

TABLE A1. Genes with significantly increased expression of at least 2.5-fold in this study¹

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
Adaption to atypical conditions					
SA0483	<i>clpC</i>	endopeptidase	1.2	2.7	6.6
SA0659		hypothetical protein, similar to CsbB stress response protein	2.1	3.5	3.0
SA0723	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit homologue	1.3	3.0	3.4
SA0755		hypothetical protein, similar to general stress protein 170	1.7	4.0	2.8
SA0835	<i>clpB</i>	ClpB chaperone homologue	1.5	6.9	16.4
SA1146	<i>bsaA</i>	glutathione peroxidase	2.1	2.7	2.7
SA1410	<i>grpE</i>	GrpE protein	0.9	3.1	5.3
SA1549		hypothetical protein, similar to serine proteinase Do, heat-shock protein htrA	7.1	4.6	5.6
SA2175		hypothetical protein, similar to small heat shock protein	2.4	3.0	3.1
SA2336	<i>clpL</i>	ATP-dependent Clp proteinase chain clpL	0.9	4.0	1.3
Cell division					
SA1023	<i>ftsL</i>	cell division protein	2.4	1.6	3.0
Cell wall related genes					
SA0205		hypothetical protein, similar to lysostaphin precursor	6.0	4.5	13.6
SA0244		hypothetical protein, similar to teichoic acid biosynthesis protein F	1.6	1.4	2.8
SA0265	<i>lytM</i>	peptidoglycan hydrolase	4.0	2.1	1.7
SA0638	<i>bacA</i>	bacitracin resistance protein (putative undecaprenol kinase) homologue	3.0	1.9	1.8
SA1103	<i>uppS</i>	undecaprenyl pyrophosphate synthetase	2.5	3.0	2.0
SA1266		hypothetical protein, similar to cell wall enzyme EbsB	3.4	1.9	3.7
SA1283	<i>pbp2</i>	penicillin binding protein 2	3.4	2.3	3.5
SA1691	<i>sgtB</i>	hypothetical protein, similar to penicillin-binding protein 1A/1B	13.1	8.8	9.7
SA1926	<i>murZ</i>	UDP-N-acetylglucosamine 1-carboxylvinyl transferase 2	3.2	4.4	6.1
SA2481		conserved hypothetical protein	2.4	3.5	7.0
Detoxification					
SA0128	<i>sodM</i>	superoxide dismutase	1.0	X	1.0
SA0681		hypothetical protein, similar to multidrug resistance protein	1.2	3.1	1.0
SA1170	<i>kata</i>	Catalase	1.6	2.7	1.9
SA1238		hypothetical protein, similar to tellurite resistance protein	2.6	3.2	3.3
SA1382	<i>sodA</i>	superoxide dismutase SodA	1.1	3.0	1.8
DNA replication, modification, recombination and repair					
SA1282	<i>recU</i>	recombination protein U homologue	3.6	2.5	2.5
SA1313		probable ATP-dependent DNA helicase RecQ	2.0	2.2	2.7
SA1485	<i>radC</i>	truncated hypothetical protein, similar to DNA repair protein	1.5	1.4	6.3
SA1711		hypothetical protein, similar to DNA-damage inducible protein P	2.2	1.6	3.4
SA2335	<i>adaB</i>	probable methylated DNA-protein cysteine methyltransferase	1.7	2.8	2.2
Membrane bioenergetics (electron transport chain and ATP synthase)					
SA0211		hypothetical protein, similar to NADH-dependent dehydrogenase	2.2	1.3	4.0
SA0411	<i>ndhF</i>	NADH dehydrogenase subunit 5	1.6	1.0	2.9
SA0817		hypothetical protein, similar to NADH-dependent flavin oxidoreductase	2.1	3.4	2.4
SA1221		thioredoxine reductase	1.2	2.6	1.2
SA2324		hypothetical protein, similar to thioredoxin	1.3	2.6	3.0
Metabolism of amino acids					
SA0011		hypothetical protein, similar to homoserine-o-acetyltransferase	1.6	2.0	2.8
SA0430	<i>gltB</i>	glutamate synthase large subunit	2.8	2.0	1.3
SA0471	<i>cysK</i>	cysteine synthase (o-acetylserine sulfhydrylase) homologue	1.6	3.4	1.8
SA0512	<i>ilvE</i>	branched-chain amino acid aminotransferase homologue	2.1	2.5	2.1
SA0829		hypothetical protein, similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase	2.1	3.2	3.1
SA0902		HisC homologue	2.2	1.8	4.2
SA0942	<i>pdfI</i>	formylmethionine deformylase homologue	1.7	1.6	2.9
SA1164	<i>dhoM</i>	homoserine dehydrogenase	2.5	2.7	6.2
SA1165	<i>thrC</i>	threonine synthase	1.6	2.0	3.9

