

Table S4 Differentially expressed proteins in the 10% NaCl group compared with the control group. The DEPs 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	0.08
A0A0D6DK32	Extracellular matrix binding protein	SAJPND1_00798	0.09
A0A0D6DCF3	Extracellular fibrinogen-binding protein	SAJPND1_01081	0.09
A0A0D6DFZ4	Leukocidin S subunit LukS	SAJPND1_01995	0.10
A0A090LXD5	Uncharacterized protein	-	0.10
A0A0D6DGW3	Gamma-hemolysin A subunit HlgA	SAJPND1_02409	0.11
OMP7	77 kDa membrane protein	SACOL2002	0.12
A0A0D1K3U3	Extracellular fibrinogen-binding protein	QU38_12095	0.13
A0A0D1JXR9	Strain SA-120 Contig630, whole genome shotgun sequence	QU38_15890	0.15
Q9AFB0	Leukocidin LukS component (Fragment)	-	0.19
SBI	Immunoglobulin-binding protein sbi	sbi	0.22
A0A0D6DFD4	Beta-lactamase regulator protein	SAJPND1_01896	0.22
A0A0C5HVE0	Pyruvate decarboxylase%3B Alpha-keto-acid decarboxylase	ipdC	0.22
A0A077TWE9	Lipoprotein	ERS094548_00195	0.22
A0A0C5HSI2	Gamma-hemolysin component B	ERS445051_01979	0.23
A0A0D6HPJ5	Lantibiotic transport ATP-binding protein	ecsA_3	0.23
A0A0D1H8B0	Threonine-tRNA ligase	A0A0D1H8B0	0.25
A7E1C4	Enterotoxin C2 (Fragment)	sec2	0.25
A0A068A489	Inhibitor	scn_2	0.25
A0A0D1I054	L-lactate dehydrogenase	ldh	0.25
A0A090LSD7	Uncharacterized protein	-	0.26
A0A077U8P9	Membrane spanning protein	ERS140026_02521	0.27
A0A090N157	Alpha-hemolysin	hly	0.28
ADH	Alcohol dehydrogenase	adh	0.29
A0A0D6DIM1	Ribokinase	SAJPND1_00306	0.29
A0A0D1HN80	Strain SA-120 Contig620, whole genome shotgun sequence	-	0.29
A0A077U1D0	Amino acid permease	steT	0.30
A0A0B6XPE8	Pyruvate carboxylase	cfiB_1	0.30
A0A0E0VS19	Carboxylic ester hydrolase	ST398NM01_2504	0.30
A0A077VAK0	Hexose phosphate transport protein	uhpT	0.30
A0A090LUS7	AraC family transcription regulator	araC	0.30
A0A077TT97	DNA-damage repair protein	umuC	0.30
A0A0D6DGG6	Uncharacterized protein	-	0.31
A0A0B6XL12	Pseudouridine-5'-phosphate glycosidase	psuG	0.32
A0A077U927	Pseudouridine-5'-phosphate glycosidase	psuG	0.32
A0A077V7K3	ABC transporter substrate-binding protein	psaA	0.33
A0A090LUS6	Lipoprotein	yehR	0.33
A0A0C2HZY8	Pyrimidine-nucleoside phosphorylase	pdp	0.33
A0A0D1GJW4	Arsenate reductase family protein	QU38_11110	0.33

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A0A0D6FNQ5	Immunoglobulin G-binding protein A	<i>spa</i>	0.33
A0A0D1HEF4	6,7-dimethyl-8-ribityllumazine synthase	<i>ribH</i>	0.33
A0A0D1JQX0	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.35
Q9S2Z4	Cell surface protein map-w	<i>map-w</i>	0.35
Q7DK27	ABC transporter ATP-binding protein	<i>stpA</i>	0.35
A0A0D6DN91	Thymidine phosphorylase	<i>SAJPND1_02113</i>	0.35
A0A077VMN9	Peptide methionine sulfoxide reductase MsrA	<i>msrA_1</i>	0.35
A0A090LW57	ABC transporter, permease protein	<i>SAU060112_100003</i>	0.36
A0A090LWP1	HTH-type transcriptional regulator SarS	<i>sarS</i>	0.38
A0A0D1GD88	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	<i>gpmA</i>	0.39
A0A0B6XTB4	N-acetylmuramoyl-L-alanine amidase%2C family 4	<i>ERS094548_01923</i>	0.39
A0A0D1G5I0	Strain SA-120 Contig630, whole genome shotgun sequence	<i>QU38_11030</i>	0.40
A0A0D1HCV5	Uncharacterized protein	-	0.40
A0A0D6GIM9	Autolysin	<i>atl_1</i>	0.40
A0A0C5HYQ5	SepS16B protein	<i>sepS16B</i>	0.40
A0A077UDD9	3-ketoacyl-CoA thiolase%3B Acetyl-CoA acetyltransferase	<i>ERS140248_02364</i>	0.40
A0A077VSV4	Peptide ABC transporter permease	<i>oppB_1</i>	0.40
A0A0D3QBH3	Peptide synthetase	<i>grsB</i>	0.40
A0A0A0Q4N9	HtrA-like serine protease	<i>htrA</i>	0.41
A0A0D1IIH6	Uncharacterized protein	-	0.42
A0A0D1GTD3	Strain SA-120 Contig622, whole genome shotgun sequence	<i>QU38_05245</i>	0.42
A0A0D6DDK7	Uncharacterized protein	<i>SAJPND1_01250</i>	0.42
A0A069GEF6	Threonine--tRNA ligase	<i>thrS_1</i>	0.42
A0A0D1HUP1	Nucleoside transporter	<i>QU38_09615</i>	0.43
A0A0E1AGE4	Uncharacterized protein	-	0.44
A0A090M2J3	Uncharacterized protein	<i>SAU060112_70120</i>	0.44
