

Table S5 Differentially expressed proteins in the 20% NaCl group compared with the control group. The DEPs in Figure 5 with fold change ≥ 2 or ≤ 0.5 are labelled in red.

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1IXJ7	Gamma-hemolysin B subunit HlgB	SAJPND1_02412	0.04
A0A0D1J6H7	Strain SA-120 Contig629, whole genome shotgun sequence	-	0.05
A0A0D6DCF3	Extracellular fibrinogen-binding protein	SAJPND1_01081	0.05
OMP7	77 kDa membrane protein	SACOL2002	0.04
A0A0D6DK32	Extracellular matrix binding protein	SAJPND1_00798	0.05
A0A0D6DFZ4	Leukocidin S subunit LukS	SAJPND1_01995	0.05
A0A077U1D0	Amino acid permease	steT	0.05
A0A0D6DIM1	Ribokinase	SAJPND1_00306	0.08
A0A0D1JXR9	Strain SA-120 Contig630, whole genome shotgun sequence	-	0.09
A0A0D1K3U3	Extracellular fibrinogen-binding protein	QU38_12095	0.10
A7E1C4	Enterotoxin C2 (Fragment)	sec2	0.10
A0A068A489	Inhibitor	scn_2	0.10
A0A0B6XPE8	Pyruvate carboxylase	cfiB_1	0.10
A0A090LXD5	Uncharacterized protein	-	0.10
A0A0D1HN80	Strain SA-120 Contig620, whole genome shotgun sequence	-	0.10
A0A0D6DGW3	Gamma-hemolysin A subunit HlgA	SAJPND1_02409	0.11
SBI	Immunoglobulin-binding protein sbi	sbi	0.11
A0A0D6DFD4	Beta-lactamase regulator protein	SAJPND1_01896	0.11
Q9AFB0	Leukocidin LukS component (Fragment)	-	0.11
A0A0C5HVE0	Pyruvate decarboxylase%3B Alpha-keto-acid decarboxylase	ipdC	0.11
A0A090N157	Alpha-hemolysin	hly	0.11
A0A0D6GYJ2	Alanine dehydrogenase	ald1	0.11
A0A0B6XPE8	Pyruvate carboxylase	cfiB_1	0.12
A0A0B6XL12	Pseudouridine-5'-phosphate glycosidase	psuG	0.13
A0A0D1I054	L-lactate dehydrogenase	ldh	0.13
A0A0B6XMG3	Argininosuccinate synthase	argG	0.14
A0A0D1I054	L-lactate dehydrogenase	ldh	0.14
A0A0E1VRD5	Threonine ammonia-lyase	ilvA	0.14
A0A0E0VS19	Carboxylic ester hydrolase	ST398NM01_2504	0.14
A0A0B6XL12	Pseudouridine-5'-phosphate glycosidase	psuG	0.14
ADH	Alcohol dehydrogenase	adh	0.14
A0A0B6XMG3	Argininosuccinate synthase	argG	0.14
A0A0C5HSI2	Gamma-hemolysin component B	ERS445051_01979	0.15
A0A0D6DGG6	Uncharacterized protein	-	0.15
A0A077TWE9	Lipoprotein	ERS094548_00195	0.15
A0A0E1VQA6	Immunoglobulin-binding protein sbi	sbi	0.15
A7E1C4	Enterotoxin C2 (Fragment)	sec2	0.15
A0A0E0VS19	Carboxylic ester hydrolase	ST398NM01_2504	0.15
Q7DK27	ABC transporter ATP-binding protein	stpA	0.15

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D6DN91	Thymidine phosphorylase	SAJPND1_02113	0.15
A0A0D1HD00	Universal stress protein	uspA	0.15
A0A090LW13	Argininosuccinate lyase	argH	0.15
A0A077U1A4	Oligopeptide transporter putative substrate binding domain protein	opp-1A	0.15
A0A0E1VRD5	Threonine ammonia-lyase	ilvA	0.15
A0A0C5HVE0	Pyruvate decarboxylase%3B Alpha-keto-acid decarboxylase	ipdC	0.16
A0A0D1JQX0	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.17
A0A090LUS6	Lipoprotein	yehR	0.17
A0A0C5HSI2	Gamma-hemolysin component B	ERS445051_01979	0.18
A0A090LW57	ABC transporter, permease protein	SAU060112_100003	0.18
A0A0C2HZY8	Pyrimidine-nucleoside phosphorylase	pdp	0.18
A0A090LW57	ABC transporter, permease protein	SAU060112_100003	0.18
A0A077U1A4	Oligopeptide transporter putative substrate binding domain protein	opp-1A	0.19
A0A0D1G5I0	Strain SA-120 Contig630, whole genome shotgun sequence	-	0.19
A0A0E1VKR4	ABC transporter, ATP-binding protein	HMPREF0776_1978	0.19
A0A090LUS6	Lipoprotein	yehR	0.19
A0A0D6DDK7	Uncharacterized protein	-	0.19
A0A0C5HUH7	Carbamate kinase	arcC	0.20
A0A0B6XTB4	N-acetylmuramoyl-L-alanine amidase%2C family 4	ERS094548_01923	0.20
A0A077U4E2	2-oxoglutarate/malate translocator-like protein	ttdT	0.20
A0A090N246	Formate/nitrite transporter	nirC	0.20
A0A077U927	Pseudouridine-5'-phosphate glycosidase	psuG	0.20
A0A077VAK0	Hexose phosphate transport protein	uhpT	0.20
A0A0D6DN91	Thymidine phosphorylase	SAJPND1_02113	0.20
A0A0D6GIM9	Autolysin	atl_1	0.20
A0A0D6DA07	Iron-sulfur cluster repair protein ScdA	scdA	0.20
A0A0B6XP33	Oligopeptide transport ATP-binding protein oppD	oppD_1	0.21
A0A077VAK0	Hexose phosphate transport protein	uhpT	0.21
A0A0B6XTB4	N-acetylmuramoyl-L-alanine amidase%2C family 4	ERS094548_01923	0.21
A0A0C2HZY8	Pyrimidine-nucleoside phosphorylase	pdp	0.22
A0A0D1GJW4	Arsenate reductase family protein	QU38_11110	0.22
A0A0D1K2N9	GlnQ protein	glnQ	0.22
A0A0D6HPJ5	Lantibiotic transport ATP-binding protein	ecsA_3	0.23
A0A0D6GIM9	Autolysin	atl_1	0.23
A0A0D6DA07	Iron-sulfur cluster repair protein ScdA	scdA	0.23
A0A090LSD7	Uncharacterized protein	-	0.23
A0A0D1HUP1	Nucleoside transporter	QU38_09615	0.23
A0A077V7K3	ABC transporter substrate-binding protein	psaA	0.23
A0A033UCK9	Biotin synthase	bioB	0.23
A0A090LQD2	Glycerophosphoryl diester phosphodiesterase	glpQ	0.23

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1GTD3	Strain SA-120 Contig622, whole genome shotgun sequence	-	0.24
Q9S2Z4	Cell surface protein map-w	<i>map-w</i>	0.24
A0A090LUS7	AraC family transcription regulator	<i>araC</i>	0.25
A0A090LQ06	Uncharacterized protein	-	0.25
A0A0D6FS99	Putative polyribitolphosphotransferase	<i>tagF_1</i>	0.25
A0A0B6XNX0	Alanine dehydrogenase	<i>ald2_1</i>	0.25
A0A0C5HYQ5	SepS16B protein	<i>sepS16B</i>	0.25
A0A0D1GJW4	Arsenate reductase family protein	<i>QU38_11110</i>	0.25
A0A0D1H8B0	Threonine-tRNA ligase	<i>thrS</i>	0.25
A0A0C5HYQ5	SepS16B protein	<i>sepS16B</i>	0.25
A0A090N246	Formate/nitrite transporter	<i>nirC</i>	0.25
A0A077U4E2	2-oxoglutarate/malate translocator-like protein	<i>ttdT</i>	0.25
A0A0B6XNX0	Alanine dehydrogenase	<i>ald2_1</i>	0.25
A0A033UCK9	Biotin synthase	<i>bioB</i>	0.25
A0A0C5HUH7	Carbamate kinase	<i>arcC</i>	0.25
A0A090LWP1	HTH-type transcriptional regulator SarS	<i>sarS</i>	0.26
A0A077TYC4	Similar to putative sodium/glucose cotransporter	<i>sglT</i>	0.26
A0A0B6XKT1	Aldehyde-alcohol dehydrogenase	<i>adhE</i>	0.26
A0A090M2J3	Uncharacterized protein	-	0.26
A0A090LR99	CobW/HypB/UreG, nucleotide-binding domain protein	<i>SAU060112_10579</i>	0.27
A0A077U8P9	Membrane spanning protein	<i>ERS140026_02521</i>	0.27
A0A077VSV4	Peptide ABC transporter permease	<i>oppB_1</i>	0.27
A0A077TT97	DNA-damage repair protein	<i>umuC</i>	0.27
A0A033V8J0	Pyruvate carboxylase	<i>V070_00063</i>	0.27
A0A077U8P9	Membrane spanning protein	<i>ERS140026_02521</i>	0.27
A0A0B6XP33	Oligopeptide transport ATP-binding protein oppD	<i>oppD_1</i>	0.27
A0A090LVY0	Aspartate carbamoyltransferase	<i>pyrB</i>	0.28
A0A0D1H6Z1	Nitric oxide synthase oxygenase	<i>QU38_06960</i>	0.28
A0A0D1JKL8	Carbamate kinase	<i>QU38_12170</i>	0.28
A0A077V7K3	ABC transporter substrate-binding protein	<i>psaA</i>	0.28
A0A0D1JA14	Esterase	<i>QU38_16465</i>	0.28
A0A0D1HUP1	Nucleoside transporter	<i>QU38_09615</i>	0.29
A0A0D1HEF4	6,7-dimethyl-8-ribityllumazine synthase	<i>ribH</i>	0.29
A0A0D1HQ98	Histidine kinase	<i>QU38_10565</i>	0.29
A0A077VMN9	Peptide methionine sulfoxide reductase MsrA	<i>msrA_1</i>	0.29
A0A0D1JLL3	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	<i>bioA</i>	0.29
A0A0D6FNQ5	Immunoglobulin G-binding protein A	<i>spa</i>	0.29
A0A0D1HEF4	6,7-dimethyl-8-ribityllumazine synthase	<i>ribH</i>	0.29
A0A090LQD2	Glycerophosphoryl diester phosphodiesterase	<i>glpQ</i>	0.29
A0A0A0Q4N9	HtrA-like serine protease	<i>htrA1</i>	0.30
A0A077V9M9	Response regulator SaeR	<i>saeR</i>	0.30

