

AirSR, a [2Fe-2S] Cluster-Containing Two-Component System, Mediates Global Oxygen Sensing and Redox Signaling in *Staphylococcus aureus*

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Supporting Information

EXPERIMENTAL METHODS

Electrophoretic Mobility Shift Assays (EMSA). DNA probes corresponding to the promoter region of three genes (*agr*, *sae*, and *cap5A*) were PCR-amplified from *S. aureus* chromosomal DNA using primers shown in Table S2. The various amount of AirR was incubated with 2 ng of 5'- γ -³²P-end labeled DNA probe in 25 μ l of the gel shift loading buffer (10 mM Tris-HCl, pH = 7.4, 50 mM KCl, 5 mM MgCl₂, 10% Glycerol, and 3 μ g/ml sheared salmon sperm DNA). After being incubated at room temperature for 10 min, the samples were analyzed by 6% polyacrylamide gel electrophoresis (100V for pre-run, 85 V for 85 min for sample separation). The gels were dried and subjected to autoradiography on a phosphor screen (BAS-IP, Fuji).

SUPPORTING FIGURE CAPTIONS

Figure S1. X-band EPR spectrum of AirS isolated from *E. coli* after dithionite reduction. Simulation of this signal gives $g = [2.025, 1.917, 1.872]$, which is identical to the 35 GHz Q-band result ($g = [2.023, 1.915, 1.870]$) within experimental and simulation precision.

Figure S2. Quantitative analysis of the X-band EPR spectra at 17 K of the isolated AirS and the reconstituted AirS in comparison to the standard *Aae* Fd1. (A) Quantitative comparison of the X-band spectra shows that the isolated, dithionite reduced AirS (40 μM) contains approximately 15–25 μM of $[2\text{Fe-2S}]^+$ (38-62%), and that the reconstituted AirS (13 μM) contains 10–15 μM of $[2\text{Fe-2S}]^+$ (77-115%). (B) SDS-PAGE analysis shows the relative amounts of the isolated and the reconstituted AirS.

Figure S3. Effects of atmospheric O_2 on the autokinase activity of the reconstituted AirS. The freshly reconstituted AirS was bubbled with air for 3 min or 1 h, followed by the addition of $\gamma\text{-}^{32}\text{P-ATP}$. The phosphorylation reactions were incubated inside anaerobic chamber at room temperature. At the indicated time points (2 min, and 5 min) aliquots of 10 μl of the reaction mixture were taken and quenched with 10 μl of 2 \times SDS loading buffer. The samples were analyzed by SDS-PAGE followed by autoradiography.

Figure S4. The *airSR* loci in the ΔairS mutant (A) and ΔairR mutant (B). The *bursa aurealis* transposon insert is shown as a reversed triangle.

Figure S5. AirR binds to the promoter regions of *agr* (A), *sae* (B), and *cap5A* (C). In a typical assay, 2 ng of 5'- $\gamma\text{-}^{32}\text{P}$ -end labeled DNA probe was incubated with the indicated concentration of protein in the presence of 3 $\mu\text{g/ml}$ salmon sperm DNA at room temperature for 10 minutes. Free DNA was indicated by an arrow.

Figure S6. No growth defect was observed in Newman *airS* antisense strain (Newman/pYJ335-anti-*airS*) during anhydrotetracycline (ATc) induction. Overnight cultures of *S. aureus* were serially diluted (10-fold) and plated onto TSA-chloramphenicol plates with or without ATc (1 $\mu\text{g/ml}$) and incubated at 37°C for 36 h. The strain Newman carrying empty pYJ335 (Newman/pYJ335) was used as a control.

