Supplementary information

Multi-omics characterization of the osmotic stress resistance and protease activities of the halophilic bacterium *Pseudoalteromonas phenolica* in response to salt stress

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Table S1. List of identified proteins in the intracellular protein analysis

Protein names	**Majority protein IDs**	**Fold change (high-salt/normal-salt)**	***p* value**
Bifunctional protein PutA	A0A0S2JZ14	0.0361	0.0000
Alkaline phosphatase	A0A0S2K8F1	0.0698	0.0000
Putative Fe transport outer membrane receptor protein	A0A0S2JYS5	0.0749	0.0000
Chemotaxis protein	A0A0S2JZE9	0.0852	0.0000
Peptidase dimerization domain-containing protein	A0A0S2K5X0	0.0914	0.0000
Alkaline phosphatase	A0A0S2K730	0.1010	0.0000
Putative signal transduction protein	A0A0S2K4T3	0.1100	0.0012
3-ketoacyl-(Acyl-carrier-protein) reductase	A0A0S2K1U5	0.1212	0.0001
Glucose-6-phosphate 1-dehydrogenase	A0A0S2K0G6	0.1431	0.0001
TonB-dependent receptor	A0A0S2K3G6	0.1478	0.0016
Glucan endo-1,3-beta-D-glucosidase	A0A0S2K2H7	0.1626	0.0002
Phage shock protein	A0A0S2K449	0.1690	0.0003
Glutamate--tRNA ligase	A0A0S2JZH4	0.1705	0.0549
Transaldolase	A0A0S2K4C6	0.1706	0.0014
Pyruvate kinase	A0A0S2K267	0.2088	0.0005
GTP-binding protein TypA/BipA	A0A0S2K5M9	0.2181	0.0006
Transcriptional regulator	A0A0S2JY35	0.2483	0.0000
Glyceraldehyde-3-phosphate dehydrogenase	A0A0S2K154	0.2515	0.0001
Aminotransferase	A0A0S2K3S2	0.2517	0.0001
Phenylalanine--tRNA ligase beta subunit	A0A0S2K451	0.2663	0.0217
Aspartate--tRNA ligase	A0A0S2K0R7	0.2705	0.0001
Alpha-1,4 glucan phosphorylase	A0A0S2K8T5	0.2726	0.0000
Elongation factor G	A0A0S2JX62	0.2743	0.0020
SpoOM family protein	A0A0S2K199	0.2749	0.0093
Uncharacterized protein	A0A0S2K4R6	0.2753	0.0138
Acetoacetyl-CoA reductase	A0A0S2K3T5	0.2769	0.0000

Nitrogen regulatory protein P-II	A0A0S2JZB8	0.2831	0.0004
Acetyl-CoA carboxylase, biotin carboxylase subunit	A0A0S2JX88	0.2860	0.0011
Orotate phosphoribosyltransferase	A0A0S2K5C4	0.2867	0.0117
Uncharacterized protein	A0A0S2K337	0.2953	0.0015
Glyoxalase	A0A0S2K6L7	0.3002	0.0009
Uncharacterized protein	A0A0S2JZM2	0.3005	0.0005
GMP synthase [glutamine-hydrolyzing]	A0A0S2K4D2	0.3006	0.0016
Site-determining protein	A0A0S2K985	0.3024	0.0001
Phosphoserine aminotransferase	A0A0S2K1T7	0.3191	0.0167
Phosphoglucomutase	A0A0S2K1V0	0.3239	0.0244
Phosphopentomutase	A0A0S2K7M7	0.3305	0.0076
RNA polymerase-binding transcription factor DksA	A0A0S2JY46	0.3306	0.0147
Protein phosphatase CheZ	A0A0S2K0D8	0.3381	0.0054
DNA gyrase subunit A	A0A0S2K1X3	0.3381	0.0391
Anti-RNA polymerase sigma 70 factor	A0A0S2JXP1	0.3392	0.0007
PhoH-like protein	A0A0S2K4C2	0.3434	0.0543
Regulator of ribonuclease activity A	A0A0S2K581	0.3539	0.0103
Purine nucleoside phosphorylase DeoD-type	A0A0S2K7Y0	0.3605	0.0001
TonB-dependent receptor	A0A0S2JZG5	0.3655	0.0315
Proline--tRNA ligase	A0A0S2K1V5	0.3885	0.0050
GTP-binding protein	A0A0S2K313	0.3921	0.0001
Alanine dehydrogenase	A0A0S2K1V8	0.3939	0.0000
Putative manganese binding agmatinase (SpeB)	A0A0S2K911	0.3966	0.0043
Isoleucine--tRNA ligase	A0A0S2JZD6	0.3983	0.0151
Uncharacterized protein	A0A0S2K9M7	0.3998	0.0000
Argininosuccinate synthase	A0A0S2K5T5	0.4086	0.0503
Enoyl-[acyl-carrier-protein] reductase [NADH]	A0A0S2K4A1	0.4105	0.0000
Bifunctional purine biosynthesis protein PurH	A0A0S2K4T8	0.4124	0.0627
Aminopeptidase YpdF (MP-, MA-, MS-,AP-,NP-specific)	A0A0S2K1S1	0.4143	0.0280

Urea carboxylase	A0A0S2K291	0.4151	0.0004
Glycine--tRNA ligase alpha subunit	A0A0S2JWM8	0.4219	0.0003
UPF0234 protein PP2015_2926	A0A0S2K520	0.4299	0.0003
ATP-dependent Clp protease ATP-binding subunit ClpX	A0A0S2K4H5	0.4315	0.0017
Uncharacterized protein	A0A0S2K201	0.4421	0.0017
Peptidyl-prolyl cis-trans isomerase	A0A0S2K2U1	0.4453	0.1200
Ornithine cyclodeaminase	A0A0S2K2E9	0.4466	0.0742
Putative enzyme related to lactoylglutathione lyase	A0A0S2K601	0.4491	0.0961
Valine--tRNA ligase	A0A0S2K4S3	0.4529	0.0064
5-methylthioadenosine/S-adenosylhomocysteine nucleosidase	A0A0S2K4E8	0.4591	0.0276
S-adenosylmethionine synthase	A0A0S2K4F2	0.4595	0.0004
50S ribosomal protein L30	A0A0S2K6N1	0.4606	0.0333
Putative glucose-6-phosphate 1-epimerase	A0A0S2K640	0.4625	0.0346
Threonine--tRNA ligase	A0A0S2K1A2	0.4663	0.0289
Putative Fe transport outer membrane receptor protein	A0A0S2K8L7	0.4709	0.0000
Cytochrome c oxidase, cbb3-type, subunit I	A0A0S2K0R3	0.4714	0.1255
Oligopeptidase A	A0A0S2K4W4	0.4779	0.0104
Tyrosine--tRNA ligase	A0A0S2K5P6	0.4819	0.0621
Phosphoribosylformylglycinamidine cyclo-ligase	A0A0S2K1D1	0.4838	0.0328
Quinol oxidase, subunit I	A0A0S2K7T0	0.4870	0.0144
Glutathione synthetase	A0A0S2K4G0	0.4880	0.0098
Outer membrane protein with a TonB box	A0A0S2K8B9	0.4918	0.0000
Cell division topological specificity factor	A0A0S2K8P7	0.4959	0.0038
Nicotinate-nucleotide pyrophosphorylase	A0A0S2JYH4	0.4973	0.0003
Glucose-1-phosphate adenylyltransferase	A0A0S2K8F3	0.4992	0.0003
Histidine--tRNA ligase	A0A0S2JY03	0.5031	0.0135
Acetyl-CoA acetyltransferase	A0A0S2K293	0.5070	0.0001
Uncharacterized protein	A0A0S2K8F4	0.5147	0.2428
Phenylalanine--tRNA ligase alpha subunit	A0A0S2K366	0.5227	0.0081

Transcription termination/antitermination protein NusA	A0A0S2JZV0	0.5280	0.0036
Fumarate/nitrate reduction transcriptional regulator	A0A0S2K1D4	0.5288	0.0455
Chemotaxis response regulator protein-glutamate methylesterase	A0A0S2K661	0.5367	0.0231
Superoxide dismutase	A0A0S2K2R9	0.5400	0.0002
Phospho-2-dehydro-3-deoxyheptonate aldolase	A0A0S2K8K1	0.5428	0.0625
Trigger factor	A0A0S2K3H0	0.5437	0.0000
DNA-directed RNA polymerase subunit omega	A0A0S2K5T2	0.5454	0.0713
Succinate--CoA ligase [ADP-forming] subunit beta	A0A0S2K2T2	0.5468	0.0000
Uncharacterized protein	A0A0S2K4P9	0.5477	0.0019
Periplasmic calcium binding protein	A0A0S2K6S5	0.5509	0.0003
Bacterioferritin	A0A0S2K7X9	0.5522	0.0045
Manganese-dependent inorganic pyrophosphatase	A0A0S2K594	0.5560	0.0051
Bacterioferritin	A0A0S2K830	0.5592	0.0272
Isopenicillin N synthase related dioxygenase	A0A0S2K2T7	0.5605	0.0000
Uridylate kinase	A0A0S2K414	0.5645	0.0002
Dihydroxy-acid dehydratase	A0A0S2K5K3	0.5677	0.0369
Arginine N-succinyltransferase	A0A0S2K551	0.5701	0.0017
Asparagine--tRNA ligase	A0A0S2K254	0.5725	0.0316
Chemotaxis protein methyltransferase	A0A0S2K018	0.5760	0.0085
DksA-type zinc finger protein	A0A0S2K1Z7	0.5826	0.0005
Queuine tRNA-ribosyltransferase	A0A0S2JXZ5	0.5834	0.2980
Malic enzyme	A0A0S2K641	0.5836	0.0009
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	A0A0S2K5Q0	0.5852	0.1079
Acyl-CoA dehydrogenase	A0A0S2K984	0.5852	0.2486
CBS domain containing membrane protein	A0A0S2K1I3	0.5885	0.0017
ATP-dependent Clp protease proteolytic subunit	A0A0S2K479	0.5888	0.0526
Uncharacterized protein	A0A0S2K597	0.5894	0.0497
Response regulator	A0A0S2K487	0.5912	0.0002
Succinate--CoA ligase [ADP-forming] subunit alpha	A0A0S2K1X7	0.5925	0.0003

Cysteine synthase	A0A0S2K3E9	0.5948	0.0004
Leucyl aminopeptidase	A0A0S2K958	0.5989	0.0079
Response regulator in two-component regulatory system with PhoQ	A0A0S2K345	0.6046	0.0080
UPF0502 protein PP2015_43	A0A0S2JWY1	0.6063	0.0253
Chaperone protein HtpG	A0A0S2K203	0.6153	0.0004
Chaperone protein ClpB	A0A0S2JZ80	0.6156	0.0074
Protein RecA	A0A0S2K534	0.6247	0.0000
Glutamate dehydrogenase	A0A0S2K1A4	0.6273	0.0001
Helix-turn-helix protein	A0A0S2K3Z5	0.6279	0.0545
Elongation factor Tu	A0A0S2JXI1	0.6281	0.0000
TonB system transporter ExbD2	A0A0S2K2I9	0.6310	0.4639
PrkA family serine protein kinase	A0A0S2K2I6	0.6318	0.0143
Transcription termination/antitermination protein NusG	A0A0S2JXX4	0.6376	0.0001
Ribosome-binding ATPase YchF	A0A0S2K3S0	0.6376	0.0006
Peroxiredoxin/glutaredoxin protein	A0A0S2JZD1	0.6431	0.0066
Glutathione peroxidase	A0A0S2JZA2	0.6447	0.0013
Citrate synthase	A0A0S2K238	0.6447	0.0004
Methylmalonate-semialdehyde dehydrogenase	A0A0S2K298	0.6450	0.0613
Leucine--tRNA ligase	A0A0S2K3R9	0.6466	0.0208
Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	A0A0S2K693	0.6469	0.2318
Phosphoribosylformylglycinamidine synthase	A0A0S2JZQ2	0.6545	0.0032
Shikimate kinase	A0A0S2K5G3	0.6552	0.0473
Uncharacterized protein	A0A0S2K9A2	0.6556	0.1493
ATP-dependent protease ATPase subunit HslU	A0A0S2K5T7	0.6557	0.0001
dUTP diphosphatase	A0A0S2K672	0.6559	0.0576
Uridine phosphorylase	A0A0S2K8B1	0.6569	0.0002
50S ribosomal protein L18	A0A0S2K5P4	0.6579	0.0565
Glycine--tRNA ligase beta subunit	A0A0S2JWZ9	0.6582	0.0079

Hydroxyproline-2-epimerase	A0A0S2K1Q7	0.6594	0.0006
RNA polymerase sigma factor RpoD	A0A0S2K5S8	0.6627	0.0546
50S ribosomal protein L14	A0A0S2K582	0.6678	0.0020
Protein-export protein SecB	A0A0S2JY60	0.6697	0.0745
Isocitrate dehydrogenase	A0A0S2K8G3	0.6727	0.3382
Glutathione-disulfide reductase	A0A0S2K5Z1	0.6752	0.0086
Flavodoxin	A0A0S2K2Q9	0.6759	0.0702
NAD-dependent epimerase/dehydratase	A0A0S2JY85	0.6779	0.0535
NH(3)-dependent NAD(+) synthetase	A0A0S2JWZ7	0.6791	0.1134
Delta-aminolevulinic acid dehydratase	A0A0S2K6J5	0.6806	0.0007
Polyhydroxyalkanoic acid synthase	A0A0S2K4H2	0.6838	0.0033
Two-component response regulator	A0A0S2K4J3	0.6858	0.3431
Acyltransferase	A0A0S2K5R9	0.6861	0.1100
Serine--tRNA ligase	A0A0S2K0N1	0.6865	0.0027
Peptidase M16	A0A0S2K3K3	0.6909	0.0190
Ribose-5-phosphate isomerase A	A0A0S2K5C2	0.6926	0.5064
30S ribosomal protein S11	A0A0S2K5L1	0.6947	0.0006
Elongation factor G	A0A0S2K5U1	0.6969	0.0018
Glycine cleavage system H protein	A0A0S2JZF6	0.6985	0.0482
Carbamoyl-phosphate synthase large chain	A0A0S2K2X6	0.6999	0.1683
Branched-chain-amino-acid aminotransferase	A0A0S2K5I1	0.7010	0.3371
TIGR02647 family protein	A0A0S2K9A1	0.7060	0.0251
Aminomethyltransferase	A0A0S2JYK1	0.7067	0.0000
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	A0A0S2K423	0.7069	0.0111
Twitching motility protein PilT	A0A0S2K4A5	0.7076	0.0040
Fe/S biogenesis protein NfuA	A0A0S2K595	0.7076	0.1831
30S ribosomal protein S10	A0A0S2K565	0.7156	0.0056
Purine-binding chemotaxis protein	A0A0S2JZ72	0.7171	0.1513
Peroxiredoxin 2	A0A0S2K526	0.7173	0.0006

