

Table 6. Results of *P. aeruginosa* membrane fraction ICAT analysis

PA#	Protein name	Gene	Alt gene	Function	n	u-ICAT	Fold induction	SD	Alt ORF
4635	conserved hypothetical protein		mgtC	Hypothetical, unclassified, unknown	2	1	20.50	9.50	
4825	Mg(2+) transport ATPase, P-type 2	mgtA		Transport of small molecules	63	3	8.11	3.32	
3553	probable glycosyl transferase		pmrF	Adaptation, protection; Putative enzymes	4	2	6.58	0.43	
1941	hypothetical protein			Hypothetical, unclassified, unknown	1	1	6.25	na	
2137	hypothetical protein			Hypothetical, unclassified, unknown	1	1	5.00	na	
1432	autoinducer synthesis protein LasI	lasI		Adaptation, protection	2	1	4.77	0.32	
4824	hypothetical protein			Hypothetical, unclassified, unknown	4	2	4.17	0.14	
1770	phosphoenolpyruvate synthase	ppsA		Carbon compound catabolism	6	1	3.41	1.07	
1179	two-component response regulator PhoP	phoP		Transcriptional regulators	2	1	3.28	0.60	
4456	probable ATP-binding component of ABC transporter		yrbF	Transport of small molecules	3	2	3.15	0.32	
126	hypothetical protein			Hypothetical, unclassified, unknown	2	1	3.03	0.13	
1585	2-oxoglutarate dehydrogenase (E1 subunit)	sucA		Amino acid biosynthesis and metabolism	10	3	2.97	0.59	
4666	glutamyl-tRNA reductase	hemA	hem1; glutR	Amino acid biosynthesis and metabolism	2	1	2.71	0.21	
2540	conserved hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.69	0.18	
2789	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.50	na	
4241	30S ribosomal protein S13	rpsM		Translation	5	1	2.42	0.05	
4266	elongation factor G	fusA1		Translation	9	1	2.41	0.22	
603	probable ATP-binding component of ABC transporter			Transport of small molecules	1	1	2.38	na	
4656	conserved hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.26	0.45	
1583	succinate dehydrogenase (A subunit)	sdhA		Energy metabolism	3	2	2.24	0.40	
1584	succinate dehydrogenase (B subunit)	sdhB		Energy metabolism	7	3	2.20	0.28	
4239	30S ribosomal protein S4	rpsD		Translation	9	2	2.19	0.22	
2953	electron transfer flavoprotein-ubiquinone oxidoreductase			Energy metabolism	9	1	2.19	0.31	
4246	30S ribosomal protein S5	rpsE		Translation	6	1	2.18	0.24	
5300	cytochrome c5	cycB		Energy metabolism	5	1	2.18	0.17	
2071	elongation factor G	fusA2		Translation	2	1	2.17	0.30	
1459	probable methyltransferase		cheB	Chemotaxis	1	1	2.16	0.90	
5557	ATP synthase delta chain	atpH	uncH papE	Energy metabolism	5	1	2.15	0.08	
4670	ribose-phosphate pyrophosphokinase	prs	prsA	Carbon compound catabolism	23	2	2.13	0.22	
3068	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.13	na	
3666	tetrahydrodipicolinate succinylase	dapD		Cell wall / LPS / capsule	1	1	2.10	na	
3656	30S ribosomal protein S2	rpsB		Translation	6	1	2.01	0.32	
5556	ATP synthase alpha chain	atpA	uncA papA	Energy metabolism	4	1	2.00	0.32	
3716	hypothetical protein			Hypothetical, unclassified, unknown	5	1	2.00	0.17	
5555	ATP synthase gamma chain	atpG	uncG papC	Energy metabolism	2	1	1.98	0.03	
4756	carbamoylphosphate synthetase large subunit	carB		Nucleotide biosynthesis and metabolism	3	1	1.90	0.41	
4005	conserved hypothetical protein		ybeB	Hypothetical, unclassified, unknown	2	1	1.83	0.24	
2302	probable non-ribosomal peptide synthetase			Putative enzymes	7	2	1.83	0.23	
892	arginine/ornithine transport protein AotP	aotP		Transport of small molecules	6	1	1.82	0.22	
1504	probable transcriptional regulator			Transcriptional regulators	1	1	1.82	na	
3481	conserved hypothetical protein		mrp	Hypothetical, unclassified, unknown	5	1	1.82	0.04	
4260	50S ribosomal protein L2	rplB		Translation	1	1	1.80	na	