A0A0E1AHK4	Foldase protein PrsA	<i>prsA</i>	0.44
A0A0D1HQ98	Histidine kinase	<i>QU38_10565</i>	0.45
A0A090LTY1	Uncharacterized protein	-	0.45
A0A0E1AMS3	Uncharacterized protein	-	0.45
A0A0E1VQA6	Immunoglobulin-binding protein sbi	-	0.45
A0A0D1HD00	Universal stress protein	<i>uspA</i>	0.45
A0A090LR99	CobW/HypB/UreG, nucleotide-binding domain protein	<i>SAU060112_10579</i>	0.45
A0A077U988	Pyrimidine nucleoside transport protein	<i>nupC_2</i>	0.45
A0A0D1JLL3	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	<i>bioA</i>	0.45
A0A0B6XN73	3-oxoadipate enol-lactonase	<i>dehH1</i>	0.45
A0A0E1AE25	Phosphoglycolate phosphatase	<i>SAZ172_0574</i>	0.45
A0A0D1H739	Strain SA-120 Contig625, whole genome shotgun sequence	-	0.46
A0A0D1IB15	Strain SA-120 Contig624, whole genome shotgun sequence	-	0.46
A0A077UJ82	Uncharacterized protein	-	0.46
A0A0D1I600	Uncharacterized N-acetyltransferase QU38_12215	-	0.46

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A0A0D1K2N9	GlnQ protein	<i>glnQ</i>	0.47
A0A090LX90	Probable transcriptional regulatory protein yeeN	<i>yeeN</i>	0.47
A0A0D1IJC4	Strain SA-120 Contig621, whole genome shotgun sequence	-	0.47
A0A0B6XP33	Oligopeptide transport ATP-binding protein oppD	<i>oppD_1</i>	0.47
A0A0D1IXM8	Small heat shock protein	<i>QU38_07680</i>	0.48
A0A077TYE1	Uncharacterized protein	-	0.49
A0A0B6XRG8	Lipoprotein	<i>ERS094548_00892</i>	0.49
A0A077W0Q5	UPF0365 protein ERS140167_00916	-	0.49
A0A090N246	Formate/nitrite transporter	<i>nirC</i>	0.50
A0A068W8S1	Ribosomal RNA large subunit methyltransferase H	<i>orfX</i>	0.50
A0A0D1GJ10	Strain SA-120 Contig630, whole genome shotgun sequence	<i>QU38_15345</i>	0.50
A0A0D1JPH9	Strain SA-120 Contig629, whole genome shotgun sequence	<i>QU38_12985</i>	0.50
A0A090LVY0	Aspartate carbamoyltransferase	<i>pyrB</i>	0.50
A0A0B6XKT1	Aldehyde-alcohol dehydrogenase	<i>adhE</i>	0.50
A0A077V9M9	Response regulator SaeR	<i>saeR</i>	0.50
A0A0D1JT33	Cardiolipin synthase	<i>QU38_06435</i>	0.50
A0A077TYE7	Uncharacterized protein conserved in bacteria	<i>ERS140095_00284</i>	0.50
A0A090M2D6	Oligoendopeptidase F	<i>SAU060112_70075</i>	0.50
A0A0D6DGT6	Cystine-binding protein	<i>SAJPND1_02402</i>	0.50
A0A0D1HBY5	Pyridoxal 5'-phosphate synthase subunit PdxT	<i>pdxT</i>	0.50
A0A0D1G640	Arginine repressor	<i>argR</i>	0.50
A0A090LY09	GTPase Obg	<i>obg</i>	0.50
A0A077UJ58	Pyridoxal 5'-phosphate synthase subunit PdxS	<i>pdxS</i>	0.51
A0A098H232	Chromosome replication initiation protein dnaD	<i>dnaD</i>	0.51
A0A090LXQ9	Uncharacterized protein	-	0.51
A0A0B6XNE5	Hydrolase (HAD superfamily)	<i>ERS094548_00694</i>	0.52
A0A0D6FS99	Putative polyribitolphosphotransferase	<i>tagF_1</i>	0.52
A0A090LZA4	Chorismate mutase I/2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I beta%2C AroH/AroA I beta	<i>aroA</i>	0.52
A0A0D1GN53	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.53
A0A090LXT5	Peptidase C45	<i>SAU060112_110028</i>	0.53
A0A090LZI4	Uncharacterized protein	-	0.53
X5IX38	DNA-binding protein	<i>SAU060112_10479</i>	0.54
A0A0D1H4D9	Strain SA-120 Contig627, whole genome shotgun sequence	-	0.54
A0A077UDM1	Manganese ABC transporter%2C ATP-binding protein SitB	<i>sitB</i>	0.54
A0A0B6XP73	Lipoate-protein ligase	<i>lplJ_2</i>	0.54
A0A077U4E2	2-oxoglutarate/malate translocator-like protein	<i>ttdT</i>	0.54
A0A090M283	Catalase	<i>katA</i>	0.54
A0A077UZP7	Transcriptional repressor NrdR	<i>nrdR</i>	0.55
A0A0D1FF77	Coenzyme A disulfide reductase	<i>cdr</i>	0.55
A0A0D1HKP9	Arginase	<i>SAJPND1_02140</i>	0.55

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A0A090N1I7	Putative aldehyde dehydrogenase YwdH	<i>ywdH</i>	0.55
A0A090LRF4	Uncharacterized protein	-	0.55
A0A090LYD3	Uncharacterized protein	-	0.56
A0A0D1HIC5	L-threonine 3-dehydrogenase	<i>QU38_09780</i>	0.56
A0A077UYW0	Uncharacterized protein	-	0.56
A0A0B6XQC4	Serine hydroxymethyltransferase	<i>glyA</i>	0.56