Methionine--tRNA ligase	A0A0S2K186	0.7175	0.0205
Elongation factor P	A0A0S2JXP7	0.7177	0.0720
2-amino-3-ketobutyrate coenzyme A ligase	A0A0S2JZP1	0.7178	0.0002
Ribonucleotide-diphosphate reductase subunit beta	A0A0S2K1S9	0.7183	0.2017
Adenylosuccinate synthetase	A0A0S2K5G4	0.7186	0.0235
Phosphoglycerate kinase	A0A0S2JYY8	0.7203	0.0006
Decarboxylase family protein	A0A0S2K8I2	0.7212	0.1519
30S ribosomal protein S2	A0A0S2K342	0.7213	0.0000
Flagellin	A0A0S2JZ74	0.7276	0.0011
Chemotaxis protein	A0A0S2JZN8	0.7324	0.0076
Peptidyl-prolyl cis-trans isomerase	A0A0S2JYW9	0.7338	0.0001
Adenylosuccinate lyase	A0A0S2K1N6	0.7348	0.0039
Cell division protein FtsZ	A0A0S2JXT4	0.7371	0.0007
Acyl-CoA dehydrogenase	A0A0S2K1R4	0.7381	0.0934
RNA polymerase sigma factor RpoS	A0A0S2K4Q1	0.7394	0.1459
Transcriptional regulator	A0A0S2JYH8	0.7405	0.0186
Nucleoside diphosphate kinase	A0A0S2JZ01	0.7411	0.0009
3-oxoacyl-ACP synthase	A0A0S2K1F8	0.7464	0.0008
Aspartyl-tRNA amidotransferase subunit B	A0A0S2K4H6	0.7477	0.3353
DNA gyrase subunit B	A0A0S2JWX9	0.7478	0.0558
50S ribosomal protein L13	A0A0S2JYE6	0.7503	0.0329
Peptidase M14, carboxypeptidase A	A0A0S2K4X4	0.7516	0.4917
Acetyl-CoA carboxylase, carboxyltransferase component (Subunits alpha and beta)	A0A0S2K2K1	0.7529	0.3305
Glutamine--tRNA ligase	A0A0S2K287	0.7569	0.3360
30S ribosomal protein S6 modification protein	A0A0S2JZV4	0.7579	0.3104
Uncharacterized protein	A0A0S2K160	0.7624	0.0355
Glutamate-1-semialdehyde 2,1-aminomutase	A0A0S2K4G3	0.7626	0.0060
tRNA (cytidine/uridine-2-O-)-methyltransferase TrmJ	A0A0S2K4S8	0.7670	0.4481

Transcription termination factor Rho	A0A0S2JX09	0.7690	0.0003
Ribonucleoside-diphosphate reductase	A0A0S2K0W0	0.7740	0.5219
Fructose-1,6-bisphosphatase class 1	A0A0S2K580	0.7762	0.2351
Uncharacterized protein	A0A0S2K0X9	0.7776	0.5503
Lipoprotein	A0A0S2K4G6	0.7858	0.0034
Dihydroorotase	A0A0S2JZT8	0.7864	0.0088
Phosphoribosylaminoimidazole-succinocarboxamide synthase	A0A0S2K516	0.7886	0.1093
50S ribosomal protein L23	A0A0S2K6F3	0.7901	0.0166
Uroporphyrinogen decarboxylase	A0A0S2JY40	0.7913	0.0200
SapC	A0A0S2K0Q9	0.7919	0.0048
Rod shape-determining protein MreB	A0A0S2JY94	0.7936	0.1097
Transcription elongation factor GreA	A0A0S2K3J0	0.7959	0.0138
Ribonuclease PH	A0A0S2K533	0.8030	0.1380
Bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	A0A0S2K1C4	0.8057	0.0004
Putative Tol protein	A0A0S2K8L1	0.8078	0.0151
30S ribosomal protein S1	A0A0S2K0J0	0.8140	0.0104
Ribosome-recycling factor	A0A0S2K3J6	0.8145	0.0267
Peptidase M14, carboxypeptidase A	A0A0S2K236	0.8148	0.1700
10 kDa chaperonin	A0A0S2JXP4	0.8188	0.0236
Inosine-5-monophosphate dehydrogenase	A0A0S2K433	0.8196	0.0079
Ferric uptake regulation protein	A0A0S2K2H4	0.8198	0.0097
TonB-denpendent receptor	A0A0S2K734	0.8236	0.0259
Phosphoenolpyruvate synthase	A0A0S2K932	0.8244	0.0260
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	A0A0S2JXL1	0.8244	0.5084
Lysine--tRNA ligase	A0A0S2JYZ1	0.8282	0.1801
50S ribosomal protein L5	A0A0S2K6D0	0.8293	0.0170
3-ketoacyl-ACP reductase	A0A0S2K2X1	0.8313	0.0050
Glycine dehydrogenase (decarboxylating)	A0A0S2JZ77	0.8352	0.0279
Phosphate-specific transport system accessory protein PhoU	A0A0S2JXY3	0.8442	0.2027

Thioredoxin	A0A0S2JX84	0.8457	0.0007
Elongation factor Ts	A0A0S2K422	0.8479	0.0409
50S ribosomal protein L25	A0A0S2K4R4	0.8489	0.0170
Type IV pilus assembly PilZ	A0A0S2K184	0.8511	0.6371
Carbamoyl-phosphate synthase small chain	A0A0S2K416	0.8513	0.1757
Protein yhgF	A0A0S2K4U6	0.8519	0.7568
Pyruvate dehydrogenase E1 component	A0A0S2K383	0.8521	0.0713
50S ribosomal protein L22	A0A0S2K5M8	0.8548	0.0035
6-phosphogluconolactonase	A0A0S2K0L2	0.8562	0.5436
DNA-binding protein HU-beta	A0A0S2K9A9	0.8584	0.1758
NAD-dependent aldehyde dehydrogenase	A0A0S2K1Z1	0.8605	0.1331
3-ketoacyl-CoA thiolase	A0A0S2JWX5	0.8606	0.4769
50S ribosomal protein L27	A0A0S2K5C7	0.8623	0.6696
S-(hydroxymethyl)glutathione dehydrogenase	A0A0S2K652	0.8639	0.2927
30S ribosomal protein S4	A0A0S2K5N3	0.8648	0.0117
30S ribosomal protein S18	A0A0S2JY33	0.8649	0.1707
Glucose-1-phosphate thymidylyltransferase	A0A0S2JYR5	0.8665	0.1291
Glutamine synthetase	A0A0S2K4Y1	0.8674	0.1047
Peptidase M3	A0A0S2K0T8	0.8706	0.0552
Cytidylate kinase	A0A0S2K155	0.8736	0.5273
2-oxoglutarate dehydrogenase, E1 component	A0A0S2K2F8	0.8743	0.1059
Biopolymer transport protein	A0A0S2K8K7	0.8790	0.4070
Acetyltransferase component of pyruvate dehydrogenase complex	A0A0S2K3V4	0.8813	0.2341
50S ribosomal protein L19	A0A0S2K4L4	0.8817	0.2928
50S ribosomal protein L20	A0A0S2K1P0	0.8858	0.2927
30S ribosomal protein S7	A0A0S2JXN4	0.8898	0.2781
Phosphoribosylamine--glycine ligase	A0A0S2K578	0.8902	0.1558

Succinate dehydrogenase hydrophobic membrane anchor subunit	A0A0S2K164	0.8909	0.6500
Stringent starvation protein A	A0A0S2JXJ2	0.8910	0.7016
Malonyl CoA-acyl carrier protein transacylase	A0A0S2K2N3	0.8917	0.0392
DNA-binding protein	A0A0S2K410	0.8984	0.4695
Fumarate hydratase class I	A0A0S2K0P2	0.9007	0.0572
Multidrug resistance protein	A0A0S2K5V5	0.9020	0.7612
50S ribosomal protein L15	A0A0S2K6E8	0.9032	0.4070
Chaperone protein DnaK	A0A0S2K8D5	0.9092	0.1080
Universal stress protein E	A0A0S2K0T6	0.9093	0.2453
Thiol peroxidase	A0A0S2K2Y1	0.9134	0.8489
30S ribosomal protein S9	A0A0S2JXX0	0.9150	0.2130
Oxoacyl-(Acyl carrier protein) reductase	A0A0S2K1S6	0.9163	0.5732
BarA-associated response regulator UvrY	A0A0S2K3Z9	0.9194	0.5662
Adenylate kinase	A0A0S2K2Y7	0.9203	0.3341
Flagellar motor switch protein FliN	A0A0S2JZ56	0.9218	0.7853
Thioredoxin reductase	A0A0S2K0T0	0.9306	0.3721
DNA topoisomerase 1	A0A0S2K068	0.9315	0.8835
Integration host factor subunit alpha	A0A0S2K444	0.9335	0.5041
50S ribosomal protein L17	A0A0S2K5X6	0.9336	0.5679
50S ribosomal protein L24	A0A0S2K5V1	0.9338	0.5482
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	A0A0S2K3P3	0.9406	0.5863
TonB-dependent receptor	A0A0S2JZP9	0.9420	0.5600
30S ribosomal protein S17	A0A0S2K5U6	0.9436	0.6397
Uncharacterized protein	A0A0S2K7R0	0.9450	0.7512
1-deoxy-D-xylulose-5-phosphate synthase	A0A0S2K497	0.9457	0.7934
60 kDa chaperonin	A0A0S2JY23	0.9497	0.3708
Malate dehydrogenase	A0A0S2K5D6	0.9502	0.0430
Cadherin	A0A0S2K198	0.9510	0.8048

Hypoxanthine-guanine phosphoribosyltransferase	A0A0S2K4H8	0.9516	0.7764
Flagellin	A0A0S2K074	0.9549	0.4848
Negative regulator of flagellin synthesis	A0A0S2K021	0.9643	0.8773
Protein translocase subunit SecA	A0A0S2JYN5	0.9704	0.9358
Acyl-CoA dehydrogenase	A0A0S2K1Q5	0.9711	0.8638
TonB-dependent receptor	A0A0S2K274	0.9720	0.5465
DNA-directed RNA polymerase subunit beta	A0A0S2JY49	0.9724	0.7462
Xaa-Pro dipeptidase	A0A0S2JXA1	0.9725	0.7150
Outer membrane protein W	A0A0S2K058	0.9731	0.7567
50S ribosomal protein L9	A0A0S2JYC4	0.9736	0.6939
Methyl-accepting chemotaxis protein	A0A0S2K6D3	0.9755	0.8929
dTDP-glucose 4,6-dehydratase	A0A0S2JY86	0.9779	0.7949
ABC transporter, ATP-binding protein	A0A0S2K216	0.9798	0.9420
Peptidyl-prolyl cis-trans isomerase	A0A0S2K2X2	0.9800	0.8780
3-oxoacyl-[acyl-carrier-protein] synthase 2	A0A0S2K2F0	0.9807	0.8317
Arginine--tRNA ligase	A0A0S2K4V5	0.9807	0.9528
Isocitrate dehydrogenase	A0A0S2K1B6	0.9808	0.7903
Na(+)-translocating NADH-quinone reductase subunit F	A0A0S2K400	0.9816	0.8403
Enoyl-CoA hydratase	A0A0S2K1I9	0.9821	0.8825
Fructose-1,6-bisphosphate aldolase	A0A0S2JYJ4	0.9821	0.8200
Serine hydroxymethyltransferase	A0A0S2K4F8	0.9852	0.8092
TonB system biopolymer transport component Chromosome segregation ATPase	A0A0S2K8X7	0.9859	0.8253
N-succinylglutamate 5-semialdehyde dehydrogenase	A0A0S2K574	0.9862	0.8105
Glyceraldehyde-3-phosphate dehydrogenase	A0A0S2K223	0.9889	0.7995
Uncharacterized protein	A0A0S2K4Z8	0.9895	0.9493
Transketolase	A0A0S2K469	0.9913	0.9069
3,4-dihydroxy-2-butanone 4-phosphate synthase	A0A0S2K5F6	0.9919	0.9245
Polyribonucleotide nucleotidyltransferase	A0A0S2K0E7	0.9953	0.9019