2247	2-oxoisovalerate dehydrogenase (alpha subunit)	bkdA1		Amino acid biosynthesis and metabolism	3	1	1.79	0.24	
1262	probable MFS transporter			Membrane proteins	1	1	1.74	na	
4935	30S ribosomal protein S6	rpsF		Translation	12	1	1.74	0.20	
5554	ATP synthase beta chain	atpD	uncD papB	Energy metabolism	4	1	1.74	0.18	
2976	ribonuclease E	rne	ams	Transcription, RNA processing and degradation	8	1	1.72	0.22	
85	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.71	0.02	
998	hypothetical protein			Putative enzymes	7	1	1.68	0.28	
302	polyamine transport protein PotG	potG		Transport of small molecules	8	1	1.68	0.22	
70	hypothetical protein			Hypothetical, unclassified, unknown	14	4	1.67	0.20	
4053	6,7-dimethyl-8-ribitylumazine synthase	ribE	ribH	Biosynthesis of cofactors	5	1	1.66	0.19	
3263	conserved hypothetical protein		yaiD	Hypothetical, unclassified, unknown	3	1	1.66	0.10	
2991	soluble pyridine nucleotide transhydrogenase	sth		Nucleotide biosynthesis and metabolism	1	1	1.64	na	
5108	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.64	na	
4408	cell division protein FtsA	ftsA		Cell division	6	1	1.63	0.20	
3831	leucine aminopeptidase	pepA	phpA	Translation, post-translational modification	6	3	1.61	0.41	
4407	cell division protein FtsZ	ftsZ		Cell division	1	1	1.59	na	
5307	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.59	na	
2014	probable acyl-CoA carboxyltransferase beta chain			Putative enzymes	3	1	1.59	0.43	
4254	30S ribosomal protein S17	rpsQ		Translation, post-translational modification	4	1	1.58	0.07	
4760	DnaJ protein	dnaJ		Adaptation, protection; Chaperones	2	1	1.56	0.32	
3328	probable FAD-dependent monooxygenase			Putative enzymes	2	1	1.56	0.63	
2641	NADH dehydrogenase I chain F	nuoF		Energy metabolism	4	2	1.55	0.13	
4270	DNA-directed RNA polymerase beta chain	rpoB		Transcription, RNA processing and degradation	4	2	1.54	0.25	
4268	30S ribosomal protein S12	rpsL	str	Translation, post-translational modification	18	2	1.54	0.13	
5316	50S ribosomal protein L28	rplM		Translation, post-translational modification	5	1	1.54	0.08	
2776	conserved hypothetical protein		ordL	Hypothetical, unclassified, unknown	1	1	1.53	na	
4429	probable cytochrome c1 precursor			Energy metabolism	1	1	1.52	na	
4431	probable iron-sulfur protein			Putative enzymes	1	1	1.52	na	
2248	2-oxoisovalerate dehydrogenase (beta subunit)	bkdA2		Amino acid biosynthesis and metabolism	2	1	1.48	0.02	
715	hypothetical protein			Related to phage, transposon, or plasmid	1	1	1.47	na	
936	hypothetical protein			Hypothetical, unclassified, unknown	3	1	1.45	0.00	
3465	conserved hypothetical protein		yfiS	Hypothetical, unclassified, unknown	3	1	1.43	0.21	
1889	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.43	na	
5146	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.43	na	
4307	chemotactic transducer PctC	pctC		Adaptation, protection; Chemotaxis	6	2	1.42	0.14	4309, 4310
1064	hypothetical protein			Hypothetical, unclassified, unknown	7	2	1.42	0.19	
3694	hypothetical protein			Hypothetical, unclassified, unknown	3	1	1.38	0.08	
652	transcriptional regulator Vfr	vfr		Transcriptional regulators	6	1	1.36	0.10	
782	proline dehydrogenase PutA	putA	pruA; pruB	Amino acid biosynthesis and metabolism	4	2	1.34	0.12	
1072	branched-chain amino acid transport protein BraE	braE		Membrane proteins; Transport	1	1	1.33	na	
4957	phosphatidylserine decarboxylase	psd		Amino acid biosynthesis and metabolism	2	1	1.32	0.05	
4054	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase	ribB	ribA	Biosynthesis of cofactors, prosthetic groups	1	1	1.30	na	
