

Table S4. Functional classification of *A. baumannii* protein spots over or under-expressed in response to SA treatment during late stationary phase.

Protein description	Gene	Locus	Spot no.	Cellular fraction ^{a)}	Change (<i>n</i> -fold) in protein expression ^{b)}	No. of peptides	Coverage (%)	Score ^{c)}	NCBI nr accession no.
Amino acid transport and metabolism									
urocanase		A1S_3407	142	T	-3,32	3	13	122	gi 126643414
Carbohydrate metabolism									
dihydrolipoamide dehydrogenase		A1S_2717	202	T	2,46	3	13	129	gi 193078183
dihydrolipoamide dehydrogenase		A1S_2717	205	T	2,39	11	36	83	gi 193078183
dihydrolipoamide dehydrogenase		A1S_2717	212	T	2,12	8	34	446	gi 193078183
dihydrolipoamide dehydrogenase		A1S_2717	214	T	2,07	7	35	409	gi 193078183
succinyl-CoA synthetase alpha chain		A1S_2719	316	M	<i>de novo</i>	2	12	69	gi 126642750
succinyl-CoA synthetase alpha chain		A1S_2719	503	T	2,14	2	14	90	gi 126642750
Cell envelope biogenesis and transport, outer membrane									
Protein tolB	<i>tolB</i>	A1S_2594	274	M	<i>de novo</i>	2	5	92	gi 126642629
outer membrane protein A	<i>ompA</i>	A1S_2840	484	M	4,23	2	7	79	gi 126642864
putative outer membrane protein		A1S_0884	530	M	<i>de novo</i>	5	37	199	gi 126640934
outer membrane protein A	<i>ompA</i>	A1S_2840	536	M	-5,03	16	16	348	gi 126642864
preprotein translocase subunit SecB	<i>secB</i>	A1S_0528	777	T	<i>de novo</i>	2	18	107	gi 126640599

outer membrane protein A	<i>ompA</i>	A1S_2840	889	T	ND	9	23	615	gi 126642864
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Cell division

cell division inhibitor, a membrane ATPase, activates minC	<i>minD</i>	ABSDF2556	503	T	2,14	3	16	85	gi 169634045
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Energy metabolism - oxidative phosphorylation

F0F1 ATP synthase subunit alpha	<i>atpA</i>	A1S_0153	197	M	<i>de novo</i>	6	14	223	gi 162286757
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NADH dehydrogenase I chain B	<i>nuoB</i>	ABSDF2713	431	M	3,71	3	9	100	gi 169634180
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Environmental information processing, signal transduction

two-component response regulator		A1S_3229	516	T	4,05	18	77	98	gi 126643237
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Iron ion homeostasis

bacterioferritin		A1S_0800	567	M	-2,03	2	17	59	gi 126640856
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bacterioferritin		A1S_0800	568	M	ND	4	29	230	gi 126640856
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Lipid metabolism

multifunctional fatty acid oxidation complex subunit alpha	<i>fadB</i>	ABSDF3220	85	T	6,27	9	18	410	gi 169634578
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Putative propionyl-CoA carboxylase beta subunit		A1S_1375	88	M	3,01	4	10	233	gi 126641421
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Putative uncharacterized protein/acetyl-/propionyl-CoA carboxylase		A1S_1270	131	T	<i>de novo</i>	1	3	77	gi 126641316
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Short-chain dehydrogenase/reductase SDR		A1S_1858	883	T	-9,45	4	37	113	gi 126641903
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Metabolism of cofactors and vitamins