Accession Number	Protein Name	Gene Name	Fold Change
A0A077VMN9	Peptide methionine sulfoxide reductase MsrA	<i>msrA_1</i>	0.30
A0A077UDD9	3-ketoacyl-CoA thiolase%3B Acetyl-CoA acetyltransferase	<i>ERS140248_02364</i>	0.30
A0A077VSV4	Peptide ABC transporter permease	<i>oppB_1</i>	0.30
A0A090LR99	CobW/HypB/UreG, nucleotide-binding domain protein	<i>SAU060112_10579</i>	0.30
A0A068W8S1	Ribosomal RNA large subunit methyltransferase H	<i>orfX</i>	0.30
A0A090LVY0	Aspartate carbamoyltransferase	<i>pyrB</i>	0.30
A0A0B6XKT1	Aldehyde-alcohol dehydrogenase	<i>adhE</i>	0.30
A0A077TYC4	Similar to putative sodium/glucose cotransporter	<i>sglT</i>	0.30
A0A0D1HCV5	Uncharacterized protein	-	0.31
A0A090M1C4	Dihydroorotate dehydrogenase (quinone)	-	0.31
A0A0D6FNQ5	Immunoglobulin G-binding protein A	<i>spa</i>	0.31
A0A090LWP1	HTH-type transcriptional regulator SarS	<i>sarS</i>	0.31
A0A0C5HTL6	Dihydroxyacetone kinase	<i>dhaL</i>	0.31
A0A0A0Q4N9	HtrA-like serine protease	<i>htrA</i>	0.32
A0A0D1JGI6	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	<i>ispD</i>	0.32
A0A077U988	Pyrimidine nucleoside transport protein	<i>nupC_2</i>	0.32
A0A0C5HMT4	GntR family transcriptional regulator	<i>treR_1</i>	0.32
A0A0D1JRN5	Strain SA-120 Contig627, whole genome shotgun sequence	-	0.32
A0A077U7R1	Cytochrome d ubiquinol oxidase subunit I	<i>cydA</i>	0.32
A0A068W8S1	Ribosomal RNA large subunit methyltransferase H	<i>orfX</i>	0.32
A0A090N1L4	Diacetyl reductase ((S)-acetoin forming)	<i>butA</i>	0.33
A0A077U2Q8	Quinol oxidase polypeptide I QoxB	<i>qoxB</i>	0.33
A0A0D1GVJ7	Poly (Glycerol-phosphate) alpha-glucosyltransferase	<i>SAJPND1_00558</i>	0.33
A0A0D1HQ98	Histidine kinase	<i>QU38_10565</i>	0.33
A0A090M1C4	Dihydroorotate dehydrogenase (quinone)	<i>pyrD</i>	0.33
A0A077U2Q8	Quinol oxidase polypeptide I QoxB	<i>qoxB</i>	0.33
T1Y8N9	Ornithine carbamoyltransferase	<i>SAKOR_01090</i>	0.34
A0A0B6XNE5	Hydrolase (HAD superfamily)	<i>ERS094548_00694</i>	0.34
A0A0D1IIH6	Uncharacterized protein	-	0.34
A0A0D1HUW5	Threonine synthase	<i>SAJPND1_01270</i>	0.34
A0A077TT97	DNA-damage repair protein	<i>umuC</i>	0.35
A0A0D3QBH3	Peptide synthetase	<i>grsB</i>	0.35
A0A077U988	Pyrimidine nucleoside transport protein	<i>nupC_2</i>	0.35
A0A0D1JLL3	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	<i>bioA</i>	0.35
A0A077V9M9	Response regulator SaeR	<i>saeR</i>	0.35
A0A077U7R1	Cytochrome d ubiquinol oxidase subunit I	<i>cydA</i>	0.35
A0A0C5HMT4	GntR family transcriptional regulator	<i>treR_1</i>	0.35
A0A0D1H6Z1	Nitric oxide synthase oxygenase	<i>QU38_06960</i>	0.35
A0A0D6DD63	Peptide methionine sulfoxide reductase MsrA	<i>msrA</i>	0.35
A0A0E1VQA5	MOSC domain protein	<i>HMPREF0776_0387</i>	0.35
A0A069G7V7	Putative N-acetyltransferase YedL	<i>CO98_1080</i>	0.35

Accession Number	Protein Name	Gene Name	Fold Change
A0A077VDA6	Lipoprotein	<i>metQ_1</i>	0.35
A0A0D1GBS9	Signal transduction protein TRAP	SAJPND1_01796	0.36
A0A0D1INB5	Arginine deiminase	<i>arcA</i>	0.36
A0A0D1JT33	Cardiolipin synthase	<i>QU38_06435</i>	0.36
A0A077TYE1	Uncharacterized protein	-	0.36
A0A090LXY5	Uncharacterized protein	-	0.36
A0A077TYE7	Uncharacterized protein conserved in bacteria	<i>ERS140095_00284</i>	0.38
A0A090M283	Catalase	<i>katA</i>	0.38
A0A0D1JGI6	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	<i>ispD</i>	0.38
A0A0D6DIR5	Protein-arginine kinase	<i>mcsB</i>	0.38
X5IX38	DNA-binding protein	<i>SAU060112_10479</i>	0.38
A0A090LW12	Poly(Glycerol-phosphate) alpha-glucosyltransferase	<i>SAU060112_10705</i>	0.38
A0A0D1G1J9	Cytochrome c oxidase polypeptide II	<i>SAJPND1_00987</i>	0.38
A0A077UIM6	Polysaccharide intercellular adhesin (PIA) biosynthesis N-glycosyltransferase IcaA	<i>icaA</i>	0.38
A0A090LPS1	Uncharacterized protein	-	0.38
A0A0D1GD88	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	<i>gpmA</i>	0.39
A0A090N1L4	Diacetyl reductase ((S)-acetoin forming)	<i>butA</i>	0.39
A0A090N1D1	ABC transporter	<i>yfmR</i>	0.39
A0A0E1XJY5	Abi-like protein	<i>HMPREF0769_10093</i>	0.39
A0A0D1GC10	Strain SA-120 Contig629, whole genome shotgun sequence	-	0.39
A0A0D6GKV9	UPF0637 protein ERS157365_00537	-	0.39
A0A0D6GUT2	Cardiolipin synthase	-	0.39
A0A0D6DNZ9	Extracellular matrix binding protein	<i>SAJPND1_02136</i>	0.39
A0A0D1GN53	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.39
A0A090LZI4	Uncharacterized protein	-	0.39
A0A0B6XN73	3-oxoadipate enol-lactonase	<i>dehH1</i>	0.40
A0A090M057	Putative ATP-dependent helicase DinG homolog	<i>dinG</i>	0.40
A0A090N1W4	Uncharacterized AAA domain-containing protein YrvN	-	0.40
A0A0E1AE46	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase, dihydroxyacetone binding subunit DhaK	<i>SAZ172_0661</i>	0.40
A0A090LVS1	Potassium-transporting ATPase B chain	<i>kdpB</i>	0.40
A0A090LXT5	Peptidase C45	<i>SAU060112_110028</i>	0.40
A0A077UJH0	DNA-binding response regulator	<i>bvgA</i>	0.40
A0A0D1EST2	Pyruvate formate-lyase-activating enzyme	<i>QU38_14695</i>	0.40
A0A077UZP7	Transcriptional repressor NrdR	<i>nrdR</i>	0.41
A0A0D1FF77	Coenzyme A disulfide reductase	<i>cdr</i>	0.41
A0A077UJ82	Uncharacterized protein	-	0.41
A0A0B6XL00	Lipoprotein	<i>metQ_1</i>	0.41
A0A090LR26	Uncharacterized oxidoreductase YcsN	-	0.41
A0A077U7Z6	Antiholin-like protein LrgA	<i>lrgA</i>	0.41
A0A090M2D6	Oligoendopeptidase F	<i>SAU060112_70075</i>	0.42