SUPPORTING FIGURES

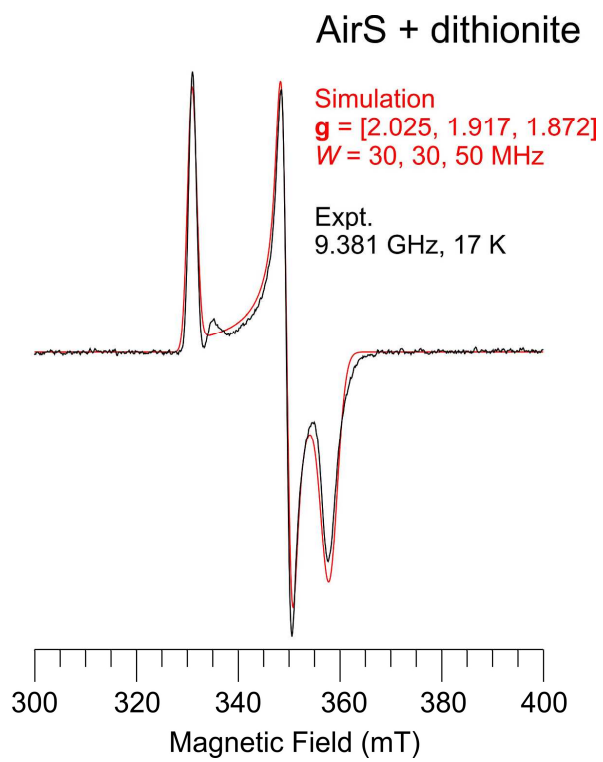


Figure S1. Sun et al

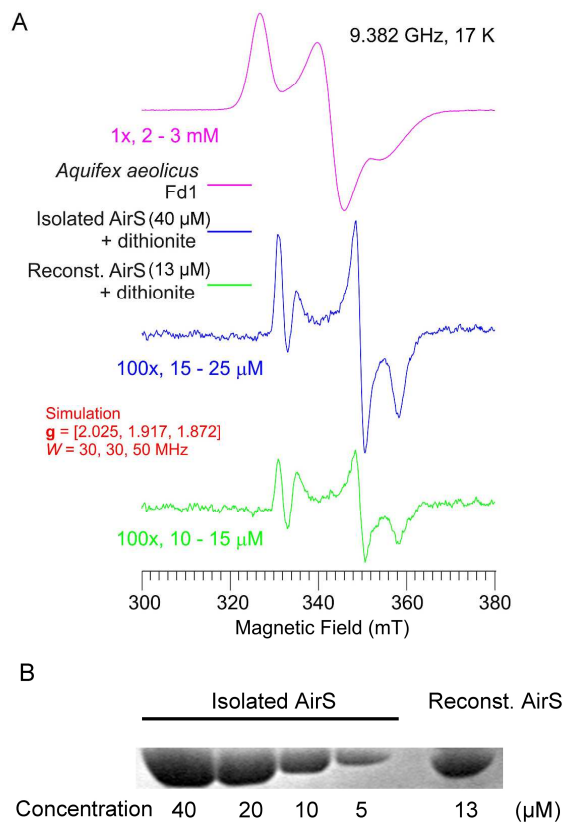


Figure S2. Sun et al

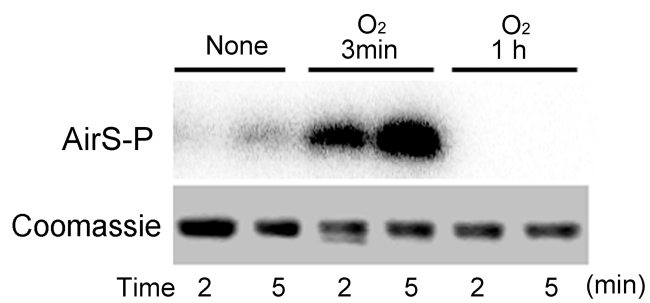


Figure S3. Sun et al

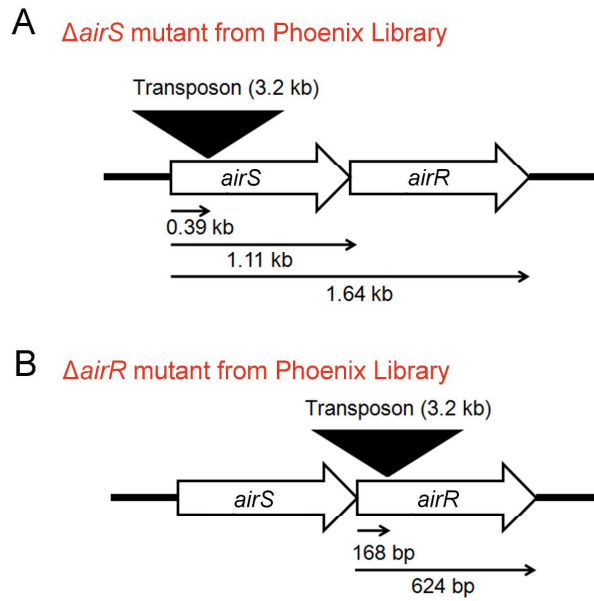


Figure S4. Sun et al

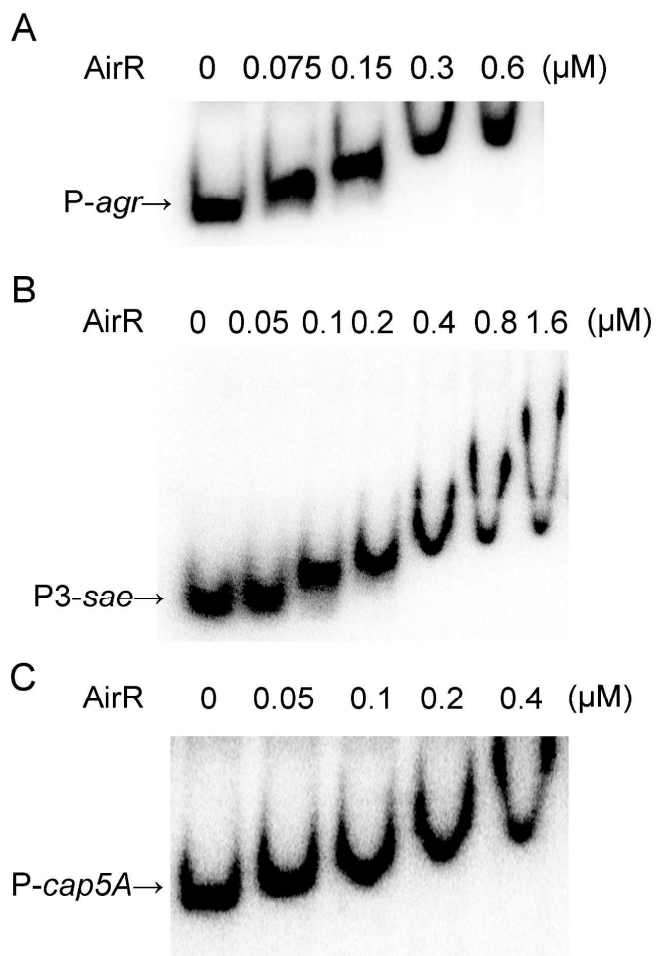


Figure S5. Sun et al



Figure S6. Sun et al

SUPPORTING TABLES

Table S1. Bacterial strains and plasmids used in this study

Strain/Plasmid	Relevant Characteristics	Source
<i>E. coli</i>		
DH5 α		Stratagene
BL21 star(DE3)		Invitrogen
<i>S. aureus</i>		
RN4220	restriction deficient, prophage-cured	1
Newman	a clinical isolate	2
Newman Δ <i>airR</i>	strain Newman with the <i>bursa aurealis</i> transposon insertion in <i>airR</i> , Em ^r	Phoenix library 3
Newman Δ <i>airS</i>	strain Newman with the <i>bursa aurealis</i> transposon	Phoenix library

	insertion in <i>airS</i> , Em ^r	3
Plasmids		
pCL55	single-copy integration plasmid, Cmr	4
pCL55- <i>airSR</i>	pCL55 carrying <i>airSR</i> operon	this study
pYJ335	Tet-inducible promoter; Ap ^r in <i>E. coli</i> ; Cm ^r in <i>S. aureus</i>	5
pYJ335-anti- <i>airS</i>	pYJ335 carrying antisense <i>airS</i> (353-bp)	6
pMCSG7	Ligation-independent-cloning (LIC) vector	7

Em^r: resistant to erythromycin; Cm^r, resistant to chloramphenicol.