nicotinate-nucleotide pyrophosphorylase		A1S_0044	420	T	<i>de novo</i>	2	10	65	gi 126640157
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dihydropteroate synthase type-2	<i>sul2</i>	*	566	T	-3,17	10	55	83	gi 224555949
Multifunctional									
aspartate carbamoyltransferase catalytic subunit	<i>pyrB</i>	A1S_1190	297	M	2,17	4	15	141	gi 162286738
putative enoyl-CoA hydratase II		A1S_1342	515	T	-2,58	2	10	58	gi 126641388
Nucleotide metabolism									
deoxyuridine 5'-triphosphate nucleotidohydrolase	<i>dut</i>	ABSDF2550	770	T	<i>de novo</i>	2	19	108	gi 169634039
Response to stress									
universal stress family protein		A1S_2072	791	T	-5,40	6	65	465	gi 126642117
universal stress family protein		A1S_2072	802	T	-4,95	7	73	602	gi 126642117
universal stress family protein		A1S_2072	845	T	<i>ND</i>	2	40	231	gi 126642117
universal stress family protein		A1S_2072	846	T	<i>ND</i>	6	65	544	gi 126642117
universal stress family protein		A1S_2072	850	T	<i>ND</i>	5	63	520	gi 126642117
universal stress family protein		A1S_2072	886	T	-7,08	5	63	465	gi 126642117
Regulation of transcription									
nitrogen assimilation regulatory protein P-II 2		A1S_0218	605	M	9,13	2	20	134	gi 126640311
host factor I for bacteriophage Q beta replication, a growth-related protein	<i>hfq</i>	ABSDF1625	632	M	-12,84	2	12	99	gi 169633286

regulatory protein, P-II 2, for
nitrogen assimilation by
glutamine synthetase,
regulates GlnL (NRII) and
GlnE (ATase)

<i>glnK</i>	ABAYE3549	830	T	4,04	8	77	532	gi 169797513
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Translation, ribosomal structure and biogenesis

30S ribosomal protein S1	<i>rpsA</i>	ACIAD2347	97	T	<i>de novo</i>	7	17	322	gi 50085438
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elongation factor Tu	<i>tuf1/tuf2</i>	A1S_0279/A1S_0869	157	M	3,94	3	12	115	gi 162286746
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phenylalanyl-tRNA synthetase alpha-subunit		A1S_0601	391	T	<i>de novo</i>	21	71	143	gi 126640670
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50S ribosomal protein L10	<i>rplJ</i>	ABSDF3245	563	M	2,00	3	21	189	gi 16963459
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50S ribosomal protein L4	<i>rplD</i>	A1S_3079	666	T	<i>de novo</i>	4	22	253	gi 126643094
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30S ribosomal protein S15	<i>rpsO</i>	A1S_0360	841	T	<i>ND</i>	2	28	82	gi 126640438
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30S ribosomal protein S15	<i>rpsO</i>	A1S_0360	842	T	-4,54	3	58	118	gi 126640438
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Others

oxidoreductase		A1S_1181	406	T	4,03	18	52	89	gi 126641229
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putative protease		A1S_2785	487	M	-3,01	10	68	78	gi 126642815
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short chain dehydrogenase		ABSDF0043	559	T	-2,95	7	37	375	gi 169632063
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putative carbonic anhydrase		A1S_0984	614	T	-2,4	4	29	132	gi 126641034
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putative protease		A1S_2785	680	T	-2,22	3	18	136	gi 193078237
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putative oxidoreductase		A1S_1929	699	T	-3,41	1	7	61	gi 126641974
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hypothetical protein A1S_3149		A1S_3149	844	T	<i>ND</i>	2	17	94	gi 126643164
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Unknown function

putative protein (DcaP-like)	<i>dcaP-like</i>	A1S_2753	161	M	2,87	2	6	109	gi 126642784
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hypothetical protein A1S_0015		A1S_0015	406	M	2,77	3	7	125	gi 126640130
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hypothetical protein A1S_2406	A1S_2406	493	M	-3,71	2	8	100	gi 126642443
hypothetical protein A1S_2843	A1S_2843	800	T	-4,84	5	33	247	gi 193078285

a) Refer to membrane enriched (M) and total (T) protein fractions

b) Positive values indicates protein up-regulation with the fold-change calculated using the ratio SA-treated/non-treated samples. Negative values indicate protein down-regulation with fold-change calculated using the ratio non- treated/SA-treated samples. de novo: protein spot detected on SA-treated samples only; ND: protein spot detected on non-treated samples only

c) The minimum score value considered for protein identification through MASCOT was 58

**blood isolate of Escherichia coli*