisomerase	ilvC	Amino acid biosynthesis and metabolism	51	4	1.04	0.13	
387	conserved hypothetical protein	yggV	Hypothetical, unclassified, unknown	6	2	1.04	0.11	
1642	selenophosphate synthetase	selD	Translation	1	1	1.03	na	
2999	Na <sup>+</sup> -translocating NADH:ubiquinone oxidoreductase subunit Nrq1nqrA		Energy metabolism	1	1	1.03	na	
5426	phosphoribosylaminoimidazole carboxylase, catalytic subunit	purE	Nucleotide biosynthesis and metabolism	1	1	1.03	na	
1459	probable methyltransferase	cheB	Chemotaxis	6	2	1.03	0.15	
4484	Glu-tRNA(Gln) amidotransferase subunit B	gatB	Translation, post-translational modification	7	2	1.03	0.16	
4848	biotin carboxylase	accC	Fatty acid and phospholipid metabolism	11	1	1.03	0.11	
3159	probable UDP-glucose/GDP-mannose dehydrogenase WbpA	wbpA	Cell wall / LPS / capsule; Putative enzymes	2	1	1.02	0.03	
4957	phosphatidylserine decarboxylase	psd	Amino acid biosynthesis and metabolism	2	1	1.02	0.00	
5225	hypothetical protein		Hypothetical, unclassified, unknown	2	1	1.02	0.10	
3158	probable oxidoreductase WpbB	wpbB	Cell wall / LPS / capsule; Putative enzymes	34	3	1.02	0.07	
871	pterin-4-alpha-carbinolamine dehydratase	phhB	Amino acid biosynthesis and metabolism	20	2	1.02	0.19	
1307	conserved hypothetical protein	yafJ	Fatty acid and phospholipid metabolism	13	2	1.02	0.25	
2553	probable acyl-CoA thiolase		Putative enzymes	24	3	1.02	0.12	
899	succinylarginine dihydrolase	aruB	Amino acid biosynthesis and metabolism	3	1	1.02	0.13	
1587	lipamide dehydrogenase-glc	lpdG	Energy metabolism	24	2	1.01	0.11	
3861	ATP-dependent RNA helicase RhlB	rhlB	Transcription, RNA processing and degradation	12	2	1.01	0.08	
105	cytochrome c oxidase, subunit II	coxB	coll	1	1	1.01	na	
3068	conserved hypothetical protein		Hypothetical, unclassified, unknown	6	1	1.01	0.05	
3226	probable hydrolase		Putative enzymes	1	1	1.01	na	
1162	succinyl-diaminopimelate desuccinylase	dapE	Amino acid biosynthesis and metabolism	10	2	1.01	0.11	
3017	conserved hypothetical protein		Hypothetical, unclassified, unknown	5	1	1.01	0.16	
1010	dihydrodipicolinate synthase	dapA	Amino acid biosynthesis and metabolism	6	3	1.01	0.16	
3987	leucyl-tRNA synthetase	leuS	Translation	14	3	1.00	0.25	
5015	pyruvate dehydrogenase	aceA	Energy metabolism	7	1	1.00	0.07	
3164	still frameshift 3-PHOSPHOSHIKIMATE							
	1-CARBOXYVINYLTRANSFERASE prephenate dehydrogenase		Amino acid biosynthesis and metabolism	1	1	1.00	na	
3295	probable HIT family protein		Putative enzymes	1	1	1.00	na	
3471	probable malic enzyme	sfcA	Central intermediary metabolism	2	2	1.00	0.06	
3657	methionine aminopeptidase	map	Translation	3	1	1.00	0.07	
5564	glucose inhibited division protein B	gidB	Cell division	2	1	1.00	0.01	
1	chromosomal replication initiator protein DnaA	dnaA	DNA replication, recombination, modification	7	1	1.00	0.15	
4502	probable binding protein component of ABC transporter		Transport of small molecules	4	2	0.99	0.01	
4744	translation initiation factor IF-2	infB	Translation	6	1	0.99	0.07	
1202	probable hydrolase	ycaC	Putative enzymes	3	1	0.99	0.03	
3635	enolase	eno	Energy metabolism	12	1	0.99	0.14	