Table S2. Primers used in this study

Primer	Sequence	Application
<i>capA</i> -F	5' TTTTATCTAAAGCAGACGGTACAGC 3'	qRT-PCR
<i>capA</i> -R	5' AAATCCACTTTTGATGAACGATATT 3'	qRT-PCR
<i>spa</i> -F	5'GGTACATTACTTATATCTGGTGGCG 3'	qRT-PCR
<i>spa</i> -R	5' TCAACATATCGACGTCATGATTACT 3'	qRT-PCR
<i>RNAIII</i> -F	5' ACAAGATATCATTTCAACAATCGGT3'	qRT-PCR
<i>RNAIII</i> -R	5' CTTTGATCCATAGCCACAATGTAAT3'	qRT-PCR
<i>hlgC</i> -F	5' TACAAAGTGGATTAAACCCTTCATT3'	qRT-PCR
<i>hlgC</i> -R	5' AGCGCAAGAGATAAGAAAATACCTA3'	qRT-PCR
<i>airSR</i> -BamHI -F	5'GTGTACAGGATCCCTTAAGTCATTAAGTTTTCTGGTAT T3'	Complementa tion test

<i>iscS</i> -F-LIC	5'TACTTCCAATCCAATGCCATGGAAATTTATGCAGATTATGCTG3'	IscS cloning
<i>iscS</i> -R-LIC	5'TTATCCACTTCCAATGTTATTATGACTCCTCCTTAAATTTAAAATAT3'	IscS cloning
<i>airR</i> -F-LIC	5'TACTTCCAATCCAATGCCATGAACAAAGTAATATTAGTAGATGAC3'	AirR cloning
<i>airR</i> -R-LIC	5'TTATCCACTTCCAATGTTACTAAATCAACTTATTTTCCATTGCATAAATTG3'	AirR cloning
<i>airS</i> -F-LIC	5'TACTTCCAATCCAATGCCATGGAACAAAGGACGCGACTAGCTTTATTA AAAAG	AirS cloning
<i>airS</i> -R-LIC	5'TTATCCACTTCCAATGTTACTATTTTATAGGAATTGTGAATTGTATTTG3'	AirS cloning
<i>airSC79S/C8</i> 1S-F	5'CTATATTAAAGATGGGTCTTCTTGGTCTGTGAAAGCATT TAATCAAC3'	Mutagenesis
<i>airSC79S/C8</i> 1S-R	5'GTTGATTAAATGCTTTCACAGACCAAGAAGACCCATCTTT AATATAG3'	Mutagenesis
<i>Cap5A-F</i>	5'TCATCTAACTCACCTGAAATTACAAAA3'	EMSA
<i>Cap5A-R</i>	5'TTCCATTATTTACCTCCCTTAAAAA3'	EMSA
<i>agr-F</i>	5'CATTAAAACATGCTAAAAGCATTATTTTCC3'	EMSA
<i>agr-R</i>	5'CACCACTCTCCTCACTGTCATTATACGATTTAG3'	EMSA
<i>sae-P3-F</i>	5'GTCAGAATTCTTATTGTGGCAAAAGGTTTATAAA3'	EMSA
<i>sae-P3-R</i>	5'GTCATCTAGACAATTTGATAAGTTAAGTTTAAAA3'	EMSA
anti- <i>airS</i> -F	5' CTAGGAAATGCTTTAGAGG CTAAG 3'	Antisense <i>airS</i>
anti- <i>airS</i> -R	5' TGAATTGGAGCGATTTGATGGAAC 3'	Antisense

		<i>airS</i>
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Table S3. Genes differentially expressed in mid-exponential phase in *S. aureus airR* mutant compared to wild-type Newman.

Gene name (synonym)	Function/similarity	Transcriptome analysis
		<i>ΔairR</i> /Newman expression ratio
Virulence/Defence/Drug resistance		
NWMN_0095	<i>cap5A</i> capsular polysaccharide biosynthesis protein Cap5A	4.92
NWMN_0096	<i>cap5B</i> capsular polysaccharide biosynthesis protein Cap5B	4.51
NWMN_0097	<i>cap5C</i> capsular polysaccharide biosynthesis protein Cap5C	2.85
NWMN_0098	<i>cap5D</i> capsular polysaccharide biosynthesis protein Cap5D	4.31
NWMN_0099	<i>cap5E</i> capsular polysaccharide biosynthesis protein Cap5E	3.08
NWMN_0101	<i>capF</i> capsular polysaccharide synthesis enzyme Cap5F	2.77
NWMN_0102	<i>cap5G</i> capsular polysaccharide biosynthesis protein Cap5G	3.24
NWMN_0103	<i>capI</i> capsular polysaccharide synthesis enzyme Cap5I	2.52
NWMN_0104	<i>capJ</i> capsular polysaccharide synthesis enzyme Cap5J	2.37
NWMN_0105	<i>capK</i> capsular polysaccharide synthesis enzyme Cap5K	2.10
NWMN_0210	<i>lytM</i> peptidoglycan hydrolase	2.07
NWMN_1084	antibacterial protein	4.06
NWMN_1085	antibacterial protein	3.74
NWMN_1664	arsenical resistance operon repressor homolog	2.19
NWMN_1665	aesenical pump membrane protein homolog	2.01
NWMN_2624	<i>rnalIII</i> delta-hemolysin precursor	3.57
NWMN_0055	<i>spa</i> Immunoglobulin G binding protein A precursor	-2.20
NWMN_0388	superantigen-like protein	-3.94
NWMN_0389	<i>set7</i> superantigen-like protein	-3.11
NWMN_0391	superantigen-like protein	-2.13
NWMN_0394	<i>set11</i> exotoxin 11	-9.13
NWMN_0395	superantigen-like protein	-3.91
NWMN_0396	<i>set13</i> exotoxin 13	-2.55
NWMN_0397	<i>set14</i> exotoxin 14	-2.59
NWMN_0524	<i>sdrD</i> Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	-2.59
NWMN_0758	<i>ssp</i> extracellular ECM and plasma binding protein	-2.55
NWMN_1069	<i>fib</i> fibrinogen-binding protein precursor	-2.16
NWMN_1826	<i>map</i> map protein	-2.54
NWMN_2318	<i>hlgA</i> gamma-hemolysin chain II precursor	-2.16
NWMN_2319	<i>hlgC</i> gamma-hemolysin component C	-2.97
NWMN_2320	<i>hlgB</i> gamma-hemolysin component C precursor	-2.15
NWMN_2529	fibrinogen and keratin-10 binding surface anchored	-2.28