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D6GK28	Uncharacterized protein	-	0.42
A0A077W0Q5	UPF0365 protein ERS140167_00916	-	0.42
A0A0B6XPU6	Acetyltransferase AcuA%2C acetyl-CoA synthetase inhibitor	<i>acuA</i>	0.42
A0A0B6XP73	Lipoate--protein ligase	<i>lplJ_2</i>	0.43
A0A0B6XNT6	Bifunctional ligase/repressor BirA	<i>birA</i>	0.43
A0A0D6DHW6	Glycosyltransferase	<i>SAJPND1_00237</i>	0.43
A0A090LTY1	Uncharacterized protein	-	0.43
A0A0E7DTW4	Putative lipoprotein	<i>ERS157365_00280</i>	0.44
A0A090LX90	Probable transcriptional regulatory protein yeeN	<i>yeeN</i>	0.44
A0A0E1VQ76	Biotin synthase	<i>bioB</i>	0.44
A0A0B6XKT2	Ribose operon repressor%2C putative	<i>degA</i>	0.45
A0A0B6XPW9	Sodium/proline symporter	<i>putP</i>	0.45
A0A0D6HWL4	ATP-dependent helicase/deoxyribonuclease subunit B	<i>addB</i>	0.45
A0A0E1VI43	Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	<i>carB</i>	0.45
A0A069G2X1	Methicillin resistance regulatory protein MecI	<i>mecI</i>	0.45
A0A077U153	Gluconate permease	<i>gntP</i>	0.45
A0A077U0H9	Pantothenate synthetase	<i>panC</i>	0.45
A0A0D6HMD3	General stress protein 26	<i>ydaG</i>	0.45
A0A0B6XRK6	Nicotinate phosphoribosyltransferase	<i>ERS094548_02369</i>	0.45
A0A0D6FNA4	ATPase	<i>CH51_00375</i>	0.45
A0A0D1HUW5	Threonine synthase	<i>SAJPND1_01270</i>	0.45
A0A077UDM1	Manganese ABC transporter%2C ATP-binding protein SitB	<i>sitB</i>	0.45
A0A077UDM4	Ketol-acid reductoisomerase	<i>ilvC</i>	0.45
A0A090LZD2	Putative permease of an ABC transporter	<i>ybbM</i>	0.45
A0A077UG02	Acid phosphatase	<i>hel</i>	0.46
A0A077TZL7	Modification methylase MboII	<i>mboIIM</i>	0.46
A0A090N216	Uncharacterized protein	-	0.46
A0A0D1IUP6	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.46
A0A0D1GU53	Uncharacterized protein	-	0.47
A0A0D1HYC8	Nitrite reductase [NAD(P)H] large subunit	<i>SAJPND1_02388</i>	0.47
A0A0D1KA16	Strain SA-120 Contig620, whole genome shotgun sequence	-	0.48
A0A0D1HKS5	Chromosomal replication initiator protein DnaA	<i>dnaA</i>	0.48
A0A0D1FNA8	Uncharacterized protein	-	0.48
A0A0E1AMS3	Uncharacterized protein	-	0.49
A0A0D6DGY8	Uroporphyrin-III C-methyltransferase	<i>SAJPND1_02386</i>	0.49
A0A080V4N7	Membrane spanning protein	<i>yhhT_1</i>	0.49
A0A090LXQ9	Uncharacterized protein	-	0.49
A0A0D6DGT6	Cystine-binding protein	<i>SAJPND1_02402</i>	0.50
A0A0D1IB15	Strain SA-120 Contig624, whole genome shotgun sequence	-	0.50
A0A090LRF4	Uncharacterized protein	-	0.50
A0A077VJX6	Deblocking aminopeptidase	<i>ysdC_1</i>	0.50
A0A0D1I5J3	Ribulose-phosphate 3-epimerase	<i>QU38_12445</i>	0.50

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1J363	Uracil phosphoribosyltransferase	<i>upp</i>	0.50
A0A0E1VLF4	TIGR01777 family protein	<i>HMPREF0776_1780</i>	0.50
A0A090LUN7	Urocanate hydratase	<i>hutU</i>	0.50
A0A077UP25	Membrane-bound serine protease	<i>ERS140159_00273</i>	0.50
A0A0D1IBW0	Strain SA-120 Contig620, whole genome shotgun sequence	-	0.50
A0A090N1M7	Type-1 restriction enzyme R protein	<i>hsdR</i>	0.50
A0A077TXE8	L-threonine 3-dehydrogenase	<i>ERS140248_00818</i>	0.50
A0A0D6DGE5	Acriflavin resistance plasma membrane protein	<i>SAJPND1_02233</i>	0.50
A0A0D6DPK7	Staphyloxanthin biosynthesis protein CrtP	<i>SAJPND1_02566</i>	0.50
A0A0D1K8W2	Bifunctional protein PyrR	<i>pyrR</i>	0.50
A0A0B6XPT4	D-3-phosphoglycerate dehydrogenase	<i>serA</i>	0.50
A0A0D6DDT0	Homoserine dehydrogenase	<i>SAJPND1_01269</i>	0.50
A0A077UPQ0	Antiholin-like protein LrgB	<i>lrgB</i>	0.50
A0A090LX68	Tagatose-6-phosphate kinase	<i>fruK</i>	0.50
A0A0D1G9T6	Tautomerase	<i>QU38_13190</i>	0.50
A0A077V1P6	Methionine ABC transporter ATP-binding protein	<i>ybbL</i>	0.50
A0A077U7R0	3-isopropylmalate dehydratase large subunit	<i>leuC</i>	0.50
A0A0B6XP11	Aldo/keto reductase family protein	<i>yvgN</i>	0.50
A0A090LXW3	Ferritin	<i>ftnA</i>	0.50
A0A090LVJ3	Ornithine carbamoyltransferase	<i>arcB</i>	0.50
A0A0D6HVT0	ATP-dependent helicase/nuclease subunit A	<i>addA</i>	0.51
A0A0D1H334	Putative kinase associated protein B family protein	<i>QU38_11380</i>	0.51
A0A090LWR0	Phosphoglycerate mutase	<i>gpmA_1</i>	0.51
A0A0E1VIJ7	HTH-type transcriptional regulator rot	<i>HMPREF0776_2797</i>	0.51
A0A0D1JYJ4	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.51
A0A077V172	Respiratory nitrate reductase gamma chain	<i>narI</i>	0.52
A0A069FW70	Fructose-1,6-bisphosphatase class 3	<i>fbp</i>	0.52
A0A090LXB7	Luciferase-like monooxygenase	<i>SAU060112_20273</i>	0.52
A0A0D1G640	Arginine repressor	<i>argR</i>	0.52
A0A077U0D7	Protein of pXO2-46	<i>ERS140095_00709</i>	0.53
A0A0D1H5M4	Transaldolase	<i>QU38_04770</i>	0.53
A0A0D1HBY5	Pyridoxal 5'-phosphate synthase subunit PdxT	<i>pdxT</i>	0.54
A0A090LUF4	Ribose-5-phosphate isomerase A	<i>rpiA</i>	0.54
A0A090LRU6	Regulatory protein RecX	<i>recX</i>	0.54
A0A077UNV8	Glycosyltransferase	<i>pimB</i>	0.54
A0A077UUV1	Hydrogen peroxide-inducible genes activator	<i>oxyR</i>	0.54
A0A0E1AE25	Phosphoglycolate phosphatase	<i>SAZ172_0574</i>	0.55
A0A0D1HKP9	Arginase	<i>SAJPND1_02140</i>	0.55
A0A0D1I632	Carbamoyl-phosphate synthase small chain	<i>carA</i>	0.55
A0A090LUN9	6-carboxyhexanoate-CoA ligase	<i>bioW</i>	0.55
A0A090LVM4	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase	<i>icaB</i>	0.55
A0A090LVR9	Uncharacterized protein	-	0.55