A0A090N1L4	Diacetyl reductase ((S)-acetoin forming)	<i>butA</i>	0.56
A0A0D1H5M4	Transaldolase	<i>QU38_04770</i>	0.56
A0A0D1JGI6	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	<i>ispD</i>	0.56
A0A0B6XMG3	Argininosuccinate synthase	<i>argG</i>	0.57
A0A0D1GBS9	Signal transduction protein TRAP	<i>SAJPND1_01796</i>	0.57
A0A0E0VRM5	TenA	<i>ST398NM01_2137</i>	0.57
A0A0D1G1J9	Cytochrome c oxidase polypeptide II	<i>SAJPND1_00987</i>	0.58
A0A0D6DAQ1	6-phospho-beta-glucosidase	<i>SAJPND1_00245</i>	0.58
A0A077UG02	Acid phosphatase	<i>hel</i>	0.58
A0A077TZL7	Modification methylase MboII	<i>mboIIM</i>	0.58
A0A077VJX6	Deblocking aminopeptidase	<i>ysdC_1</i>	0.58
A0A090N1X3	Chaperone protein DnaK	<i>dnaK</i>	0.58
A0A090LW12	Poly (Glycerol-phosphate) alpha-glucosyltransferase	<i>SAU060112_10705</i>	0.58
A0A090LXY5	Uncharacterized protein	<i>SAU060112_120007</i>	0.58
A0A0D1GVJ7	Poly (Glycerol-phosphate) alpha-glucosyltransferase	<i>SAJPND1_00558</i>	0.59
A0A0D6DJ43	Teichoic acid biosynthesis protein X	<i>SAJPND1_00639</i>	0.59
A0A090LR26	Uncharacterized oxidoreductase YcsN	<i>ycsN</i>	0.60
A0A080V4N7	Membrane spanning protein	<i>yhhT_1</i>	0.60
A0A0E1VKR4	ABC transporter, ATP-binding protein	<i>HMPREF0776_1978</i>	0.60
A0A0D1IUP6	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.60
A0A090LWI3	Argininosuccinate lyase	<i>argH</i>	0.60
A0A077TYC4	Similar to putative sodium/glucose cotransporter	<i>sglT</i>	0.60
A0A090M057	Putative ATP-dependent helicase DinG homolog	<i>dinG</i>	0.60
A0A0B6XKT2	Ribose operon repressor%2C putative	<i>degA</i>	0.60
A0A0D1I5J3	Ribulose-phosphate 3-epimerase	<i>QU38_12445</i>	0.60
A0A069FTI7	Hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase	<i>thiD_1</i>	0.60
A0A090LUN2	Na ⁺ /H ⁺ antiporter family protein	<i>SAU060112_40163</i>	0.60
A0A0D1IL35	NAD kinase	<i>ppnK</i>	0.60
A0A0D1FA95	Negative regulator of genetic competence clpC	<i>QU38_09635</i>	0.60
A0A0B4NAS5	30S ribosomal protein S1	<i>rpsA</i>	0.60
A0A077W554	Membrane associated protein	<i>ERS140026_02425</i>	0.60
A0A090M1C4	Dihydroorotate dehydrogenase (quinone)	<i>pyrD</i>	0.61
A0A0B6XL00	Lipoprotein	<i>metQ_1</i>	0.61
A0A0D6GYJ2	Alanine dehydrogenase	<i>ald1</i>	0.61
A0A0C5HTL6	Dihydroxyacetone kinase	<i>dhaL</i>	0.63

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A0A0E0VSZ0	GTP pyrophosphokinase	<i>ST398NM01_2559</i>	0.63
A0A069GA97	30S ribosomal protein S1	-	0.63
A0A077U7R1	Cytochrome d ubiquinol oxidase subunit I	<i>cydA</i>	0.63
A0A0B6XNT6	Bifunctional ligase/repressor BirA	<i>birA</i>	0.64
A0A0E1VLF4	TIGR01777 family protein	<i>HMPREF0776_1780</i>	0.64
A0A090LUN7	Urocanate hydratase	<i>hutU</i>	0.64
A0A0D1J363	Uracil phosphoribosyltransferase	<i>upp</i>	0.64
A0A0D6DNP1	Uncharacterized protein	-	0.65
A0A090LUL7	DeoR-like helix-turn-helix domain protein	<i>SAU060112_40148</i>	0.67
A0A0E1VIJ7	HTH-type transcriptional regulator rot	<i>HMPREF0776_2797</i>	0.67
A0A0D6GAR1	Carboxylesterase	<i>est_2</i>	0.67
A0A0D6DK53	Glyoxylated reductase	<i>SAJPND1_00846</i>	0.67
A0A0B6XRM8	Glycine betaine transport ATP-binding protein	<i>proV_2</i>	0.67
A0A0D1HL09	Redox-sensing transcriptional repressor Rex	<i>rex</i>	0.67
A0A077U2Q8	Quinol oxidase polypeptide I QoxB	<i>qoxB</i>	0.67
A0A0D1GC10	Strain SA-120 Contig629, whole genome shotgun sequence	-	0.67
A0A0C5HTQ6	Oxidoreductase of aldo/keto reductase family%2C subgroup 1	<i>yvgN_1</i>	0.68
A0A0D1GID9	Strain SA-120 Contig630, whole genome shotgun sequence	-	0.68
A0A090N216	Uncharacterized protein	-	0.68
A0A0D1JYJ4	Strain SA-120 Contig628, whole genome shotgun sequence	<i>QU38_10035</i>	0.68
A0A077UFT7	Lipoprotein	<i>ERS140147_00473</i>	0.68
A0A0D6H2B5	Salicylate hydroxylase	<i>nagX</i>	0.68
A0A0D1HD94	Serine acetyltransferase	<i>sat</i>	0.69
A0A0B6XQW2	2-oxoisovalerate dehydrogenase subunit alpha	<i>bfmBAA</i>	0.69
A0A0E8GI61	GTPase Der	<i>engA</i>	0.69
