

Table 3. *Pseudomonas aeruginosa* magnesium stress-induced proteins

PA#	Protein name	Gene	Alt gene	Function	n	u-ICAT	Fold induction	SD	Alt ORF
8	glycyl-tRNA synthetase beta chain	glyS		Amino acid biosynthesis and metabolism	11	1	2.74	0.36	
70	hypothetical protein			Hypothetical, unclassified, unknown	14	4	1.67	0.20	
85	conserved hypothetical protein			Hypothetical, unclassified, unknown	12	1	1.78	0.11	
100	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.20	na	
126	hypothetical protein, OMP			Hypothetical, unclassified, unknown	2	1	3.03	0.13	
302	polyamine transport protein PotG	potG		Transport of small molecules	8	1	1.68	0.22	
603**	probable ATP-binding component of ABC transporter			Transport of small molecules	1	1	2.38	na	
604	probable binding protein component of ABC transporter			Transport of small molecules	2	1	1.66	0.16	
704	probable amidase			Putative enzymes	1	1	1.77	na	
858	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.94	na	
865	4-hydroxyphenylpyruvate dioxygenase	hpd		Amino acid biosynthesis and metabolism	12	1	2.12	0.24	
934	GTP pyrophosphokinase	relA		Adaptation, protection	2	1	1.53	0.00	
996	probable coenzyme A ligase			Putative enzymes	1	1	1.57	na	
997	hypothetical protein			Hypothetical, unclassified, unknown	16	2	1.57	0.26	
998	hypothetical protein			Putative enzymes	6	2	2.04	0.24	
999	3-oxoacyl-[acyl-carrier-protein] synthase III	fabH1		Fatty acid and phospholipid metabolism	4	1	1.63	0.13	
1091	hypothetical protein			Hypothetical, unclassified, unknown	1	1	3.27	na	
1163	probable glucosyl transferase	ndvB		Putative enzymes	1	1	5.06	na	
1179**	two-component response regulator PhoP	phoP		Transcriptional regulators	6	1	10.34	0.96	
1262	probable MFS transporter			Membrane proteins	1	1	1.74	na	
1432	autoinducer synthesis protein LasI	lasI		Adaptation, protection	2	1	3.10	0.05	
1504	probable transcriptional regulator			Transcriptional regulators	1	1	1.82	na	
1520	probable transcriptional regulator			Transcriptional regulators	4	1	1.51	0.06	
1563	conserved hypothetical protein	ygdE		Hypothetical, unclassified, unknown	2	1	3.55	0.39	
1574	conserved hypothetical protein	yaiE		Hypothetical, unclassified, unknown	7	1	2.06	0.22	
1579	hypothetical protein			Hypothetical, unclassified, unknown	5	1	1.68	0.33	
1941	hypothetical protein			Hypothetical, unclassified, unknown	1	1	6.25	na	
2036	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.71	na	
2040	probable glutamine synthetase			Putative enzymes	5	1	2.61	0.47	
2127**	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.79	na	
2137	hypothetical protein			Hypothetical, unclassified, unknown	1	1	5.00	na	
2343	xylulose kinase	mtlY		Carbon compound catabolism	1	1	2.44	na	
2400	probable non-ribosomal peptide synthetase			Adaptation, protection	11	2	3.29	0.55	2402
2405	hypothetical protein			Hypothetical, unclassified, unknown	2	1	2.59	0.14	
2491	probable oxidoreductase			Putative enzymes	9	1	1.54	0.08	
2540	conserved hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.69	0.18	
2641	NADH dehydrogenase I chain F	nuoF		Energy metabolism	2	1	1.50	0.01	
2735	probable restriction-modification system protein			Putative enzymes	1	1	7.27	na	
2789	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.50	na	
2953	electron transfer flavoprotein-ubiquinone oxidoreductase			Energy metabolism	9	4	1.66	0.13	
2968	malonyl-CoA-[acyl-carrier-protein] transacylase	fabD		Fatty acid and phospholipid metabolism	1	1	1.81	na	
3179	conserved hypothetical protein	tmNRP	yciL	Hypothetical, unclassified, unknown	2	1	2.54	0.20	