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1GS08	GTP-sensing transcriptional pleiotropic repressor CodY	<i>codY</i>	0.55
A0A090LUQ0	Glycerate kinase	<i>glxK</i>	0.55
A0A0D6GUT9	Dehydrosqualene desaturase	<i>crtN</i>	0.55
A0A077UJ58	Pyridoxal 5'-phosphate synthase subunit PdxS	<i>pdxS</i>	0.56
A0A0B6XQC4	Serine hydroxymethyltransferase	<i>glyA</i>	0.56
A0A0B6XMC2	Lipoprotein	<i>metQ_2</i>	0.56
A0A077UYA4	Glycerol uptake facilitator protein	<i>glpF</i>	0.56
A0A0D6DAW8	Long-chain-fatty-acid-CoA ligase	<i>SAJPND1_00209</i>	0.56
A0A0D1HXA7	D-alanine aminotransferase	<i>SAJPND1_01699</i>	0.56
A0A0D3QB94	Fructose-1,6-bisphosphatase class 3	<i>fbp</i>	0.56
A0A0D1IG60	2-dehydropantoate 2-reductase	<i>SAJPND1_02437</i>	0.56
A0A077UPJ4	Phosphopentomutase	<i>deoB</i>	0.57
A0A090N1I7	Putative aldehyde dehydrogenase YwdH	<i>ywdH</i>	0.57
A0A077UPJ4	Phosphopentomutase	<i>deoB</i>	0.57
A0A0D1JMD6	Ribokinase	<i>QU38_14445</i>	0.57
A0A0D1HYD3	Strain SA-120 Contig626, whole genome shotgun sequence	-	0.57
A0A077VJX6	Deblocking aminopeptidase	<i>ysdC_1</i>	0.57
A0A0D1JPH9	Strain SA-120 Contig629, whole genome shotgun sequence	-	0.58
A0A0D1HD94	Serine acetyltransferase	<i>sat</i>	0.58
A0A0D1GS08	GTP-sensing transcriptional pleiotropic repressor CodY	<i>codY</i>	0.58
A0A090LSG7	L-lactate dehydrogenase	<i>ldhA</i>	0.58
A0A0D1K078	Nitrite reductase [NAD(P)H] small subunit	<i>QU38_07730</i>	0.59
A0A077U7M7	Two component transcriptional regulator VraR%2C LuxR family	<i>vraR_2</i>	0.59
A0A0D3Q7P5	3-phosphoshikimate 1-carboxyvinyltransferase	<i>aroA_2</i>	0.59
A0A0D1HPS7	SdhB protein	<i>sdhB</i>	0.59
A0A090LVS0	DNA replication and repair protein RecF	<i>recF</i>	0.59
A0A090LUN2	Na ⁺ /H ⁺ antiporter family protein	<i>SAU060112_40163</i>	0.60
A0A0E0VRM5	TenA	<i>ST398NM01_2137</i>	0.60
A0A090M1B5	KR domain protein	<i>SAU060112_40411</i>	0.60
EBH	Extracellular matrix-binding protein ebh	<i>ebh</i>	0.60
A0A077USJ8	Putative lipoprotein	<i>ERS140159_00666</i>	0.60
A0A090LYD3	Uncharacterized protein	-	0.60
A0A0B6XKQ5	Deoxyribose-phosphate aldolase	<i>dra_1</i>	0.60
A0A090LVS0	DNA replication and repair protein RecF	<i>recF</i>	0.60
A0A077UYA4	Glycerol uptake facilitator protein	<i>glpF</i>	0.60
A0A0D1JK42	Methionine import ATP-binding protein MetN	<i>metN</i>	0.60
A0A0D6GUT9	Dehydrosqualene desaturase	<i>crtN</i>	0.60
A0A090M1B5	KR domain protein	<i>SAU060112_40411</i>	0.60
A0A090LYP3	Protein EsaA	<i>esaA</i>	0.60
A0A0D1H4D9	Strain SA-120 Contig627, whole genome shotgun sequence	-	0.61
A0A077VIK6	Monofunctional glycosyltransferase	<i>mgt</i>	0.61

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1JK42	Methionine import ATP-binding protein MetN	<i>metN</i>	0.61
A0A0D1H739	Strain SA-120 Contig625, whole genome shotgun sequence	-	0.61
A0A0B6XQ25	Aspartokinase	<i>lysC2</i>	0.61
A0A077UG73	Lactose phosphotransferase system repressor	<i>lacR</i>	0.61
A0A0D1HPS7	SdhB protein	<i>sdhB</i>	0.62
A0A0B6XKQ5	Deoxyribose-phosphate aldolase	<i>dra_1</i>	0.62
A0A0E1AIF3	Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit	<i>bfmBAB</i>	0.62
A0A0D1HFA7	Type II pantothenate kinase	<i>coaW</i>	0.62
A0A0A0R7J1	RepL	-	0.62
A0A0D6DK53	Glyoxylated reductase	<i>SAJPND1_00846</i>	0.62
A0A0D1FJV3	Glucose-6-phosphate 1-dehydrogenase	<i>zwf</i>	0.62
A0A0D1I792	Strain SA-120 Contig624, whole genome shotgun sequence	-	0.62
A0A077U8X5	ResD	<i>srrA</i>	0.63
A0A0E1VKG9	Endonuclease MutS2	<i>mutS2</i>	0.63
A0A077U597	Histidine kinase	<i>walk</i>	0.63
A0A090LUE4	Pseudouridine synthase	<i>ylyB</i>	0.63
A0A077UQK7	Small integral membrane protein	<i>ERS140095_02392</i>	0.64
A0A077UJ41	3-methyl-2-oxobutanoate hydroxymethyltransferase	<i>panB</i>	0.64
A0A077VQ84	NADP-dependent malic enzyme	<i>maeB</i>	0.64
A0A077U828	Serine-protein kinase RsbW	<i>rsbW</i>	0.64
A0A0D6DB70	Staphylococcal accessory regulator-like protein	<i>SAJPND1_00668</i>	0.64
A0A0D1FJV3	Glucose-6-phosphate 1-dehydrogenase	<i>zwf</i>	0.64
A0A0D1HST0	Putative sporulation transcription regulator WhiA	<i>whiA</i>	0.65
A0A0D6GTK5	3-hydroxy-3-methylglutaryl coenzyme A reductase	<i>mvaA</i>	0.65
A0A090LZA4	Chorismate mutase I / 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase	<i>aroA</i>	0.65
A0A077TXN4	Ncharacterized conserved protein	<i>ERS140095_00443</i>	0.65
A0A090N186	Putative sodium/proton-dependent alanine carrier protein YrbD	<i>yrbD</i>	0.65
A0A0D6DMA3	2-succinylbenzoate--CoA ligase	<i>menE</i>	0.66
A0A0D1FA95	Negative regulator of genetic competence clpC	<i>QU38_09635</i>	0.66
A0A0B6XKE6	Type I restriction-modification system DNA methylase	<i>hsdM</i>	0.66
A0A0D1HJP2	Ribosomal large subunit pseudouridine synthase D	<i>SAJPND1_01814</i>	0.67
A0A0B6XRG6	Teichoic acid export ATP-binding protein TagH	<i>tagH_2</i>	0.67
A0A0D1H8Y0	Glucose-6-phosphate isomerase	<i>pgi</i>	0.67
A0A0D6DMP1	Putative exported protein	<i>SAJPND1_01686</i>	0.67
A0A0D6DK53	Glyoxylated reductase	<i>SAJPND1_00846</i>	0.67
A0A0E1VKG9	Endonuclease MutS2	<i>mutS2</i>	0.67
A0A0D1HJP2	Ribosomal large subunit pseudouridine synthase D	<i>SAJPND1_01814</i>	0.67
A0A0C5HUP1	Endoglucanase M	<i>ysdC_2</i>	0.67
A0A0E1AI63	Peptide methionine sulfoxide reductase MsrB	<i>msrB</i>	0.67
A0A0E1AGM7	PTS system, glucose-specific IIA component	<i>SAZ172_1435</i>	0.67

