

Table S1. Proteins associated with purified *F. tularensis* ribosomes. LC-MS/MS analysis of four samples of ribosomes purified from wild-type cells by sucrose cushions. Total spectral counts (columns F-I) were filtered with the following parameters: 99% protein threshold, 95% peptide threshold, minimum of 2 peptides. Hypothetical proteins with no known function were not categorized as transcription or translation-related. Proteins were primarily ribosomal (69%) or associated with transcription and translation processes (10%).

| Accession Number | Molecular Weight (kDa) | Gene Locus | Gene Name | Identified Proteins (245) |
|------------------|------------------------|------------|--------------|-----------------------------------|
| YP_514345.1 | 57 | FTL_1714 | <i>groEL</i> | chaperonin GroEL |
| YP_514522.1 | 62 | FTL_1912 | <i>rpsA</i> | 30S ribosomal protein S1 |
| YP_513037.1 | 25 | FTL_0242 | <i>rpsC</i> | 30S ribosomal protein S3 |
| YP_513727.1 | 16 | FTL_1026 | <i>rplI</i> | 50S ribosomal protein L9 |
| YP_513045.1 | 14 | FTL_0250 | <i>rpsH</i> | 30S ribosomal protein S8 |
| YP_514378.1 | 25 | FTL_1747 | <i>rplA</i> | 50S ribosomal protein L1 |
| YP_513101.1 | 100 | FTL_0309 | <i>aceE</i> | pyruvate dehydrogenase subunit E1 |
| YP_514376.1 | 13 | FTL_1745 | <i>rplL</i> | 50S ribosomal protein L7/L12 |
| YP_513044.1 | 12 | FTL_0249 | <i>rpsN</i> | 30S ribosomal protein S14 |
| YP_514377.1 | 19 | FTL_1746 | <i>rplJ</i> | 50S ribosomal protein L10 |
| YP_513055.1 | 23 | FTL_0260 | <i>rpsD</i> | 30S ribosomal protein S4 |
| YP_513032.1 | 23 | FTL_0237 | <i>rplD</i> | 50S ribosomal protein L4 |

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|------------------|------------------------|------------|-------------|---|
| YP_513043.1 | 20 | FTL_0248 | <i>rplE</i> | 50S ribosomal protein L5 |
| YP_513030.1 | 12 | FTL_0235 | <i>rpsJ</i> | 30S ribosomal protein S10 |
| YP_513019.1 | 26 | FTL_0224 | <i>rpsB</i> | 30S ribosomal protein S2 |
| YP_513031.1 | 22 | FTL_0236 | <i>rplC</i> | 50S ribosomal protein L3 |
| YP_513041.1 | 13 | FTL_0246 | <i>rplN</i> | 50S ribosomal protein L14 |
| YP_513102.1 | 57 | FTL_0310 | - | dihydrolipoamide acetyltransferase |
| YP_513036.1 | 12 | FTL_0241 | <i>rplV</i> | 50S ribosomal protein L22 |
| YP_513046.1 | 19 | FTL_0251 | <i>rplF</i> | 50S ribosomal protein L6 |
| YP_513048.1 | 18 | FTL_0253 | <i>rpsE</i> | 30S ribosomal protein S5 |
| YP_513034.1 | 30 | FTL_0239 | <i>rplB</i> | 50S ribosomal protein L2 |
| YP_514399.1 | 103 | FTL_1772 | - | aconitate hydratase |
| YP_513039.1 | 8 | FTL_0244 | - | 50S ribosomal protein L29 |
| YP_514411.1 | 66 | FTL_1786 | - | succinate dehydrogenase, catalytic and NAD/flavoprotein subunit |
| YP_513870.1 | 16 | FTL_1187 | <i>rplM</i> | 50S ribosomal protein L13 |
| YP_513042.1 | 11 | FTL_0247 | <i>rplX</i> | 50S ribosomal protein L24 |
| YP_513869.1 | 15 | FTL_1186 | <i>rpsI</i> | 30S ribosomal protein S9 |
| YP_513057.1 | 17 | FTL_0262 | <i>rplQ</i> | 50S ribosomal protein L17 |
| YP_513468.1 | 96 | FTL_0717 | <i>rne</i> | ribonuclease E |
| YP_513038.1 | 16 | FTL_0243 | <i>rplP</i> | 50S ribosomal protein L16 |
| YP_514420.1 | 50 | FTL_1795 | - | FOF1 ATP synthase subunit beta |
| YP_513028.1 | 18 | FTL_0233 | <i>rpsG</i> | 30S ribosomal protein S7 |
| YP_513345.1 | 83 | FTL_0585 | <i>fadE</i> | acyl-CoA dehydrogenase |