2991	soluble pyridine nucleotide transhydrogenase	sth	Nucleotide biosynthesis and metabolism	3	1	0.99	0.05	
296	probable glutamine synthetase		Putative enzymes	2	1	0.99	0.03	
1796	5,10-methylene-tetrahydrofolate dehydrogenase / cyclohydrolaseI	folD	Biosynthesis of cofactors, prosthetic groups	4	1	0.99	0.00	
2412	conserved hypothetical protein		Hypothetical, unclassified, unknown	6	1	0.99	0.15	
3637	CTP synthase	pyrG	Nucleotide biosynthesis and metabolism	4	1	0.99	0.10	
3686	adenylate kinase	adk	Nucleotide biosynthesis and metabolism	4	2	0.99	0.12	
4389	probable short-chain dehydrogenase		Putative enzymes	17	2	0.98	0.11	
747	probable aldehyde dehydrogenase		Putative enzymes	1	1	0.98	na	
2304	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.98	na	
3769	GMP synthase	guaA	Amino acid biosynthesis and metabolism	3	1	0.98	0.06	
5245	conserved hypothetical protein	yhbL	Hypothetical, unclassified, unknown	15	3	0.97	0.13	
2	DNA polymerase III, beta chain	dnaN	DNA replication, recombination, modification	12	2	0.97	0.15	
3356	conserved hypothetical protein		Hypothetical, unclassified, unknown	4	1	0.97	0.15	
4075	hypothetical protein		Hypothetical, unclassified, unknown	2	1	0.97	0.11	
4740	polyribonucleotide nucleotidyltransferase	pnp	Transcription, RNA processing and degradation	2	1	0.97	0.04	
1707	regulatory protein PcrH	pcrH	Protein secretion/export apparatus	1	1	0.97	na	
4889	probable oxidoreductase		Putative enzymes	1	1	0.97	na	
4496	probable binding protein component of ABC transporter		Transport of small molecules	3	1	0.96	0.10	
3525	argininosuccinate synthase	argG	Amino acid biosynthesis and metabolism	19	1	0.96	0.16	
956	prolyl-tRNA synthetase	proS	Translation	11	2	0.96	0.06	
4235	bacterioferritin	bfrA	Adaptation, protection	5	1	0.96	0.10	
4995	probable acyl-CoA dehydrogenase		Putative enzymes	1	1	0.95	na	
5313	probable pyridoxal-dependent aminotransferase	paat	Putative enzymes	2	1	0.95	na	
447	glutaryl-CoA dehydrogenase	gcdH	Carbon compound catabolism	10	1	0.95	0.10	
1074	branched-chain amino acid transport protein BraC	braC	Transport of small molecules	2	1	0.95	0.11	
4916	hypothetical protein		Hypothetical, unclassified, unknown	5	1	0.95	0.22	
5224	aminopeptidase P	pepP	Translation	3	2	0.95	0.20	
2069	probable carbamoyl transferase		Putative enzymes	2	2	0.94	0.11	
4513	probable oxidoreductase		Putative enzymes	1	1	0.94	na	
4723	suppressor protein DksA	dksA	DNA replication, recombination, modification	1	1	0.94	na	
795	citrate synthase 2	prpC	Carbon compound catabolism	20	2	0.94	0.08	
5119	glutamine synthetase	glhA	Amino acid biosynthesis and metabolism	18	1	0.94	0.10	
2623	isocitrate dehydrogenase	icd	Energy metabolism	89	3	0.94	0.21	
4874	conserved hypothetical protein	psiF	Hypothetical, unclassified, unknown	102	4	0.94	0.14	
317	hypothetical protein		Hypothetical, unclassified, unknown	8	1	0.93	0.10	
4922	azurin precursor	azu	Energy metabolism	42	2	0.93	0.10	
2302	probable non-ribosomal peptide synthetase		Putative enzymes	5	2	0.93	0.09	
3978	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.93	na	
4920	NH3-dependent NAD synthetase	nadE	Biosynthesis of cofactors, prosthetic groups	23	2	0.93	0.08	
