

Table 7. *P. aeruginosa* stress-response proteins not induced by magnesium limitation

PA#	Protein name	Gene	Alt gene	Function	n	u-ICAT	Fold induction	SD	Alt ORF
4236	catalase	katA	catA	Adaptation, protection	5	1	1.25	0.04	
4542	CipB protein	cipB		Translation	5	1	1.19	0.16	
1801	ATP-dependent Clp protease proteolytic subunit	cipP		Chaperones & heat shock proteins	8	1	0.92	0.08	
2620	ATP-binding protease component ClpA	cipA		Translation	1	1	1.35	na	
4760	DnaJ protein	dnaJ		Adaptation, protection; Chaperones	13	1	1.19	0.08	
2399	pyoverdine synthetase D	pvdD		Adaptation, protection; Secreted Factors	4	1	0.78	0.25	
2386	L-ornithine N5-oxygenase	pvdA		Adaptation, protection	2	1	1.00	0.04	
4231	salicylate biosynthesis isochorismate synthase	pchA		Secreted Factors	1	1	0.45	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	

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.