Uncharacterized protein	A0A0S2K2H1	0.9986	0.9919
Nucleoid-associated protein PP2015_2029	A0A0S2K388	1.0004	0.9951
Collagenase	A0A0S2K3Q9	1.0005	0.9954
UDP-galactose-4-epimerase	A0A0S2JYM3	1.0020	0.9912
Uncharacterized protein	A0A0S2K1Z2	1.0022	0.9891
30S ribosomal protein S3	A0A0S2K5F9	1.0024	0.9753
Proline dipeptidase	A0A0S2K2G0	1.0027	0.9639
CTP synthase	A0A0S2K3G3	1.0027	0.9616
30S ribosomal protein S16	A0A0S2K3C3	1.0057	0.9697
Methionyl-tRNA formyltransferase	A0A0S2JXH6	1.0058	0.9878
Glutaredoxin	A0A0S2JYG6	1.0059	0.9744
Dihydrodipicolinate synthetase	A0A0S2K0N2	1.0061	0.9200
Isoaspartyl dipeptidase	A0A0S2K351	1.0100	0.9819
DNA-directed RNA polymerase subunit beta	A0A0S2JXY9	1.0171	0.8295
50S ribosomal protein L3	A0A0S2K5T4	1.0178	0.8056
Na(+)-translocating NADH-quinone reductase subunit B	A0A0S2K555	1.0188	0.9577
Peptidase M28	A0A0S2K135	1.0190	0.9008
50S ribosomal protein L16	A0A0S2K6L0	1.0203	0.8784
dTDP-4-dehydrorhamnose 3,5-epimerase	A0A0S2JXS8	1.0225	0.7636
Signal recognition particle protein	A0A0S2K432	1.0230	0.9266
Phasin family protein	A0A0S2K4T7	1.0231	0.7176
Cation/multidrug efflux pump	A0A0S2K1D5	1.0239	0.9786
Acetylornithine aminotransferase	A0A0S2K5E5	1.0248	0.7343
Methyl-accepting chemotaxis sensory transducer	A0A0S2K8F7	1.0252	0.8437
30S ribosomal protein S8	A0A0S2K6H1	1.0267	0.6580
50S ribosomal protein L6	A0A0S2K6R3	1.0291	0.7026
2-hydroxy-3-oxopropionate reductase	A0A0S2K2Z6	1.0293	0.8300
Fumarylacetoacetase	A0A0S2JZA9	1.0330	0.5184
2-dehydro-3-deoxyphosphooctonate aldolase	A0A0S2K4V1	1.0340	0.7962

50S ribosomal protein L21	A0A0S2K4G4	1.0340	0.8705
50S ribosomal protein L32	A0A0S2K2D1	1.0344	0.8372
Cytochrome c4	A0A0S2K495	1.0359	0.8158
Bmp1	A0A0S2JY74	1.0376	0.9219
5-nucleotidase SurE	A0A0S2K5Q2	1.0400	0.8299
30S ribosomal protein S14	A0A0S2K6H4	1.0401	0.7990
50S ribosomal protein L4	A0A0S2K6C0	1.0419	0.7744
Uncharacterized protein	A0A0S2K7T8	1.0445	0.8292
30S ribosomal protein S12	A0A0S2JY34	1.0541	0.5440
Cytochrome c oxidase subunit CcoO	A0A0S2K1E4	1.0639	0.5281
30S ribosomal protein S5	A0A0S2K5H5	1.0645	0.3960
Phosphoglucosamine mutase	A0A0S2K0E3	1.0670	0.5601
Ribose-phosphate pyrophosphokinase	A0A0S2K3Q4	1.0681	0.3253
Bifunctional protein FolD	A0A0S2K3Y6	1.0701	0.6397
Glycosyl transferase	A0A0S2JY43	1.0706	0.8594
Transcription antitermination protein NusB	A0A0S2K450	1.0726	0.6556
Peptidase M17, leucyl aminopeptidase domain-containing protein	A0A0S2K3H8	1.0767	0.2559
Acetyl-coenzyme A synthetase	A0A0S2JYE8	1.0776	0.5354
Enolase	A0A0S2K3G8	1.0784	0.0515
50S ribosomal protein L28	A0A0S2JXA5	1.0812	0.5716
Anti-sigma factor antagonist	A0A0S2K4K0	1.0815	0.5268
Uncharacterized protein	A0A0S2JY21	1.0853	0.7891
Sulfate permease	A0A0S2K208	1.0875	0.6212
Amidohydrolase	A0A0S2JZQ5	1.0893	0.7943
UDP-galactopyranose mutase	A0A0S2JX61	1.0946	0.6339
Beta-propeller domain-containing protein	A0A0S2K7C3	1.0958	0.6731
50S ribosomal protein L29	A0A0S2K6D8	1.1010	0.0939
DUF1696 domain-containing protein	A0A0S2K1H3	1.1030	0.7646

Dihydrolipoyl dehydrogenase	A0A0S2K4G9	1.1042	0.2055
Bmp7	A0A0S2JYW1	1.1160	0.8183
Cbb3-type cytochrome c oxidase subunit	A0A0S2K1H6	1.1174	0.4921
Beta-1,6-galactofuranosyltransferase	A0A0S2JX64	1.1196	0.5014
Bacterial putative lipoprotein (DUF940)	A0A0S2JYW2	1.1230	0.7406
Prolyl oligopeptidase family	A0A0S2JY98	1.1240	0.1616
Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	A0A0S2K6F2	1.1259	0.3101
Chemotaxis sensory transducer	A0A0S2K5X4	1.1273	0.6693
Putative protease with the C-terminal PDZ domain protein	A0A0S2K8N7	1.1310	0.7590
Oxaloacetate decarboxylase	A0A0S2K6X1	1.1353	0.2864
Uncharacterized protein	A0A0S2K6L6	1.1377	0.4859
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	A0A0S2K326	1.1377	0.4858
Triosephosphate isomerase	A0A0S2K0V0	1.1396	0.0134
Phosphoenolpyruvate carboxykinase (ATP)	A0A0S2K519	1.1457	0.0181
Alanine--tRNA ligase	A0A0S2K7D1	1.1508	0.2901
6,7-dimethyl-8-ribityllumazine synthase	A0A0S2K4D6	1.1510	0.1084
Two-component system, chemotaxis family, sensor kinase CheA	A0A0S2K0B8	1.1523	0.3584
AcrB/AcrD/AcrF family protein	A0A0S2K6V6	1.1573	0.3040
Aminopeptidase B	A0A0S2JZ46	1.1598	0.0222
2-oxoisovalerate dehydrogenase subunit beta	A0A0S2K153	1.1644	0.7846
Uncharacterized protein	A0A0S2JYU3	1.1664	0.0094
TonB-dependent receptor	A0A0S2K0N7	1.1745	0.0530
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	A0A0S2K2I8	1.1746	0.2220
Outer membrane receptor for ferrienterochelin and colicin	A0A0S2K885	1.1747	0.0906
Leucine dehydrogenase	A0A0S2K2B3	1.1893	0.0737
Ribonuclease E	A0A0S2K334	1.1906	0.2143
Pyridoxine 5-phosphate synthase	A0A0S2K2F5	1.1907	0.0232

Methyl-accepting chemotaxis protein	A0A0S2JWW6	1.1913	0.4327
Adenine phosphoribosyltransferase	A0A0S2K2N4	1.1953	0.5560
3-hydroxyisobutyrate dehydrogenase	A0A0S2K114	1.1998	0.3630
Uncharacterized protein	A0A0S2JXM1	1.2024	0.1587
Cold shock domain protein CspD	A0A0S2K0H8	1.2047	0.0781
RNA chaperone ProQ	A0A0S2K2W4	1.2048	0.5560
Protein GrpE	A0A0S2K1V2	1.2101	0.0184
Uncharacterized protein	A0A0S2JZQ1	1.2172	0.6268
50S ribosomal protein L2	A0A0S2K6F9	1.2234	0.1005
Fatty aldehyde dehydrogenase	A0A0S2K169	1.2244	0.0006
Partitioning protein B	A0A0S2K697	1.2260	0.3752
Putative pterin-4-alpha-carbinolamine dehydratase	A0A0S2K402	1.2282	0.2556
Glutamate carboxypeptidase II	A0A0S2K1A5	1.2283	0.2815
Translational regulator CsrA	A0A0S2K6K6	1.2349	0.0022
Collagenase	A0A0S2JYX1	1.2386	0.0032
Flagellin	A0A0S2K038	1.2409	0.0669
UPF0246 protein PP2015_2708	A0A0S2K4D7	1.2445	0.1447
Peptide deformylase	A0A0S2JXG4	1.2488	0.2918
Ribosome hibernation promoting factor HPF	A0A0S2JYH0	1.2507	0.4621
Putative salt-induced outer membrane protein	A0A0S2JY72	1.2528	0.0221
Protein TonB	A0A0S2K8Q5	1.2542	0.5023
Dipeptidyl peptidase IV	A0A0S2K558	1.2549	0.3594
Thiol:disulfide interchange protein	A0A0S2K6G8	1.2624	0.0495
Probable cytosol aminopeptidase	A0A0S2K5F2	1.2662	0.1650
50S ribosomal protein L31	A0A0S2K626	1.2681	0.3700
HTH-type transcriptional regulator	A0A0S2K9I7	1.2694	0.4775
Methyl-accepting chemotaxis protein	A0A0S2JZ97	1.2732	0.0390
CBS domain-containing protein	A0A0S2JZ75	1.2794	0.5116
50S ribosomal protein L10	A0A0S2JXN5	1.2820	0.0000

50S ribosomal protein L11	A0A0S2JY63	1.2884	0.0039
TonB-dependent receptor	A0A0S2K7I0	1.2919	0.0002
Single-stranded DNA-binding protein	A0A0S2JXG7	1.3039	0.0086
Thioredoxin-dependent thiol peroxidase	A0A0S2K2G8	1.3070	0.0000
N5-carboxyaminoimidazole ribonucleotide mutase	A0A0S2K194	1.3100	0.1017
50S ribosomal protein L1	A0A0S2JX69	1.3121	0.0457
30S ribosomal protein S19	A0A0S2K6P6	1.3153	0.0812
Cytochrome b	A0A0S2JXS7	1.3182	0.0912
50S ribosomal protein L7/L12	A0A0S2JY81	1.3210	0.0854
Translation initiation factor IF-3	A0A0S2K276	1.3233	0.0469
30S ribosomal protein S6	A0A0S2JXH8	1.3234	0.0095
Bmp2	A0A0S2JXW2	1.3260	0.5836
ABC transporter ATP-binding protein	A0A0S2JXH2	1.3287	0.1073
DNA-directed RNA polymerase subunit alpha	A0A0S2K570	1.3391	0.0000
RNA-binding protein Hfq	A0A0S2K5V4	1.3433	0.1085
50S ribosomal protein L35	A0A0S2K288	1.3487	0.2259
Translation initiation factor IF-2	A0A0S2JZT1	1.3578	0.0220
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	A0A0S2JY55	1.3598	0.3458
Hydrolase	A0A0S2JXD1	1.3733	0.0714
TonB-denpendent receptor	A0A0S2K084	1.3738	0.0002
Aspartate-semialdehyde dehydrogenase	A0A0S2K3E4	1.3749	0.5353
Uncharacterized protein	A0A0S2JY08	1.3780	0.1572
Orotidine 5-phosphate decarboxylase	A0A0S2K165	1.3850	0.0259
50S ribosomal protein L33	A0A0S2JXN0	1.3899	0.1666
Arsenate reductase	A0A0S2K2Z5	1.3960	0.4597
Putative signal transduction protein with CBS domains	A0A0S2K148	1.4105	0.0248
Phosphotyrosine protein phosphatase	A0A0S2JY36	1.4189	0.3105
Anti-sigma-E factor RseA	A0A0S2K2L8	1.4194	0.1286
Flagellar protein FliL	A0A0S2K078	1.4256	0.1083

Monooxygenase FAD/NAD(P)-binding subunit	A0A0S2JY90	1.4258	0.0769
Secreted hydrolase	A0A0S2K2Y3	1.4438	0.3276
30S ribosomal protein S21	A0A0S2K5E0	1.4447	0.0016
Porphobilinogen deaminase	A0A0S2JX10	1.4545	0.3100
Ferritin	A0A0S2K0E1	1.4577	0.0174
Fimbrial protein	A0A0S2JY64	1.4647	0.0007
Sulfate adenylyltransferase subunit 1	A0A0S2JXG6	1.4748	0.4986
2-methylisocitrate lyase	A0A0S2K6S8	1.4774	0.0176
MR-MLE family protein	A0A0S2K5I5	1.4867	0.1528
Chemotaxis response regulator	A0A0S2K636	1.4904	0.0132
ATP synthase subunit a	A0A0S2K5T1	1.4920	0.2105
Peptidyl-prolyl cis-trans isomerase	A0A0S2K1C3	1.4951	0.0001
Citrate synthase	A0A0S2K7M1	1.4983	0.0034
Phosphate ABC transporter permease	A0A0S2JYA0	1.5109	0.0956
Flagellar hook protein FlgE	A0A0S2JZH9	1.5125	0.0821
Uncharacterized protein	A0A0S2K4K6	1.5139	0.0107
Uncharacterized protein	A0A0S2K6X9	1.5247	0.0003
Uncharacterized protein	A0A0S2K1S2	1.5278	0.0972
Methyl-accepting chemotaxis protein	A0A0S2K4Q5	1.5371	0.0365
Phosphate binding protein	A0A0S2JYF0	1.5497	0.0000
Amino acid/peptide transporter	A0A0S2JZU2	1.5599	0.2577
Uncharacterized protein	A0A0S2K2R1	1.5655	0.0444
Uncharacterized protein	A0A0S2JXW5	1.5662	0.1268
Peptidase M23/M37 protein	A0A0S2JZS0	1.5738	0.2346
ATP synthase subunit delta	A0A0S2K5S2	1.5739	0.0000
Na(+)-translocating NADH-quinone reductase subunit A	A0A0S2K572	1.5790	0.0002
MotA/TolQ/ExbB proton channel protein	A0A0S2K2S7	1.5814	0.0000
Glycerol-3-phosphate cytidylyltransferase	A0A0S2JYU6	1.5939	0.1816
Putative lipoprotein	A0A0S2K0G3	1.5950	0.1283