2008	fumarylacetoacetase	fahA	Carbon compound catabolism	17	4	0.93	0.10	
3977	glutamate-1-semialdehyde 2,1-aminomutase	hemL	Biosynthesis of cofactors, prosthetic groups	8	1	0.92	0.11	
4854	phosphoribosylaminoimidazolecarboxamide formyltransferase	purH	Nucleotide biosynthesis and metabolism	6	1	0.92	0.04	
4472	PmbA protein	pmbA	Adaptation, protection; Translation	9	1	0.92	0.12	
1801	ATP-dependent Clp protease proteolytic subunit	clpP	Chaperones & heat shock proteins	8	1	0.92	0.08	
1843	methionine synthase	metH	Amino acid biosynthesis and metabolism	1	1	0.92	na	
3043	conserved hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.92	na	
3345	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.92	na	
139	alkyl hydroperoxide reductase subunit C	ahpC	Adaptation, protection	41	1	0.92	0.09	
4676	probable carbonic anhydrase	yadF	Putative enzymes	3	1	0.91	0.14	
1754	transcriptional regulator CysB	cysB	Amino acid biosynthesis and metabolism	2	1	0.91	0.00	
3582	glycerol kinase	glpK	Central intermediary metabolism	20	3	0.91	0.17	
1772	probable methyltransferase	menG	Biosynthesis of cofactors, prosthetic groups	3	1	0.90	0.04	
5435	probable transcarboxylase subunit	oadA	Central intermediary metabolism	2	2	0.90	0.09	
5334	ribonuclease PH	rph	Transcription, RNA processing and degradation	3	1	0.90	0.12	
917	potassium uptake protein Kup	kup	Transport of small molecules	2	1	0.90	0.01	
963	aspartyl-tRNA synthetase	aspS	syd	Transcription, RNA processing and degradation	30	2	0.90	0.05
1455	sigma factor FlIA	flIA	rpoF	Transcriptional regulators	2	1	0.90	0.10

3640	DNA polymerase III, alpha chain	dnaE	polC	DNA replication, recombination, modification	1	1	0.90	na	
1097	transcriptional regulator FleQ	fleQ		Motility & Attachment; Transcriptional regulators	5	1	0.89	0.13	
2990	probable phosphodiesterase	ugpQ		Central intermediary metabolism	9	2	0.89	0.06	
5317	probable binding protein component of ABC dipeptide transporter			Transport of small molecules	3	1	0.89	0.14	
1618	conserved hypothetical protein	ybdB		Hypothetical, unclassified, unknown	2	1	0.89	0.06	
469	hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.88	0.00	
3797	conserved hypothetical protein	yafV		Hypothetical, unclassified, unknown	2	1	0.88	0.00	
4434	probable oxidoreductase			Putative enzymes	3	1	0.88	0.05	
1681	chorismate synthase	aroC		Amino acid biosynthesis and metabolism	5	2	0.88	0.05	
3628	probable esterase	yeiG		Putative enzymes	5	1	0.87	0.09	
3117	aspartate semialdehyde dehydrogenase	asd		Amino acid biosynthesis and metabolism	7	1	0.87	0.05	
1160	hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.87	0.01	
1584	succinate dehydrogenase (B subunit)	sdhB		Energy metabolism	2	1	0.87	0.07	
5179	probable transcriptional regulator			Transcriptional regulators	1	1	0.87	na	
5223	ubiH protein	ubiH	visB	Biosynthesis of cofactors, prosthetic groups	2	1	0.87	0.00	
5304	D-amino acid dehydrogenase, small subunit	dadA		Amino acid biosynthesis and metabolism	3	1	0.86	0.08	
5349	probable rubredoxin reductase			Carbon compound catabolism	2	1	0.86	0.01	
2248	2-oxoisovalerate dehydrogenase (beta subunit)	bkdA2		Amino acid biosynthesis and metabolism	17	3	0.86	0.11	