A0A0D1K8W2	Bifunctional protein PyrR	<i>pyrR</i>	0.70
A0A0C5HMT4	GntR family transcriptional regulator	<i>treR_1</i>	0.70
A0A0D1H6Z1	Nitric oxide synthase oxygenase	<i>QU38_06960</i>	0.70
A0A0E1AE46	Phosphoenolpyruvate-dihydroxyacetone phosphotransferase, dihydroxyacetone binding subunit DhaK	<i>SAZ172_0661</i>	0.70
A0A077UP25	Membrane-bound serine protease	<i>ERS140159_00273</i>	0.70
A0A069FW70	Fructose-1,6-bisphosphatase class 3	<i>fbp</i>	0.70
A0A0B6XKQ5	Deoxyribose-phosphate aldolase	<i>dra_1</i>	0.70
A0A0D6DGV1	Staphyloxanthin biosynthesis protein CrtQ	<i>SAJPND1_02565</i>	0.70
A0A077U1Q7	Oxidoreductase%2C aldo/keto reductase family	<i>ERS140248_01341</i>	0.70
A0A0D1JZ91	General stress protein	<i>QU38_08215</i>	0.70
A0A090N275	Transcriptional regulator, TetR family	<i>SAU060112_40385</i>	0.70
A0A090M109	Gluconate operon transcriptional repressor	<i>gntR</i>	0.70
A0A090LYF9	Acetoin dehydrogenase E1 component beta-subunit	<i>acoB</i>	0.70
A0A0B6XKM4	Histidine ammonia-lyase	<i>hutH</i>	0.70
A0A0D6DEP2	Beta-lactamase	<i>SAJPND1_01897</i>	0.70
A0A0D1IUZ1	Citrate synthase	<i>QU38_08465</i>	0.70

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A0A077U7M7	Two component transcriptional regulator VraR%2C LuxR family	<i>vraR_2</i>	0.70
A0A0B6XL04	PTS system trehalose-specific transporter subunit IIBC	<i>treB</i>	0.71
A0A0B6XRJ3	Riboflavin biosynthesis protein RibD	<i>ribD</i>	0.71
A0A0D1JNX0	Glutamate racemase	<i>murI</i>	0.71
A0A0B6XRK6	Nicotinate phosphoribosyltransferase	<i>ERS094548_02369</i>	0.71
A0A0D1EZS5	Proline dehydrogenase	<i>SAJPND1_01717</i>	0.71
A0A0D1FPR0	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	<i>fabZ</i>	0.72
A0A090LVA4	Sulfite reductase [NADPH] flavoprotein alpha-component	<i>cysJ</i>	0.72
A0A0D6DMA3	2-succinylbenzoate-CoA ligase	<i>menE</i>	0.72
A0A0D6DPK7	Staphyloxanthin biosynthesis protein CrtP	<i>SAJPND1_02566</i>	0.73
A0A090LYL9	Teichoic acid biosynthesis protein F	<i>SAU060112_20185</i>	0.73
A0A0B6XL97	Periplasmic binding protein	<i>btuF</i>	0.73
A0A0B6XPW9	Sodium/proline symporter	<i>putP</i>	0.73
A0A0B6XQ10	Exported protein	<i>ERS094548_02603</i>	0.73
A0A077UAU6	Transcription regulator (Contains diacylglycerol kinase catalytic domain)	<i>dagK</i>	0.73
A0A0B6XQX6	Bifunctional protein: zinc-containing alcohol dehydrogenase%3B quinone oxidoreductase (NADPH:quinone reductase)	<i>ERS094548_01069</i>	0.73
A0A0E1X794	DEAD/DEAH box helicase	<i>HMPREF0769_12121</i>	0.73
A0A077UUV1	Hydrogen peroxide-inducible genes activator	<i>oxyR</i>	0.73
A0A0A0R7J1	RepL	-	0.73
A0A0D1I4D2	Oligoendopeptidase F	<i>QU38_11615</i>	0.74
A0A077UNV6	Pseudouridine synthase	<i>rluB</i>	0.74
A0A090LUF4	Ribose-5-phosphate isomerase A	<i>rpiA</i>	0.74
A0A090LUE4	Pseudouridine synthase	<i>ylyB</i>	0.75
A0A0D1HRD3	Strain SA-120 Contig627, whole genome shotgun sequence	-	0.75
A0A0D1JST6	Peroxide operon regulator	<i>QU38_07270</i>	0.75
A0A0D1GUW7	GTPase Era	<i>era</i>	0.75
A0A0D1IPW1	DNA polymerase III subunit beta	<i>QU38_15525</i>	0.75
A0A0B6XMZ2	Succinate dehydrogenase flavoprotein subunit	<i>sdhA_1</i>	0.75
A0A090LZZ7	Uncharacterized peptidase YqhT	<i>YqhT</i>	0.76
A0A077UYI3	Ribonuclease 3	<i>rnc</i>	0.76
A0A077UJ41	3-methyl-2-oxobutanoate hydroxymethyltransferase	<i>panB</i>	0.76
A0A090LVR9	Uncharacterized protein	<i>SAU060112_10595</i>	0.76
A0A077U7P6	Sugar phosphate isomerase/epimerase	<i>ERS140159_00782</i>	0.76
A0A0D1IP31	Septation ring formation regulator EzrA	<i>ezrA</i>	0.76
A0A0D1IBM2	DEAD-box ATP-dependent RNA helicase CshA	<i>cshA</i>	0.77
A0A0D6H5T9	NAD-dependent protein deacetylase	<i>cobB</i>	0.77
A0A0D6DD44	Glycerophosphoryl diester phosphodiesterase	<i>SAJPND1_01047</i>	0.77
A0A0D1IBW0	Strain SA-120 Contig620, whole genome shotgun sequence	<i>QU38_04480</i>	0.77

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A0A0D1G9T6	Tautomerase	<i>QU38_13190</i>	0.77
