

Table 4. *P. aeruginosa* magnesium stress-repressed proteins

PA#	Protein name	Gene	Alt gene	Function	n	u-ICAT	Fold repression	SD	Alt ORF
35	tryptophan synthase alpha chain	trpA		Amino acid biosynthesis and metabolism	1	1	1.76	na	
39	hypothetical protein			Hypothetical, unclassified, unknown	38	1	2.08	0.20	
122**	conserved hypothetical protein			Hypothetical, unclassified, unknown	6	2	2.40	0.19	
364	probable oxidoreductase			Putative enzymes	1	1	3.91	na	
399	cystathionine beta-synthase			Amino acid biosynthesis and metabolism	6	1	2.14	0.13	
400	probable cystathionine gamma-lyase	metB metC		Amino acid biosynthesis and metabolism	12	1	1.74	0.08	
407	glutathione synthetase	gshB		Amino acid biosynthesis and metabolism	1	1	1.76	na	
408	twitching motility protein PilG	pilG		Chemotaxis; Motility & Attachment	1	1	2.26	na	
430	5,10-methylenetetrahydrofolate reductase	metF		Central intermediary metabolism	10	2	1.56	0.12	
432	S-adenosyl-L-homocysteine hydrolase	sahH	ahcY	Amino acid biosynthesis and metabolism	5	1	1.54	0.03	
554	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.39	na	
588**	conserved hypothetical protein	yeaG		Hypothetical, unclassified, unknown	27	5	1.56	0.16	
744**	probable enoyl-CoA hydratase/isomerase			Putative enzymes	21	3	1.69	0.17	
745	probable enoyl-CoA hydratase/isomerase			Putative enzymes	5	2	1.81	0.06	
746**	probable acyl-CoA dehydrogenase			Putative enzymes	7	3	1.83	0.14	
792	propionate catabolic protein PrpD	prpD		Carbon compound catabolism	43	4	2.00	0.13	
888	arginine/ornithine binding protein AotJ	aotJ		Transport of small molecules	1	1	2.00	na	
1049	pyridoxine 5'-phosphate oxidase	pdxH		Biosynthesis of cofactors	2	1	1.54	0.13	
1155	ribonucleoside reductase, small chain	nrdB		Nucleotide biosynthesis and metabolism	6	1	1.81	0.06	
1238	probable outer membrane component of multidrug efflux pump	opmJ		Transport of small molecules	1	1	1.91	na	
1484	probable transcriptional regulator			Transcriptional regulators	1	1	1.65	na	
1529	DNA ligase	lig	dnaL ligA	DNA metabolism	1	1	1.79	na	
1803	Lon protease	lon		Translation, degradation	1	1	3.44	na	
1899**	probable phenazine biosynthesis protein	phzA2		Secreted Factors (toxins, enzymes, alginate)	2	2	2.69	0.00	4210
1900	probable phenazine biosynthesis protein	phzB2		Secreted Factors (toxins, enzymes, alginate)	8	2	1.70	0.10	
1903**	phenazine biosynthesis protein PhzE	phzE2		Secreted Factors (toxins, enzymes, alginate)	1	1	2.70	na	4214
1904**	probable phenazine biosynthesis protein	phzF2		Secreted Factors (toxins, enzymes, alginate)	2	1	1.85	0.01	4215
2222	hypothetical protein			Hypothetical, unclassified, unknown	1	1	12.29	na	
2290	glucose dehydrogenase	gcd		Carbon compound catabolism	8	2	2.09	0.16	
2367	hypothetical protein			Hypothetical, unclassified, unknown	4	1	3.34	0.18	
2394	probable aminotransferase			Putative enzymes	2	1	2.32	0.36	
2395**	hypothetical protein			Hypothetical, unclassified, unknown	4	1	3.04	0.20	
2413**	probable class III aminotransferase			Putative enzymes	93	3	1.92	0.25	
2424	probable non-ribosomal peptide synthetase			Adaptation, protection	90	7	1.56	0.14	
2764	hypothetical protein			Hypothetical, unclassified, unknown	1	1	2.05	na	
3083	aminopeptidase N	pepN		Translation, post-translational modification	3	1	2.10	0.15	
3120	3-isopropylmalate dehydratase small subunit			Amino acid biosynthesis and metabolism	1	1	3.58	na	
3331	cytochrome P450			Carbon compound catabolism	5	1	2.00	0.08	