3999	D-ala-D-ala-carboxypeptidase	dacC	dacD	Cell wall / LPS / capsule	10	1	1.30	0.06	
2994	Na+-translocating NADH:quinone oxidoreductase, subunit Nqr6	nqrF		Energy metabolism	3	1	1.30	0.08	
1482	cytochrome C-type biogenesis protein CcmH	ccmH	ccl2 cycL	Energy metabolism	4	1	1.30	0.15	
4265	elongation factor Tu	tufA		Translation, post-translational modification	9	3	1.29	0.16	4277
2232	probable phosphomannose isomerase/GDP-mannose pyrophosphorylase			Cell wall / LPS / capsule	10	2	1.27	0.15	
4	DNA gyrase subunit B	gyrB		DNA replication, recombination, modification	8	1	1.26	0.10	
3611	hypothetical protein			Hypothetical, unclassified, unknown	3	1	1.26	0.15	
4525	type 4 fimbrial precursor PilA	pilA		Motility & Attachment	4	2	1.26	0.05	
1587	lipamide dehydrogenase-glc	lpdG	lpdA	Amino acid biosynthesis and metabolism	10	2	1.23	0.44	
1339	probable ATP-binding component of ABC transporter			Transport of small molecules	4	2	1.22	0.07	
3247	hypothetical protein			Hypothetical, unclassified, unknown	3	1	1.20	0.16	
3349	probable chemotaxis protein			Adaptation, protection; Chemotaxis	3	1	1.20	0.02	
867	hypothetical protein			Hypothetical, unclassified, unknown	13	2	1.19	0.06	
1475	heme exporter protein CcmA	ccmA	cycV, helA	Transport of small molecules	1	1	1.18	na	
1814	hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.17	0.07	
3150	LPS biosynthesis protein WbpG	wbpG		Cell wall / LPS / capsule	1	1	1.14	na	
3584	glycerol-3-phosphate dehydrogenase	glpD		Central intermediary metabolism	11	2	1.13	0.14	
5011	heptosyltransferase I	wacC	rfaC	Cell wall / LPS / capsule	3	1	1.12	0.04	
11	probable 2-OH-lauroyltransferase			Cell wall / LPS / capsule	2	1	1.11	0.09	

4717	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.11	0.05
2725	probable chaperone			Chaperones & heat shock proteins; Translation	1	1	1.11	na
5152	probable ATP-binding component of ABC transporter			Transport of small molecules	1	1	1.11	na
2945	conserved hypothetical protein		cobW	Biosynthesis of cofactors	1	1	1.10	na
5119	glutamine synthetase	glnA		Amino acid biosynthesis and metabolism	11	1	1.10	0.14
3582	glycerol kinase	glpK		Central intermediary metabolism	2	2	1.09	0.17
1057	conserved hypothetical protein		phaE	Hypothetical, unclassified, unknown	2	1	1.08	0.16
5049	50S ribosomal protein L31	rpmE		Translation, post-translational modification	1	1	1.08	na
2402	probable non-ribosomal peptide synthetase			Putative enzymes	19	7	1.06	0.23
4874	conserved hypothetical protein		psIF	Hypothetical, unclassified, unknown	3	1	1.06	0.01
4633	probable chemotaxis transducer			Adaptation, protection; Chemotaxis	4	1	1.05	0.03
2042	probable transporter (membrane subunit)		ygjU	Transport of small molecules	5	2	1.04	0.07
2195	hydrogen cyanide synthase HcnC	hcnC		Central intermediary metabolism	1	1	1.04	na
4565	glutamate 5-kinase	proB		Amino acid biosynthesis and metabolism	1	1	1.02	na
917	potassium uptake protein Kup	kup		Transport of small molecules	4	1	1.02	0.08
172	hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.01	0.08
5304	D-amino acid dehydrogenase, small subunit	dadA		Amino acid biosynthesis and metabolism	12	1	1.00	0.21
2386	L-ornithine N5-oxygenase	pvdA		Adaptation, protection	2	1	1.00	0.04
4751	cell division protein FtsH	ftsH	hflB	Fatty acid and phospholipid metabolism	1	1	0.98	na
1969	hypothetical protein			Hypothetical, unclassified, unknown	4	1	0.96	0.15
2399	pyoverdine synthetase D	pvdD		Adaptation, protection; Secreted Factors	4	1	0.95	0.09
5028	conserved hypothetical protein			Hypothetical, unclassified, unknown	4	2	0.92	0.05
2728	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.89	na