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TABLE A1 - Continued

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA1166	<i>thrB</i>	homoserine kinase homologue	1.4	1.7	3.9
SA1216		hypothetical protein, similar to oligoendopeptidase	1.8	1.7	2.8
SA1226	<i>asd</i>	aspartate semialdehyde dehydrogenase	2.2	3.8	2.2
SA1227	<i>dapA</i>	dihydrodipicolinate synthase	2.3	3.0	2.0
SA1228	<i>dapB</i>	dihydrodipicolinate reductase	2.3	2.6	1.9
SA1232	<i>lysA</i>	diaminopimelate decarboxylase	2.1	2.4	2.7
SA1531	<i>ald</i>	alanine dehydrogenase	2.1	1.5	4.2
SA1545	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	2.1	1.6	2.8
SA1861	<i>ilvC</i>	alpha-keto-beta-hydroxyacyl reductoisomerase	1.9	2.5	1.2
SA2341	<i>rocA</i>	1-pyrroline-5-carboxylate dehydrogenase	1.2	1.4	3.1
Metabolism of carbohydrates					
SA0528		hypothetical protein, similar to hexulose-6-phosphate synthase	1.5	3.4	3.3
SA0658		hypothetical protein, similar to plant-metabolite dehydrogenases	1.5	3.3	2.6
SA0958		myo-inositol-1(or 4)-monophosphatase homologue	1.8	3.1	3.1
SA1142	<i>glpD</i>	aerobic glycerol-3-phosphate dehydrogenase	1.4	2.0	3.8
SA1566		endo-1,4-beta-glucanase homologue	2.0	2.9	2.4
SA1599		hypothetical protein, similar to transaldolase	1.7	2.7	3.1
SA1736	<i>aldH</i>	aldehyde dehydrogenase	2.0	2.3	3.3
SA1924		hypothetical protein, similar to aldehyde dehydrogenase	1.3	3.4	2.4
SA1925		conserved hypothetical protein	3.5	3.8	4.7
SA2104		hypothetical protein, similar to suppressor protein SuhB	1.4	2.0	2.9
SA2266		hypothetical protein, similar to oxidoreductase	2.0	3.4	1.6
SA2346		hypothetical protein, similar to D-specific D-2-hydroxyacid dehydrogenase ddh homologue	1.9	2.2	3.8
SA2490		hypothetical protein, similar to N-hydroxyarylamine O-acetyltransferase	3.6	6.0	5.4
Metabolism of coenzymes and prosthetic groups					
SA0915	<i>folD</i>	FolD bifunctional protein	1.3	2.7	1.8
SA2412		hypothetical protein, similar to uroporphyrin-III C-methyltransferase	1.9	2.3	2.7
SA2438		hypothetical protein, similar to N-carbamoylsarcosine amidohydrolase	2.3	2.7	3.7
Metabolism of lipids					
SA0534	<i>vraB</i>	acetyl-CoA c-acetyltransferase	18.5	8.5	12.9
SA0572		hypothetical protein, similar to esterase/lipase	0.9	3.3	1.8
SA1435		hypothetical protein, similar to acetyl-CoA carboxylase (biotin carboxyl carrier subunit), <i>accB</i> homologue	0.9	1.3	3.4
SA1542		hypothetical protein, similar to glycerophosphoryl diester phosphodiesterase	2.3	2.8	4.6
SA2240		hypothetical protein, similar to para-nitrobenzyl esterase chain A	1.8	4.1	2.2
Metabolism of nucleotides and nucleic acids					
SA0864		GTP pyrophosphokinase	1.6	1.8	2.8
SA1172		hypothetical protein, similar to GMP reductase	1.8	3.0	2.4
SA1308		30S ribosomal protein S1	2.0	3.5	3.2
SA2297		hypothetical protein, similar to GTP-pyrophosphokinase	9.1	14.1	10.3
Metabolism of phosphate					
SA1237		hypothetical protein, similar to 5-bromo-4-chloroindolyl phosphate hydrolysis protein XpaC	2.5	4.1	6.0
SA2301		hypothetical protein, similar to alkaline phosphatase	2.7	2.7	3.3
Pathogenic factors (toxins and colonization factors)					
SA0382	<i>set6</i>	exotoxin 6 [Pathogenicity island SaPI _n 2]	2.4	2.7	5.1
SA0610		hypothetical protein, similar to lipase LipA	1.2	0.7	3.9
SA0909	<i>fntA</i>	FntA, autolysis and methicillin resistant-related protein	9.3	3.8	6.3
SA2006		hypothetical protein, similar to MHC class II analogue	3.4	7.3	4.4
SA2323		conserved hypothetical protein	1.9	2.4	2.9
Phage-related functions					
SA1760		holin homologue [Bacteriophage phiN315]	3.8	3.2	17.5