2400	probable non-ribosomal peptide synthetase			Adaptation, protection	3	2	0.86	0.11	
2001	acetyl-CoA acetyltransferase	atoB		Central intermediary metabolism	18	1	0.86	0.13	
1287	probable glutathione peroxidase			Putative enzymes	3	1	0.86	0.03	
3975	phosphomethylpyrimidine kinase	thiD		Biosynthesis of cofactors, prosthetic groups	2	1	0.85	0.01	
4336	conserved hypothetical protein			Hypothetical, unclassified, unknown	6	1	0.85	0.14	
4053	6,7-dimethyl-8-ribityllumazine synthase	ribE	ribH	Biosynthesis of cofactors, prosthetic groups	5	1	0.85	0.09	
4242	50S ribosomal protein L36	rpmJ		Translation	27	1	0.85	0.09	
3568	probable acetyl-coa synthetase	ymmS		Putative enzymes	1	1	0.85	na	
318	conserved hypothetical protein	hpcE		Hypothetical, unclassified, unknown	8	1	0.85	0.04	
67	oligopeptidase A	prlC	opdA	Translation	3	2	0.84	0.18	
1344	probable short-chain dehydrogenase	yvaG		Putative enzymes	5	1	0.84	0.08	
2612	seryl-tRNA synthetase	serS		Translation, post-translational modification	8	2	0.84	0.16	
5172	ornithine carbamoyltransferase, catabolic	arcB		Amino acid biosynthesis and metabolism	27	2	0.84	0.12	
2402	probable non-ribosomal peptide synthetase			Putative enzymes	21	4	0.84	0.10	
1969	hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.83	0.01	
2952	electron transfer flavoprotein beta-subunit	etfB		Energy metabolism	42	1	0.83	0.10	
3286	hypothetical protein			Hypothetical, unclassified, unknown	4	1	0.83	0.11	
2815	probable acyl-CoA dehydrogenase	yafH		Putative enzymes	4	1	0.82	0.07	
3182	conserved hypothetical protein	pgl		Hypothetical, unclassified, unknown	3	1	0.82	0.12	
2532	thiol peroxidase	tpx		Adaptation, protection	83	3	0.82	0.14	
5174	probable beta-ketoacyl synthase			Fatty acid and phospholipid metabolism	2	1	0.82	0.19	
4425	probable phosphotriose isomerase			Putative enzymes	5	1	0.82	0.12	
4402	glutamate N-acetyltransferase	argJ	yraO	Amino acid biosynthesis and metabolism	4	2	0.81	0.07	
3862	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.81	na	
4168	probable TonB-dependent receptor			Transport of small molecules	1	1	0.81	na	
5192	phosphoenolpyruvate carboxykinase	pckA		Carbon compound catabolism	2	1	0.81	0.08	
2116	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.80	0.01	
4971	conserved hypothetical protein	yrqIE		Hypothetical, unclassified, unknown	1	1	0.80	na	
5208	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.80	na	
5239	transcription termination factor Rho	rho		Transcription, RNA processing and degradation	2	1	0.80	0.03	
1794	glutaminyl-tRNA synthetase	glnS		Amino acid biosynthesis and metabolism	27	3	0.80	0.12	
36	tryptophan synthase beta chain	trpB		Amino acid biosynthesis and metabolism	1	1	0.79	na	
3613	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.79	na	
1913	hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.79	0.07	
2012	probable acyl-CoA carboxylase alpha chain	accA		Fatty acid and phospholipid metabolism	8	1	0.79	0.09	
3112	acetyl-CoA carboxylase beta subunit	accD	dedB	Fatty acid and phospholipid metabolism	2	2	0.79	0.01	
4732	glucose-6-phosphate isomerase	pgi		Carbon compound catabolism	6	1	0.79	0.09	