Ribosomal RNA small subunit methyltransferase H	A0A0S2JYI9	1.6088	0.1463
Ribosome-binding factor A	A0A0S2JZQ0	1.6104	0.1141
Hemolysin D	A0A0S2JYC6	1.6169	0.0998
23S rRNA (guanosine-2-O-)-methyltransferase RlmB	A0A0S2JXQ8	1.6171	0.2563
TIGR00266 family protein	A0A0S2K6W5	1.6192	0.2020
UPF0250 protein PP2015_2666	A0A0S2K4C1	1.6257	0.2832
Uncharacterized protein	A0A0S2K046	1.6314	0.0029
Phosphate transport system permease protein PstA	A0A0S2JZ10	1.6386	0.0813
Outer membrane protein	A0A0S2K5P1	1.6449	0.0001
Cytochrome C biogenesis protein	A0A0S2K0D4	1.6489	0.0902
Succinate dehydrogenase flavoprotein subunit	A0A0S2K1T8	1.6519	0.0000
Hemagglutinin	A0A0S2K6H7	1.6632	0.1803
Electron transfer flavoprotein subunit beta	A0A0S2K1E5	1.6705	0.0003
Response regulator receiver domain protein (CheY-like)	A0A0S2K6I5	1.6720	0.0940
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	A0A0S2K794	1.6756	0.0025
Tryptophan--tRNA ligase	A0A0S2K576	1.6829	0.2691
4-hydroxythreonine-4-phosphate dehydrogenase	A0A0S2K0D6	1.6955	0.2596
Multidrug resistance efflux pump	A0A0S2JYN0	1.6983	0.0131
AcnD-accessory protein PrpF	A0A0S2K7F8	1.7023	0.1097
Na(+)-linked D-alanine glycine permease	A0A0S2K1K1	1.7082	0.0226
Ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit	A0A0S2JXU0	1.7165	0.0005
Collagenase	A0A0S2K6X3	1.7243	0.0744
Phosphate import ATP-binding protein PstB	A0A0S2JYX5	1.7257	0.0039
Putative ring-cleavage extradiol dioxygenase	A0A0S2K875	1.7315	0.0762
ATP synthase subunit alpha	A0A0S2K6C7	1.7417	0.0000
Uncharacterized protein	A0A0S2K2I7	1.7534	0.0000
Peptidase	A0A0S2K1Z0	1.7608	0.0018
Cell division coordinator CpoB	A0A0S2K1Y9	1.7695	0.0002

Peptide methionine sulfoxide reductase MsrA	A0A0S2JY88	1.7826	0.0953
Outer membrane channel protein	A0A0S2K3M7	1.7911	0.0001
Uncharacterized protein	A0A0S2K333	1.8172	0.0192
Glycine betaine aldehyde dehydrogenase	A0A0S2K0C8	1.8355	0.1455
Amidohydrolase	A0A0S2JXX3	1.8657	0.0000
ATP synthase gamma chain	A0A0S2K6U0	1.8725	0.0000
Peptidase M13	A0A0S2K1X2	1.8730	0.0001
Uncharacterized protein	A0A0S2K2H6	1.8807	0.2448
Major outer membrane protein	A0A0S2K8P4	1.9015	0.0007
Membrane protein	A0A0S2JZX4	1.9109	0.0514
RND family efflux transporter MFP subunit	A0A0S2K6H2	1.9110	0.0335
Propionyl CoA synthase	A0A0S2K7N8	1.9130	0.1075
AcrB/acrD/acrF acriflavin resistance protein	A0A0S2JYC3	1.9188	0.0144
Translation initiation factor IF-1	A0A0S2K142	1.9553	0.1996
Peptidase S9	A0A0S2K930	1.9603	0.0000
Mechanosensitive channel protein	A0A0S2JXS0	1.9694	0.0036
50S ribosomal protein L34	A0A0S2K5T8	1.9884	0.0043
Preprotein translocase subunit YajC	A0A0S2JY73	2.0597	0.0001
Periplasmic protein	A0A0S2JY32	2.0664	0.0000
Tyrosine-protein kinase	A0A0S2JYU8	2.0700	0.0444
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	A0A0S2K408	2.0871	0.0170
Lipoprotein NlpI	A0A0S2JZL2	2.0938	0.0012
Amidohydrolase	A0A0S2JZF2	2.0947	0.0000
Peptidoglycan-associated protein	A0A0S2K2C8	2.0949	0.0015
Putative Cobalt-zinc-cadmium resistance protein (Cation efflux system protein)	A0A0S2K8G7	2.1060	0.1704
Acyl carrier protein	A0A0S2K1T6	2.1076	0.2157
O-methyltransferase	A0A0S2K482	2.1078	0.0000

Outer membrane protein assembly factor BamB	A0A0S2JYB9	2.1250	0.0230
Ribosomal subunit interface protein	A0A0S2JZ31	2.1293	0.0518
Alcohol dehydrogenase	A0A0S2K3L0	2.1327	0.0001
Amidohydrolase	A0A0S2K1U3	2.1343	0.0000
Isoaspartyl peptidase	A0A0S2K0S2	2.1367	0.0532
ATP synthase subunit b	A0A0S2K6N7	2.1528	0.0000
Electron transfer flavoprotein, alpha subunit	A0A0S2K0J8	2.1943	0.1154
Small heat shock protein	A0A0S2K292	2.1947	0.0003
Succinate dehydrogenase iron-sulfur subunit	A0A0S2K2G4	2.2070	0.0002
Xaa-Pro aminopeptidase family protein	A0A0S2K784	2.2260	0.0576
TIGR00153 family protein	A0A0S2JYE2	2.2317	0.0252
Peptidase M16	A0A0S2JZ16	2.2390	0.0060
RNA-binding protein	A0A0S2K5N5	2.2411	0.0634
ATP synthase subunit beta	A0A0S2K724	2.2565	0.0000
Protein HflC	A0A0S2K5G9	2.2572	0.0004
Aminopeptidase	A0A0S2K6B9	2.2596	0.1551
Na(+)-translocating NADH-quinone reductase subunit C	A0A0S2K4M7	2.2598	0.0000
Outer membrane protein assembly factor BamD	A0A0S2JYZ6	2.2688	0.0062
Aconitate hydratase	A0A0S2K7G2	2.3019	0.0470
Ubiquinol-cytochrome c reductase iron-sulfur subunit	A0A0S2JXH4	2.3031	0.0001
Uncharacterized protein	A0A0S2K2S8	2.3108	0.0038
Rhodanese sulfur transferase	A0A0S2JYG4	2.3283	0.0080
Membrane protein insertase YidC	A0A0S2K739	2.3456	0.0193
Methyl-accepting chemotaxis protein	A0A0S2K4S6	2.3569	0.0375
Uncharacterized protein	A0A0S2JZY6	2.3583	0.0001
Cytochrome c4	A0A0S2K5R4	2.3817	0.0000
Outer membrane protein (Porin)	A0A0S2K4H1	2.4291	0.0000
ATP-dependent zinc metalloprotease FtsH	A0A0S2K1B1	2.4384	0.0000
Protein HflK	A0A0S2K4K4	2.4460	0.0008

UDP-N-acetylglucosamine 1-carboxyvinyltransferase	A0A0S2JXI4	2.4579	0.1849
AsmA protein	A0A0S2K5P8	2.4816	0.0060
3-ketoacyl-CoA thiolase	A0A0S2K494	2.4823	0.0437
Probable cytosol aminopeptidase	A0A0S2K1Y7	2.4855	0.0000
Putative TonB-dependent receptor	A0A0S2JZ59	2.4920	0.0001
General secretion pathway protein D	A0A0S2K6C1	2.5089	0.0096
ATP synthase subunit c	A0A0S2K6M2	2.5265	0.0000
Uncharacterized protein	A0A0S2K384	2.5363	0.0000
30S ribosomal protein S20	A0A0S2JZA6	2.5629	0.0232
Cytochrome c5	A0A0S2K6D1	2.5796	0.0001
Protein translocase subunit SecD	A0A0S2JYA5	2.5898	0.0365
Uncharacterized protein	A0A0S2K7T6	2.5948	0.2203
Uncharacterized protein	A0A0S2K5P5	2.6823	0.0000
Glutamate 5-kinase	A0A0S2K6P1	2.8199	0.0115
Carboxy-terminal protease	A0A0S2K209	2.8202	0.0000
Uncharacterized protein	A0A0S2K5Y9	2.8336	0.0000
Chaperone SurA	A0A0S2K0B0	2.8408	0.0342
General secretion pathway protein G	A0A0S2K5A8	2.9683	0.0000
D-alanyl-D-alanine carboxypeptidase, penicillin-binding protein 5	A0A0S2K434	2.9728	0.0326
Chaperone protein DnaJ	A0A0S2K8F6	3.0044	0.0012
TonB-dependent receptor	A0A0S2K6M5	3.0076	0.0007
ABC transporter substrate-binding protein	A0A0S2JXM9	3.0339	0.0244
Bmp5	A0A0S2JY87	3.0699	0.0744
Thiol:disulfide interchange protein	A0A0S2K6B4	3.0722	0.0178
Protein translocase subunit SecY	A0A0S2K5W0	3.1206	0.0155
Bifunctional protein GlmU	A0A0S2K680	3.1394	0.0002
Uncharacterized protein	A0A0S2K0P4	3.1697	0.0139
ABC transporter ATP-binding protein	A0A0S2K5Q8	3.1735	0.0009
Peptidyl-prolyl cis-trans isomerase	A0A0S2JXG3	3.2971	0.0001

ABC transporter	A0A0S2JXT7	3.3157	0.0001
BatD	A0A0S2K3U2	3.3178	0.0895
Peptidase S46	A0A0S2JZP6	3.3642	0.0003
ATP synthase epsilon chain	A0A0S2K727	3.3980	0.0002
Cytochrome c	A0A0S2JXJ0	3.4244	0.0000
Uncharacterized protein	A0A0S2K593	3.4532	0.0004
Uroporphyrinogen-III synthase	A0A0S2JWZ6	3.5438	0.0033
Outer membrane protein OmpH	A0A0S2K2S0	3.8136	0.0047
Amidohydrolase	A0A0S2K1V6	3.8284	0.0002
D-amino-acid dehydrogenase	A0A0S2K1W7	4.0284	0.0020
Membrane protein	A0A0S2K7U7	4.0803	0.0004
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	A0A0S2K421	4.3555	0.0000
Signal peptidase I	A0A0S2K315	4.3860	0.0003
Uncharacterized protein	A0A0S2K125	4.4374	0.0006
Peptidase S9	A0A0S2K6T8;A0A0S2K5S7	4.4964	0.0047
TPR repeat-containing protein	A0A0S2K2T9	4.4999	0.0002
Uncharacterized protein	A0A0S2K8Y4	4.7235	0.0003
Acyl-peptide hydrolase	A0A0S2K2R5	4.8420	0.0067
2-oxoisovalerate dehydrogenase subunit alpha	A0A0S2K1P4	4.8507	0.0065
Anti-sigma B factor antagonist	A0A0S2JYD7	4.9622	0.0039
Uncharacterized protein	A0A0S2K7S2	5.4298	0.0003
Membrane-bound lytic murein transglycosylase C	A0A0S2K244	5.5077	0.0004
Uncharacterized protein	A0A0S2JZA0	5.6551	0.0001
Collagen-binding surface adhesin SpaP (Antigen I/II family)	A0A0S2K346	5.6772	0.0148
TPR-like domain-containing protein	A0A0S2JYB7	5.8072	0.0063
TonB-dependent receptor	A0A0S2K4P7	5.9073	0.0015
Tol-Pal system protein TolQ	A0A0S2K2X9	6.0372	0.0008
Uncharacterized protein	A0A0S2K813	6.6413	0.0005
Porin	A0A0S2JYA3	6.9819	0.0011

Uncharacterized protein	A0A0S2JYI5	7.1456	0.0000
Putative Polyphosphate kinase 2	A0A0S2K1J9	7.4462	0.0001
Lipoprotein	A0A0S2K843	7.5605	0.0000
Outer membrane protein assembly factor BamA	A0A0S2K3W3	8.3540	0.0002
Uncharacterized protein	A0A0S2K7J6	10.2881	0.0008
Peptidylprolyl isomerase	A0A0S2K4M9	10.3638	0.0005
Uncharacterized protein	A0A0S2K1M1	10.7719	0.0000
Dihydroorotate dehydrogenase (quinone)	A0A0S2K252	11.1037	0.0000
Putative stomatin/prohibitin-family membrane protease subunit YbbK	A0A0S2K7B7	12.4932	0.0000
Tol-Pal system protein TolB	A0A0S2K380	13.0778	0.0000
Carboxypeptidase	A0A0S2K4K5	14.3760	0.0000
Uncharacterized protein	A0A0S2K1K7	21.1365	0.0000
TonB-dependent receptor	A0A0S2JZN4	24.8862	0.0004
Periplasmic serine endoprotease DegP-like	A0A0S2JYI3	26.6078	0.0000
Tricorn protease homolog	A0A0S2K7Y2	29.6843	0.0000
OmpA domain-containing protein	A0A0S2K429	51.3789	0.0000
Gamma-glutamyl phosphate reductase	A0A0S2K703	76.9250	0.0000

Table S2. List of identified proteins in the extracellular protein analysis

Protein names	**Majority protein IDs**	**Fold change (high-salt/normal-salt)**	***p* value**
Bifunctional protein PutA	A0A0S2JZ14	0.0367	0.0002
Alkaline phosphatase	A0A0S2K730	0.0476	0.0000
Putative Fe transport outer membrane receptor protein	A0A0S2JYS5	0.0669	0.0000
Alkaline phosphatase	A0A0S2K8F1	0.0674	0.0000
TonB-dependent receptor	A0A0S2K3G6	0.0776	0.0000
Glucan endo-1,3-beta-D-glucosidase	A0A0S2K2H7	0.1005	0.0000
Peptidase dimerization domain-containing protein	A0A0S2K5X0	0.1128	0.0000
TonB system biopolymer transport component Chromosome segregation ATPase	A0A0S2K8X7	0.1618	0.0049
Uncharacterized protein	A0A0S2K0D9	0.1713	0.0000
RimK domain-containing protein ATP-grasp	A0A0S2K545	0.1735	0.0004
Phage shock protein	A0A0S2K449	0.1757	0.0040
Peptidase S8/S53 subtilisin kexin sedolisin	A0A0S2K7G7	0.1972	0.0015
Cytochrome c4	A0A0S2K495	0.1990	0.0454
Glucose-6-phosphate 1-dehydrogenase	A0A0S2K0G6	0.2017	0.0009
Biopolymer transport protein	A0A0S2K8K7	0.2080	0.0051
Polyhydroxyalkanoic acid synthase	A0A0S2K4H2	0.2112	0.0010
Alpha-1,4 glucan phosphorylase	A0A0S2K8T5	0.2116	0.0017
GTP-binding protein	A0A0S2K313	0.2119	0.0072
Bacterioferritin	A0A0S2K7X9	0.2222	0.1149
Transaldolase	A0A0S2K4C6	0.2314	0.0018
Quinol oxidase, subunit I	A0A0S2K7T0	0.2360	0.0177
UPF0234 protein PP2015_2926	A0A0S2K520	0.2483	0.0344
Integration host factor subunit alpha	A0A0S2K444	0.2504	0.0390
Phasin family protein	A0A0S2K4T7	0.2677	0.0068
PhoH-like protein	A0A0S2K4C2	0.3024	0.0302