3348	probable chemotaxis protein methyltransferase	cheR1		Adaptation, protection; Chemotaxis	4	1	1.67	0.21	
3478**	rhamnosyltransferase chain B	rhIB		Secreted Factors (toxins, enzymes, alginate)	4	1	1.57	0.15	
3569	3-hydroxyisobutyrate dehydrogenase	mmsB		Carbon compound catabolism	16	1	2.07	0.04	
3570**	methylmalonate-semialdehyde dehydrogenase	mmsA		Amino acid biosynthesis and metabolism	4	1	2.15	0.12	
3751	phosphoribosylglycinamide formyltransferase 2	purT		Amino acid biosynthesis and metabolism	1	1	1.62	na	
3792	2-isopropylmalate synthase	leuA		Amino acid biosynthesis and metabolism	9	2	2.76	0.30	
4025	probable ethanolamine ammonia-lyase light chain	eutC		Carbon compound catabolism	1	1	1.72	na	
4211	probable phenazine biosynthesis protein	phzB1		Secreted Factors (toxins, enzymes, alginate)	2	1	1.93	0.07	
4224	hypothetical protein	pchG		Hypothetical, unclassified, unknown	21	2	5.23	0.25	
4225**	pyochelin synthetase	pchF		Transport of small molecules; Secreted Factors	4	3	1.97	0.14	
4226**	dihydroaeruginic acid synthetase	pchE		Transport of small molecules; Secreted Factors	15	3	4.23	0.19	
4228**	pyochelin biosynthesis protein PchD	pchD		Transport of small molecules; Secreted Factors	30	5	4.07	0.19	
4230**	salicylate biosynthesis protein PchB	pchB		Transport of small molecules; Secreted Factors	17	2	4.42	0.36	
4231**	salicylate biosynthesis isochorismate synthase	pchA		Secreted Factors (toxins, enzymes, alginate)	1	1	2.21	na	
4385	GroEL protein	groEL	mopA	Chaperones & heat shock proteins	3	1	3.07	0.21	
4464	nitrogen regulatory IIA protein	ptsN		Transport of small molecules	2	1	1.58	0.12	
4579	hypothetical protein			Hypothetical, unclassified, unknown	1	1	1.69	na	
4588	glutamate dehydrogenase	gdhA		Amino acid biosynthesis and metabolism	1	1	1.87	na	
4607	hypothetical protein			Hypothetical, unclassified, unknown	16	1	2.10	0.16	
4715	probable aminotransferase	yfdZ		Putative enzymes	3	1	1.77	0.10	
4847**	biotin carboxyl carrier protein (BCCP)	accB	fabE	Fatty acid and phospholipid metabolism	11	1	2.30	0.09	
4876	osmotically inducible lipoprotein OsmE	osmE	osmE	Membrane proteins; Adaptation, protection	7	2	1.52	0.18	
4988	3-deoxy-D-manno-octulosonic-acid (KDO) transferase	waaA	kdtA	Cell wall / LPS / capsule	1	1	4.55	na	
5091	N-formylglutamate amidohydrolase	hutG		Amino acid biosynthesis and metabolism	4	1	2.16	0.15	
5092	imidazolone-5-propionate hydrolase HutI	hutI		Amino acid biosynthesis and metabolism	1	1	1.83	na	
5291	probable choline transporter		bet2	Transport of small molecules	1	1	1.65	na	
5316	50S ribosomal protein L28	rpmB		Translation, post-translational modification	12	1	1.81	0.14	
5323	acetylglutamate kinase	argB		Amino acid biosynthesis and metabolism	2	1	1.54	0.09	
5355	glycolate oxidase subunit GlcD	glcD		Central intermediary metabolism	1	1	1.72	na	
5359	hypothetical protein			Hypothetical, unclassified, unknown	9	1	1.87	0.08	
5436	probable biotin carboxylase subunit of a transcarboxylase			Central intermediary metabolism	1	1	2.50	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 repression, average ratios of all quantified peptides for each protein; na, not applicable; alt ORF, identified peptides are identical in both ORFs.

** Authors contributing equally were arranged alphabetically, per PNAS style. Corresponding genes were also shown to be repressed by transcriptional profiling analysis (R. K. Ernst and S.I.M., unpublished results). Values >1.5 represent decreased 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.