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|------------------|------------------------|------------|-------------|--|
| YP_514379.1 | 15 | FTL_1748 | <i>rplK</i> | 50S ribosomal protein L11 |
| YP_513047.1 | 13 | FTL_0252 | <i>rplR</i> | 50S ribosomal protein L18 |
| YP_513103.1 | 51 | FTL_0311 | - | dihydrolipoamide dehydrogenase |
| YP_513874.1 | 69 | FTL_1191 | <i>dnaK</i> | molecular chaperone DnaK |
| YP_514408.1 | 53 | FTL_1783 | <i>sucB</i> | dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex |
| YP_514115.1 | 71 | FTL_1464 | - | ATP-dependent metalloprotease |
| YP_514366.1 | 13 | FTL_1735 | <i>rplS</i> | 50S ribosomal protein L19 |
| YP_513053.1 | 13 | FTL_0258 | <i>rpsM</i> | 30S ribosomal protein S13 |
| YP_513054.1 | 14 | FTL_0259 | - | 30S ribosomal protein S11 |
| YP_514198.1 | 70 | FTL_1552 | - | hypothetical protein FTL_1552 |
| YP_514374.1 | 157 | FTL_1743 | - | DNA-directed RNA polymerase subunit beta |
| YP_513622.1 | 40 | FTL_0903 | <i>hflK</i> | FtsH protease activity modulator |
| YP_514409.1 | 106 | FTL_1784 | <i>sucA</i> | 2-oxoglutarate dehydrogenase E1 component |
| YP_514108.1 | 12 | FTL_1453 | <i>rplU</i> | 50S ribosomal protein L21 |
| YP_513726.1 | 8 | FTL_1025 | <i>rpsR</i> | 30S ribosomal protein S18 |
| YP_513661.1 | 11 | FTL_0950 | - | 50S ribosomal protein L25 |
| YP_514446.1 | 87 | FTL_1824 | - | NADH dehydrogenase subunit G |
| YP_514059.1 | 13 | FTL_1404 | <i>rplT</i> | 50S ribosomal protein L20 |
| YP_513725.1 | 13 | FTL_1024 | <i>rpsF</i> | 30S ribosomal protein S6 |
| YP_514184.1 | 10 | FTL_1538 | <i>rpsO</i> | 30S ribosomal protein S15 |

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|------------------|------------------------|------------|--------------|---|
| YP_513559.1 | 53 | FTL_0837 | <i>metIQ</i> | D-methionine binding transport protein, ABC transporter, membrane and periplasmic protein |
| YP_513050.1 | 15 | FTL_0255 | <i>rplO</i> | 50S ribosomal protein L15 |
| YP_514183.1 | 76 | FTL_1537 | <i>pnp</i> | polynucleotide phosphorylase/polyadenylase |
| YP_513639.1 | 19 | FTL_0926 | - | Ferritin-like protein |
| YP_513033.1 | 11 | FTL_0238 | <i>rplW</i> | 50S ribosomal protein L23 |
| YP_513788.1 | 40 | FTL_1096 | <i>dsbA</i> | Disulfide bond formation protein A / FipB |
| YP_514154.1 | 81 | FTL_1504 | <i>katG</i> | peroxidase/catalase |
| YP_514517.1 | 40 | FTL_1907 | - | cell division protein FtsZ |
| YP_514539.1 | 34 | FTL_1936 | - | periplasmic solute binding family protein |
| YP_512944.1 | 49 | FTL_0146 | - | ABC transporter ATP-binding protein |
| YP_513027.1 | 14 | FTL_0232 | <i>rpsL</i> | 30S ribosomal protein S12 |
| YP_514375.1 | 151 | FTL_1744 | <i>rpoB</i> | DNA-directed RNA polymerase subunit beta |
| YP_514422.1 | 56 | FTL_1797 | - | FOF1 ATP synthase subunit alpha |
| YP_513291.1 | 9 | FTL_0522 | <i>rpmB</i> | 50S ribosomal protein L28 |
| YP_513974.2 | 8 | FTL_1303 | <i>rpmE</i> | 50S ribosomal protein L31 |
| YP_513035.1 | 10 | FTL_0240 | <i>rpsS</i> | 30S ribosomal protein S19 |
| YP_514307.1 | 113 | FTL_1672 | - | AcrB/AcrD/AcrF family transporter |
| YP_513615.1 | 55 | FTL_0896 | - | peptidyl-prolyl cis-trans isomerase D |
| YP_514047.1 | 64 | FTL_1392 | <i>deaD</i> | cold-shock DEAD-box protein A |
| YP_514382.1 | 43 | FTL_1751 | - | elongation factor Tu |
| YP_514071.1 | 45 | FTL_1416 | <i>capB</i> | capsule biosynthesis protein capB |