3584	glycerol-3-phosphate dehydrogenase	glpD		Central intermediary metabolism	10	2	0.79	0.11	
1292	probable 3-mercaptopyruvate sulfurtransferase			Putative enzymes	4	1	0.78	0.10	
3029	molybdopterin biosynthetic protein B2	moaB2		Biosynthesis of cofactors, prosthetic groups	2	1	0.78	0.04	
2444	serine hydroxymethyltransferase	glyA2		Amino acid biosynthesis and metabolism	15	2	0.78	0.14	
2399	pyoverdine synthase D	pvdD		Adaptation, protection; Secreted Factors	4	1	0.78	0.25	
5022	conserved hypothetical protein	aefA		Hypothetical, unclassified, unknown	1	1	0.78	na	
2401	probable non-ribosomal peptide synthetase			Adaptation, protection	3	1	0.78	0.07	
4936	probable rRNA methylase	yjFH	spoU	Transcription, RNA processing and degradation	5	1	0.78	0.05	
5277	diaminopimelate decarboxylase	lysA		Amino acid biosynthesis and metabolism	12	2	0.78	0.09	
586	conserved hypothetical protein	ycgB		Hypothetical, unclassified, unknown	8	2	0.77	0.13	
5128	secretion protein SecB	secB		Protein secretion/export apparatus	14	2	0.76	0.12	
870	aromatic amino acid aminotransferase	phhC	tyrB	aspC	Amino acid biosynthesis and metabolism	44	2	0.76	0.15
3011	DNA topoisomerase I	topA		DNA replication, recombination, modification	7	3	0.76	0.03	
3195	glyceraldehyde 3-phosphate dehydrogenase	gapA		Energy metabolism	8	1	0.76	0.03	
1072	branched-chain amino acid transport protein BraE	braE		Transport of small molecules	2	1	0.76	0.01	
3723	probable FMN oxidoreductase	yrqJM		Putative enzymes	1	1	0.76	na	
4547	two-component response regulator PiIR	piIR		Motility & Attachment; Transcriptional regulator	1	1	0.76	na	
5344	probable transcriptional regulator			Transcriptional regulators	2	1	0.76	0.00	
5163	glucose-1-phosphate thymidyltransferase	rmlA	rfbA		Cell wall / LPS / capsule	13	1	0.76	0.10
3148	probable UDP-N-acetylglucosamine 2-epimerase WbpI	wbpI		Cell wall / LPS / capsule; Putative enzymes	4	2	0.75	0.08	
652	transcriptional regulator Vfr	vfr		Transcriptional regulators	1	1	0.74	na	
1412	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.74	na	
902	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.73	na	
5171	arginine deiminase	arcA		Amino acid biosynthesis and metabolism	9	2	0.73	0.09	
4180	probable acetolactate synthase large subunit			Amino acid biosynthesis and metabolism	2	1	0.73	0.05	
4329	pyruvate kinase II	pykA	pyk-II		Energy metabolism	1	1	0.72	na
5320	DNA/pantothenate metabolism flavoprotein	dtp		DNA replication, recombination, modification	2	1	0.72	0.00	
947	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	0.72	0.02	
3366	aliphatic amidase	amiE		Carbon compound catabolism	1	1	0.71	na	
3919	conserved hypothetical protein			Hypothetical, unclassified, unknown	5	1	0.70	0.13	
4199	probable acyl-CoA dehydrogenase	ylaK		Putative enzymes	2	1	0.70	0.06	
2312	probable transcriptional regulator			Transcriptional regulators	1	1	0.70	na	
3332	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.70	na	
3088	conserved hypothetical protein	yfjB		Hypothetical, unclassified, unknown	3	1	0.69	0.08	
4268	30S ribosomal protein S12	rpsL	str		Translation	1	1	0.69	na
5100	urocanase	hutU		Amino acid biosynthesis and metabolism	27	3	0.68	0.07	