		protein	
NWMN_2537	<i>isaB</i>	immunodominant antigen B	-2.20
NWMN_2439	<i>cidB</i>	Holin-like protein cidB	-2.55
Transcriptional regulation			
NWMN_1946	<i>agrA</i>	accessory gene regulator protein A	1.96
Translation			
NWMN_0509	<i>fusA</i>	translation elongation factor G	-2.39
NWMN_2137	<i>rplF</i>	50S ribosomal protein L6	-2.18
Transporter			
NWMN_2059	<i>mltA</i>	PTS system, mannitol specific IIA component	2.15
NWMN_0118		ABC transporter, permease protein	-2.21
NWMN_1347		amino acid permease	-2.39
Metabolism			
NWMN_1209	<i>glpD</i>	glycerol-3-phosphate dehydrogenase	3.30
NWMN_0933	<i>purE</i>	phosphoribosylaminoimidazole carboxylase, catalytic subunit	2.02
NWMN_1216	<i>glnR</i>	glutamine synthetase repressor	2.09
NWMN_1217	<i>glnA</i>	glutamine-ammonia ligase	2.01
NWMN_1348		threonine dehydratase	-2.26
NWMN_1349	<i>ald</i>	alanine dehydrogenase	-2.21
NWMN_2111		alpha-acetolactate synthase	-4.88
Cell wall/surface protein			
NWMN_2545		putative surface anchored protein	2.03
NWMN_2392		cell wall surface anchor family protein	-2.27
Unknown function			
NWMN_0233		hypothetical protein	2.17
NWMN_0408	<i>lpl5</i>	hypothetical protein	2.30
NWMN_0767		hypothetical protein	1.93
NWMN_0904		hypothetical protein	1.99
NWMN_0995		prophage L54a, antirepressor, putative	2.16
NWMN_1039		amidase	1.87
NWMN_1249		hypothetical protein	2.21
NWMN_1894		hypothetical protein	2.29
NWMN_1913		hypothetical protein	2.03
NWMN_1999		similar to SceD precursor	5.16
NWMN_2109		hypothetical protein	3.11
NWMN_0116		hypothetical protein	-2.33
NWMN_0117		hypothetical protein	-2.99

NWMN_0119	hypothetical protein	-2.14
NWMN_0362	hypothetical protein	-2.23
NWMN_0759	hypothetical protein	-2.62
NWMN_2110	hypothetical protein	-3.54
NWMN_2440	hypothetical protein	-3.12

Table S4. Genes differentially expressed in stationary phase in *S. aureus airR* mutant compared to wild-type Newman.

Gene name (synonym)	Function/similarity	Transcriptome analysis
		$\Delta airR$ /Newman expression ratio
Virulence/Defence/Drug resistance		
NWMN_0095	<i>cap5A</i> capsular polysaccharide biosynthesis protein Cap5A	45.71
NWMN_0096	<i>cap5B</i> capsular polysaccharide biosynthesis protein Cap5B	11.92
NWMN_0097	<i>cap5C</i> capsular polysaccharide biosynthesis protein Cap5C	18.02
NWMN_0098	<i>cap5D</i> capsular polysaccharide biosynthesis protein Cap5D	8.06
NWMN_0099	<i>cap5E</i> capsular polysaccharide biosynthesis protein Cap5E	4.51
NWMN_0101	<i>capF</i> capsular polysaccharide synthesis enzyme Cap5F	5.73
NWMN_0102	<i>capH</i> capsular polysaccharide synthesis enzyme O-acetyl transferase Cap5H	12.99
NWMN_0103	<i>capI</i> capsular polysaccharide synthesis enzyme Cap5I	6.39
NWMN_0104	<i>capJ</i> capsular polysaccharide synthesis enzyme Cap5J	36.27
NWMN_0105	<i>capK</i> capsular polysaccharide synthesis enzyme Cap5K	7.19
NWMN_0106	<i>capL</i> capsular polysaccharide synthesis enzyme Cap5L	3.01
NWMN_0107	<i>cap5</i> capsular polysaccharide biosynthesis protein Cap5M <i>M</i>	6.46
NWMN_0108	<i>capN</i> capsular polysaccharide synthesis enzyme Cap5N	2.45
NWMN_0109	<i>capO</i> capsular polysaccharide synthesis enzyme Cap8O	4.13
NWMN_0110	capsular polysaccharide synthesis enzyme	3.72
NWMN_0196	murein hydrolase regulator LrgA	1.93
NWMN_0197	<i>lrgB</i> antiholin-like protein LrgB	1.94
NWMN_0461	regulatory protein SpoVG	4.64
NWMN_0756	<i>clfA</i> fibrinogen-binding protein A, clumping factor	2.34
NWMN_0761	cold shock protein	2.32
NWMN_0791	hemolysin	1.94
NWMN_1091	<i>pbpA</i> penicillin-binding protein 1	2.32
NWMN_1084	antibacterial protein	3.98
NWMN_1085	antibacterial protein	4.94
NWMN_1184	similar to metallo-beta-lactamase family protein	2.21
NWMN_1709	<i>epiG</i> lantibiotic epidermin immunity protein G	1.85
NWMN_1710	<i>epiE</i> lantibiotic epidermin immunity protein F	2.23