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|------------------|------------------------|------------|--------------|--|
| YP_513570.1 | 70 | FTL_0848 | <i>secD</i> | preprotein translocase subunit SecD |
| YP_513438.1 | 38 | FTL_0687 | - | HlyD family secretion protein |
| YP_514229.1 | 25 | FTL_1590 | - | hypothetical protein FTL_1590 |
| YP_513040.1 | 10 | FTL_0245 | <i>rpsQ</i> | 30S ribosomal protein S17 |
| YP_514410.1 | 27 | FTL_1785 | <i>sdhB</i> | succinate dehydrogenase iron-sulfur subunit |
| YP_514303.1 | 67 | FTL_1668 | <i>msbA</i> | lipid A transport protein ABC transporter ATP-binding protein/permease |
| YP_514421.1 | 33 | FTL_1796 | - | F0F1 ATP synthase subunit gamma |
| YP_513829.1 | 7 | FTL_1143 | <i>rpmF</i> | 50S ribosomal protein L32 |
| YP_513965.1 | 31 | FTL_1294 | - | short-chain dehydrogenase |
| YP_514434.1 | 92 | FTL_1809 | <i>infB</i> | translation initiation factor IF-2 |
| YP_513610.1 | 50 | FTL_0891 | <i>tig</i> | trigger factor |
| YP_513260.1 | 57 | FTL_0488 | - | 4-alpha-glucanotransferase |
| YP_513919.1 | 50 | FTL_1239 | <i>ffh</i> | signal recognition particle protein, Ffh |
| YP_513652.1 | 26 | FTL_0939 | - | aldolase/adducin class II family protein |
| YP_514069.1 | 44 | FTL_1414 | <i>capA</i> | hypothetical membrane protein, capA |
| YP_513862.1 | 11 | FTL_1179 | <i>hfp</i> | ribosome hibernation-promoting factor |
| YP_512874.1 | 10 | FTL_0070 | <i>rpsT</i> | 30S ribosomal protein S20 |
| YP_513049.1 | 7 | FTL_0254 | <i>rpmD</i> | 50S ribosomal protein L30 |
| YP_513747.1 | 8 | FTL_1047 | <i>rpsU2</i> | 30S ribosomal protein S21-2 |
| YP_514109.1 | 104 | FTL_1458 | <i>secA</i> | preprotein translocase subunit SecA |
| YP_513144.1 | 22 | FTL_0361 | - | LemA-like protein |
| YP_514369.1 | 9 | FTL_1738 | <i>rpsP</i> | 30S ribosomal protein S16 |

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|------------------|------------------------|------------|-------------|--|
| YP_513551.1 | 30 | FTL_0829 | - | glycerophosphoryl diester phosphodiesterase |
| YP_513790.1 | 15 | FTL_1100 | <i>rsfS</i> | ribosomal silencing factor RsfS |
| YP_514488.1 | 37 | FTL_1874 | <i>obgE</i> | GTPase ObgE |
| YP_514310.1 | 38 | FTL_1678 | - | hypothetical protein FTL_1678 |
| YP_514129.1 | 52 | FTL_1478 | <i>guaB</i> | inosine-5-monophosphate dehydrogenase |
| YP_513623.1 | 35 | FTL_0904 | <i>hflC</i> | protease modulator HflC |
| YP_514140.1 | 115 | FTL_1489 | - | FAD-binding family protein |
| YP_512961.1 | 30 | FTL_0166 | - | universal stress protein |
| YP_514306.1 | 50 | FTL_1671 | - | RND efflux transporter |
| YP_513537.1 | 150 | FTL_0805 | - | bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase |
| YP_512931.1 | 81 | FTL_0133 | <i>feoB</i> | ferrous iron transport protein |
| YP_512973.1 | 62 | FTL_0178 | <i>yidC</i> | inner-membrane protein |
| YP_513113.1 | 47 | FTL_0325 | - | OmpA family protein |
| YP_513349.1 | 33 | FTL_0589 | - | hypothetical membrane protein FTL_0589 |
| YP_513560.1 | 39 | FTL_0838 | <i>metN</i> | D-methionine transport protein, ABC transporter,ATP-binding subunit |
| YP_514354.1 | 24 | FTL_1723 | - | hypothetical protein FTL_1723 |
| YP_513202.1 | 33 | FTL_0430 | - | hypothetical protein FTL_0430 |
| YP_514185.1 | 63 | FTL_1539 | <i>ftsI</i> | penicillin binding protein (peptidoglycan synthetase) |