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TABLE A1 - Continued

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
Protein modification, folding and secretion					
SA0825	<i>spsA</i>	type-I signal peptidase	2.2	1.4	3.9
SA0826	<i>spsB</i>	type-1 signal peptidase 1B	2.4	1.5	2.9
SA1257		peptide methionine sulfoxide reductase MsrA2	6.0	11.0	17.1
SA1530		Xaa-Pro dipeptidase homologue	1.8	3.1	2.2
SA1409	<i>dnaK</i>	DnaK protein	0.9	2.1	4.6
SA1659	<i>prsA</i>	peptidyl-prolyl cis/trans isomerase homologue	10.8	18.1	33.3
SA1836	<i>groEL</i>	GroEL protein	1.2	3.9	4.5
Protein transport and binding					
SA0166		hypothetical protein, similar to nitrate transporter	2.0	2.4	2.6
SA0531	<i>proP</i>	proline/betaine transporter homologue	2.4	2.7	0.6
SA0640		hypothetical protein, similar to ABC transporter required for expression of cytochrome bd	1.6	1.5	2.6
SA0677		hypothetical protein, similar to choline transport ATP-binding protein	1.2	1.1	2.8
SA0769		ABC transporter ATP-binding protein homologue	0.9	1.4	3.6
SA0845	<i>oppB</i>	oligopeptide transport system permease protein	1.4	3.6	3.5
SA0846		hypothetical protein, similar to oligopeptide transport system permease protein OppC	1.8	3.1	3.4
SA0847	<i>oppD</i>	oligopeptide transport system ATP-binding protein OppD homologue	1.5	3.0	2.6
SA0848	<i>oppF</i>	oligopeptide transport system ATP-binding protein OppF homologue	2.3	3.9	2.1
SA1255		PTS system, glucose-specific enzyme IIA component	4.7	10.7	13.1
SA1478		hypothetical protein, similar to transporter PAB2175 from <i>Pyrococcus abyssi</i>	3.8	3.7	4.9
SA1654		hypothetical protein, similar to ABC transporter EcsB	2.3	2.0	2.9
SA1655		ABC transporter EcsA homologue	1.5	2.4	5.1
SA1848	<i>nrgA</i>	probabale ammonium transporter	1.4	1.4	4.1
SA1948	<i>czrB</i>	cation-efflux system membrane protein homologue	0.9	1.9	2.7
SA2112		hypothetical protein, similar to sodium-dependent transporter	1.9	1.3	2.9
SA2114	<i>glvC</i>	PTS system, arbutin-like IIBC component	3.7	5.6	4.7
SA2148		hypothetical protein, similar to membrane protein	1.4	1.6	4.1
SA2396		hypothetical protein, similar to amino acid transporter	1.9	1.3	3.0
SA2416		hypothetical protein, similar to ABC transporter (ATP-binding protein)	2.3	2.3	2.7
SA2492	<i>vraD</i>	hypothetical protein, similar to ABC transporter	59.4	72.2	52.7
SA2493	<i>vraE</i>	hypothetical protein, similar to ABC transporter (permease)	52.7	39.6	42.4
RNA synthesis - regulation					
SA0480	<i>ctsR</i>	transcription repressor of class III stress genes homologue	1.1	4.2	5.0
SA1195	<i>msrR</i>	peptide methionine sulfoxide reductase regulator MsrR	4.2	3.6	5.5
SA1411	<i>hrcA</i>	Heat-inducible transcriptional repressor	1.3	3.3	5.1
SA1700	<i>vraR</i>	two-component response regulator	13.3	8.0	17.3
SA1947	<i>czrA</i>	repressor protein	1.2	2.5	3.5
SA2103		hypothetical protein, similar to lyt divergon expression attenuator LytR	6.4	6.1	8.0
SA2159		hypothetical protein, similar to transcription repressor of sporulation, septation and degradation PaiA	1.8	2.1	3.4
SA2296		hypothetical protein, similar to transcriptional regulator, MerR family	8.1	10.4	5.5
SA2458	<i>icaR</i>	<i>ica</i> operon transcriptional regulator IcaR	1.4	2.6	1.6
Sensors (signal transduction)					
SA1701	<i>vraS</i>	two-component sensor histidine kinase	11.7	8.9	17.0
Transformation competence					
SA0857		hypothetical protein, similar to negative regulator of genetic competence MecA	3.0	3.4	7.0
Hypothetical proteins					
SA0165		hypothetical protein, similar to alpha-helical coiled-coil protein SrpF	1.8	3.4	3.5
SA0192		hypothetical protein, similar to ABC transporter ATP-binding protein	23.6	31.7	26.6
SA0358		conserved hypothetical protein	10.6	15.4	39.3
SA0359		conserved hypothetical protein	1.9	6.1	4.3