4372	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.89	na
4578	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.89	na
1222	probable membrane-bound lytic murein transglycosylase A	mltA		Cell wall / LPS / capsule	1	1	0.88	na
2345	conserved hypothetical protein			Hypothetical, unclassified, unknown	9	2	0.87	0.15
1944	hypothetical protein			Hypothetical, unclassified, unknown	3	2	0.87	0.02
4385	GroEL protein	groEL	mopA	Chaperones & heat shock proteins	3	1	0.86	0.02
2424	probable non-ribosomal peptide synthetase			Adaptation, protection	40	11	0.86	0.14
2413	probable class III aminotransferase			Putative enzymes	7	2	0.84	0.18
5172	ornithine carbamoyltransferase, catabolic	arcB		Amino acid biosynthesis and metabolism	9	1	0.84	0.21
1641	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.81	na
3617	RecA protein	recA		DNA replication, recombination, modification	5	1	0.80	0.03
4168	probable TonB-dependent receptor			Transport of small molecules	1	1	0.80	na
5308	leucine-responsive regulatory protein	lrp		Central intermediary metabolism	1	1	0.80	na
4744	translation initiation factor IF-2	infB		Translation, post-translational modification	1	1	0.77	na
3158	probable oxidoreductase WpbB	wpbB		Cell wall / LPS / capsule; Putative enzymes	3	1	0.73	0.06
5015	pyruvate dehydrogenase	aceE	aceA	Amino acid biosynthesis and metabolism	5	2	0.73	0.03
1860	hypothetical protein			Putative enzymes	2	1	0.72	0.00
3179	conserved hypothetical protein		yciL	Hypothetical, unclassified, unknown	3	1	0.70	0.05
4916	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.68	na
3148	probable UDP-N-acetylglucosamine 2-epimerase Wbpl	wbpl		Cell wall / LPS / capsule; Putative enzymes	3	1	0.66	0.04
4694	ketol-acid reductoisomerase	ilvC		Amino acid biosynthesis and metabolism	2	2	0.63	0.10
4876	osmotically inducible lipoprotein OsmE	osmE	osmE	Membrane proteins; Adaptation, protection	3	1	0.60	0.05
4579	hypothetical protein			Hypothetical, unclassified, unknown	1	1	0.59	na
2290	glucose dehydrogenase	gcd		Carbon compound catabolism	3	1	0.56	0.03
4226	dihydroaeruginic acid synthetase	pchE		Transport of small molecules; Secreted Factors	9	3	0.56	0.05
3331	cytochrome P450			Adaptation, protection	5	1	0.50	0.04
4230	salicylate biosynthesis protein PchB	pchB		Transport of small molecules; Secreted Factors	3	1	0.48	0.04
4224	hypothetical protein		pchG	Hypothetical, unclassified, unknown	2	1	0.45	0.07
139	alkyl hydroperoxide reductase subunit C	ahpC		Adaptation, protection	7	1	0.45	0.04
4228	pyochelin biosynthesis protein PchD	pchD		Transport of small molecules; Secreted Factors	2	1	0.44	0.00
4607	hypothetical protein			Hypothetical, unclassified, unknown	6	1	0.44	0.09
5436	probable biotin carboxylase subunit of a transcarboxylase			Central intermediary metabolism	1	1	0.40	na
1903	phenazine biosynthesis protein PhzE		phzE2	Secreted Factors (toxins, enzymes, alginate)	1	1	0.37	na or 4214
4231	salicylate biosynthesis isochorismate synthase		pchA	Secreted Factors (toxins, enzymes, alginate)	2	1	0.36	0.06
1899	probable phenazine biosynthesis protein		phzA2	Secreted Factors (toxins, enzymes, alginate)	3	1	0.34	0.02 or 4210
4988	3-deoxy-D-manno-octulosonic-acid (KDO) transferase	waaA	kdtA	Cell wall / LPS / capsule	1	1	0.22	na
2069	probable carbamoyl transferase			Putative enzymes	3	1	0.11	0.02

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 μM Mg^{2+} ; na, not applicable; alt ORF, identified peptides are identical in both ORFs. Values >1.5 represent increased relative abundance upon growth in low magnesium, values <0.66 represent decreased relative abundance.