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|------------------|------------------------|------------|-------------|--|
| YP_514040.1 | 13 | FTL_1384 | - | hypothetical protein FTL_1384 |
| YP_514107.1 | 9 | FTL_1452 | <i>rpmA</i> | 50S ribosomal protein L27 |
| YP_514451.1 | 17 | FTL_1829 | - | NADH dehydrogenase subunit B |
| YP_514447.1 | 46 | FTL_1825 | - | NADH dehydrogenase I subunit F |
| YP_512984.1 | 64 | FTL_0189 | - | cytochrome d terminal oxidase, polypeptide subunit I |
| YP_514250.1 | 36 | FTL_1611 | - | glycosyl transferase family protein |
| YP_514336.1 | 92 | FTL_1705 | <i>ftsK</i> | cell division protein |
| YP_513572.1 | 20 | FTL_0850 | - | hypothetical protein FTL_0850 |
| YP_513208.1 | 107 | FTL_0436 | <i>ileS</i> | isoleucyl-tRNA synthetase |
| YP_513322.1 | 86 | FTL_0556 | <i>rnr</i> | ribonuclease R |
| YP_513187.1 | 52 | FTL_0414 | <i>engA</i> | GTP-binding protein EngA |
| YP_514341.1 | 28 | FTL_1710 | - | ProP osmoprotectant transporter, fragment, partial |
| YP_513409.1 | 45 | FTL_0656 | - | hypothetical membrane protein FTL_0656 |
| YP_514524.1 | 21 | FTL_1914 | <i>ripA</i> | hypothetical membrane protein, ripA |
| YP_513957.1 | 15 | FTL_1286 | - | hypothetical membrane protein FTL_1286 |
| YP_513310.1 | 22 | FTL_0541 | - | hypothetical membrane protein FTL_0541 |
| YP_513309.1 | 43 | FTL_0540 | <i>lpxB</i> | lipid-A-disaccharide synthase |
| YP_513875.1 | 41 | FTL_1192 | - | chaperone protein DnaJ |
| YP_514424.1 | 17 | FTL_1799 | - | FOF1 ATP synthase subunit B |
| YP_513352.1 | 66 | FTL_0592 | <i>wbtA</i> | dTDP-glucose 4,6-dehydratase |
| YP_513408.1 | 40 | FTL_0655 | - | hypothetical membrane protein FTL_0655 |

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|------------------|------------------------|------------|--------------|--|
| YP_514276.1 | 38 | FTL_1637 | - | lipoprotein |
| YP_512895.1 | 96 | FTL_0094 | <i>clpB</i> | ClpB protein |
| YP_513246.1 | 48 | FTL_0474 | - | lipoprotein releasing system, subunit C, putative membrane protein |
| YP_513660.1 | 35 | FTL_0949 | - | ribose-phosphate pyrophosphokinase |
| YP_513029.1 | 78 | FTL_0234 | - | elongation factor G |
| YP_513426.1 | 31 | FTL_0674 | <i>panB</i> | 3-methyl-2-oxobutanoate hydroxymethyltransferase |
| YP_514060.1 | 7 | FTL_1405 | <i>rpmI</i> | 50S ribosomal protein L35 |
| YP_514346.1 | 10 | FTL_1715 | <i>groES</i> | co-chaperonin GroES |
| YP_513375.1 | 35 | FTL_0616 | <i>rpoA2</i> | DNA-directed RNA polymerase subunit alpha |
| YP_514221.1 | 45 | FTL_1582 | <i>potF</i> | putrescine-binding periplasmic protein |
| YP_513354.1 | 30 | FTL_0594 | <i>wbtC</i> | UDP-glucose 4-epimerase |
| YP_513364.1 | 33 | FTL_0604 | <i>wbtK</i> | glycosyltransferase |
| YP_512987.1 | 76 | FTL_0192 | - | cytochrome O ubiquinol oxidase subunit I |
| YP_513211.1 | 58 | FTL_0439 | - | hypothetical protein FTL_0439 |
| YP_513381.1 | 36 | FTL_0625 | <i>gtrB</i> | glycosyl transferase family protein |
| YP_513890.1 | 31 | FTL_1207 | - | MRP like protein |
| YP_513662.1 | 47 | FTL_0951 | - | hypothetical membrane protein FTL_0951 |
| YP_513519.1 | 67 | FTL_0784 | - | lipoprotein |
| YP_513617.1 | 12 | FTL_0898 | <i>hfq</i> | host factor I for bacteriophage Q beta replication |
| YP_512875.1 | 66 | FTL_0071 | - | GTP-binding protein LepA |