5173	carbamate kinase	arcC		Amino acid biosynthesis and metabolism	1	1	0.67	na	
1087	osmotically inducible lipoprotein OsmE	osmE	osmE		Membrane proteins; Adaptation, protection	7	2	0.66	0.12
1049	pyridoxine 5'-phosphate oxidase	pdxH		Biosynthesis of cofactors, prosthetic groups	2	1	0.65	0.08	
5323	acetylglutamate kinase	argB		Amino acid biosynthesis and metabolism	2	1	0.65	0.06	
432	S-adenosyl-L-homocysteine hydrolase	sahH	ahcY		Amino acid biosynthesis and metabolism	5	1	0.65	0.02
430	5,10-methylenetetrahydrofolate reductase	metF		Central intermediary metabolism	10	2	0.64	0.08	
588	conserved hypothetical protein	yeaG		Hypothetical, unclassified, unknown	27	5	0.64	0.10	
2424	probable non-ribosomal peptide synthetase			Adaptation, protection	90	7	0.64	0.09	
3478	rhamnosyltransferase chain B	rhIB		Secreted Factors (toxins, enzymes, alginate)	4	1	0.64	0.10	
4464	nitrogen regulatory IIA protein	ptsN		Transport of small molecules	2	1	0.63	0.08	
3751	phosphoribosylglycinamide formyltransferase 2	purT		Nucleotide biosynthesis and metabolism	1	1	0.62	na	
1484	probable transcriptional regulator			Transcriptional regulators	1	1	0.60	na	
5291	probable choline transporter	betT2		Transport of small molecules	1	1	0.60	na	
3348	probable chemotaxis protein methyltransferase	cheR1		Adaptation, protection; Chemotaxis	4	1	0.60	0.12	
744	probable phenyl-CoA hydratase/isomerase			Putative enzymes	21	3	0.59	0.10	
1900	probable phenazine biosynthesis protein	phzB2		Secreted Factors (toxins, enzymes, alginate)	8	2	0.59	0.06	
4025	probable ethanolamine ammonia-lyase light chain	eutC		Carbon compound catabolism	1	1	0.58	na	
5355	glycolate oxidase subunit GlcD	glcD		Carbon compound catabolism	1	1	0.58	na	
400	probable cystathionine gamma-lyase	metB	metC		Amino acid biosynthesis and metabolism	12	1	0.57	0.04
35	tryptophan synthase alpha chain	trpA		Amino acid biosynthesis and metabolism	1	1	0.57	na	
407	glutathione synthetase	gshB		Biosynthesis of cofactors, prosthetic groups	1	1	0.57	na	

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4715	probable aminotransferase	yfdZ	Putative enzymes	3	1	0.57	0.06	
1529	DNA ligase	lig	dnaL ligA	1	1	0.56	na	
1155	ribonucleoside reductase, small chain	nrdB	Nucleotide biosynthesis and metabolism	6	1	0.55	0.04	
5316	50S ribosomal protein L28	rpmB	Translation	12	1	0.55	0.08	
745	probable enoyl-CoA hydratase/isomerase		Putative enzymes	5	2	0.55	0.04	
5092	imidazolone-5-propionate hydrolase HutI	hutI	Amino acid biosynthesis and metabolism	1	1	0.55	na	
746	probable acyl-CoA dehydrogenase		Putative enzymes	7	3	0.55	0.08	
1904	probable phenazine biosynthesis protein	phzF2	Secreted Factors (toxins, enzymes, alginate)	2	1	0.54	0.01	4215
5359	hypothetical protein		Hypothetical, unclassified, unknown	9	1	0.54	0.04	
4588	glutamate dehydrogenase	gdhA	Amino acid biosynthesis and metabolism	1	1	0.53	na	
1238	probable outer membrane component of multidrug efflux pump	opmJ	Transport of small molecules	1	1	0.52	na	
2413	probable class III aminotransferase		Putative enzymes	93	3	0.52	0.13	
4225	pyochelin synthetase	pchF	Transport of small molecules; Secreted Factors	4	3	0.51	0.07	
3049	ribosome modulation factor	rnf	Translation	2	1	0.51	0.32	