A0A0D1IKK8	10 kDa chaperonin	<i>groS</i>	0.77
A0A0D1JZP5	DNA repair protein RecN	<i>QU38_09335</i>	0.78
A0A0E1VKG9	Endonuclease MutS2	<i>mutS2</i>	0.78
A0A0D1HJ56	Strain SA-120 Contig628, whole genome shotgun sequence	-	0.78
A0A090LXX3	DNA polymerase	<i>polA</i>	0.78
A0A0D6DLY3	Pyrroline-5-carboxylate reductase	<i>proC</i>	0.78
A0A0D6DJB9	Histidinol-phosphate aminotransferase	<i>hisC</i>	0.78
A0A0D1HJP2	Ribosomal large subunit pseudouridine synthase D	<i>SAJPND1_01814</i>	0.78
A0A0D1HWP8	Dephospho-CoA kinase	<i>coaE</i>	0.78
A0A0D6DM29	5-formyltetrahydrofolate cyclo-ligase	<i>SAJPND1_01504</i>	0.78
A0A0D1JR64	Accessory regulator a	<i>QU38_10110</i>	0.78
A0A068A8Z0	Protein GrpE	<i>grpE</i>	0.78
A0A0D1HZ15	Cell division protein divic	<i>QU38_03180</i>	0.78
A0A0D1FJV3	Glucose-6-phosphate 1-dehydrogenase	<i>zwf</i>	0.79
A0A090LXP9	Uroporphyrinogen decarboxylase	<i>hemE</i>	0.79
A0A0D3Q7P5	3-phosphoshikimate 1-carboxyvinyltransferase	<i>aroA_2</i>	0.79
A0A090LXB7	Luciferase-like monooxygenase	<i>SAU060112_20273</i>	0.79
A0A0D6DFF7	Uncharacterized protein	-	0.80
A0A090LVS1	Potassium-transporting ATPase B chain	<i>kdpB</i>	0.80
A0A0D6HWL4	ATP-dependent helicase/deoxyribonuclease subunit B	<i>addB</i>	0.80
A0A0E1VI43	Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	<i>carB</i>	0.80
A0A090N1M7	Type-1 restriction enzyme R protein	<i>hsdR</i>	0.80
CCA	CCA-adding enzyme	<i>cca</i>	0.80
A0A0D1J100	Ribosomal-protein-alanine acetyltransferase	<i>SAJPND1_02696</i>	0.80
A0A0B6XMQ8	Myo-inositol-1(Or 4)-monophosphatase	<i>suhB_1</i>	0.80
A0A0D6DHW6	Glycosyltransferase	<i>SAJPND1_00237</i>	0.80
A0A077UBB6	Type I restriction modification DNA specificity domain protein	<i>hsdS</i>	0.80
A0A0D1K8D2	Tyrosine recombinase XerD	<i>xerD</i>	0.80
A0A090LYW3	Molybdopterine molybdenumtransferase	<i>moeA</i>	0.80
A0A0D6GHE7	Protease	<i>ERS445051_00905</i>	0.80
A0A0E1AFV2	Non-canonical purine NTP pyrophosphatase	<i>SAZ172_1150</i>	0.80
A0A0D1JJX2	Mevalonate kinase	<i>QU38_09960</i>	0.80
A0A069G475	Pyridine nucleotide-disulfide oxidoreductase	<i>CO98_1154</i>	0.80
A0A090LQG8	Protein dltD	<i>SAU060112_10398</i>	0.80
A0A0C5I2R4	Peptidase propeptide and YPEB domain-containing protein	<i>ERS445051_01691</i>	0.80
A0A0D1JKT6	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	<i>queA</i>	0.80
A0A0D1HD79	tRNA binding domain protein	<i>SAJPND1_01690</i>	0.80
A0A0D1I2B3	Chaperone protein DnaJ	<i>dnaJ</i>	0.80
A0A0D1HV16	Putative cytosolic protein	<i>QU38_12695</i>	0.81
A0A0D6DEN2	Uncharacterized protein	-	0.81

Accession Number	Protein Name	Gene Name	Fold Change
A0A090LYF0	Acetyl-CoA carboxylase, biotin carboxylase subunit	<i>accC</i>	0.82
A0A0D1I4Q5	Strain SA-120 Contig630, whole genome shotgun sequence	-	0.82
A0A0D1G9L3	Adenylosuccinate lyase	<i>QU38_06995</i>	0.82
A0A077U409	Protein GrpE	<i>grpE</i>	0.82
A0A0D6GTK5	3-hydroxy-3-methylglutaryl coenzyme A reductase	<i>mvaA</i>	0.83
A0A0B6XM19	Signal peptidase I	<i>spsB</i>	0.83
A0A077ULT9	Ribonuclease R	<i>rnr</i>	0.83
A0A0D1JS50	Strain SA-120 Contig626, whole genome shotgun sequence	<i>QU38_07375</i>	0.83
A0A0E1XJY5	Abi-like protein	<i>HMPREF0769_10093</i>	0.83
A0A033ULT9	ATP synthase subunit c	<i>V070_02071</i>	1.20
A0A0B6XRB8	Sodium export permease protein	<i>yhaP</i>	1.20
A0A0C5HFW6	Aromatic amino acid aminotransferase	<i>patA</i>	1.20
A0A0B6XM00	Iron binding protein from the HesB_IscA_SufA family	<i>ERS094548_00056</i>	1.20
A0A090LQ01	Putative DNA-binding protein	<i>SAU060112_10164</i>	1.20
A0A077W129	30S ribosomal protein S13	<i>rpsM</i>	1.20
A0A069FUU4	30S ribosomal protein S11	<i>rpsK</i>	1.20
A5X5X2	RNA polymerase-beta subunit (Fragment)	<i>rpoB</i>	1.20
A0A0D1FKQ9	30S ribosomal protein S9	<i>rpsI</i>	1.20
A0A090LTG7	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	<i>accD</i>	1.21
A0A0D1H0K7	50S ribosomal protein L23	<i>rplW</i>	1.21
A0A0C5HKE6	Hypothetical esterase/lipase	<i>pip</i>	1.21