Phosphate-specific transport system accessory protein PhoU	A0A0S2JXY3	0.3037	0.0516
RNA polymerase sigma factor RpoS	A0A0S2K4Q1	0.3053	0.0285
Protein TonB	A0A0S2K8Q5	0.3100	0.0003
Uncharacterized protein	A0A0S2K4Z8	0.3184	0.0031
6-phosphogluconolactonase	A0A0S2K0L2	0.3203	0.0291
Uncharacterized protein	A0A0S2K337	0.3270	0.0008
Uncharacterized protein	A0A0S2K201	0.3293	0.0148
5-methylthioadenosine/S-adenosylhomocysteine nucleosidase	A0A0S2K4E8	0.3381	0.0066
Uncharacterized protein	A0A0S2K7J6	0.3390	0.0619
Transcriptional regulator	A0A0S2JY35	0.3422	0.0344
Putative signal transduction protein	A0A0S2K4T3	0.3467	0.0115
Anti-RNA polymerase sigma 70 factor	A0A0S2JXP1	0.3506	0.0026
Ribosome modulation factor	A0A0S2K181	0.3608	0.0008
Putative Tol protein	A0A0S2K8L1	0.3688	0.0000
ATP synthase subunit b	A0A0S2K6N7	0.3738	0.2241
Glucan 1,4-beta-glucosidase	A0A0S2K2Y6	0.3747	0.0204
Bacterioferritin	A0A0S2K830	0.3790	0.1061
Uncharacterized protein	A0A0S2K9M7	0.3892	0.0000
Uncharacterized protein	A0A0S2K160	0.3916	0.0011
30S ribosomal protein S21	A0A0S2K5E0	0.3942	0.0663
Outer membrane protein with a TonB box	A0A0S2K8B9	0.3947	0.0000
SpoOM family protein	A0A0S2K199	0.3999	0.0128
TIGR02647 family protein	A0A0S2K9A1	0.4059	0.1115
Histone family protein nucleoid-structuring protein H-NS	A0A0S2K0K0	0.4065	0.0002
Putative Fe transport outer membrane receptor protein	A0A0S2K8L7	0.4078	0.0000
Oxaloacetate decarboxylase	A0A0S2K6X1	0.4139	0.0776
Helix-turn-helix protein	A0A0S2K3Z5	0.4173	0.0592
RND family efflux transporter MFP subunit	A0A0S2K6H2	0.4174	0.0758
Periplasmic calcium binding protein	A0A0S2K6S5	0.4225	0.0000

Putative phosphohistidine phosphatase, SixA	A0A0S2K868	0.4229	0.0224
Acetoacetyl-CoA reductase	A0A0S2K3T5	0.4231	0.0000
30S ribosomal protein S20	A0A0S2JZA6	0.4234	0.0779
Aminotransferase	A0A0S2K3S2	0.4258	0.0003
Glycosyl transferase	A0A0S2K1Q2	0.4259	0.0947
Glyceraldehyde-3-phosphate dehydrogenase	A0A0S2K154	0.4274	0.0091
DNA gyrase subunit A	A0A0S2K1X3	0.4284	0.0012
Cation/multidrug efflux pump	A0A0S2K1D5	0.4307	0.1615
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	A0A0S2K3P3	0.4421	0.0321
TonB-denpendent receptor	A0A0S2K734	0.4454	0.0001
Orotate phosphoribosyltransferase	A0A0S2K5C4	0.4507	0.0012
Nucleoid-associated protein PP2015_2029	A0A0S2K388	0.4527	0.1275
Pyruvate kinase	A0A0S2K267	0.4587	0.0003
Cytochrome c oxidase subunit CcoO	A0A0S2K1E4	0.4692	0.0000
Alanine dehydrogenase	A0A0S2K1V8	0.4718	0.0000
Lipoprotein	A0A0S2K4G6	0.4725	0.0001
Argininosuccinate synthase	A0A0S2K5T5	0.4725	0.1174
Phosphodiesterase/alkaline phosphatase D	A0A0S2K5P9	0.4778	0.0567
Twitching motility protein PilT	A0A0S2K4A5	0.4779	0.0118
Aminopeptidase YpdF (MP-, MA-, MS-,AP-,NP-specific)	A0A0S2K1S1	0.4794	0.2664
1,4-alpha-glucan branching enzyme GlgB	A0A0S2K8E2	0.4815	0.1738
Uncharacterized protein	A0A0S2K4P9	0.4826	0.0113
TPR repeat-containing protein	A0A0S2K2T9	0.4849	0.0248
TonB-dependent receptor	A0A0S2JZG5	0.4866	0.0111
NH(3)-dependent NAD(+) synthetase	A0A0S2JWZ7	0.4868	0.0279
DksA-type zinc finger protein	A0A0S2K1Z7	0.4895	0.0410
Small heat shock protein	A0A0S2K292	0.4924	0.1046
Cytochrome c	A0A0S2JXJ0	0.4928	0.1360
Phosphate ABC transporter permease	A0A0S2JYA0	0.5017	0.0137

General secretion pathway protein G	A0A0S2K5A8	0.5021	0.1836
Nitrogen regulatory protein P-II	A0A0S2JZB8	0.5044	0.0362
50S ribosomal protein L29	A0A0S2K6D8	0.5097	0.2235
Chemotaxis response regulator protein-glutamate methylesterase	A0A0S2K661	0.5115	0.1800
Regulator of ribonuclease activity A	A0A0S2K581	0.5126	0.0692
Methyl-accepting chemotaxis protein	A0A0S2K6D3	0.5129	0.0074
50S ribosomal protein L34	A0A0S2K5T8	0.5145	0.0548
Aspartate--tRNA ligase	A0A0S2K0R7	0.5160	0.0297
Zn-finger domain associated with topoisomerase type I	A0A0S2JX22	0.5173	0.0003
Chemotaxis protein	A0A0S2JZN8	0.5279	0.2204
GTP-binding protein TypA/BipA	A0A0S2K5M9	0.5297	0.0006
Collagenase	A0A0S2JYX1	0.5304	0.0004
GMP synthase [glutamine-hydrolyzing]	A0A0S2K4D2	0.5331	0.0038
Uncharacterized protein	A0A0S2JXM1	0.5334	0.1798
Cbb3-type cytochrome c oxidase subunit	A0A0S2K1H6	0.5363	0.0006
Integration host factor subunit beta	A0A0S2K1M9	0.5376	0.2530
Beta-propeller domain-containing protein	A0A0S2K7C3	0.5475	0.2898
Uncharacterized protein	A0A0S2K2I4	0.5512	0.0245
Uncharacterized protein	A0A0S2JY21	0.5525	0.1792
Threonine--tRNA ligase	A0A0S2K1A2	0.5536	0.0930
Phosphate import ATP-binding protein PstB	A0A0S2JYX5	0.5598	0.0210
Response regulator in two-component regulatory system with PhoQ	A0A0S2K345	0.5604	0.1513
RNA-binding protein Hfq	A0A0S2K5V4	0.5621	0.0161
DNA topoisomerase 1	A0A0S2K068	0.5658	0.2178
30S ribosomal protein S19	A0A0S2K6P6	0.5680	0.0081
Phosphoglucomutase	A0A0S2K1V0	0.5690	0.1328
Arginine--tRNA ligase	A0A0S2K4V5	0.5707	0.1983
Glutathione peroxidase	A0A0S2JZA2	0.5716	0.0020

CBS domain containing membrane protein	A0A0S2K1I3	0.5720	0.0043
Malic enzyme	A0A0S2K641	0.5732	0.0002
Glucose-1-phosphate adenylyltransferase	A0A0S2K8F3	0.5745	0.0016
Putative enzyme related to lactoylglutathione lyase	A0A0S2K601	0.5768	0.1548
Acyltransferase	A0A0S2JZX6	0.5771	0.0633
Site-determining protein	A0A0S2K985	0.5855	0.0001
Cytochrome c oxidase, cbb3-type, subunit I	A0A0S2K0R3	0.5876	0.0463
Phosphate transport system permease protein PstA	A0A0S2JZ10	0.5877	0.1185
Carboxyl-terminal protease	A0A0S2JXY2	0.5884	0.2406
Nicotinate-nucleotide pyrophosphorylase	A0A0S2JYH4	0.5898	0.0199
Lipoprotein	A0A0S2K1N4	0.5934	0.2479
TonB system transporter ExbD2	A0A0S2K2I9	0.5935	0.1209
Uncharacterized protein	A0A0S2K0P4	0.6001	0.0337
Uncharacterized protein	A0A0S2K5P5	0.6068	0.2458
Uncharacterized protein	A0A0S2K4R6	0.6088	0.1482
Uncharacterized protein	A0A0S2JY08	0.6130	0.1160
Stringent starvation protein A	A0A0S2JXJ2	0.6162	0.2923
Translation initiation factor IF-3	A0A0S2K276	0.6183	0.3219
50S ribosomal protein L20	A0A0S2K1P0	0.6191	0.1800
30S ribosomal protein S14	A0A0S2K6H4	0.6252	0.0527
Protein RecA	A0A0S2K534	0.6286	0.0004
Uridylate kinase	A0A0S2K414	0.6316	0.0028
Nucleoside diphosphate kinase	A0A0S2JZ01	0.6321	0.0292
DNA-directed RNA polymerase subunit omega	A0A0S2K5T2	0.6338	0.3192
Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	A0A0S2K6F2	0.6342	0.1715
Rod shape-determining protein MreB	A0A0S2JY94	0.6346	0.1791
RNA polymerase-binding transcription factor DksA	A0A0S2JY46	0.6354	0.1078
Cell division topological specificity factor	A0A0S2K8P7	0.6358	0.0306
Isopenicillin N synthase related dioxygenase	A0A0S2K2T7	0.6358	0.0000

ATP-dependent protease ATPase subunit HslU	A0A0S2K5T7	0.6366	0.1339
dUTP diphosphatase	A0A0S2K672	0.6412	0.1120
Acetyl-CoA carboxylase, biotin carboxylase subunit	A0A0S2JX88	0.6417	0.0008
Peptidase M3	A0A0S2K0T8	0.6425	0.4125
Transcription antitermination protein NusB	A0A0S2K450	0.6436	0.1745
Tail Collar domain protein	A0A0S2K2F9	0.6491	0.1136
Glutathione synthetase	A0A0S2K4G0	0.6497	0.1973
Prolyl oligopeptidase family	A0A0S2JY98	0.6589	0.0639
HoxA-like transcriptional regulator	A0A0S2K525	0.6712	0.2589
Glycine--tRNA ligase beta subunit	A0A0S2JWZ9	0.6714	0.3304
Chemotaxis protein	A0A0S2JZE9	0.6724	0.0014
50S ribosomal protein L18	A0A0S2K5P4	0.6739	0.3049
HTH-type transcriptional regulator	A0A0S2K9I7	0.6766	0.2298
Cytochrome c4	A0A0S2K5R4	0.6831	0.2140
M48 family peptidase	A0A0S2K2T5	0.6878	0.3154
Phosphoserine aminotransferase	A0A0S2K1T7	0.6889	0.1132
Superoxide dismutase	A0A0S2K2R9	0.6897	0.0324
Arsenate reductase	A0A0S2K2Z5	0.6907	0.3190
Glutamate dehydrogenase	A0A0S2K1A4	0.6963	0.0002
Elongation factor G	A0A0S2JX62	0.6983	0.3615
3-ketoacyl-(Acyl-carrier-protein) reductase	A0A0S2K1U5	0.6988	0.0439
Putative glucose-6-phosphate 1-epimerase	A0A0S2K640	0.6989	0.1192
Hydrolase	A0A0S2JX50	0.7009	0.0622
Purine nucleoside phosphorylase DeoD-type	A0A0S2K7Y0	0.7011	0.0422
30S ribosomal protein S18	A0A0S2JY33	0.7019	0.1665
DNA-binding protein HU-beta	A0A0S2K9A9	0.7022	0.0241
Acetyl-CoA acetyltransferase	A0A0S2K293	0.7062	0.0013
Peptidyl-prolyl cis-trans isomerase	A0A0S2K2U1	0.7064	0.5826
Ornithine cyclodeaminase	A0A0S2K2E9	0.7125	0.0098