NWMN_1718	<i>lukD</i>	leukotoxin LukD	2.19
NWMN_1826	<i>map</i>	map protein	3.01
NWMN_1873	<i>hlyB</i>	beta hemolysin precursor	2.05
NWMN_2086	<i>asp23</i>	alkaline shock protein 23	4.68
NWMN_2624		delta-hemolysin precursor	3.39
NWMN_0050		putative myosin-crossreactive antigen	-4.17
NWMN_0055	<i>spa</i>	Immunoglobulin G binding protein A precursor	-3.96
NWMN_0166	<i>coa</i>	staphylocoagulase precursor	-3.78
NWMN_0345	<i>ltrA</i>	low temperature requirement protein LtrA	-2.10
NWMN_0388		superantigen-like protein	-3.69
NWMN_0394	<i>set11</i>	exotoxin 11	-3.10
NWMN_0400		superantigen-like protein	-5.68
NWMN_0757		putative staphylocoagulase	-3.72
NWMN_0844	<i>clpB</i>	ClpB chaperone homolog	-2.48
NWMN_1876		staphylococcal complement inhibitor SCIN	-2.12
NWMN_1877		chemotaxis-inhibiting protein CHIPS	-2.50
NWMN_1604		universal stress protein family	-2.80
NWMN_2199	<i>ssaA</i>	secretory antigen precursor SsaA homolog	-2.05
NWMN_2317	<i>sbi</i>	IgG-binding protein SBI	-2.40
NWMN_2319	<i>hlyC</i>	gamma-hemolysin component C precursor	-2.08
NWMN_2398	<i>fnb</i>	fibronectin-binding protein homolog	-3.97
NWMN_2399	<i>fnbA</i>	fibronectin binding protein A	-3.99
NWMN_2461	<i>crtN</i>	squalene synthase	-3.15
<i>Stress-associated genes</i>			
NWMN_0771		OsmC/Ohr family protein	2.01
NWMN_0779		putative thioredoxin	3.42
NWMN_0321		putative oxidoreductase	5.05
NWMN_0930		quinol oxidase polypeptide II QoxA	2.01
NWMN_0980	<i>ctaA</i>	cytochrome oxidase assembly protein	2.09
NWMN_1060	<i>sdhC</i>	succinate dehydrogenase, cytochrome b-558 subunit	3.47
NWMN_1061	<i>sdhA</i>	succinate dehydrogenase	2.27
NWMN_1062	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	1.84
NWMN_1326	<i>odhA</i>	oxoglutarate dehydrogenase	2.00
NWMN_1326	<i>odhA</i>	2-oxoglutarate dehydrogenase E1	2.71
NWMN_1412		glucose-6-phosphate 1-dehydrogenase	1.88
NWMN_1603	<i>ald</i>	alanine dehydrogenase	1.95
NWMN_1659	<i>ribH</i>	riboflavin synthase, beta subunit	3.39
NWMN_1660	<i>ribA</i>	riboflavin biosynthesis protein	2.74
NWMN_1748		similar to iron-sulfur cluster-binding protein	2.06
NWMN_2026		aldehyde dehydrogenase family protein	4.54
NWMN_2060	<i>mitD</i>	mannitol-1-phosphate 5-dehydrogenase	2.41
NWMN_2369		glucose 1-dehydrogenase-like protein	3.18
NWMN_2454	<i>rocA</i>	1-pyrroline-5-carboxylate dehydrogenase	1.89

NWMN_2464		similar to phytoene dehydrogenase	4.34
NWMN_2515		anaerobic ribonucleoside triphosphate reductase	2.06
NWMN_2605		cold shock protein	2.56
NWMN_0071		acetoin reductase	-2.28
NWMN_0077	<i>sodM</i>	superoxide dismutase	-2.19
NWMN_0156		similar to NADH-dependent dehydrogenase	-3.42
NWMN_0175		flavoheмоprotein	-1.79
NWMN_0332		similar to NADH-dependent FMN reductase	-2.00
NWMN_0371	<i>ahpF</i>	alkyl hydroperoxide reductase subunit F	-2.09
NWMN_0372	<i>ahpC</i>	Alkyl hydroperoxide reductase subunit C	-1.95
NWMN_0387		similar to oxidoreductase	-2.18
NWMN_0418		NADH dehydrogenase subunit L	-2.16
NWMN_1199		2-oxoglutarate ferredoxin oxidoreductase subunit beta	-2.73
NWMN_1392		ferredoxin	-2.88
NWMN_1456		superoxide dismutase	-2.19
NWMN_2090		putative zinc-binding dehydrogenase	-2.05
NWMN_2274		pyridine nucleotide-disulfide oxidoreductase	-2.13
NWMN_2299	<i>nasE</i>	assimilatory nitrite reductase	-2.01
NWMN_2300	<i>nirB</i>	nitrite reductase [NAD(P)H], large subunit	-2.12
NWMN_2422		2-hydroxyacid dehydrogenase	-2.10
NWMN_2488	<i>pyrD</i>	dihydroorotate dehydrogenase 2	-2.05
NWMN_2518		sulfite reductase flavoprotein	-2.47