Accession Number	Protein Name	Gene Name	Fold Change
A0A090N275	Transcriptional regulator, TetR family	SAU060112_40385	0.68
A0A090LV62	D-lactate dehydrogenase	<i>ldhD</i>	0.68
A0A0D1HWP8	Dephospho-CoA kinase	<i>coaE</i>	0.68
A0A0B6XMX7	DNA mismatch repair protein MutL	<i>mutL</i>	0.68
A0A0D1JNT4	ATP synthase subunit alpha	<i>atpA</i>	0.68
A0A0D1K6G2	Putative NmrA family protein	SAJPND1_02580	0.68
A0A0D1I997	Strain SA-120 Contig626, whole genome shotgun sequence	-	0.68
A0A0D1EZS5	Proline dehydrogenase	SAJPND1_01717	0.68
A0A090LTX6	HTH-type transcriptional regulator MalR	<i>malR</i>	0.69
A0A077U2I8	FMN-dependent NADH-azoreductase	<i>azoR</i>	0.69
A0A0D1J368	ATP synthase subunit b	<i>atpF</i>	0.69
A0A077U8C2	ATP synthase subunit beta	<i>atpD</i>	0.69
A0A068DT57	Phosphoesterase%2C DHH family protein	<i>nrnA_1</i>	0.70
A0A0D1F682	Staphylococcal accessory regulator-like protein SarV	QU38_05105	0.70
A0A0E8GI61	GTPase Der	<i>engA</i>	0.70
A0A090N2D7	Low molecular weight protein-tyrosine-phosphatase PtpB	<i>ptpB</i>	0.70
A0A0D6DD85	DNA Polymerase X family	SAJPND1_01069	0.70
A0A090LY09	GTPase Obg	<i>obg</i>	0.70
A0A077UBB6	Type I restriction modification DNA specificity domain protein	<i>hsdS</i>	0.70
A0A0D6DMA3	2-succinylbenzoate-CoA ligase	<i>menE</i>	0.70
A0A0D1JZP5	DNA repair protein RecN	QU38_09335	0.70
A0A077U1Q7	Oxidoreductase%2C aldo/keto reductase family	ERS140248_01341	0.70
A0A077UBB6	Type I restriction modification DNA specificity domain protein	<i>hsdS</i>	0.70
A0A0C5HTQ6	Oxidoreductase of aldo/keto reductase family%2C subgroup 1	<i>yvgN_1</i>	0.70
A0A090N2D7	Low molecular weight protein-tyrosine-phosphatase PtpB	<i>ptpB</i>	0.70
A0A0B6XM36	Peptidase T	<i>pepT_1</i>	0.70
A0A090LUJ0	Protease synthase and sporulation negative regulatory protein PAI 1	<i>paiA</i>	0.70
A0A0D1H8Y0	Glucose-6-phosphate isomerase	<i>pgi</i>	0.70
A0A077U2Q7	Cell division protein ftsA	<i>ftsA</i>	0.70
A0A0D1JNT4	ATP synthase subunit alpha	<i>atpA</i>	0.70
A0A0B6XRG6	Teichoic acid export ATP-binding protein TagH	<i>tagH_2</i>	0.70
A0A077TUN9	Siderophore staphylobactin ABC transporter%2C substrate-binding protein SirA	<i>sirA</i>	0.70
A0A077TXN4	Ncharacterized conserved protein	ERS140095_00443	0.70
A0A0B6XQ25	Aspartokinase	<i>lysC2</i>	0.70
A0A0D1JFQ2	Glutathione peroxidase	QU38_12880	0.71
A0A0E8IKP1	GMP synthase [glutamine-hydrolyzing]	<i>guaA</i>	0.71
A0A0D6FMN0	Putative cytosolic protein	ERS445051_00083	0.71
A0A0D1H3K1	Phosphoglucosamine mutase	<i>glmM</i>	0.72
A0A0D6WD10	Acetyltransferase	<i>paiA</i>	0.72
A0A0D1GUW7	GTPase Era	<i>era</i>	0.72

Accession Number	Protein Name	Gene Name	Fold Change
A0A090M224	Transcription termination factor	<i>rho</i>	0.72
A0A0D1I3S9	Outer membrane protein	<i>SAJPND1_01920</i>	0.72
A0A0D1EZE3	Putative pyruvate, phosphate dikinase regulatory protein	<i>QU38_09115</i>	0.72
A0A090LQ50	Isochorismate synthase family protein	<i>SAU060112_10293</i>	0.73
A0A0D1GMN8	Hydrolase	<i>QU38_11475</i>	0.73
A0A0D1JNW2	Strain SA-120 Contig624, whole genome shotgun sequence	-	0.73
A0A077UC86	PTS family glucose/glucoside (Glc) porter component IIABC	<i>glcB</i>	0.73
A0A0C5HKH2	PTS-dependent dihydroxyacetone kinase phosphotransfer protein	<i>dhaM</i>	0.73
A0A077U828	Serine-protein kinase RsbW	<i>rsbW</i>	0.73
A0A0E8H010	Cell shape-determining protein MreC	<i>ERS094548_00451</i>	0.73
A0A0D6HD63	DNA repair protein Rad50	<i>CH51_09905</i>	0.73
A0A0D1IP31	Septation ring formation regulator EzrA	<i>ezrA</i>	0.73
A0A0B6XL97	Periplasmic binding protein	<i>btuF</i>	0.73
A0A0B6XPA0	Pyruvate kinase	<i>pykA</i>	0.73
A0A077U9J9	Replicative DNA helicase	<i>dnaC_1</i>	0.74
A0A090LYW3	Molybdopterin molybdenumtransferase	<i>moeA</i>	0.74
A0A0D1H3K1	Phosphoglucosamine mutase	<i>glmM</i>	0.75
A0A068DT57	Phosphoesterase%2C DHH family protein	<i>nrnA_1</i>	0.75
A0A0D6FKA0	DNA gyrase subunit B	<i>gyrB</i>	0.75
A0A090LTA2	PTS system N-acetylglucosamine-specific EIICB component	<i>nagP</i>	0.75
A0A0D6DEQ9	Phosphoesterase, DHH family protein	<i>SAJPND1_01651</i>	0.75
A0A077UMA1	Copper-translocating P-type ATPase	<i>copA</i>	0.75
A0A0B6XPB4	Proline dipeptidase	<i>ERS094548_00400</i>	0.75
A0A0D1GSA9	Strain SA-120 Contig630, whole genome shotgun sequence	-	0.76
A0A0D1HWI2	tRNA-specific 2-thiouridylase MnmA	<i>mnmA</i>	0.76
A0A0D1I4D2	Oligoendopeptidase F	<i>QU38_11615</i>	0.77
A0A0D1JNX0	Glutamate racemase	<i>murI</i>	0.77
A0A090LUT3	Uncharacterized protein	-	0.77
A0A090LR04	Substrate binding domain of ABC-type glycine betaine transport system family protein	<i>SAU060112_10543</i>	0.77
A0A0D1HL09	Redox-sensing transcriptional repressor Rex	<i>rex</i>	0.78
A0A0D6DM29	5-formyltetrahydrofolate cyclo-ligase	<i>SAJPND1_01504</i>	0.78
A0A077UYI3	Ribonuclease 3	<i>rnc</i>	0.78
A0A0D6DC64	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	<i>SAJPND1_00699</i>	0.78
A0A0B6XN18	Ribulokinase	<i>araB</i>	0.78
A0A077UHU0	Membrane spanning protein	<i>ERS140147_01129</i>	0.78
A0A0D6GX81	Cell wall surface anchor family protein	<i>ERS445052_00900</i>	0.78
A0A0D6DE64	Putative cytosolic protein	<i>SAJPND1_01441</i>	0.79
A0A077W554	Membrane associated protein	<i>ERS140026_02425</i>	0.80
A0A0D6DDB0	Dihydrofolate reductase	<i>SAJPND1_01369</i>	0.80
A0A068A3K4	Histidine kinase	<i>srrB</i>	0.80

Accession Number	Protein Name	Gene Name	Fold Change
A0A077UH28	LytR family transcriptional regulator	<i>lytR_2</i>	0.80
A0A0D1JZ91	General stress protein	<i>QU38_08215</i>	0.80
A0A090N275	Transcriptional regulator, TetR family	<i>SAU060112_40385</i>	0.80
A0A0E1AFV2	Non-canonical purine NTP pyrophosphatase	<i>SAZ172_1150</i>	0.80
A0A0B6XRB8	Sodium export permease protein	<i>yhaP</i>	0.80
A0A077U2I8	FMN-dependent NADH-azoreductase	<i>azoR</i>	0.80
A0A0C5HIW4	Thiamine-phosphate synthase	<i>thiE</i>	0.80
A0A090M224	Transcription termination factor	<i>rho</i>	0.80
A0A090LPK8	DNA polymerase III PolC-type	<i>polC</i>	0.80
A0A0E1VK91	Primosomal protein N'	<i>priA</i>	0.80
A0A077VMD2	Trigger factor	<i>tig</i>	0.80
A0A077UEH0	ATP synthase subunit a	<i>atpB</i>	0.80
A0A090LTA4	Pyridine nucleotide-disulfide oxidoreductase family protein	<i>SAU060112_30030</i>	0.80
A0A0D1I3S9	Outer membrane protein	<i>SAJPND1_01920</i>	0.80
A0A0D6DGB0	Energy-coupling factor transporter ATP-binding protein EcfA	<i>ecfA</i>	0.80
A0A0B6XMX7	DNA mismatch repair protein MutL	<i>mutL</i>	0.80
A0A068DXM4	Magnesium transporter MgtE	<i>mgtE</i>	0.81
A0A077U5J7	Ribonuclease Y	<i>rny</i>	0.81
A0A0B6XQ10	Exported protein	<i>ERS094548_02603</i>	0.82
A0A077UNV6	Pseudouridine synthase	<i>rluB</i>	0.82
A0A090LQ68	Peptide chain release factor 3	<i>prfC</i>	0.82
A0A0D1ICI0	Pur operon repressor	<i>QU38_03120</i>	0.82
A0A0D6GRP2	tRNA pseudouridine synthase B	<i>truB</i>	0.82
METN1	Methionine import ATP-binding protein MetN 1	<i>metN1</i>	0.82
A0A077UF55	Purine nucleoside phosphorylase DeoD-type	<i>deoD_2</i>	0.82
A0A090LRA1	Uncharacterized protein	-	1.20
A0A090LWG8	Chaperone protein ClpB	<i>clpB</i>	1.20
A0A0D1GUG3	Protein RecA	<i>recA</i>	1.20
A0A0D6DL16	Virulence factor expression protein CvfB	<i>SAJPND1_01333</i>	1.20
A0A090N2E4	Cof-like hydrolase	<i>SAU060112_60089</i>	1.20
A0A0C5HQR7	Radical activating enzyme protein	<i>ERS445051_00968</i>	1.20
A0A0B6XT76	Fructose-bisphosphate aldolase class 1	<i>fda</i>	1.20
A0A0E0VN86	Nitropropane dioxygenase	<i>ST398NM01_0904</i>	1.20
A0A0D1G285	CDP-ribitol ribitolphosphotransferase	<i>QU38_14515</i>	1.20
A0A033UZD3	Chaperone protein DnaK	<i>dnaK</i>	1.21
A0A090LW80	CTP synthase	<i>pyrG</i>	1.22
A0A0D1HWG7	Ribonuclease J	<i>QU38_12735</i>	1.22
A0A090LWD8	Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B	<i>gatB</i>	1.22
A0A0C5I0G0	Aspartate aminotransferase	<i>aspC</i>	1.22
A0A090LQ19	Bifunctional purine biosynthesis protein PurH	<i>purH</i>	1.23
A0A0E8HN36	DNA topoisomerase 4 subunit B	<i>parE</i>	1.23
A0A069G7B5	UPF0473 protein CO98_1354	-	1.25