50S ribosomal protein L10	A0A0S2JXN5	0.7127	0.2919
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	A0A0S2JXL1	0.7128	0.5780
Acyl-CoA dehydrogenase	A0A0S2K1R4	0.7164	0.0243
Fimbrial protein	A0A0S2JY64	0.7170	0.0006
Phospho-2-dehydro-3-deoxyheptonate aldolase	A0A0S2K8K1	0.7184	0.1654
Ribonuclease E	A0A0S2K334	0.7228	0.1931
Succinate--CoA ligase [ADP-forming] subunit alpha	A0A0S2K1X7	0.7229	0.0036
Enoyl-[acyl-carrier-protein] reductase [NADH]	A0A0S2K4A1	0.7236	0.0566
Uncharacterized protein	A0A0S2K2H1	0.7263	0.4139
TonB-dependent receptor	A0A0S2JZP9	0.7314	0.0022
Purine-binding chemotaxis protein	A0A0S2JZ72	0.7322	0.0667
Asparagine synthetase	A0A0S2JXT6	0.7329	0.4568
TonB-dependent receptor	A0A0S2K274	0.7358	0.0002
Succinyl-CoA transferase, beta subunit	A0A0S2K0Z8	0.7362	0.1560
Uncharacterized protein	A0A0S2K5S9	0.7430	0.3912
Outer membrane protein assembly factor BamB	A0A0S2JYB9	0.7450	0.4189
Histidine triad protein	A0A0S2JXB7	0.7455	0.3041
Uncharacterized protein	A0A0S2K560	0.7461	0.4636
MR-MLE family protein	A0A0S2K5I5	0.7517	0.5135
Succinate--CoA ligase [ADP-forming] subunit beta	A0A0S2K2T2	0.7544	0.0029
Uncharacterized protein	A0A0S2K4E4	0.7563	0.1994
BarA-associated response regulator UvrY	A0A0S2K3Z9	0.7569	0.6460
Leucine--tRNA ligase	A0A0S2K3R9	0.7581	0.1536
Phosphoribosylformylglycinamidine synthase	A0A0S2JZQ2	0.7625	0.5082
DNA gyrase subunit B	A0A0S2JWX9	0.7630	0.2846
Putative outer membrane protein TIGR02001 family	A0A0S2K5X2	0.7675	0.3988
Delta-aminolevulinic acid dehydratase	A0A0S2K6J5	0.7691	0.0554
Tyrosine-protein kinase	A0A0S2JYU8	0.7714	0.3615
50S ribosomal protein L33	A0A0S2JXN0	0.7733	0.2565

Uncharacterized protein	A0A0S2JZQ1	0.7759	0.1093
NAD-dependent epimerase/dehydratase	A0A0S2JY85	0.7771	0.0578
SapC	A0A0S2K0Q9	0.7773	0.0616
Tyrosine--tRNA ligase	A0A0S2K5P6	0.7793	0.4525
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	A0A0S2K423	0.7794	0.0542
Uncharacterized protein	A0A0S2K2B2	0.7800	0.2407
Collagenase	A0A0S2K3Q9	0.7822	0.0232
Histidine--tRNA ligase	A0A0S2JY03	0.7854	0.4419
Uncharacterized protein	A0A0S2K2R1	0.7872	0.2151
Cytochrome c5	A0A0S2K6D1	0.7877	0.2548
Protein translocase subunit SecA	A0A0S2JYN5	0.7885	0.4464
Glutamine--tRNA ligase	A0A0S2K287	0.7928	0.5160
Outer membrane protein W	A0A0S2K058	0.7986	0.0396
Uncharacterized protein	A0A0S2JYS7	0.7997	0.4414
Elongation factor G	A0A0S2K5U1	0.7997	0.0157
Isocitrate dehydrogenase	A0A0S2K8G3	0.8024	0.3566
Protein phosphatase CheZ	A0A0S2K0D8	0.8028	0.5980
Ribonucleoside-diphosphate reductase	A0A0S2K0W0	0.8032	0.6496
Universal stress protein E	A0A0S2K0T6	0.8038	0.1546
Peptidase M14, carboxypeptidase A	A0A0S2K4X4	0.8044	0.6414
Putative signal transduction protein with CBS domains	A0A0S2K148	0.8064	0.2012
Hydroxyproline-2-epimerase	A0A0S2K1Q7	0.8065	0.0121
Putative salt-induced outer membrane protein	A0A0S2JY72	0.8112	0.0473
ABC transporter substrate-binding protein	A0A0S2JYD0	0.8119	0.2757
Putative lipoprotein	A0A0S2K0G3	0.8129	0.3480
Phosphoribosylaminoimidazole-succinocarboxamide synthase	A0A0S2K516	0.8132	0.4608
Na(+)-translocating NADH-quinone reductase subunit F	A0A0S2K400	0.8134	0.0550
Acetyl-CoA carboxylase, carboxyltransferase component (Subunits alpha and beta)	A0A0S2K2K1	0.8162	0.3993

CBS domain-containing protein	A0A0S2JZ75	0.8185	0.6241
Glutaredoxin	A0A0S2JYG6	0.8194	0.6002
Multidrug resistance efflux pump	A0A0S2JYN0	0.8279	0.4599
Glucose-1-phosphate thymidylyltransferase	A0A0S2JYR5	0.8329	0.2345
Protein HflC	A0A0S2K5G9	0.8338	0.2474
Transcription termination factor Rho	A0A0S2JX09	0.8360	0.0122
Uncharacterized protein	A0A0S2K7T6	0.8366	0.6097
Glutamate carboxypeptidase II	A0A0S2K1A5	0.8377	0.1727
Ribonuclease PH	A0A0S2K533	0.8387	0.0904
Peptidyl-prolyl cis-trans isomerase	A0A0S2JYW9	0.8404	0.2263
Transcription termination/antitermination protein NusA	A0A0S2JZV0	0.8406	0.1295
Putative manganese binding agmatinase (SpeB)	A0A0S2K911	0.8435	0.2168
Outer membrane receptor for ferrienterochelin and colicin	A0A0S2K885	0.8444	0.0341
Ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit	A0A0S2JXU0	0.8460	0.0845
PrkA family serine protein kinase	A0A0S2K2I6	0.8482	0.2225
Amidophosphoribosyltransferase	A0A0S2K3C4	0.8495	0.5796
50S ribosomal protein L31	A0A0S2K626	0.8520	0.4568
10 kDa chaperonin	A0A0S2JXP4	0.8533	0.0239
ATP synthase gamma chain	A0A0S2K6U0	0.8558	0.2524
ATP synthase subunit delta	A0A0S2K5S2	0.8599	0.3598
Aminomethyltransferase	A0A0S2JYK1	0.8604	0.0370
Cytochrome b	A0A0S2JXS7	0.8607	0.1894
Thiol peroxidase	A0A0S2K2Y1	0.8634	0.3091
Elongation factor Tu	A0A0S2JXI1	0.8664	0.0008
Protein GrpE	A0A0S2K1V2	0.8681	0.6136
50S ribosomal protein L7/L12	A0A0S2JY81	0.8710	0.6418
Methionine--tRNA ligase	A0A0S2K186	0.8715	0.2765
Methyl-accepting chemotaxis protein	A0A0S2JZ97	0.8716	0.2873
Glycosyl transferase	A0A0S2JY43	0.8720	0.6427

Phosphate binding protein	A0A0S2JYF0	0.8737	0.0605
Lysine--tRNA ligase	A0A0S2JYZ1	0.8775	0.2033
Flagellin	A0A0S2JZ74	0.8775	0.0447
Inosine-5-monophosphate dehydrogenase	A0A0S2K433	0.8785	0.0560
50S ribosomal protein L28	A0A0S2JXA5	0.8788	0.5479
RNA polymerase sigma factor RpoD	A0A0S2K5S8	0.8797	0.4795
Peptide deformylase	A0A0S2JXG4	0.8807	0.6016
Glyoxalase	A0A0S2K6L7	0.8848	0.4797
Ribosome-binding ATPase YchF	A0A0S2K3S0	0.8896	0.1156
Uncharacterized protein	A0A0S2K7U8	0.8902	0.6068
Ribose-5-phosphate isomerase A	A0A0S2K5C2	0.8904	0.7744
Transcription termination/antitermination protein NusG	A0A0S2JXX4	0.8911	0.3576
ATP-dependent Clp protease proteolytic subunit	A0A0S2K479	0.8936	0.3727
3-phosphoshikimate 1-carboxyvinyltransferase	A0A0S2K1S8	0.8940	0.7158
Calmodulin	A0A0S2JY01	0.8941	0.3870
Ribosome-recycling factor	A0A0S2K3J6	0.8943	0.4435
Flagellar motor switch protein FliN	A0A0S2JZ56	0.8986	0.7490
TIGR00153 family protein	A0A0S2JYE2	0.8995	0.7249
ATP-dependent Clp protease ATP-binding subunit ClpX	A0A0S2K4H5	0.9034	0.2900
Elongation factor Ts	A0A0S2K422	0.9038	0.0940
Phenylalanine--tRNA ligase beta subunit	A0A0S2K451	0.9072	0.6410
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	A0A0S2K326	0.9073	0.4725
RNA chaperone ProQ	A0A0S2K2W4	0.9079	0.5243
Ribonuclease (Endoribonuclease L-PSP)	A0A0S2K4I6	0.9111	0.7786
Fumarate/nitrate reduction transcriptional regulator	A0A0S2K1D4	0.9111	0.5902
Cysteine synthase	A0A0S2K3E9	0.9121	0.4600
Uncharacterized protein	A0A0S2K0X9	0.9135	0.8180
DNA-binding protein	A0A0S2K410	0.9157	0.4821

Uncharacterized protein	A0A0S2JYU3	0.9170	0.3250
Ribosome hibernation promoting factor HPF	A0A0S2JYH0	0.9181	0.7683
Glycine--tRNA ligase alpha subunit	A0A0S2JWM8	0.9186	0.6424
ATP synthase subunit c	A0A0S2K6M2	0.9187	0.7519
Aminopeptidase	A0A0S2K6B9	0.9200	0.8456
30S ribosomal protein S4	A0A0S2K5N3	0.9208	0.1481
Ferric uptake regulation protein	A0A0S2K2H4	0.9226	0.7597
Methyl-accepting chemotaxis sensory transducer	A0A0S2K8F7	0.9229	0.4283
Pyruvate dehydrogenase E1 component	A0A0S2K383	0.9235	0.1510
Glutamate-1-semialdehyde 2,1-aminomutase	A0A0S2K4G3	0.9251	0.5747
30S ribosomal protein S1	A0A0S2K0J0	0.9253	0.2155
Bacterial putative lipoprotein (DUF940)	A0A0S2JYW2	0.9254	0.6920
Methylmalonate-semialdehyde dehydrogenase	A0A0S2K298	0.9324	0.5018
Cadherin	A0A0S2K198	0.9416	0.6131
3-oxoacyl-ACP synthase	A0A0S2K1F8	0.9428	0.4099
Citrate synthase	A0A0S2K238	0.9450	0.4995
Uncharacterized protein	A0A0S2K597	0.9465	0.7416
Amidohydrolase	A0A0S2JZQ5	0.9473	0.6445
Glutathione-disulfide reductase	A0A0S2K5Z1	0.9486	0.8546
UPF0246 protein PP2015_2708	A0A0S2K4D7	0.9490	0.8667
30S ribosomal protein S2	A0A0S2K342	0.9492	0.5567
Oligopeptidase A	A0A0S2K4W4	0.9501	0.6541
Adenylosuccinate lyase	A0A0S2K1N6	0.9507	0.8009
Chaperone protein HtpG	A0A0S2K203	0.9514	0.4661
Thioredoxin-dependent thiol peroxidase	A0A0S2K2G8	0.9545	0.8380
Acyl carrier protein	A0A0S2K1T6	0.9556	0.9206
Asparagine--tRNA ligase	A0A0S2K254	0.9577	0.7869
Cell division coordinator CpoB	A0A0S2K1Y9	0.9611	0.9222
50S ribosomal protein L17	A0A0S2K5X6	0.9639	0.7548

Two-component response regulator	A0A0S2K4J3	0.9653	0.8505
Branched-chain-amino-acid aminotransferase	A0A0S2K5I1	0.9665	0.7499
Uncharacterized protein	A0A0S2JZM2	0.9666	0.7713
Manganese-dependent inorganic pyrophosphatase	A0A0S2K594	0.9677	0.7606
Protein-export protein SecB	A0A0S2JY60	0.9691	0.7744
2-oxoglutarate dehydrogenase, E1 component	A0A0S2K2F8	0.9723	0.4631
Na(+)-translocating NADH-quinone reductase subunit A	A0A0S2K572	0.9753	0.7729
50S ribosomal protein L16	A0A0S2K6L0	0.9787	0.8683
Uridine phosphorylase	A0A0S2K8B1	0.9827	0.8886
Probable cytosol aminopeptidase	A0A0S2K5F2	0.9834	0.8768
BatD	A0A0S2K3U2	0.9835	0.9666
Two-component system, chemotaxis family, sensor kinase CheA	A0A0S2K0B8	0.9850	0.9318
30S ribosomal protein S3	A0A0S2K5F9	0.9853	0.7763
ATP-dependent RNA helicase DeaD	A0A0S2K006	0.9855	0.9794
30S ribosomal protein S7	A0A0S2JXN4	0.9904	0.9114
Outer membrane channel protein	A0A0S2K3M7	0.9904	0.8402
Hypoxanthine-guanine phosphoribosyltransferase	A0A0S2K4H8	0.9919	0.9842
dTDP-glucose 4,6-dehydratase	A0A0S2JY86	0.9925	0.9306
Outer membrane protein	A0A0S2K5P1	0.9933	0.7612
D-amino-acid dehydrogenase	A0A0S2K1W7	0.9933	0.9866
Uncharacterized protein	A0A0S2JXH9	1.0000	0.9999
Ferritin	A0A0S2K0E1	1.0019	0.9954
Peroxiredoxin 2	A0A0S2K526	1.0086	0.8751
Acetyltransferase component of pyruvate dehydrogenase complex	A0A0S2K3V4	1.0087	0.8983
TonB-dependent receptor	A0A0S2K7I0	1.0097	0.8432
MotA/TolQ/ExbB proton channel protein	A0A0S2K2S7	1.0112	0.8569
Na(+)-translocating NADH-quinone reductase subunit C	A0A0S2K4M7	1.0127	0.8788
Trigger factor	A0A0S2K3H0	1.0133	0.7641