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TABLE A1 - *Continued*

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA0481		conserved hypothetical protein	1.8	5.3	8.0
SA0482		hypothetical protein, similar to creatine kinase	1.2	4.5	5.8
SA0509		conserved hypothetical protein	1.1	2.8	0.8
SA0529		conserved hypothetical protein	1.4	3.0	3.7
SA0530		hypothetical protein, similar to indigoidine synthesis protein	2.5	2.4	1.3
SA0535	<i>vraC</i>	hypothetical protein	25.7	11.3	18.9
SA0536		hypothetical protein	30.2	17.1	26.6
SA0591		hypothetical protein	11.3	8.9	10.9
SA0608		hypothetical protein	2.7	3.8	9.2
SA0611		hypothetical protein	1.2	0.8	4.6
SA0612		conserved hypothetical protein	2.0	2.5	2.4
SA0637		conserved hypothetical protein	2.5	4.0	1.5
SA0647		hypothetical protein	2.3	1.2	3.6
SA0648		conserved hypothetical protein	2.4	1.5	3.6
SA0707		conserved hypothetical protein	4.8	9.7	2.5
SA0721		conserved hypothetical protein	1.0	3.1	1.9
SA0725		conserved hypothetical protein	2.9	2.9	1.8
SA0750		conserved hypothetical protein	1.9	1.7	4.9
SA0770		conserved hypothetical protein	0.8	1.2	3.8
SA0771		conserved hypothetical protein	1.2	1.4	2.8
SA0772		conserved hypothetical protein	2.4	4.5	0.8
SA0782		conserved hypothetical protein	2.1	1.6	2.9
SA0824		conserved hypothetical protein	4.1	2.4	3.9
SA0833		conserved hypothetical protein	1.8	2.6	1.8
SA0856		conserved hypothetical protein	2.0	2.6	2.1
SA0903		conserved hypothetical protein	3.2	1.4	5.3
SA0908		conserved hypothetical protein	2.2	1.5	3.1
SA0914		hypothetical protein, similar to chitinase B	14.2	3.9	15.3
SA0931		hypothetical protein	4.9	3.2	6.2
SA0943		conserved hypothetical protein	3.2	3.2	4.5
SA0957		conserved hypothetical protein	1.8	2.2	3.2
SA0962		conserved hypothetical protein	1.8	1.4	2.8
SA1018		conserved hypothetical protein	1.7	2.2	3.0
SA1019		conserved hypothetical protein	3.9	6.9	6.5
SA1022		conserved hypothetical protein	2.2	2.1	2.8
SA1050		conserved hypothetical protein	2.0	2.6	1.1
SA1173		conserved hypothetical protein	2.7	2.8	3.7
SA1185		conserved hypothetical protein	2.0	1.9	3.2
SA1186		conserved hypothetical protein	1.9	1.4	3.4
SA1256		conserved hypothetical protein	7.9	16.1	18.8
SA1280		conserved hypothetical protein	1.7	2.8	2.8
SA1281		conserved hypothetical protein	1.9	3.0	2.9