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1I3W4	ATP-dependent Clp protease proteolytic subunit	<i>clpP</i>	1.25
A0A0D1I8Z9	Mechanosensitive ion channel	<i>SAJPND1_00360</i>	1.25
A0A0B6XNU4	DNA primase	<i>dnaG</i>	1.25
A0A090LQZ8	Ribonucleoside-diphosphate reductase subunit beta	<i>nrdF</i>	1.25
A0A077VBV0	Methionine aminopeptidase	<i>map_3</i>	1.26
A0A0D1H1Q3	Glyoxalase family protein	<i>QU38_12370</i>	1.26
A0A069G7F5	UPF0374 protein CO98_2312	-	1.26
A0A0C2HEJ1	Translation initiation factor IF-2	<i>infB</i>	1.27
A0A090LTG7	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	<i>accD</i>	1.27
A0A0D1JLY3	Strain SA-120 Contig625, whole genome shotgun sequence	-	1.28
A0A0D1I8U1	30S ribosomal protein S4	-	1.28
A0A0D1H2U8	1,4-dihydroxy-2-naphthoyl-CoA synthase	<i>menB</i>	1.28
A0A0D1I4Y4	Strain SA-120 Contig630, whole genome shotgun sequence	-	1.29
A0A0D1IJ21	Peroxiredoxin	<i>QU38_04455</i>	1.29
A0A077ULL5	LPXTG surface protein	<i>sdrD</i>	1.30
A0A0D1I5P8	High-affinity zinc uptake system ATP-binding protein znuC	<i>SAJPND1_01510</i>	1.30
DRP35	Lactonase drp35	<i>drp35</i>	1.30
A0A0D6GCQ1	Phosphoglycerate mutase	<i>gpmA_1</i>	1.30
A0A0E1AIF5	2-amino-3-ketobutyrate coenzyme A ligase	<i>kbl</i>	1.30
A0A0E1AJI0	Ferredoxin-dependent glutamate synthase	<i>SAZ172_2563</i>	1.30
A0A0B6XMB1	Branched-chain alpha-keto acid dehydrogenase subunit E2	<i>pdhC</i>	1.30
A0A090N1T0	Uncharacterized protein	-	1.30
A0A0E1VGD1	Fumarate hydratase class II	<i>fumC</i>	1.31
SYI	Isoleucine-tRNA ligase	<i>ileS</i>	1.32
A0A0D1G603	RNA polymerase sigma factor SigA	<i>sigA</i>	1.32
A0A0D1EUJ0	Cytidylate kinase	<i>cmk</i>	1.32
A0A069FS69	Phosphocarrier protein HPr	<i>ptsH</i>	1.33
A0A0D6DLY3	Pyrroline-5-carboxylate reductase	<i>proC</i>	1.33
A0A0D1FPD0	Elongation factor G	<i>fusA</i>	1.33
A0A0D1IQB7	Enoyl-[acyl-carrier-protein] reductase [NADPH]	<i>QU38_11665</i>	1.33
A0A0D1K0Z5	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	<i>murA</i>	1.34
A0A0D1GZ06	Putative septation protein SpoVG	<i>spoVG</i>	1.35
A0A068A8I1	Serine/threonine protein kinase	<i>prkC</i>	1.36
A0A0D6DKR6	Bifunctional protein FOLD	<i>fold</i>	1.36
A0A077UEH9	Thymidine kinase	<i>tdk</i>	1.36
A0A0D1GQ94	Transcriptional regulator IcaR	<i>SAJPND1_02678</i>	1.36
A0A0D1I5C0	Methionyl-tRNA formyltransferase	<i>fnt</i>	1.36
A0A0C5HRP6	Peptidase family U32	<i>yhbU_2</i>	1.36
A0A0D1JCM4	50S ribosomal protein L11	-	1.37
A0A0E1AFG8	Peptide deformylase	<i>def</i>	1.38
A0A0E0VNX4	Ribosome-associated factor Y	<i>ST398NM01_0828</i>	1.38

Accession Number	Protein Name	Gene Name	Fold Change
A0A0C2L9V4	Putative N-acetylmannosamine-6-phosphate 2-epimerase	<i>nanE</i>	1.38
A0A0D1JJZ3	Central glycolytic protein regulator	<i>QU38_10935</i>	1.39
A0A0D1J8V1	Glycerophosphoryl diester phosphodiesterase	<i>SAJPND1_01669</i>	1.39
A0A0D6DEH7	Dimethylallyltransferase	<i>SAJPND1_01475</i>	1.40
A0A0D6HUF4	Phosphoenolpyruvate-protein phosphotransferase	<i>ptsI</i>	1.40
A0A090LUA2	Ribosome biogenesis GTPase A	<i>rbgA</i>	1.40
A0A090LW97	EVE domain protein	<i>ERS094548_02511</i>	1.40
A0A0C5HQ19	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	<i>accA</i>	1.40
A0A077USS5	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	<i>ispD2</i>	1.40
A0A0D1H6R9	Aconitate hydratase	<i>SAJPND1_01292</i>	1.40
A0A077USL8	L-lactate permease	<i>lctP_1</i>	1.41
A0A0D1IKI9	Strain SA-120 Contig619, whole genome shotgun sequence	-	1.41
A0A090LXW9	Isocitrate dehydrogenase [NADP]	<i>icd</i>	1.41
D7RM11	Translation elongation factor Tu (Fragment)	-	1.42
A0A0D1HD79	tRNA binding domain protein	<i>SAJPND1_01690</i>	1.42
A0A090N220	Cyclic pyranopterin monophosphate synthase accessory protein	<i>moaC</i>	1.42
A0A0D6DJ51	50S ribosomal protein L25	<i>rplY</i>	1.42
A0A069FMB9	DNA-directed RNA polymerase subunit alpha	<i>rpoA</i>	1.43
A0A077VNY2	Teichoic acids export ATP-binding protein TagH	<i>tagH_1</i>	1.44
A0A0D1JI56	Cell division initiation protein DivIVA	<i>QU38_12295</i>	1.44
A0A077TZY1	Thioredoxin reductase	<i>trxB_2</i>	1.45
A0A090N127	GTPase HflX	<i>hflX</i>	1.46
A0A077W129	30S ribosomal protein S13	<i>rpsM</i>	1.47
A0A0D1I5C9	Strain SA-120 Contig629, whole genome shotgun sequence	-	1.47
A0A0B6XQV4	Alpha-amylase	<i>mala</i>	1.48
A0A0D1GT36	RNA polymerase sigma factor	<i>SAJPND1_02037</i>	1.48
A0A0D6H5T9	NAD-dependent protein deacetylase	<i>cobB</i>	1.49
A0A0D1H4E0	Strain SA-120 Contig630, whole genome shotgun sequence	-	1.49
A0A0D1IHY2	50S ribosomal protein L29	-	1.50
A0A090LU21	Fe(3+)-citrate-binding protein YfmC	<i>yfmC</i>	1.50
A0A077U027	1-acyl-sn-glycerol-3-phosphate acyltransferase	<i>plsC</i>	1.50
A0A077UXQ0	UTP-glucose-1-phosphate uridylyltransferase	<i>gtaB</i>	1.50
A0A0D1IPU6	Adenylosuccinate synthetase	<i>purA</i>	1.52
A0A0D6DKC9	UPF0738 protein SAJPND1_00926	-	1.52
A0A0E1AI69	Uncharacterized protein	-	1.52
A0A0D1I2B3	Chaperone protein DnaJ	<i>dnaJ</i>	1.53
A0A090LRD1	Molecular chaperone Hsp31 and glyoxalase 3	<i>hchA</i>	1.53
A0A0D1JMR1	Acyl carrier protein	<i>acpP</i>	1.54
A0A0B6XSS6	Molybdate-binding protein	<i>modA</i>	1.54
A0A0D1K1G7	Phosphopantetheine adenylyltransferase	<i>coaD</i>	1.55
A0A0C5I8L9	Malonyl CoA-acyl carrier protein transacylase	<i>fabD</i>	1.55