A0A0B6XLD2	Sporulation protein	<i>yaaT</i>	1.21
A0A0E1AM34	Uncharacterized protein	-	1.21
A0A077U0Z6	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	<i>accB</i>	1.22
A0A0D1JM30	Ribosomal silencing factor RsfS	<i>rsfS</i>	1.22
A0A0B6XLK3	Haloacid dehalogenase-like hydrolase	<i>ppaX</i>	1.22
A0A0D1I5G9	50S ribosomal protein L19	-	1.22
A0A090LVT9	DNA topoisomerase 1	<i>topA</i>	1.22
A0A0D1G616	Putative cytosolic protein	<i>QU38_09200</i>	1.23
A0A0D1H8Z3	3-oxoacyl-[acyl-carrier-protein] synthase 3	<i>fabH</i>	1.23
A0A0D1GMH3	50S ribosomal protein L17	-	1.23
A0A0D1K0H1	30S ribosomal protein S16	-	1.24
A0A0D1HQY5	Nucleoside diphosphate kinase	<i>ndk</i>	1.24
A0A0B6XQS8	Valine--tRNA ligase	<i>valS</i>	1.24
A0A0D1HT39	NADH dehydrogenase	<i>QU38_11305</i>	1.24
A0A0D1I3J5	Urease accessory protein UreE	<i>ureE</i>	1.25
A0A0E0VNZ9	Glyceraldehyde-3-phosphate dehydrogenase	<i>ST398NM01_0851</i>	1.25
A0A0D1HT84	50S ribosomal protein L5	-	1.25
A0A0E0VM51	Acetate CoA-transferase YdiF	<i>ST398NM01_0245</i>	1.25
A0A090LTN7	Adenine phosphoribosyltransferase	<i>apt</i>	1.25

Accession Number	Protein Name	Gene Name	Fold Change
A0A090N220	Cyclic pyranopterin monophosphate synthase accessory protein	<i>moaC</i>	1.25
A0A0B6XL55	Hydrolase (HAD superfamily)	<i>ywpJ_1</i>	1.25
A0A0D6HKP6	Asparaginase	<i>ansA</i>	1.25
A0A0D1HYX5	50S ribosomal protein L14	<i>rplN</i>	1.25
A0A0E1XGI2	Uncharacterized protein	-	1.26
A0A090LQH4	Protein NagD homolog	<i>nagD</i>	1.27
A0A0D1HVU3	Strain SA-120 Contig623, whole genome shotgun sequence	-	1.28
A0A090N2E5	Mannitol-specific phosphotransferase enzyme IIA component	<i>mtlF</i>	1.28
A0A0E1AJ22	Probable thiol peroxidase	<i>tpx</i>	1.28
A0A0D1GW14	50S ribosomal protein L4	<i>rplD</i>	1.28
A0A0D6DCH6	Scaffold protein sufB	<i>SAJPND1_00832</i>	1.29
A0A0D1IW07	Histidine-tRNA ligase	<i>hisS</i>	1.29
A0A0D6HFE5	Repressor-like protein	<i>ERS445051_01972</i>	1.30
A0A0D1JPL9	Strain SA-120 Contig616, whole genome shotgun sequence	-	1.30
A0A0D1HF64	30S ribosomal protein S18	-	1.30
A0A0E1AHK5	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase-related deacylase	<i>SAZ172_1765</i>	1.30
A0A0B6XLN0	Uracil-DNA glycosylase	<i>ung</i>	1.30
A0A0E8GH95	Phage protein	<i>ERS195391_00924</i>	1.31
A0A0C2HDA0	Glycerol-3-phosphate dehydrogenase	<i>glpD</i>	1.33
A0A090LRD1	Molecular chaperone Hsp31 and glyoxalase 3	<i>hchA</i>	1.33
A0A0D1I6P2	Diaminopimelate decarboxylase	<i>lysA</i>	1.33
A0A0B6XNR9	Probable glycine dehydrogenase (decarboxylating) subunit 2	<i>gcvPB</i>	1.33
A0A0D1GNJ9	Putative pit accessory protein	<i>QU38_10340</i>	1.33
A0A077V1V2	50S ribosomal protein L10	<i>rplJ</i>	1.33
A0A0D1HI29	Putative tRNA (cytidine(34)-2'-O)-methyltransferase	<i>QU38_03970</i>	1.33
A0A0D1IHK1	50S ribosomal protein L20	<i>rplT</i>	1.33
A0A0D1HT50	Adenylate kinase	<i>adk</i>	1.34
A0A077VUG4	Hypoxanthine-guanine phosphoribosyltransferase	<i>hpt</i>	1.35
A0A0B6XN60	Probable dual-specificity RNA methyltransferase RlmN	<i>rlmN</i>	1.35
A0A0D1H0B5	50S ribosomal protein L27	<i>rpmA</i>	1.36
A0A0B6XP80	Similar to oxidoreductase	<i>yhdN</i>	1.36
A0A0B6XPL1	Aldo/keto reductase family protein	<i>yvgN</i>	1.36
A0A0D1HQV9	30S ribosomal protein S6	<i>rpsF</i>	1.38
A0A0D1J193	30S ribosomal protein S12	-	1.38
A0A068DY65	DNA ligase	<i>lig</i>	1.39
A0A0C5HKH2	PTS-dependent dihydroxyacetone kinase phosphotransfer protein	<i>dhaM</i>	1.40
A0A0D1FBM5	6-phosphogluconolactonase	<i>SAJPND1_01893</i>	1.40
A0A077W1K8	Pyrrolidone-carboxylate peptidase	<i>pcp</i>	1.40
A0A0B6XSS6	Molybdate-binding protein	<i>modA</i>	1.40

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D6DDB0	Dihydrofolate reductase	<i>SAJPND1_01369</i>	1.41
A0A0D1FXV8	Succinyl-CoA ligase [ADP-forming] subunit beta	<i>sucC</i>	1.42
A0A090LYX3	Inosine-uridine preferring nucleoside hydrolase	<i>SAU060112_40119</i>	1.42
A0A0D1J2E1	Translation initiation factor IF-3	<i>infC</i>	1.43