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|------------------|------------------------|------------|-------------|---|
| YP_513308.1 | 28 | FTL_0539 | - | UDP-N-acetylglucosamine acyltransferase |
| YP_513332.1 | 52 | FTL_0572 | - | hypothetical protein FTL_0572 |
| YP_513433.1 | 42 | FTL_0681 | <i>potG</i> | polyamine transporter, ABC transporter, ATP-binding protein |
| YP_513288.1 | 30 | FTL_0519 | <i>minD</i> | septum site-determining protein MinD |
| YP_512888.1 | 28 | FTL_0087 | - | acetyltransferase protein |
| YP_512910.1 | 58 | FTL_0112 | <i>iglB</i> | intracellular growth locus, subunit B |
| YP_513180.1 | 64 | FTL_0407 | <i>ubiB</i> | 2-polyprenylphenol 6-hydroxylase |
| YP_512982.1 | 28 | FTL_0187 | - | cyclohexadienyl dehydratase |
| YP_513955.1 | 37 | FTL_1284 | - | glutathione synthetase |
| YP_514168.1 | 84 | FTL_1521 | - | chitinase family 18 protein |
| YP_513056.1 | 35 | FTL_0261 | - | DNA-directed RNA polymerase subunit alpha |
| YP_514174.1 | 50 | FTL_1527 | <i>eno</i> | phosphopyruvate hydratase |
| YP_513398.1 | 15 | FTL_0645 | - | lipoprotein |
| YP_514518.1 | 45 | FTL_1908 | - | cell division protein FtsA |
| YP_514423.1 | 19 | FTL_1798 | - | F0F1 ATP synthase subunit delta |
| YP_513109.1 | 12 | FTL_0317 | - | hypothetical protein FTL_0317 |
| YP_513716.1 | 20 | FTL_1015 | - | AhpC/TSA family protein |
| YP_512923.1 | 128 | FTL_0125 | <i>pdpB</i> | Type VI Secretion protein PdpB |
| YP_513117.1 | 30 | FTL_0329 | <i>pssA</i> | CDP-alcohol phosphatidyltransferase |
| YP_514293.1 | 49 | FTL_1658 | <i>fimV</i> | hypothetical protein, fimV |
| YP_513437.1 | 55 | FTL_0686 | - | outer membrane efflux protein |

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|------------------|------------------------|------------|-------------|---|
| YP_514231.1 | 16 | FTL_1592 | <i>accB</i> | Acetyl-CoA carboxylase, biotin carboxyl carrier protein subunit |
| YP_513413.1 | 60 | FTL_0661 | - | hypothetical protein FTL_0661 |
| YP_512889.1 | 29 | FTL_0088 | - | acetyltransferase protein |
| YP_512998.1 | 37 | FTL_0203 | - | hypothetical protein FTL_0203 |
| YP_513823.1 | 44 | FTL_1137 | - | 3-oxoacyl-ACP synthase |
| YP_513977.1 | 40 | FTL_1306 | - | hypothetical protein FTL_1306 |
| YP_514130.1 | 52 | FTL_1479 | <i>pepA</i> | cytosol aminopeptidase |
| YP_513886.1 | 55 | FTL_1203 | - | cardiolipin synthetase |
| YP_513427.1 | 27 | FTL_0675 | <i>panG</i> | hypothetical protein, putative ketopantoate reductase |
| YP_512975.1 | 36 | FTL_0180 | <i>htrB</i> | acyltransferase |
| YP_513912.1 | 15 | FTL_1231 | - | hypothetical protein, FeS assembly SUF system regulator |
| YP_513348.1 | 82 | FTL_0588 | - | isocitrate dehydrogenase |
| YP_513908.1 | 26 | FTL_1225 | - | hypothetical protein FTL_1225 |
| YP_514514.1 | 37 | FTL_1904 | - | peptide chain release factor 2 |
| YP_513506.1 | 18 | FTL_0761 | <i>smpB</i> | SsrA-binding protein |
| YP_513194.1 | 16 | FTL_0421 | <i>tul4</i> | lipoprotein |
| YP_513994.1 | 41 | FTL_1328 | <i>fopA</i> | outer membrane associated protein |
| YP_513290.1 | 6 | FTL_0521 | <i>rpmG</i> | 50S ribosomal protein L33 |
| YP_514444.1 | 19 | FTL_1822 | - | NADH dehydrogenase subunit I |
| YP_514449.1 | 48 | FTL_1827 | - | NADH dehydrogenase subunit D |