Glycine cleavage system H protein	A0A0S2JZF6	1.0147	0.8972
Response regulator	A0A0S2K487	1.0181	0.9353
3,4-dihydroxy-2-butanone 4-phosphate synthase	A0A0S2K5F6	1.0190	0.5669
Outer membrane protein assembly factor BamA	A0A0S2K3W3	1.0277	0.9533
2-amino-3-ketobutyrate coenzyme A ligase	A0A0S2JZP1	1.0279	0.7780
TIGR00266 family protein	A0A0S2K6W5	1.0293	0.9189
Translational regulator CsrA	A0A0S2K6K6	1.0297	0.8465
Inositol-1-monophosphatase	A0A0S2K511	1.0366	0.7817
Protein HflK	A0A0S2K4K4	1.0397	0.4690
Signal peptidase I	A0A0S2K315	1.0419	0.8895
Uncharacterized protein	A0A0S2K013	1.0430	0.8752
60 kDa chaperonin	A0A0S2JY23	1.0448	0.6212
Decarboxylase family protein	A0A0S2K8I2	1.0517	0.6534
Sulfate adenylyltransferase subunit 2	A0A0S2JXI2	1.0554	0.6490
Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	A0A0S2K693	1.0555	0.4538
Dihydrolipoyl dehydrogenase	A0A0S2K4G9	1.0589	0.1547
TonB-dependent receptor	A0A0S2K0N7	1.0612	0.5258
Phosphoglycerate kinase	A0A0S2JYY8	1.0619	0.4901
Phage shock protein A (IM30), suppresses sigma54-dependent transcription	A0A0S2K6P9	1.0626	0.8800
Uncharacterized protein	A0A0S2JZY6	1.0640	0.8435
50S ribosomal protein L23	A0A0S2K6F3	1.0644	0.6542
DNA-directed RNA polymerase subunit alpha	A0A0S2K570	1.0657	0.2001
NAD-dependent aldehyde dehydrogenase	A0A0S2K1Z1	1.0699	0.4036
30S ribosomal protein S10	A0A0S2K565	1.0707	0.6882
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	A0A0S2K2I8	1.0716	0.7411
Translation initiation factor IF-2	A0A0S2JZT1	1.0722	0.2276
Polyribonucleotide nucleotidyltransferase	A0A0S2K0E7	1.0729	0.3343

Succinate dehydrogenase flavoprotein subunit	A0A0S2K1T8	1.0755	0.1089
Malonyl CoA-acyl carrier protein transacylase	A0A0S2K2N3	1.0772	0.3675
Phenylalanine--tRNA ligase alpha subunit	A0A0S2K366	1.0782	0.5535
Secreted hydrolase	A0A0S2K2Y3	1.0798	0.7772
Peptidase	A0A0S2K1Z0	1.0828	0.4097
UDP-galactopyranose mutase	A0A0S2JX61	1.0858	0.7264
Fe/S biogenesis protein NfuA	A0A0S2K595	1.0860	0.7495
Ribose-phosphate pyrophosphokinase	A0A0S2K3Q4	1.0901	0.2212
50S ribosomal protein L9	A0A0S2JYC4	1.0911	0.0698
Uncharacterized protein	A0A0S2K384	1.0929	0.1271
Ubiquinol-cytochrome c reductase iron-sulfur subunit	A0A0S2JXH4	1.0935	0.3172
3-ketoacyl-ACP reductase	A0A0S2K2X1	1.0951	0.0675
ATP synthase subunit alpha	A0A0S2K6C7	1.0951	0.0825
2-dehydro-3-deoxyphosphooctonate aldolase	A0A0S2K4V1	1.0954	0.4064
Mechanosensitive channel protein	A0A0S2JXS0	1.0974	0.4495
Peptidyl-prolyl cis-trans isomerase	A0A0S2K2X2	1.0976	0.3964
Fructose-1,6-bisphosphate aldolase	A0A0S2JYJ4	1.0994	0.2643
Calmodulin	A0A0S2JXR6	1.1083	0.8400
30S ribosomal protein S12	A0A0S2JY34	1.1098	0.2235
50S ribosomal protein L35	A0A0S2K288	1.1120	0.8475
Serine hydroxymethyltransferase	A0A0S2K4F8	1.1133	0.0186
S-adenosylmethionine synthase	A0A0S2K4F2	1.1152	0.5809
Fructose-1,6-bisphosphatase class 1	A0A0S2K580	1.1153	0.3777
ABC transporter, ATP-binding protein	A0A0S2K216	1.1163	0.5569
Peptide chain release factor 1	A0A0S2K4Y6	1.1234	0.6144
Cold shock domain protein CspD	A0A0S2K0H8	1.1235	0.2659
2-oxoisovalerate dehydrogenase subunit beta	A0A0S2K153	1.1278	0.7962
Glutamine synthetase	A0A0S2K4Y1	1.1286	0.0966
DNA-directed RNA polymerase subunit beta	A0A0S2JY49	1.1309	0.0592

30S ribosomal protein S6	A0A0S2JXH8	1.1318	0.2503
50S ribosomal protein L1	A0A0S2JX69	1.1319	0.0865
Fumarate hydratase class I	A0A0S2K0P2	1.1331	0.0265
Anti-sigma factor antagonist	A0A0S2K4K0	1.1347	0.4027
Phosphoribosylamine--glycine ligase	A0A0S2K578	1.1358	0.2027
Phosphoglucosamine mutase	A0A0S2K0E3	1.1393	0.0878
30S ribosomal protein S9	A0A0S2JXX0	1.1394	0.0988
2-hydroxy-3-oxopropionate reductase	A0A0S2K2Z6	1.1401	0.3294
Flagellar hook protein FlgE	A0A0S2JZH9	1.1418	0.6854
Chemotaxis response regulator	A0A0S2K636	1.1422	0.0959
30S ribosomal protein S16	A0A0S2K3C3	1.1432	0.1812
Phosphopentomutase	A0A0S2K7M7	1.1448	0.6018
Putative protease with the C-terminal PDZ domain protein	A0A0S2K8N7	1.1487	0.4191
Negative regulator of flagellin synthesis	A0A0S2K021	1.1512	0.7542
Adenylate kinase	A0A0S2K2Y7	1.1544	0.1770
Serine--tRNA ligase	A0A0S2K0N1	1.1544	0.5241
50S ribosomal protein L15	A0A0S2K6E8	1.1544	0.2413
Adenine phosphoribosyltransferase	A0A0S2K2N4	1.1593	0.4162
50S ribosomal protein L2	A0A0S2K6F9	1.1612	0.0683
DNA-directed RNA polymerase subunit beta	A0A0S2JXY9	1.1624	0.0739
Thioredoxin	A0A0S2JX84	1.1645	0.1581
Carbamoyl-phosphate synthase large chain	A0A0S2K2X6	1.1646	0.0985
50S ribosomal protein L21	A0A0S2K4G4	1.1675	0.1216
Pyridoxine 5-phosphate synthase	A0A0S2K2F5	1.1722	0.0981
Cell division protein FtsZ	A0A0S2JXT4	1.1751	0.0425
Uroporphyrinogen decarboxylase	A0A0S2JY40	1.1777	0.2234
30S ribosomal protein S17	A0A0S2K5U6	1.1779	0.0943
30S ribosomal protein S8	A0A0S2K6H1	1.1785	0.0591
Carbamoyl-phosphate synthase small chain	A0A0S2K416	1.1790	0.1741

Bmp1	A0A0S2JY74	1.1807	0.7311
50S ribosomal protein L5	A0A0S2K6D0	1.1812	0.0232
Flagellin	A0A0S2K074	1.1820	0.0141
50S ribosomal protein L22	A0A0S2K5M8	1.1856	0.0316
ATP synthase subunit beta	A0A0S2K724	1.1858	0.0014
Shikimate kinase	A0A0S2K5G3	1.1870	0.2332
Iron-sulfur cluster assembly scaffold protein IscU	A0A0S2K569	1.1876	0.3954
Uncharacterized protein	A0A0S2K4K6	1.1906	0.5153
Amidohydrolase	A0A0S2K1U3	1.2023	0.0039
3-oxoacyl-[acyl-carrier-protein] synthase 2	A0A0S2K2F0	1.2027	0.0289
6-phosphogluconate dehydrogenase, decarboxylating	A0A0S2K259	1.2030	0.5379
50S ribosomal protein L19	A0A0S2K4L4	1.2065	0.0074
Succinate dehydrogenase iron-sulfur subunit	A0A0S2K2G4	1.2068	0.0359
Uncharacterized protein	A0A0S2K6X9	1.2076	0.0382
Chaperone protein DnaK	A0A0S2K8D5	1.2119	0.0006
50S ribosomal protein L30	A0A0S2K6N1	1.2140	0.1433
50S ribosomal protein L13	A0A0S2JYE6	1.2143	0.0179
Single-stranded DNA-binding protein	A0A0S2JXG7	1.2186	0.0615
Acyltransferase	A0A0S2K5R9	1.2207	0.2580
30S ribosomal protein S5	A0A0S2K5H5	1.2214	0.0103
50S ribosomal protein L6	A0A0S2K6R3	1.2236	0.0398
Peptidase M16	A0A0S2K3K3	1.2262	0.5290
Arginine N-succinyltransferase	A0A0S2K551	1.2271	0.0087
50S ribosomal protein L25	A0A0S2K4R4	1.2272	0.0199
N-succinylglutamate 5-semialdehyde dehydrogenase	A0A0S2K574	1.2344	0.0347
Lipoprotein	A0A0S2K590	1.2366	0.5369
Bmp7	A0A0S2JYW1	1.2375	0.7855
Na(+)-translocating NADH-quinone reductase subunit B	A0A0S2K555	1.2414	0.6373
Protein translocase subunit SecD	A0A0S2JYA5	1.2431	0.3185

dTDP-4-dehydrorhamnose 3,5-epimerase	A0A0S2JXS8	1.2470	0.0362
Phosphotyrosine protein phosphatase	A0A0S2JY36	1.2490	0.1748
TonB-denpendent receptor	A0A0S2K084	1.2530	0.0113
Uncharacterized protein	A0A0S2K046	1.2544	0.4546
Amidohydrolase	A0A0S2K1V6	1.2633	0.0050
O-methyltransferase	A0A0S2K482	1.2708	0.0001
Adenylosuccinate synthetase	A0A0S2K5G4	1.2727	0.0806
50S ribosomal protein L3	A0A0S2K5T4	1.2732	0.0016
Peroxiredoxin/glutaredoxin protein	A0A0S2JZD1	1.2738	0.3094
TonB-dependent receptor	A0A0S2K6M5	1.2740	0.0479
Thioredoxin reductase	A0A0S2K0T0	1.2741	0.0041
Uncharacterized protein	A0A0S2JYC5	1.2791	0.5032
Isoleucine--tRNA ligase	A0A0S2JZD6	1.2847	0.5994
50S ribosomal protein L24	A0A0S2K5V1	1.2852	0.0139
Peptidyl-prolyl cis-trans isomerase	A0A0S2K023	1.2907	0.2827
Microbial collagenase, secreted	A0A0S2K878	1.2962	0.1132
Bifunctional purine biosynthesis protein PurH	A0A0S2K4T8	1.2975	0.3519
Acetylornithine aminotransferase	A0A0S2K5E5	1.2993	0.0005
Dihydroorotase	A0A0S2JZT8	1.3003	0.1460
30S ribosomal protein S11	A0A0S2K5L1	1.3025	0.0003
Peptidoglycan-associated protein	A0A0S2K2C8	1.3030	0.0791
Amidohydrolase	A0A0S2JXX3	1.3045	0.0052
Outer membrane protein (Porin)	A0A0S2K4H1	1.3047	0.0026
Urea carboxylase	A0A0S2K291	1.3088	0.2371
Dihydrodipicolinate synthetase	A0A0S2K0N2	1.3091	0.0001
Glyceraldehyde-3-phosphate dehydrogenase	A0A0S2K223	1.3121	0.0008
50S ribosomal protein L11	A0A0S2JY63	1.3127	0.0051
Sulfate permease	A0A0S2K208	1.3161	0.4139
Amidohydrolase	A0A0S2JZF2	1.3173	0.0114

Putative pterin-4-alpha-carbinolamine dehydratase	A0A0S2K402	1.3179	0.2466
Flagellin	A0A0S2K038	1.3217	0.0009
TonB-dependent receptor	A0A0S2K700	1.3227	0.3498
Transketolase	A0A0S2K469	1.3248	0.0105
Major outer membrane protein	A0A0S2K8P4	1.3270	0.0180
Transcriptional regulator	A0A0S2JYH8	1.3312	0.2607
Thiol:disulfide interchange protein	A0A0S2K6B4	1.3421	0.0164
Malate dehydrogenase	A0A0S2K5D6	1.3457	0.0001
Enoyl-CoA hydratase	A0A0S2K1I9	1.3464	0.1520
Bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	A0A0S2K1C4	1.3474	0.0747
Valine--tRNA ligase	A0A0S2K4S3	1.3475	0.3807
Proline dipeptidase	A0A0S2K2G0	1.3501	0.0000
Fatty aldehyde dehydrogenase	A0A0S2K169	1.3536	0.0005
ATP synthase subunit a	A0A0S2K5T1	1.3576	0.3579
Uncharacterized protein	A0A0S2K333	1.3577	0.4467
Fumarylacetoacetase	A0A0S2JZA9	1.3583	0.0046
Peptidase M14, carboxypeptidase A	A0A0S2K236	1.3690	0.1279
Phosphoenolpyruvate synthase	A0A0S2K932	1.3694	0.0012
S-(hydroxymethyl)glutathione dehydrogenase	A0A0S2K652	1.3730	0.1247
Preprotein translocase subunit YajC	A0A0S2JY73	1.3756	0.0118
Phosphoenolpyruvate carboxykinase (ATP)	A0A0S2K519	1.3760	0.0008
Isocitrate dehydrogenase	A0A0S2K1B6	1.3765	0.0010
Porin	A0A0S2JYA3	1.3811	0.0612
Sulfate adenylyltransferase subunit 1	A0A0S2JXG6	1.3853	0.1056
Porphobilinogen deaminase	A0A0S2JX10	1.3932	0.2965
Peptidase M28	A0A0S2K135	1.3937	0.1442
Isoaspartyl peptidase	A0A0S2K0S2	1.3978	0.0526
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	A0A0S2JY55	1.4030	0.3758
Glutamate--tRNA ligase	A0A0S2JZH4	1.4032	0.7380