SA1293		conserved hypothetical protein	1.7	2.3	3.5
SA1419		conserved hypothetical protein	1.3	1.4	4.6
SA1436		conserved hypothetical protein	0.7	1.0	3.4
SA1476		hypothetical protein	11.5	11.3	15.9
SA1532		conserved hypothetical protein	2.5	9.1	5.5
SA1543		conserved hypothetical protein	2.8	3.9	6.0
SA1544		hypothetical protein, similar to soluble hydrogenase 42 kD subunit	1.8	2.0	4.9
SA1546		hypothetical protein	2.3	1.7	3.2
SA1606		plant metabolite dehydrogenase homologue	1.9	3.5	2.6
SA1649		conserved hypothetical protein	1.9	1.1	3.0

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TABLE A1 - *Continued*

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA1680		conserved hypothetical protein	2.3	2.7	3.0
SA1682		conserved hypothetical protein	2.4	2.9	1.8
SA1686		conserved hypothetical protein	2.1	2.1	3.5
SA1690		conserved hypothetical protein	2.0	2.1	4.0
SA1692		conserved hypothetical protein	1.3	3.1	0.8
SA1702		conserved hypothetical protein	10.4	9.4	12.2
SA1703		hypothetical protein	31.6	24.8	45.4
SA1712		conserved hypothetical protein	24.7	21.0	29.4
SA1743		hypothetical protein	2.7	4.3	2.6
SA1942		conserved hypothetical protein	1.7	3.7	2.5
SA1990		conserved hypothetical protein	1.9	2.6	3.9
SA2004		conserved hypothetical protein	2.1	2.2	2.5
SA2049		hypothetical protein	4.3	5.8	6.5
SA2113		hypothetical protein	14.9	11.8	11.4
SA2138		conserved hypothetical protein	3.1	4.2	5.3
SA2139		hypothetical protein	2.7	2.8	3.4
SA2146	<i>tcaA</i>	TcaA protein	3.3	1.6	4.0
SA2158		hypothetical protein, similar to TpgX protein	2.1	2.7	2.3
SA2220		conserved hypothetical protein	7.0	12.2	21.4
SA2221		hypothetical protein	25.6	18.3	42.7
SA2366		conserved hypothetical protein	0.9	2.7	1.1
SA2367		conserved hypothetical protein	1.0	3.3	1.1
SA2480	<i>drp35</i>	drug responsive protein 35	2.7	3.4	2.8

¹ Significant changes of gene expression were determined by implementing SAM (significance analysis of microarrays; <http://www-stat.stanford.edu/~tibs/SAM/>).

² Fold change in transcript level indicated as mean of the “median of ratios” compared to control cells. Fold change in bold = classified as “significantly” regulated in this strain by SAM. “X” indicates the deletion of this ORF in the respective strain according to Reipert et al. (2003).