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|------------------|------------------------|------------|-------------|--|
| YP_513550.1 | 67 | FTL_0828 | - | Type IV pili nucleotide binding protein, ABC transporter ATP-binding protein |
| YP_513237.1 | 43 | FTL_0465 | - | BNR/Asp-box repeat-containing protein |
| YP_513828.1 | 38 | FTL_1142 | - | putative glycerol-3-phosphate acyltransferase PlsX |
| YP_512904.1 | 14 | FTL_0105 | - | hypothetical membrane protein FTL_0105 |
| YP_513742.1 | 29 | FTL_1042 | - | FKBP-type peptidyl-prolyl cis-trans isomerase family protein |
| YP_513894.1 | 21 | FTL_1211 | - | lipoprotein |
| YP_513329.1 | 20 | FTL_0569 | - | hypothetical protein FTL_0569 |
| YP_514450.1 | 25 | FTL_1828 | - | NADH dehydrogenase I |
| YP_513757.1 | 48 | FTL_1060 | <i>dacD</i> | D-alanyl-D-alanine carboxypeptidase |
| YP_513355.1 | 42 | FTL_0595 | - | galacturonosyl transferase |
| YP_514188.1 | 79 | FTL_1542 | - | hypothetical protein FTL_1542 |
| YP_514419.1 | 16 | FTL_1794 | <i>atpC</i> | F0F1 ATP synthase subunit epsilon |
| YP_513746.1 | 51 | FTL_1046 | <i>dacB</i> | D-alanyl-D-alanine carboxypeptidase |
| YP_514074.1 | 29 | FTL_1419 | - | cyanophycinase |
| YP_513119.1 | 26 | FTL_0331 | - | TolQ protein |
| YP_513587.1 | 50 | FTL_0865 | - | major facilitator transporter |
| YP_512882.1 | 40 | FTL_0078 | - | riboflavin biosynthesis protein ribD |
| YP_513646.1 | 54 | FTL_0933 | - | DNA recombination protein RmuC family protein |

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|------------------|------------------------|---------------------|-----------------------------|--|
| YP_513540.1 | 43 | FTL_0808 | - | bifunctional 4'-phosphopantothenoylcysteine decarboxylase,phosphopantothenoylcysteine synthetase |
| YP_513532.1 | 64 | FTL_0800 | - | Type IV pilin multimeric outer membrane protein |
| YP_513376.1 | 17 | FTL_0617 | - | hypothetical protein FTL_0617 |
| YP_514146.1 | 66 | FTL_1495 | - | cysteine/glutathione ABC transporter membrane/ATP-binding protein |
| YP_514236.1 | 99 | FTL_1597 | - | organic solvent tolerance protein |
| YP_512914.1 | 156 | FTL_0116 | <i>pdpC</i> | Type VI Secretion Protein PdpC |
| YP_514242.1 | 10 | FTL_1603 | - | RNA-binding protein |
| YP_514435.1 | 55 | FTL_1810 | <i>nusA</i> | transcription elongation factor NusA |
| YP_514021.1 | 8 | FTL_0456 / FTL_1360 | <i>rpsU1</i> / <i>rpsU3</i> | 30S ribosomal protein S21 |
| YP_513087.1 | 35 | FTL_0295 | - | acetyl-CoA carboxylase carboxyltransferase subunit alpha |
| YP_512970.1 | 5 | FTL_0175 | <i>rpmH</i> | 50S ribosomal protein L34 |
| YP_513548.1 | 15 | FTL_0823 | - | hypothetical lipoprotein FTL_0823 |
| YP_513051.1 | 48 | FTL_0256 | <i>secY</i> | preprotein translocase subunit SecY |
| YP_512829.1 | 67 | FTL_0020 | <i>aspS</i> | aspartyl-tRNA synthetase |
| YP_514352.1 | 40 | FTL_1721 | <i>prfA</i> | peptide chain release factor 1 |
| YP_514097.1 | 28 | FTL_1442 | <i>fabI</i> | enoyl-[acyl-carrier-protein] reductase (NADH) |