A0A0B6XPZ7	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	<i>odhB</i>	1.43
A0A0D6H0T7	Phage protein	<i>ERS445051_01427</i>	1.43
A0A033UV78	50S ribosomal protein L36	<i>rpmJ</i>	1.44
A0A090LXL4	Glutamate-tRNA ligase	<i>gltX</i>	1.45
A0A090LYB7	UDP-N-acetyl glucosamine-2-epimerase	<i>rffE</i>	1.45
A0A077U9X8	Two-component response regulator	<i>nreC</i>	1.46
A0A0D1I1V1	50S ribosomal protein L7/L12	-	1.47
A0A0D1HES6	Strain SA-120 Contig628, whole genome shotgun sequence	-	1.48
A0A0D1IKI9	Strain SA-120 Contig619, whole genome shotgun sequence	-	1.49
A0A0D1GP04	Succinyl-CoA ligase [ADP-forming] subunit alpha	<i>SAJPND1_01177</i>	1.49
A0A0D1HKI2	Ferric uptake regulation protein	<i>QU38_09445</i>	1.50
A0A077TYV7	3-oxoacyl-[acyl-carrier-protein] synthase 2	<i>fabF</i>	1.50
A0A0B6XNS5	Aspartate-semialdehyde dehydrogenase	<i>asd</i>	1.50
A0A0B6XQU1	Molybdenum cofactor biosynthesis protein E	<i>moaE</i>	1.50
A0A0D1HN41	Phosphoenolpyruvate carboxykinase [ATP]	<i>pckA</i>	1.51
A0A069FZ92	Branched-chain-amino-acid aminotransferase	<i>ilvE</i>	1.51
A0A0D1EZR2	Strain SA-120 Contig627, whole genome shotgun sequence	<i>QU38_08415</i>	1.51
A0A0D6DE20	Alanine dehydrogenase	<i>SAJPND1_01657</i>	1.52
A0A0D1I3V2	UDP-N-acetylenolpyruvoylglucosamine reductase	<i>murB</i>	1.53
A0A0D3Q4K0	ABC transporter permease protein	<i>CH51_01470</i>	1.53
A0A0D1HTP8	Strain SA-120 Contig628, whole genome shotgun sequence	-	1.54
A0A0D1H088	50S ribosomal protein L35	<i>rpmI</i>	1.55
A0A0D1JWV4	50S ribosomal protein L28	<i>rpmB</i>	1.55
A0A0D6GUT4	Membrane protein	<i>mmpL8</i>	1.55
A0A069FS69	Phosphocarrier protein HPr	<i>ptsH</i>	1.58
A0A033UDX3	33 kDa chaperonin	<i>hslO</i>	1.60
A0A0D1FDF3	UPF0291 protein QU38_13075	-	1.63
A0A0D6DD31	4-hydroxy-tetrahydrodipicolinate synthase	<i>dapA</i>	1.65
A0A090LZN4	Biotin carboxylase 1	<i>accC</i>	1.65
A0A0D1FG95	Deoxyadenosine kinase	<i>SAJPND1_00548</i>	1.65
A0A090LTB6	Methyltransferase small domain protein	<i>SAU060112_30089</i>	1.66
A0A0D1HT96	Strain SA-120 Contig620, whole genome shotgun sequence	-	1.69
A0A0D1H7G8	Thioredoxin	<i>QU38_12030</i>	1.69
A0A077ULL5	LPXTG surface protein	<i>sdrD</i>	1.70
A0A069G344	FeS assembly protein SufD	<i>sufD</i>	1.70
A0A0D1I822	30S ribosomal protein S20	<i>rpsT</i>	1.72
A0A0D6GKH3	FAD-dependent pyridine nucleotide-disulfide oxidoreductase	<i>fccB</i>	1.73

Accession Number	Protein Name	Gene Name	Fold Change
A0A077UL50	ATP-dependent Clp protease ATP-binding subunit	<i>clpX</i>	1.73
A0A0D1JUA6	UPF0473 protein QU38_08855	-	1.74
A0A0B6XSQ4	DNA repair/chromosome segregation ATPase	<i>ERS094548_01003</i>	1.74
A0A033UZC9	30S ribosomal protein S21	<i>rpsU</i>	1.75
A0A0D1IZY7	Superoxide dismutase	<i>QU38_15115</i>	1.75
A0A0D1HPY4	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	<i>murE</i>	1.75
A0A0D1H3E1	Sced	<i>SAJPND1_02072</i>	1.75
A0A0B6XR64	Urease subunit beta	<i>ureB</i>	1.75
A0A0D6HMU5	FmhA protein of FemAB family	<i>fmhA</i>	1.76
A0A0D6FMN0	Putative cytosolic protein	<i>ERS445051_00083</i>	1.78
A0A0D1GUR6	Strain SA-120 Contig627, whole genome shotgun sequence	-	1.78
A0A0D1H1Q3	Glyoxalase family protein	<i>QU38_12370</i>	1.78
A0A090LXA3	Lipase/esterase LipA	<i>SAU060112_10612</i>	1.80
A0A033UV22	Translation initiation factor IF-1	<i>infA</i>	1.80
A0A090M065	Serine--tRNA ligase	<i>serS</i>	1.82
A0A0C5HY37	Glycine cleavage system H protein	<i>gcvH_2</i>	1.82
A0A0D1JMR1	Acyl carrier protein	<i>acpP</i>	1.83
A0A077USG2	Immunodominant staphylococcal antigen A	<i>isaA</i>	1.83
A0A068A921	Nitrate reductase	<i>narH</i>	1.85
A0A0D6DE64	Putative cytosolic protein	<i>SAJPND1_01441</i>	1.90
A0A0E0VPB3	Tripeptidase T	<i>ST398NM01_1577</i>	1.90
A0A090LUB5	Uncharacterized protein	-	1.95
A0A090N225	Secretory antigen	<i>ssaA</i>	1.95
A0A0B6XQV4	Alpha-amylase	<i>mala</i>	2.00
A0A0D1K117	Peptide methionine sulfoxide reductase MsrA	<i>msrA</i>	2.00