792	propionate catabolic protein PrpD	prpD	Carbon compound catabolism	43	4	0.50	0.06	
888	arginine/ornithine binding protein AotJ	aotJ	Transport of small molecules	1	1	0.50	na	
2764	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.49	na	
3569	3-hydroxyisobutyrate dehydrogenase	mmsB	Carbon compound catabolism	16	1	0.48	0.02	
39	hypothetical protein		Hypothetical, unclassified, unknown	38	1	0.48	0.10	
2290	glucose dehydrogenase	gcd	Carbon compound catabolism	8	2	0.48	0.08	
3083	aminopeptidase N	pepN	Translation	3	1	0.48	0.07	
4607	hypothetical protein		Hypothetical, unclassified, unknown	16	1	0.48	0.07	
399	cystathionine beta-synthase		Amino acid biosynthesis and metabolism	6	1	0.47	0.06	
3570	methylmalonate-semialdehyde dehydrogenase	mmsA	Amino acid biosynthesis and metabolism	4	1	0.47	0.05	
5091	N-formylglutamate amidohydrolase	hutG	Amino acid biosynthesis and metabolism	4	1	0.46	0.07	
4231	salicylate biosynthesis isochorismate synthase	pchA	Secreted Factors	1	1	0.45	na	
408	twitching motility protein PilG	pilG	Chemotaxis	1	1	0.44	na	
4847	biotin carboxyl carrier protein (BCCP)	accB	Fatty acid and phospholipid metabolism	11	1	0.43	0.04	
2394	probable aminotransferase	fabE	Putative enzymes	2	1	0.43	0.16	
554	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.42	na	
122	conserved hypothetical protein		Hypothetical, unclassified, unknown	6	2	0.42	0.08	
1899	probable phenazine biosynthesis protein	phzA2	Secreted Factors (toxins, enzymes, alginate)	2	2	0.37	0.00	or 4210
3792	2-isopropylmalate synthase	leuA	Amino acid biosynthesis and metabolism	9	2	0.36	0.11	
2395	hypothetical protein		Hypothetical, unclassified, unknown	4	1	0.33	0.07	
4385	GroEL protein	groEL	Chaperones & heat shock proteins	3	1	0.33	0.07	
2367	hypothetical protein	mopA	Hypothetical, unclassified, unknown	4	1	0.30	0.05	
1803	Lon protease	lon	deg	1	1	0.29	na	
3120	3-isopropylmalate dehydratase small subunit	leuD	Amino acid biosynthesis and metabolism	1	1	0.28	na	
364	probable oxidoreductase		Putative enzymes	1	1	0.26	na	
4228	pyochelin biosynthesis protein PchD	pchD	Secreted Factors (toxins, enzymes, alginate)	30	5	0.25	0.05	
4226	dihydroaeruginic acid synthetase	pchE	Secreted Factors (toxins, enzymes, alginate)	15	3	0.24	0.04	
4230	salicylate biosynthesis protein PchB	pchB	Secreted Factors (toxins, enzymes, alginate)	17	2	0.23	0.08	
4224	hypothetical protein	pchG	Hypothetical, unclassified, unknown	21	2	0.19	0.05	
2222	hypothetical protein		Hypothetical, unclassified, unknown	1	1	0.08	na	

PA#, *P. aeruginosa* gene number; alt gene, alternative gene name; *n*, number of independent identifications and quantification events for each protein; u-ICAT, number of unique peptide sequences; fold induction, average ratios of all quantified peptides for each protein representing relative increase in protein abundance during growth of *P. aeruginosa* in 8  $\mu\text{M}$   $\text{Mg}^{2+}$ ; na, not applicable; alt ORF, identified peptides are identical in both ORFs. Values >1.5 represent increased relative abundance on growth in low magnesium, values <0.66 represent decreased relative abundance.