3193	glucokinase	glk		Carbon compound catabolism	1	1	1.63	na	
3284	hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.99	0.96	
3327	probable non-ribosomal peptide synthetase			Adaptation, protection	2	1	1.55	0.00	
3330	probable short chain dehydrogenase			Putative enzymes	5	1	1.86	0.08	
3481	conserved hypothetical protein	mrp		Hypothetical, unclassified, unknown	5	1	1.82	0.04	
3504	probable aldehyde dehydrogenase			Putative enzymes	3	1	1.68	0.02	
3531	bacterioferritin	bfrB		Transport of small molecules	3	1	1.59	0.14	
3533	conserved hypothetical protein	ydhD		Hypothetical, unclassified, unknown	10	1	1.65	0.15	
3552**	conserved hypothetical protein			Hypothetical, unclassified, unknown	7	1	2.84	0.25	
3553	probable glycosyl transferase	pmrF		Adaptation, protection; Putative enzymes	1	1	2.33	na	
3554	conserved hypothetical protein			Putative enzymes	34	7	6.09	1.16	
3578	conserved hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.21	na	
3619	hypothetical protein			Hypothetical, unclassified, unknown	1	1	3.14	na	
3655	elongation factor Ts	tsf		Translation, post-translational modification	4	1	2.20	0.38	
3666	tetrahydrodipicolinate succinylase	dapD		Cell wall / LPS / capsule	1	1	2.10	na	
3716	hypothetical protein			Hypothetical, unclassified, unknown	5	1	2.00	0.17	
3735	threonine synthase	thrC		Amino acid biosynthesis and metabolism	1	1	2.71	na	
3736	homoserine dehydrogenase	hom		Amino acid biosynthesis and metabolism	1	1	1.66	na	
3925	probable acyl-CoA thiolase			Putative enzymes	6	1	2.91	1.22	
4005	conserved hypothetical protein			Hypothetical, unclassified, unknown	2	1	1.83	0.24	
4031	inorganic pyrophosphatase	ppa	ipyR	Central intermediary metabolism	6	1	2.24	0.46	
4074	probable transcriptional regulator			Transcriptional regulators	1	1	7.79	na	
4284	exodeoxyribonuclease V beta chain	recB		DNA metabolism	1	1	2.91	na	
4456	probable ATP-binding component of ABC transporter			Transport of small molecules	3	2	3.15	0.32	
4457	conserved hypothetical protein	yrbF		Secreted Factors (toxins, enzymes, alginate)	3	1	1.82	0.15	
4481	rod shape-determining protein MreB	mreB	envB rodY	Cell division; Cell wall / LPS / capsule	3	2	1.88	0.33	
4635**	conserved hypothetical protein			Hypothetical, unclassified, unknown	13	1	3.99	0.56	
4656	conserved hypothetical protein			Hypothetical, unclassified, unknown	3	1	2.26	0.45	
4774	hypothetical protein			Hypothetical, unclassified, unknown	2	1	3.48	0.19	
4824**	hypothetical protein			Hypothetical, unclassified, unknown	4	2	4.17	0.14	
4825**	Mg(2+) transport ATPase, P-type 2	mgtA		Transport of small molecules	85	3	5.80	1.75	
4935	30S ribosomal protein S6	rpsF		Translation, post-translational modification	12	1	1.74	0.20	
5108	hypothetical protein, OMP			Hypothetical, unclassified, unknown	1	1	1.64	na	
5143	imidazoleglycerol-phosphate dehydratase	hisB		Amino acid biosynthesis and metabolism	3	1	1.61	0.11	

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; na, not applicable; alt ORF, identified peptides are identical in both ORFs.

**Corresponding genes were also shown to be induced by transcriptional profiling analysis (R. K. Ernst and S.I.M., unpublished results). Values >1.5 represent increased relative abundance on growth in low magnesium. For proteins that were quantified by ICAT analysis of both the whole cell and the membrane fraction, results of the whole cell protein analysis were defined as the accurate abundance ratio for a given protein.