MURC	UDP-N-acetylmuramate-L-alanine ligase	<i>murC</i>	2.02
A0A0D1INB5	Arginine deiminase	<i>arcA</i>	2.07
A0A0D6HFI7	Succinyl-diaminopimelate desuccinylase	<i>dapE</i>	2.07
A0A077U2I8	FMN-dependent NADH-azoreductase	<i>azoR</i>	2.10
A0A0D1JQL5	Thioredoxin	<i>SAJPND1_00815</i>	2.11
A0A090LQD9	Putative peptidyl-prolyl cis-trans isomerase	<i>SAU060112_10378</i>	2.17
A0A090LUF7	DNA repair/chromosome segregation ATPase	<i>ERS445051_02217</i>	2.22
A0A0D6DD40	UPF0223 protein SAJPND1_01024	-	2.26
A0A0D1I7V8	Triosephosphate isomerase	<i>tpiA</i>	2.27
A0A077VA34	Uncharacterized protein	<i>ERS140026_01689</i>	2.28
A0A0D1FZV0	Strain SA-120 Contig626, whole genome shotgun sequence	<i>QU38_07345</i>	2.28
A0A077VL65	Succinyl-diaminopimelate desuccinylase	<i>dapE</i>	2.30
A0A0B6XKZ1	Sorbitol dehydrogenase	<i>gutB_1</i>	2.30
A0A0D1GRH1	Superoxide dismutase	<i>QU38_09165</i>	2.36
A0A077TYH3	Uncharacterized protein	-	2.37
A0A077UT21	Phage protein	<i>ERS140159_01807</i>	2.40
A0A0B4N811	3-hexulose-6-phosphate synthase	<i>CH51_02975</i>	2.40

Accession Number	Protein Name	Gene Name	Fold Change
A0A0D1I4N9	Strain SA-120 Contig630, whole genome shotgun sequence	-	2.41
A0A0D1HX32	Strain SA-120 Contig626, whole genome shotgun sequence	-	2.43
A0A090LTM2	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	<i>pfs</i>	2.44
A0A0D1IW19	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	<i>SAJPND1_01561</i>	2.44
A0A0D1HYD3	Strain SA-120 Contig626, whole genome shotgun sequence	<i>QU38_07650</i>	2.46
A0A0D6WDW6	Major tail protein	<i>ERS445051_01394</i>	2.50
A0A0D1FA44	Strain SA-120 Contig617, whole genome shotgun sequence	-	2.52
A0A077UAB9	S-ribosylhomocysteine lyase	<i>luxS</i>	2.53
A0A077UBW6	O-methyltransferase family protein	<i>ERS140162_01570</i>	2.55
A0A0D1GNT7	Strain SA-120 Contig628, whole genome shotgun sequence	-	2.55
A0A0D1IPY9	Organic hydroperoxide resistance protein	<i>SAJPND1_00812</i>	2.56
A0A0D1K2T0	Putative cytosolic protein	<i>QU38_07185</i>	2.64
A0A069G4G3	Recombination protein RecR	<i>recR</i>	2.77
A0A0C5HEJ3	Endoribonuclease L-PSP	<i>yabJ</i>	2.85
A0A0D1K3I9	Cold shock protein	<i>QU38_11035</i>	2.89
A0A0D1HB94	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	<i>gpmI</i>	2.90
A0A0D1H2E4	UPF0356 protein SAJPND1_01017	-	2.97
A0A0D1JVV7	Oxygen-dependent choline dehydrogenase	<i>betA</i>	3.00
A0A077UW75	YceI-like domain protein	<i>ERS140266_00175</i>	3.00
A0A0D1HIZ5	Putative cytosolic protein	<i>SAJPND1_01624</i>	3.01
A0A090LVJ3	Ornithine carbamoyltransferase	<i>arcB</i>	3.09
A0A0D1KAK6	Rhodanese-related sulfurtransferase	<i>SAJPND1_01707</i>	3.15
A0A0D1HYC8	Nitrite reductase [NAD(P)H] large subunit	<i>SAJPND1_02388</i>	3.17
A0A0E1VTG8	Oxidoreductase, FAD/FMN-binding protein	<i>HMPREF0776_1945</i>	3.20
A0A090M0E8	Molybdopterin synthase sulfur carrier subunit	<i>moaD</i>	3.23
A0A0D3Q462	Uncharacterised protein	<i>CH51_01290</i>	3.31
A0A0D1H4E0	Strain SA-120 Contig630, whole genome shotgun sequence	<i>QU38_15895</i>	3.40
G0XY48	Clumping factor A	<i>clfA</i>	3.45
A0A0E1X586	Phage major tail protein	<i>HMPREF0769_12240</i>	3.50
A0A0D3Q486	Uncharacterized protein	-	3.68
A0A033V5W3	Cold shock protein CspA	<i>cspA</i>	3.75
A0A0B6XQZ3	S-ribosylhomocysteine lyase	<i>luxS</i>	3.80
A0A0D6HBG6	UPF0435 protein ERS445051_01856	-	3.98
A0A0D1GFP6	Transcription elongation factor GreA	<i>greA</i>	4.06
A0A077UAB5	D-2-hydroxyacid dehydrogenase	<i>ldhD_2</i>	4.25
A0A0D1JZ55	Putative cytosolic protein	<i>SAJPND1_01294</i>	4.52
A0A0B6XLS6	UDP-2-acetamido-2%2C6-dideoxy-beta-L-talose 4-dehydrogenase	<i>ERS094548_01225</i>	5.15
A0A0D6G3W7	Serine-aspartate repeat-containing protein E	<i>sdrE</i>	5.16
A0A0B6XKR5	Capsular polysaccharide synthesis enzyme Cap5I	<i>capI</i>	5.40
A0A077UNT4	YozC	<i>ERS140026_00525</i>	6.35

Accession Number	Protein Name	Gene Name	Fold Change
A0A090N1L9	UDP-glucose 4-epimerase	<i>capD</i>	7.55