Accession Number	Protein Name	Gene Name	Fold Change
A0A0E1APW1	1-pyrroline-5-carboxylate dehydrogenase	<i>rocA</i>	1.55
A0A0B6XPW5	UDP-N-acetylmuramoylalanyl-D-glutamate-2%2C 6-diaminopimelate ligase	<i>ERS094548_02204</i>	1.55
A0A0D6DQ24	tRNA modification GTPase MnmE	<i>mnmE</i>	1.55
A0A0D1I6P2	Diaminopimelate decarboxylase	<i>lysA</i>	1.56
A0A0B6XQS8	Valine-tRNA ligase	<i>valS</i>	1.56
A0A0D1FKQ9	30S ribosomal protein S9	<i>rpsI</i>	1.57
A0A0D1JTQ6	50S ribosomal protein L15	-	1.58
A0A0D1J4E7	Glutamate dehydrogenase	<i>QU38_11405</i>	1.58
A0A0C5I0S0	Mannitol-1-phosphate 5-dehydrogenase	<i>mtlD</i>	1.59
HUTG	Formimidoylglutamase	<i>hutG</i>	1.60
A0A0D1HT84	50S ribosomal protein L5	<i>rplE</i>	1.60
A0A077UHD3	Uridine kinase	<i>udk</i>	1.60
A0A0B6XP80	Similar to oxidoreductase	<i>yhdN</i>	1.60
A0A077UEE8	Proline--tRNA ligase	<i>proS</i>	1.60
A0A077VSG0	50S ribosomal protein L9	<i>rplI</i>	1.61
A0A068DY65	DNA ligase	<i>lig</i>	1.61
A0A0C2I3Y5	Branched-chain amino acid aminotransferase	<i>ilvE</i>	1.61
A0A0B6XQ41	GMP reductase	<i>guaC</i>	1.61
A0A0C5HY37	Glycine cleavage system H protein	<i>gcvH_2</i>	1.61
A0A0D1GWI4	50S ribosomal protein L4	<i>rplD</i>	1.62
A0A0D1I3V2	UDP-N-acetylenolpyruvoylglucosamine reductase	<i>murB</i>	1.62
A0A0B6XL55	Hydrolase (HAD superfamily)	<i>ywpJ_1</i>	1.63
A0A0D1HWC8	30S ribosomal protein S2	<i>rpsB</i>	1.63
A0A069FME4	50S ribosomal protein L16	<i>rplP</i>	1.63
A0A0D1HB86	Strain SA-120 Contig627, whole genome shotgun sequence	-	1.63
A0A0D1HPJ7	DNA-directed RNA polymerase subunit omega	<i>rpoZ</i>	1.64
A0A0D1I8Q0	Tyrosine-tRNA ligase	<i>tyrS</i>	1.64
A0A033UZC9	30S ribosomal protein S21	<i>rpsU</i>	1.65
A0A0C5I321	Glutamate-1-semialdehyde 2,1-aminomutase	<i>gsaB</i>	1.65
A0A0D1FN85	Methylenetetrahydrofolate-tRNA-(uracil-5-)-methyltransferase TrmFO	<i>gid</i>	1.66
A0A0D1HXC4	Glycine-tRNA ligase	<i>glyQS</i>	1.69
A0A077VEQ5	Endonuclease III	<i>nth</i>	1.69
A0A077TYV7	3-oxoacyl-[acyl-carrier-protein] synthase 2	<i>fabF</i>	1.70
A0A0D6DDD4	Phosphate acyltransferase	<i>plsX</i>	1.70
A0A077V1V2	50S ribosomal protein L10	-	1.70
A0A0D1I5W0	Phenylalanine-tRNA ligase alpha subunit	<i>pheS</i>	1.70
A0A0D1K2T0	Putative cytosolic protein	<i>QU38_07185</i>	1.71
A0A0D1HMM2	30S ribosomal protein S3	<i>rpsC</i>	1.72
A0A090LRJ4	Ferrochelatase	<i>hemH</i>	1.72
A0A0D1JTN2	30S ribosomal protein S10	-	1.72

Accession Number	Protein Name	Gene Name	Fold Change
A0A077UA73	RNA binding protein%2C contains ribosomal protein S1 domain	<i>yugI_2</i>	1.75
A0A090M2G5	Cobalamin biosynthesis CobT VWA domain protein	<i>SAU060112_70100</i>	1.75
A0A0D1H0K7	50S ribosomal protein L23	<i>rplW</i>	1.75
A0A077U6Y9	CobB/CobQ-like glutamine amidotransferase domain-containing protein	<i>ERS140026_02417</i>	1.75
A0A0D6DCH6	Scaffold protein sufB	<i>SAJPND1_00832</i>	1.75
A0A033UV22	Translation initiation factor IF-1	<i>infA</i>	1.75
A0A0D1H7G8	Thioredoxin	<i>QU38_12030</i>	1.76
A0A090LXL4	Glutamate-tRNA ligase	<i>gltX</i>	1.77
A0A077U0Z6	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	<i>accB</i>	1.78
A0A0D1JM30	Ribosomal silencing factor RsfS	<i>rsfS</i>	1.82
A0A0D1HMF1	Exodeoxyribonuclease 7 small subunit	<i>xseB</i>	1.83
A0A0D1K1S3	50S ribosomal protein L2	<i>rplB</i>	1.83
A0A0D1J193	30S ribosomal protein S12	<i>rpsL</i>	1.83
A0A0D1HQY5	Nucleoside diphosphate kinase	<i>ndk</i>	1.83
A0A0B6XQU1	Molybdenum cofactor biosynthesis protein E	<i>moaE</i>	1.84
A0A077V9E3	Acetyltransferase	<i>ERS140254_00101</i>	1.85
A0A0D1JTT1	AspS protein	<i>aspS</i>	1.85
A0A0D1IBH8	30S ribosomal protein S5	<i>rpsE</i>	1.85
A0A0D1JQF8	NADH dehydrogenase	<i>QU38_11320</i>	1.86
A0A0D1H8Z3	3-oxoacyl-[acyl-carrier-protein] synthase 3	<i>fabH</i>	1.86
A0A0B6XLK3	Haloacid dehalogenase-like hydrolase	<i>ppaX</i>	1.86
A0A0D1JTP6	Putative cytosolic protein	<i>QU38_03765</i>	1.87
A0A077VD35	Multidrug resistance protein (Function not yet clear)	<i>ERS140254_01513</i>	1.89
A0A0D1H5H3	Phenol-soluble modulins export ABC transporter ATP-binding protein PmtC	<i>QU38_06870</i>	1.89
A0A0D1J1L9	Phosphoglycerate kinase	<i>pgk</i>	1.90
A0A077VKN4	50S ribosomal protein L1	<i>rplA</i>	1.91
A0A0B6XPU4	Ribosome maturation factor RimP	<i>rimP</i>	1.94
A0A0D1H088	50S ribosomal protein L35	-	1.94
A0A0D1HPY4	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	<i>murE</i>	1.94
A0A0D1IUZ1	Citrate synthase	<i>QU38_08465</i>	1.95
A0A077VJ87	GTP-binding protein TypA/BipA	<i>typA</i>	1.95
A0A0D1JX26	Glutamine synthetase	<i>glnA</i>	1.95
A0A090N1V7	Porphobilinogen deaminase	<i>hemC</i>	1.97
A0A0D1IHK1	50S ribosomal protein L20	<i>rplT</i>	2.00
A0A077UBW6	O-methyltransferase family protein	<i>ERS140162_01570</i>	2.00
A0A077UAB5	D-2-hydroxyacid dehydrogenase	<i>ldhD_2</i>	2.00
A0A0D1HF64	30S ribosomal protein S18	<i>rpsR</i>	2.00
A0A0D1H5C2	50S ribosomal protein L22	<i>rplV</i>	2.00
A0A090LY44	Alanine-tRNA ligase	<i>alaS</i>	2.00