Transcriptional regulation

NWMN_0459	<i>purR</i>	purine operon repressor	2.70
NWMN_0673		similar to CsbB stress response protein	3.26
NWMN_0674	<i>saeS</i>	sensor histidine kinase SaeS	3.00
NWMN_0675	<i>saeR</i>	DNA-binding response regulator SaeR	2.27
NWMN_1327	<i>arlS</i>	sensor histidine kinase protein	2.09
NWMN_1585	<i>phoR</i>	alkaline phosphatase synthesis sensor protein	2.02
NWMN_1415	<i>malR</i>	maltose operon transcriptional repressor	1.85
NWMN_1944	<i>agrD</i>	accessory gene regulator protein D	2.63
NWMN_1971		serine-protein kinase RsbW	2.77
NWMN_1973	<i>rsbU</i>	sigma-B regulation protein	1.87
NWMN_1974		similar to pemK family of DNA-binding proteins	2.23
NWMN_2291		putative response regulator	2.12
NWMN_0056	<i>sarH1</i>	staphylococcal accessory regulator	-2.09
NWMN_0205		putative ribose operon repressor	-3.36
NWMN_0667		transcriptional regulator, DeoR family	-3.99
NWMN_0740		glycolytic operon regulator	-2.45
NWMN_2258	<i>tcaR</i>	transcriptional regulator TcaR	-2.10
NWMN_2404		transcriptional regulator, MerR family	-1.92

Translation

NWMN_0460		translation initiation inhibitor homolog	3.48
NWMN_0008	<i>serS</i>	seryl-tRNA synthetase	3.44
NWMN_1180		putative tRNA pseudouridine synthase B	2.77
NWMN_1401	<i>rluB</i>	ribosomal large subunit pseudouridine synthase B	1.90
NWMN_0023	<i>orfX</i>	rRNA large subunit methyltransferase	-2.62
NWMN_0513		chaperone protein HchA	-2.97
NWMN_0501	<i>rplJ</i>	50S ribosomal protein L10	-2.09
NWMN_0502	<i>rplL</i>	50S ribosomal protein L7/L12	-2.49
NWMN_0721	<i>yfiA</i>	ribosomal subunit interface protein	-3.95
NWMN_1166	<i>rpsB</i>	30S ribosomal protein S2	-1.81
NWMN_2129	<i>rpmJ</i>	50S ribosomal protein L36	-2.13
NWMN_2130	<i>infA</i>	translation initiation factor IF-1	-2.08
NWMN_2134	<i>rpmD</i>	50S ribosomal protein L30	-2.10
NWMN_2135	<i>rpsE</i>	30S ribosomal protein S5	-2.33
NWMN_2136	<i>rplR</i>	50S ribosomal protein L18	-2.44
NWMN_2140	<i>rplE</i>	50S ribosomal protein L5	-1.98
NWMN_2141	<i>rplX</i>	50S ribosomal protein L24	-2.02
NWMN_2142	<i>rplN</i>	50S ribosomal protein L14	-2.40
NWMN_2143	<i>rpsQ</i>	30S ribosomal protein S17	-1.86
NWMN_2146	<i>rpsC</i>	30S ribosomal protein S3	-2.86
NWMN_2147	<i>rplV</i>	50S ribosomal protein L22	-2.44
NWMN_2148	<i>rpsS</i>	30S ribosomal protein S19	-2.29
NWMN_2150		50S ribosomal protein L23	-2.01
NWMN_2153	<i>rpsJ</i>	30S ribosomal protein S10	-1.78

DNA Replication

NWMN_1015		large terminase	1.95
NWMN_1469	<i>recO</i>	DNA repair protein RecO	2.28

Cell wall/surface protein

NWMN_0412		staphylococcal tandem lipoprotein	2.48
NWMN_0523		putative surface anchored protein	2.09
NWMN_0677		putative lipoprotein	3.36
NWMN_0887		similar to cell wall synthesis protein	2.06
NWMN_1394		putative lipoprotein	2.03
NWMN_2270		putative lipoprotein	2.81
NWMN_0076		polysaccharide extrusion protein	-2.32
NWMN_0078		putative surface anchored protein	-3.27
NWMN_0401		putative surface protein	-4.15
NWMN_2392		cell wall surface anchor family protein	-2.22
NWMN_2545	<i>sasF</i>	putative surface anchored protein	-2.92

Metabolism

NWMN_0007	<i>hutH</i>	histidine ammonia-lyase	3.46
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NWMN_0047		similar to aminoacylase	2.70
NWMN_1090	<i>ftsL</i>	cell division protein	2.66
NWMN_0738		cell-division inhibitor	1.97
NWMN_0949	<i>ptsH</i>	phosphocarrier protein HPr	2.24
NWMN_1162	<i>xerC</i>	site-specific recombinase XerC homolog	2.11
NWMN_1163	<i>clpQ</i>	ATP-dependent protease peptidase subunit	2.06
NWMN_2235		arginase family protein	2.78
NWMN_0129		ornithine aminotransferase	-1.92
NWMN_0167		acetyl-CoA acetyltransferase homolog	-2.13
NWMN_0475	<i>cysK</i>	cysteine synthase A	-2.18
NWMN_0486		putative ATP:guanido phosphotransferase	-2.02
NWMN_0668	<i>fruB</i>	fructose 1-phosphate kinase	-2.20
NWMN_0742	<i>pgk</i>	phosphoglycerate kinase	-2.81
NWMN_0743		triosephosphate isomerase	-2.98
NWMN_0744		phosphoglyceromutase	-2.30
NWMN_0745	<i>eno</i>	phosphopyruvate hydratase	-2.55
NWMN_0916	<i>sspC</i>	cysteine protease	-1.93
NWMN_1541	<i>tgt</i>	queuine tRNA-ribosyltransferase	-2.30
NWMN_1587		isocitrate dehydrogenase	-2.96
NWMN_1588	<i>citZ</i>	citrate synthase	-1.99
NWMN_1592	<i>pyk</i>	pyruvate kinase	-2.12
NWMN_1348	<i>ilvA</i>	threonine dehydratase	-2.13
NWMN_2031	<i>pyrG</i>	CTP synthetase	-1.78
NWMN_2131	<i>adk</i>	adenylate kinase	-2.14
NWMN_2205		glycerate dehydrogenase	-1.92
NWMN_2229		dehydrogenase	-1.82
NWMN_2232	<i>hutU</i>	urocanate hydratase	-2.54
NWMN_2315		putative phosphoglycerate mutase	-2.21
NWMN_2416		phospholipase/carboxylesterase family protein	-3.61
NWMN_2437	<i>ptsG</i>	phosphotransferase system, glucose-specific IIBC component	-2.37
NWMN_2448	<i>clpL</i>	putative ATP-dependent protease ATP-binding subunit ClpL	-2.69
NWMN_2494	<i>panD</i>	aspartate 1-decarboxylase precursor	-2.13
NWMN_2495	<i>panC</i>	pantoate--beta-alanine ligase	-1.85
NWMN_2498		similar to alpha-acetolactate decarboxylase	-2.08
NWMN_2540		fructose phosphotransferase system enzyme fruA homolog	-9.04
NWMN_2541	<i>manA</i>	mannose-6-phosphate isomerase, class I	-6.31
NWMN_2571	<i>hisF</i>	imidazole glycerol phosphate synthase subunit hisF	-1.92
NWMN_2572		1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino imidazole-4-carboxamide isomerase	-1.81
NWMN_2592		2-oxoglutarate/malate translocator	-1.81
Transport			
NWMN_0048		putative transporter protein	4.09