| Accession Number | Molecular Weight (kDa) | Gene Locus | Gene Name | Identified Proteins (245) |
|------------------|------------------------|------------|--------------|--|
| YP_513160.1 | 44 | FTL_0387 | <i>aspC1</i> | aspartate aminotransferase |
| YP_513200.1 | 35 | FTL_0428 | - | chromosome partition protein B |
| YP_513344.1 | 101 | FTL_0584 | - | bifunctional 3-hydroxacyl-CoA dehydrogenase/acyl-CoA-binding protein |
| YP_513372.1 | 34 | FTL_0612 | <i>ppx</i> | exopolyphosphatase |
| YP_512917.1 | 25 | FTL_0119 | <i>dotU</i> | Type VI Secretion Protein DotU |
| YP_514482.1 | 57 | FTL_1865 | - | outer membrane protein tolC |
| YP_513195.1 | 19 | FTL_0423 | - | hypothetical protein FTL_0423 |
| YP_514196.1 | 28 | FTL_1550 | - | lipoprotein |
| YP_512994.1 | 16 | FTL_0199 | - | hypothetical lipoprotein FTL_0199 |
| YP_513001.1 | 61 | FTL_0206 | - | hypothetical protein FTL_0206 |
| YP_513711.1 | 53 | FTL_1005 | - | hypothetical protein FTL_1005 |
| YP_513307.1 | 18 | FTL_0538 | <i>fabZ</i> | (3R)-hydroxymyristoyl-ACP dehydratase |
| YP_514160.1 | 39 | FTL_1511 | - | glycerophosphoryl diester phosphodiesterase family protein |
| YP_513896.1 | 73 | FTL_1213 | - | hypothetical protein FTL_1213 |