Acyl-peptide hydrolase	A0A0S2K2R5	1.4062	0.0536
Protein translocase subunit SecY	A0A0S2K5W0	1.4114	0.0571
Peptidase M16	A0A0S2JZ16	1.4137	0.3593
3-hydroxyisobutyrate dehydrogenase	A0A0S2K114	1.4143	0.0521
Leucyl aminopeptidase	A0A0S2K958	1.4182	0.0145
Putative ring-cleavage extradiol dioxygenase	A0A0S2K875	1.4220	0.2788
Uncharacterized protein	A0A0S2K8Y4	1.4295	0.1044
Acetyl-coenzyme A synthetase	A0A0S2JYE8	1.4318	0.0032
Peptidase M13	A0A0S2K1X2	1.4319	0.0060
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	A0A0S2K421	1.4411	0.5630
2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	A0A0S2K6M9	1.4417	0.1945
Elongation factor 4	A0A0S2K2D3	1.4485	0.1419
D-3-phosphoglycerate dehydrogenase	A0A0S2K5B5	1.4554	0.3314
50S ribosomal protein L4	A0A0S2K6C0	1.4556	0.0357
Uncharacterized protein	A0A0S2K5Y9	1.4559	0.0038
ATP-dependent zinc metalloprotease FtsH	A0A0S2K1B1	1.4593	0.2300
Chaperone protein DnaJ	A0A0S2K8F6	1.4650	0.0779
50S ribosomal protein L14	A0A0S2K582	1.4676	0.0000
6,7-dimethyl-8-ribityllumazine synthase	A0A0S2K4D6	1.4721	0.0302
Membrane-bound lytic murein transglycosylase C	A0A0S2K244	1.4949	0.0003
Hydrolase	A0A0S2JXD1	1.4989	0.1095
Ribosomal subunit interface protein	A0A0S2JZ31	1.5011	0.2285
Periplasmic protein	A0A0S2JY32	1.5126	0.0531
Glycine dehydrogenase (decarboxylating)	A0A0S2JZ77	1.5132	0.0305
Twin-arginine translocation pathway signal	A0A0S2K5R1	1.5192	0.2352
Membrane protein	A0A0S2JZX4	1.5229	0.3259
Two-component response regulator	A0A0S2K472	1.5233	0.0905
Triosephosphate isomerase	A0A0S2K0V0	1.5243	0.0080
Peptidase S9	A0A0S2K930	1.5243	0.0000

Enolase	A0A0S2K3G8	1.5370	0.0000
Translation initiation factor IF-1	A0A0S2K142	1.5487	0.3901
Aminopeptidase B	A0A0S2JZ46	1.5639	0.0000
Alanine--tRNA ligase	A0A0S2K7D1	1.5667	0.0412
Chemotaxis response regulator protein-glutamate methylesterase	A0A0S2K001	1.5790	0.0057
N5-carboxyaminoimidazole ribonucleotide mutase	A0A0S2K194	1.5793	0.3755
Elongation factor P	A0A0S2JXP7	1.5866	0.2190
Uncharacterized protein	A0A0S2K2I7	1.5968	0.0003
Flavodoxin	A0A0S2K2Q9	1.5970	0.2357
D-alanyl-D-alanine carboxypeptidase, penicillin-binding protein 5	A0A0S2K434	1.6052	0.0302
Carboxy-terminal protease	A0A0S2K209	1.6250	0.0330
Thiol:disulfide interchange protein	A0A0S2K6G8	1.6303	0.0000
Citrate synthase	A0A0S2K7M1	1.6525	0.0006
Peptidoglycan D,D-transpeptidase FtsI	A0A0S2JXN2	1.6642	0.2554
Probable cytosol aminopeptidase	A0A0S2K1Y7	1.6816	0.0000
Chaperone SurA	A0A0S2K0B0	1.6899	0.0156
Coproporphyrinogen-III oxidase	A0A0S2K648	1.6917	0.0018
TonB-dependent receptor	A0A0S2K4P7	1.6967	0.1928
Uncharacterized protein	A0A0S2K8F4	1.7190	0.0188
50S ribosomal protein L32	A0A0S2K2D1	1.7269	0.0024
Outer membrane protein OmpH	A0A0S2K2S0	1.7316	0.0004
Peptidase M17, leucyl aminopeptidase domain-containing protein	A0A0S2K3H8	1.7371	0.0031
Putative stomatin/prohibitin-family membrane protease subunit YbbK	A0A0S2K7B7	1.7682	0.1021
Xaa-Pro dipeptidase	A0A0S2JXA1	1.7787	0.0004
Glycerol-3-phosphate cytidylyltransferase	A0A0S2JYU6	1.7903	0.2343
Uncharacterized protein	A0A0S2K813	1.7952	0.0654
Dipeptidyl peptidase IV	A0A0S2K558	1.8230	0.0196

50S ribosomal protein L27	A0A0S2K5C7	1.8290	0.0075
tRNA (cytidine/uridine-2-O-)-methyltransferase TrmJ	A0A0S2K4S8	1.8343	0.0881
Collagen-binding surface adhesin SpaP (Antigen I/II family)	A0A0S2K346	1.8635	0.0362
Aspartate--ammonia ligase	A0A0S2K5E3	1.8727	0.0911
Peptidyl-prolyl cis-trans isomerase	A0A0S2K1C3	1.8960	0.0000
Uncharacterized protein	A0A0S2K125	1.9141	0.0039
Uncharacterized protein	A0A0S2JZV6	1.9173	0.1764
Acyl-CoA dehydrogenase	A0A0S2K1Q5	1.9895	0.0184
4-hydroxy-tetrahydrodipicolinate synthase	A0A0S2K8E0	1.9998	0.0067
Collagenase	A0A0S2K6X3	2.0125	0.0312
Tol-Pal system protein TolQ	A0A0S2K2X9	2.0278	0.0302
Bmp2	A0A0S2JXW2	2.0289	0.3851
Putative Cobalt-zinc-cadmium resistance protein (Cation efflux system protein)	A0A0S2K8G7	2.0300	0.0969
CTP synthase	A0A0S2K3G3	2.1256	0.1048
Uncharacterized protein	A0A0S2K2H6	2.1420	0.0012
Uncharacterized protein	A0A0S2K593	2.1587	0.0079
Propionyl CoA synthase	A0A0S2K7N8	2.1806	0.0450
2-methylisocitrate lyase	A0A0S2K6S8	2.1848	0.0023
4-hydroxyphenylpyruvate dioxygenase	A0A0S2K002	2.1907	0.0000
Leucine dehydrogenase	A0A0S2K2B3	2.2090	0.0008
Alcohol dehydrogenase	A0A0S2K3L0	2.2239	0.0001
Bmp5	A0A0S2JY87	2.2257	0.2167
Putative TonB-dependent receptor	A0A0S2JZ59	2.2280	0.0076
Aspartate-semialdehyde dehydrogenase	A0A0S2K3E4	2.2632	0.0308
Orotidine 5-phosphate decarboxylase	A0A0S2K165	2.2761	0.0000
Membrane protein	A0A0S2K7U7	2.3803	0.0004
Uncharacterized protein	A0A0S2JXC4	2.3921	0.0201
Bifunctional protein GlmU	A0A0S2K680	2.4184	0.0078

Uncharacterized protein	A0A0S2JYI5	2.4398	0.0617
Membrane protein insertase YidC	A0A0S2K739	2.4438	0.0094
Transcription elongation factor GreA	A0A0S2K3J0	2.4456	0.0308
Uncharacterized protein	A0A0S2K1K7	2.4583	0.0195
Peptidase S9	A0A0S2K6T8	2.5827	0.0028
Electron transfer flavoprotein subunit beta	A0A0S2K1E5	2.6032	0.0037
Peptidylprolyl isomerase	A0A0S2K4M9	2.6573	0.0535
Anti-sigma B factor antagonist	A0A0S2JYD7	2.6866	0.0520
TPR-like domain-containing protein	A0A0S2JYB7	2.6969	0.0156
Uncharacterized protein	A0A0S2K5M6	2.7642	0.0002
Succinylglutamate desuccinylase	A0A0S2K1N2	2.7760	0.0311
ABC transporter	A0A0S2JXT7	2.7955	0.0000
Peptidyl-prolyl cis-trans isomerase	A0A0S2JXG3	2.9670	0.1250
ATP synthase epsilon chain	A0A0S2K727	3.2037	0.0890
ABC transporter substrate-binding protein	A0A0S2JXM9	3.2427	0.0001
Tol-Pal system protein TolB	A0A0S2K380	3.5471	0.0126
Carboxypeptidase	A0A0S2K4K5	3.5730	0.0011
Electron transfer flavoprotein, alpha subunit	A0A0S2K0J8	3.7150	0.0164
Uncharacterized protein	A0A0S2K752	3.7237	0.0001
Lipoprotein	A0A0S2K843	3.8036	0.0044
UDP-galactose-4-epimerase	A0A0S2JYM3	3.8420	0.0045
Calmodulin-like protein	A0A0S2JXX2	3.9405	0.0848
Uncharacterized protein	A0A0S2K1M1	4.0266	0.0029
2-oxoisovalerate dehydrogenase subunit alpha	A0A0S2K1P4	4.1634	0.0046
Glycine betaine aldehyde dehydrogenase	A0A0S2K0C8	4.3273	0.0015
Uncharacterized protein	A0A0S2JZA0	4.4142	0.0000
Putative Polyphosphate kinase 2	A0A0S2K1J9	4.6789	0.0001
Glutamate 5-kinase	A0A0S2K6P1	4.9416	0.0000
Aconitate hydratase	A0A0S2K7G2	5.4074	0.0001

Peptidase S46	A0A0S2JZP6	6.3664	0.0001
Hemagglutinin	A0A0S2K6H7	7.1260	0.0002
Uncharacterized protein	A0A0S2K7S2	7.6040	0.0003
TonB-dependent receptor	A0A0S2JZN4	8.0852	0.0102
Periplasmic serine endoprotease DegP-like	A0A0S2JYI3	10.4123	0.0001
Tricorn protease homolog	A0A0S2K7Y2	12.3235	0.0000
OmpA domain-containing protein	A0A0S2K429	43.0423	0.0000
Gamma-glutamyl phosphate reductase	A0A0S2K703	129.6681	0.0000

Table S3. Expression changes of identified extracellular proteases in P. phenolica under salt stress ([1]NS, not significant; [2]ND, not detected in high-salt samples; [3]ND, not detected in normal-salt samples)

Group	Uniprot accession	Protein name	Fold change (High-salt/Normal-salt)	p value
Metalloprotease	A0A0S2JXA1	Xaa-Pro dipeptidase	1.78	0.0004
	A0A0S2K3H8	Peptidase M17, leucyl aminopeptidase domain-containing protein	1.74	0.003
	A0A0S2K1Y7	Probable cytosol aminopeptidase	1.68	<0.0001
	A0A0S2JZ46	Aminopeptidase B	1.56	<0.0001
	A0A0S2K1B1	ATP-dependent zinc metalloprotease FtsH	1.46	NS [1]
	A0A0S2K1X2	Peptidase M13	1.43	0.006
	A0A0S2K958	Leucyl aminopeptidase	1.42	0.01
	A0A0S2JZ16	Peptidase M16	1.41	NS [1]
	A0A0S2K135	Peptidase M28	1.39	NS [1]
	A0A0S2K236	Peptidase M14, carboxypeptidase A	1.37	NS [1]
	A0A0S2K2G0	Proline dipeptidase	1.35	NS [1]
	A0A0S2K3K3	Peptidase M16	1.23	NS [1]
	A0A0S2K5F2	Probable cytosol aminopeptidase	0.98	NS [1]
	A0A0S2K4W4	Oligopeptidase A	0.95	NS [1]
	A0A0S2K6B9	Aminopeptidase	0.92	NS [1]
	A0A0S2K4H5	ATP-dependent Clp protease ATP-binding subunit ClpX	0.9	NS [1]
	A0A0S2K0T8	Peptidase M3	0.64	NS [1]
	A0A0S2K1S1	Aminopeptidase YpdF (MP-, MA-, MS-,AP-,NP-specific)	0.48	NS [1]
	A0A0S2K4X4	Peptidase M14, carboxypeptidase A	ND in high-salt samples [2]	-
	A0A0S2K2T5	M48 family peptidase	ND in high-salt samples [2]	-

Serine protease	A0A0S2K315	Signal peptidase I	ND in normal-salt samples[3]	-
	A0A0S2K7Y2	Tricorn protease homolog	12.32	<0.0001
	A0A0S2JYI3	Periplasmic serine endoprotease DegP-like	10.41	<0.0001
	A0A0S2JZP6	Peptidase S46	6.37	0.0001
	A0A0S2K4K5	Carboxypeptidase	3.57	0.001
	A0A0S2K6T8	Peptidase S9	2.58	0.003
	A0A0S2K558	Dipeptidyl peptidase IV	1.82	0.02
	A0A0S2K209	Carboxy-terminal protease	1.63	0.03
	A0A0S2K930	Peptidase S9	1.52	<0.0001
	A0A0S2K2R5	Acyl-peptide hydrolase	1.41	NS[1]
	A0A0S2K1Z0	Peptidase	1.08	NS[1]
	A0A0S2K479	ATP-dependent Clp protease proteolytic subunit	0.89	NS[1]
	A0A0S2JXY2	Carboxyl-terminal protease	0.59	NS[1]
	A0A0S2K7G7	Peptidase S8/S53 subtilisin kexin sedolisin	0.2	0.001
Other protease	A0A0S2K7B7	Putative stomatin/prohibitin-family membrane protease subunit YbbK	1.77	NS[1]
	A0A0S2K8N7	Putative protease with the C-terminal PDZ domain protein	1.15	NS[1]
	A0A0S2K1A5	Glutamate carboxypeptidase II	0.84	NS[1]
	A0A0S2K5T7	ATP-dependent protease ATPase subunit HslU	0.64	NS[1]
	A0A0S2K0S2	Isoaspartyl peptidase	ND in high-salt samples[2]	-