NWMN_0054	<i>lctP</i>	L-lactate permease	3.05
NWMN_0057	<i>sirC</i>	iron compound ABC transporter, permease protein SirC	2.01
NWMN_0158	<i>uhpT</i>	sugar phosphate antiporter	2.00
NWMN_0536	<i>proP</i>	proline/betaine transporter homolog	3.28
NWMN_0593		putative monovalent cation/H ⁺ antiporter subunit A	2.72
NWMN_0614		putative nucleoside transporter	1.84
NWMN_0688		similar to ABC transporter ATP-binding protein	2.53
NWMN_1207	<i>glpF</i>	glycerol uptake facilitator	2.21
NWMN_1292		putative oligopeptide transport system permease	1.81
NWMN_1347		amino acid permease	2.04
NWMN_1854		similar to sodium-dependent transporter	2.00
NWMN_2351		putative transport protein	2.16
NWMN_2353		ABC transporter, ATP-binding protein	2.12
NWMN_1717		lantibiotic precursor	1.82
NWMN_0481		pyridoxine biosynthesis protein	4.64
NWMN_0527		similar to poly (glycerol-phosphate) alpha-glucosyltransferase	1.91
NWMN_0554	<i>mvaD</i>	mevalonate diphosphate decarboxylase	2.76
NWMN_1089		S-adenosyl-methyltransferase mraW	2.40
NWMN_0827	<i>rocD</i>	ornithine--oxo-acid transaminase	2.01
NWMN_1155	<i>sucC</i>	succinyl-CoA synthetase subunit beta	2.30
NWMN_1192	<i>pgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	2.68
NWMN_1254	<i>tkt</i>	transketolase	1.79
NWMN_1331		acetyltransferase, GNAT family	2.33
NWMN_1378	<i>ndk</i>	nucleoside diphosphate kinase	2.09
NWMN_1474	<i>phoH</i>	phosphate starvation-induced protein, PhoH family	2.30
NWMN_1441	<i>gcvT</i>	aminomethyltransferase (glycine cleavage system T protein)	3.06
NWMN_1470	<i>era</i>	GTP-binding protein Era	2.25
NWMN_1471	<i>cdd</i>	cytidine deaminase	2.04
NWMN_1472		putative diacylglycerol kinase	2.62
NWMN_1681	<i>pckA</i>	phosphoenolpyruvate carboxykinase	1.90
NWMN_1743	<i>citG</i>	fumarate hydratase, class-II	2.44
NWMN_2056	<i>glmS</i>	D-fructose-6-phosphate amidotransferase	2.02
NWMN_2429		putative L-serine dehydratase	3.59
NWMN_2430		putative beta-subunit of L-serine dehydratase	3.58
NWMN_2431		perfringolysin O regulator protein	3.74
NWMN_0133		glucose-specific PTS transporter protein, IIABC component	-2.05
NWMN_0153		putative sugar transport system permease	-2.01
NWMN_0154		maltose/maltodextrin transport permease homolog	-2.94
NWMN_0251		similar to ABC transporter (ATP-binding protein)	-1.88
NWMN_0177		PTS system, IIIC components	-2.08
NWMN_0322	<i>ulaA</i>	ascorbate-specific PTS system enzyme IIC	-4.34
NWMN_0323		putative sugar-specific PTS component EIIB	-3.79
NWMN_0374		putative sodium:dicarboxylate symporter protein	-1.99