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1IJS9	50S ribosomal protein L21	<i>rplU</i>	2.00
A0A0D6DK60	Uncharacterized protein	-	2.01
A0A0B6XPZ7	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	<i>odhB</i>	2.01
A0A0D1I3J5	Urease accessory protein UreE	<i>ureE</i>	2.05
A0A033UV78	50S ribosomal protein L36	<i>rpmJ</i>	2.06
A0A090LQD9	Putative peptidyl-prolyl cis-trans isomerase	<i>SAU060112_10378</i>	2.06
A0A068DWZ8	Ribosomal protein L11 methyltransferase	<i>prmA</i>	2.06
A0A0D1HYX5	50S ribosomal protein L14	<i>rplN</i>	2.06
A0A090M065	Serine-tRNA ligase	<i>serS</i>	2.06
A0A0B6XKV9	Isochorismatase	<i>yecD</i>	2.08
A0A090N2E5	Mannitol-specific phosphotransferase enzyme IIA component	<i>mtlF</i>	2.08
A0A0D6DNQ3	Transcription accessory protein	<i>SAJPND1_02036</i>	2.08
A0A090LYX3	Inosine-uridine preferring nucleoside hydrolase	<i>SAU060112_40119</i>	2.09
A0A0B6XQV6	Iron-sulfur cluster assembly/repair protein ApbC	<i>apbC</i>	2.09
A0A0D1HPY4	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	<i>murE</i>	2.10
A0A0B6XMV1	Proline/betaine transporter	<i>proP</i>	2.10
A0A090LUB5	Uncharacterized protein	-	2.10
A0A0D1FKP4	50S ribosomal protein L30	<i>rpmD</i>	2.11
A0A077UEX9	Putative cysteine ligase BshC	<i>bshC</i>	2.13
A0A0D1K117	Peptide methionine sulfoxide reductase MsrA	<i>msrA</i>	2.14
A0A0D1IZY7	Superoxide dismutase	<i>QU38_15115</i>	2.15
A0A090LUF7	DNA repair/chromosome segregation ATPase	<i>ERS445051_02217</i>	2.17
A0A0D1IW07	Histidine-tRNA ligase	<i>hisS</i>	2.18
A0A0D6WDW6	Major tail protein	<i>ERS445051_01394</i>	2.20
A0A0D1IZ12	D-alanine-poly(phosphoribitol) ligase subunit 2	<i>dltC</i>	2.22
A0A0D1J2L0	Phosphomethylpyrimidine kinase	<i>SAJPND1_00574</i>	2.25
A0A090LTM2	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	<i>pfs</i>	2.28
A0A090LPS7	Putative ribosomal protein YlxQ	<i>rplGA</i>	2.29
A0A0D1H3G2	50S ribosomal protein L31 type B	<i>rpmE2</i>	2.30
A0A0D1HTN7	50S ribosomal protein L18	<i>rplR</i>	2.31
A0A077UL50	ATP-dependent Clp protease ATP-binding subunit ClpX	<i>clpX</i>	2.39
A0A0D6DD40	UPF0223 protein SAJPND1_01024	-	2.40
A0A0D6DE20	Alanine dehydrogenase	<i>SAJPND1_01657</i>	2.42
A0A0D1IX47	Trp repressor binding protein	<i>SAJPND1_00599</i>	2.45
A0A0D1HG99	Strain SA-120 Contig630, whole genome shotgun sequence	-	2.47
A0A0D1GXI2	Strain SA-120 Contig624, whole genome shotgun sequence	-	2.47
A0A0D1JWV4	50S ribosomal protein L28	<i>rpmB</i>	2.55
A0A077W130	Iron-sulfur cluster assembly ATPase SufC	<i>yurY</i>	2.55
A0A077UKA9	50S ribosomal protein L24	<i>rplX</i>	2.55
A0A0D1I822	30S ribosomal protein S20	<i>rpsT</i>	2.56
A0A0D1JQL5	Thioredoxin	<i>SAJPND1_00815</i>	2.56

Accession Number	Protein Name	Gene Name	Fold Change
A0A0C5IA88	Formate-tetrahydrofolate ligase	<i>fhs</i>	2.57
A0A0E1VP50	Aldehyde dehydrogenase (NAD) family protein	<i>HMPREF0776_0903</i>	2.62
A0A033V5W3	Cold shock protein CspA	<i>cspA</i>	2.63
A0A0B6XR80	Glyoxylate reductase/Glyoxylate reductase/Hydroxypyruvate reductase	<i>SASCBU26_02308</i>	2.63
A0A0D1J2E1	Translation initiation factor IF-3	<i>infC</i>	2.64
A0A0E1VTG8	Oxidoreductase, FAD/FMN-binding protein	<i>HMPREF0776_1945</i>	2.65
A0A0D3Q486	Uncharacterized protein	-	2.69
A0A0B6XKR5	Capsular polysaccharide synthesis enzyme Cap5I	<i>capI</i>	2.70
A0A090LYE2	Aminomethyltransferase	<i>gcvT</i>	2.72
A0A077VL65	Succinyl-diaminopimelate desuccinylase	<i>dapE</i>	2.75
A0A0B6XSJ7	Alcohol dehydrogenase	<i>curA</i>	2.76
SYL	Leucine-tRNA ligase	<i>leuS</i>	2.77
A0A090M2S9	Uncharacterized deoxyribonuclease YabD	-	2.77
A0A0D1JCN9	Peptidyl-tRNA hydrolase	<i>pth</i>	2.85
A0A0B6XST7	Urease subunit alpha	<i>ureC</i>	3.00
A0A0E1X668	2-oxoglutarate ferredoxin oxidoreductase subunit beta	<i>HMPREF0769_12488</i>	3.00
MURC	UDP-N-acetylmuramate-L-alanine ligase	<i>murC</i>	3.00
A0A0D1GP04	Succinyl-CoA ligase [ADP-forming] subunit alpha	<i>SAJPND1_01177</i>	3.05
A0A090LT64	Uncharacterized protein	-	3.09
A0A0E1X586	Phage major tail protein	<i>HMPREF0769_12240</i>	3.15
A0A0D6DD94	Phosphoesterase	<i>SAJPND1_01079</i>	3.15
A0A0D1JZ55	Putative cytosolic protein	<i>SAJPND1_01294</i>	3.25
A0A0D1HIZ5	Putative cytosolic protein	<i>SAJPND1_01624</i>	3.29
A0A0D6GZ63	Phage protein	<i>ERS445051_01398</i>	3.35
A0A0D1IPY9	Organic hydroperoxide resistance protein	<i>SAJPND1_00812</i>	3.44
A0A0D6G3W7	Serine-aspartate repeat-containing protein E	<i>sdrE</i>	3.47
A0A0D1H5K7	Strain SA-120 Contig628, whole genome shotgun sequence	-	3.47
A0A0B6XKZ1	Sorbitol dehydrogenase	<i>gutB_1</i>	3.60
A0A0D1JVV7	Oxygen-dependent choline dehydrogenase	<i>betA</i>	3.60
A0A033V401	Ferredoxin	<i>V070_00532</i>	3.65
A0A090LXA3	Lipase/esterase LipA	<i>SAU060112_10612</i>	3.70
A0A0B6XLS6	UDP-2-acetamido-2%2C6-dideoxy-beta-L-talose 4-dehydrogenase	<i>ERS094548_01225</i>	3.80
A0A077UAB9	S-ribosylhomocysteine lyase	<i>luxS</i>	3.80
A0A0D6GUT4	Membrane protein	<i>mmpL8</i>	3.85
A0A090M0E8	Molybdopterin synthase sulfur carrier subunit	<i>moaD</i>	3.91
A0A0D6HBG6	UPF0435 protein ERS445051_01856	-	3.93
A0A0E1VYJ0	Urease accessory protein UreG	<i>ureG</i>	3.95
A0A069G4G3	Recombination protein RecR	<i>recR</i>	4.00
G0XY48	Clumping factor A	<i>clfA</i>	4.05
A0A077UT21	Phage protein	<i>ERS140159_01807</i>	4.15

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D6HFI7	Succinyl-diaminopimelate desuccinylase	<i>dapE</i>	4.18
A0A0D6DN74	Aldehyde dehydrogenase	<i>SAJPND1_02098</i>	4.30
A0A0D1KAK6	Rhodanese-related sulfurtransferase	<i>SAJPND1_01707</i>	4.40
A0A0D1HB94	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	<i>gpmI</i>	4.45
A0A0D1GFP6	Transcription elongation factor GreA	<i>greA</i>	4.50
A0A090N1L9	UDP-glucose 4-epimerase	<i>capD</i>	4.65
A0A090LXH5	3-hexulose-6-phosphate isomerase	<i>hxlB</i>	4.77
A0A0B4N811	3-hexulose-6-phosphate synthase	<i>CH51_02975</i>	4.90
A0A090LZV4	Betaine-aldehyde dehydrogenase	<i>betB</i>	5.30
A0A0D1IUM8	L-serine dehydratase beta subunit	<i>SAJPND1_02531</i>	5.63
A0A077UW75	YceI-like domain protein	<i>ERS140266_00175</i>	5.70
A0A0C5HEJ3	Endoribonuclease L-PSP	<i>yabJ</i>	5.75
A0A0D1FVH2	Strain SA-120 Contig630, whole genome shotgun sequence	-	6.06
A0A0D1HWG4	ProteaseI	<i>SAJPND1_01839</i>	6.27
A0A0B6XR64	Urease subunit beta	<i>ureB</i>	6.58
A0A0B6XQZ3	S-ribosylhomocysteine lyase	<i>luxS</i>	6.75
A0A077U0G6	Glycine betaine transporter OpuD	<i>opuD_1</i>	7.61
A0A0D1H3E1	Sced	<i>SAJPND1_02072</i>	8.25
A0A0D1FGD6	Strain SA-120 Contig629, whole genome shotgun sequence	-	8.92
A0A077UNT4	YozC	<i>ERS140026_00525</i>	9.20