NWMN_0669		PTS transport system, fructose-specific IIBC component	-1.87
NWMN_0702		FecCD transport family protein	-2.95
NWMN_0782		similar to ABC transporter substrate-binding protein	-1.92
NWMN_0813		Na ⁺ /H ⁺ antiporter family protein	-2.38
NWMN_0965	<i>potA</i>	spermidine/putrescine ABC transporter	-1.92
NWMN_1269		sodium:alanine symporter family protein	-2.16
NWMN_1290		oligopeptide transporter putative ATPase domain	-1.82
NWMN_2177	<i>modC</i>	molybdenum transport ATP-binding protein	-2.01
NWMN_2253		putative transport protein	-2.54
NWMN_2279		PTS system, sucrose-specific IIBC component	-1.82
NWMN_2298		tetrapyrrole (corrin/porphyrin) methylase family protein	-2.57
NWMN_2344		putative glycine betaine/carnitine/choline transport system permease protein	-4.38
NWMN_2345	<i>opuC</i> <i>C</i>	glycine betaine/carnitine/choline ABC transporter	-3.26
NWMN_2346	<i>opuC</i> <i>B</i>	putative glycine betaine/carnitine/choline transport system permease protein	-3.14
NWMN_2347	<i>opuC</i> <i>A</i>	glycine betaine/carnitine/choline ABC transporter	-2.58
NWMN_2401		putative gluconate permease	-3.14
NWMN_2595	<i>nixA</i>	high-affinity nickel-transporter	-1.89
Unknown function			
NWMN_0053		hypothetical protein	2.90
NWMN_0135		hypothetical protein	2.43
NWMN_0377		hypothetical protein	3.58
NWMN_0402		hypothetical protein	2.74
NWMN_0413		hypothetical protein	2.29
NWMN_0414		hypothetical protein	3.04
NWMN_0415		hypothetical protein	2.51
NWMN_0450		hypothetical protein	1.91
NWMN_0457		veg protein	2.21
NWMN_0482		hypothetical protein	5.94
NWMN_0542		hypothetical protein	3.00
NWMN_0561		hypothetical protein	2.41
NWMN_0592		phage integrase family protein	4.79
NWMN_0622		hypothetical protein	1.77
NWMN_0687		sulfatase family protein	2.89
NWMN_0710		hypothetical protein	2.41
NWMN_0765		hypothetical protein	2.57
NWMN_0766		hypothetical protein	5.82
NWMN_0767		hypothetical protein	7.03
NWMN_0778		Toprim domain protein	2.80
NWMN_0783		CsbD-like superfamily	5.97

NWMN_0825	hypothetical protein	2.57
NWMN_0885	hypothetical protein	2.09
NWMN_0912	hypothetical protein	1.99
NWMN_0948	hypothetical protein	4.44
NWMN_0956	hypothetical protein	1.88
NWMN_0983	hypothetical protein	1.86
NWMN_0983	hypothetical protein	2.09
NWMN_0984	hypothetical protein	1.99
NWMN_0995	similar to anti-repressor	2.04
NWMN_1017- 1018	hypothetical protein	1.89
NWMN_1068	hypothetical protein	2.54
NWMN_1076	hypothetical protein	1.93
NWMN_1088	<i>mraZ</i> hypothetical protein	1.91
NWMN_1100	hypothetical protein	1.86
NWMN_1190	hypothetical protein	2.25
NWMN_1191	hypothetical protein	2.28
NWMN_1238	hypothetical protein	2.97
NWMN_1263	hypothetical protein	2.45
NWMN_1360	hypothetical protein	1.99
NWMN_1397	hypothetical protein	2.01
NWMN_1473	hypothetical protein	2.24
NWMN_1504	hypothetical protein	3.13
NWMN_1526	hypothetical protein	2.57
NWMN_1527	hypothetical protein	3.79
NWMN_1552	hypothetical protein	2.06
NWMN_1627	acetoin utilization protein	2.15
NWMN_1631	hypothetical protein	2.49
NWMN_1631	hypothetical protein	2.56
NWMN_1632	hypothetical protein	2.27
NWMN_1640	hypothetical protein	1.87
NWMN_1645	hypothetical protein	2.23
NWMN_1709	truncated hypothetical protein	2.66
NWMN_1730	hypothetical protein	2.46
NWMN_1745	hypothetical protein	1.95
NWMN_1746	hypothetical protein	2.38
NWMN_1767	hypothetical protein	2.95
NWMN_1821	hypothetical protein	4.56
NWMN_1914	hypothetical protein	3.04
NWMN_1916	hypothetical protein	1.81
NWMN_1934	hypothetical protein	2.17
NWMN_2005	hypothetical protein	1.86
NWMN_2061	<i>fmtB</i> truncated FmtB protein	2.18
NWMN_2079	hypothetical protein	1.93

NWMN_2087		hypothetical protein	4.59
NWMN_2088		hypothetical protein	2.29
NWMN_2209		hypothetical protein	2.62
NWMN_2352		hypothetical protein	2.29
NWMN_2368		hypothetical protein	3.41
NWMN_2506		putative AMP-binding enzyme	1.99
NWMN_2606		hypothetical protein	2.53
NWMN_2607		hypothetical protein	2.13
NWMN_0032		hypothetical protein	-2.18
NWMN_0051		integral membrane domain protein	-2.95
NWMN_0157		hypothetical protein	-2.36
NWMN_0165		hypothetical protein	-2.15
NWMN_0219		hypothetical protein	-2.49
NWMN_0252		regulatory protein PfoR	-1.89
NWMN_0261		hypothetical protein	-3.15
NWMN_0324		hypothetical protein	-4.68
NWMN_0344		hypothetical protein	-2.12
NWMN_0386		hypothetical protein	-2.23
NWMN_0416		hypothetical protein	-3.95
NWMN_0419		hypothetical protein	-2.91
NWMN_0503		hypothetical protein	-2.60
NWMN_0566		hypothetical protein	-1.91
NWMN_0739		hypothetical protein	-1.98
NWMN_0759		hypothetical protein	-5.33
NWMN_0820	<i>mmhC</i>	hypothetical protein	-2.22
NWMN_0896		hypothetical protein	-3.63
NWMN_0900		hypothetical protein	-2.47
NWMN_1072		hypothetical protein	-2.20
NWMN_1624		hypothetical protein	-3.36
NWMN_1828		hypothetical protein	-2.22
NWMN_1861		hypothetical protein	-2.51
NWMN_1903		phi77 ORF031-like protein	-2.59
NWMN_1908		phiPVL ORF046-like protein	-2.44
NWMN_2039		hypothetical protein	-2.92
NWMN_2254		hypothetical protein	-1.80
NWMN_2265		hypothetical protein	-2.87
NWMN_2266		hypothetical protein	-2.14
NWMN_2282		similar to general stress protein	-2.60
NWMN_2307		hypothetical protein	-2.09
NWMN_2432		hypothetical protein	-1.99
NWMN_2487		hypothetical protein	-2.26
NWMN_2489		hypothetical protein	-2.02
NWMN_2597		hypothetical protein	-2.81

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