Total spectra

99% protein
threshold, 95%
peptide
threshold,
minimum of 2
peptides

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|------------------|----------|----------|----------|----------|-------------------|--|
| YP_514345.1 | 141 | 248 | 273 | 257 | NO | YES |
| YP_514522.1 | 756 | 245 | 192 | 277 | YES | YES |
| YP_513037.1 | 255 | 232 | 225 | 247 | YES | YES |
| YP_513727.1 | 295 | 220 | 228 | 228 | YES | YES |
| YP_513045.1 | 299 | 183 | 163 | 175 | YES | YES |
| YP_514378.1 | 252 | 164 | 159 | 199 | YES | YES |
| YP_513101.1 | 67 | 154 | 139 | 161 | NO | NO |
| YP_514376.1 | 414 | 151 | 165 | 212 | YES | YES |
| YP_513044.1 | 166 | 139 | 131 | 123 | YES | YES |
| YP_514377.1 | 296 | 128 | 141 | 156 | YES | YES |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513055.1 | 304 | 125 | 76 | 157 | YES | YES |
| YP_513032.1 | 385 | 123 | 142 | 128 | YES | YES |
| YP_513043.1 | 157 | 109 | 102 | 105 | YES | YES |
| YP_513030.1 | 177 | 105 | 93 | 141 | YES | YES |
| YP_513019.1 | 135 | 104 | 115 | 112 | YES | YES |
| YP_513031.1 | 173 | 101 | 108 | 109 | YES | YES |
| YP_513041.1 | 168 | 96 | 104 | 105 | YES | YES |
| YP_513102.1 | 39 | 96 | 71 | 95 | NO | NO |
| YP_513036.1 | 240 | 95 | 86 | 55 | YES | YES |
| YP_513046.1 | 283 | 82 | 128 | 93 | YES | YES |
| YP_513048.1 | 189 | 71 | 67 | 81 | YES | YES |
| YP_513034.1 | 184 | 67 | 62 | 75 | YES | YES |
| YP_514399.1 | 10 | 67 | 70 | 68 | NO | NO |
| YP_513039.1 | 24 | 65 | 67 | 63 | YES | YES |
| YP_514411.1 | 16 | 64 | 60 | 46 | NO | NO |
| YP_513870.1 | 85 | 52 | 50 | 48 | YES | YES |
| YP_513042.1 | 72 | 52 | 50 | 65 | YES | YES |
| YP_513869.1 | 64 | 50 | 53 | 42 | YES | YES |
| YP_513057.1 | 82 | 49 | 40 | 49 | YES | YES |
| YP_513468.1 | 75 | 47 | 39 | 35 | NO | YES |
| YP_513038.1 | 61 | 47 | 38 | 44 | YES | YES |
| YP_514420.1 | 25 | 47 | 60 | 62 | NO | NO |
| YP_513028.1 | 80 | 46 | 39 | 54 | YES | YES |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513345.1 | 22 | 46 | 58 | 55 | NO | NO |
| YP_514379.1 | 51 | 42 | 38 | 39 | YES | YES |
| YP_513047.1 | 192 | 41 | 35 | 35 | YES | YES |
| YP_513103.1 | 31 | 41 | 28 | 44 | NO | NO |
| YP_513874.1 | 18 | 40 | 35 | 37 | NO | YES |
| YP_514408.1 | 4 | 39 | 34 | 34 | NO | NO |
| YP_514115.1 | 7 | 36 | 39 | 34 | NO | NO |
| YP_514366.1 | 75 | 35 | 37 | 43 | YES | YES |
| YP_513053.1 | 68 | 35 | 32 | 34 | YES | YES |
| YP_513054.1 | 94 | 33 | 41 | 39 | YES | YES |
| YP_514198.1 | 4 | 33 | 34 | 34 | NO | NO |
| YP_514374.1 | 65 | 32 | 27 | 29 | NO | YES |
| YP_513622.1 | 10 | 30 | 35 | 31 | NO | NO |
| YP_514409.1 | 3 | 29 | 25 | 25 | NO | NO |
| YP_514108.1 | 321 | 27 | 25 | 30 | YES | YES |
| YP_513726.1 | 34 | 27 | 31 | 29 | YES | YES |
| YP_513661.1 | 33 | 27 | 26 | 27 | YES | YES |
| YP_514446.1 | 10 | 26 | 29 | 23 | NO | NO |
| YP_514059.1 | 84 | 25 | 30 | 33 | YES | YES |
| YP_513725.1 | 49 | 25 | 27 | 25 | YES | YES |
| YP_514184.1 | 38 | 25 | 18 | 19 | YES | YES |
| YP_513559.1 | 5 | 25 | 32 | 26 | NO | NO |
| YP_513050.1 | 110 | 24 | 25 | 27 | YES | YES |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_514183.1 | 48 | 24 | 27 | 37 | NO | YES |
| YP_513639.1 | 16 | 24 | 26 | 30 | NO | NO |
| YP_513033.1 | 115 | 23 | 28 | 30 | YES | YES |
| YP_513788.1 | 4 | 23 | 27 | 24 | NO | NO |
| YP_514154.1 | 3 | 23 | 26 | 28 | NO | NO |
| YP_514517.1 | 24 | 22 | 16 | 17 | NO | NO |
| YP_514539.1 | 11 | 22 | 27 | 30 | NO | NO |
| YP_512944.1 | 1 | 21 | 26 | 21 | NO | NO |
| YP_513027.1 | 138 | 20 | 19 | 22 | YES | YES |
| YP_514375.1 | 70 | 20 | 18 | 20 | NO | YES |
| YP_514422.1 | 7 | 20 | 30 | 22 | NO | NO |
| YP_513291.1 | 33 | 19 | 22 | 23 | YES | YES |
| YP_513974.2 | 108 | 18 | 37 | 30 | YES | YES |
| YP_513035.1 | 49 | 18 | 12 | 17 | YES | YES |
| YP_514307.1 | 5 | 18 | 17 | 16 | NO | NO |
| YP_513615.1 | 0 | 18 | 18 | 14 | NO | YES |
| YP_514047.1 | 8 | 17 | 16 | 14 | NO | YES |
| YP_514382.1 | 5 | 17 | 18 | 20 | NO | YES |
| YP_514071.1 | 1 | 17 | 16 | 17 | NO | NO |
| YP_513570.1 | 4 | 16 | 17 | 20 | NO | YES |
| YP_513438.1 | 4 | 16 | 19 | 15 | NO | NO |
| YP_514229.1 | 0 | 16 | 14 | 13 | NO | NO |
| YP_513040.1 | 38 | 15 | 14 | 15 | YES | YES |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_514410.1 | 2 | 15 | 20 | 18 | NO | NO |
| YP_514303.1 | 0 | 15 | 17 | 16 | NO | NO |
| YP_514421.1 | 0 | 15 | 22 | 18 | NO | NO |
| YP_513829.1 | 16 | 14 | 16 | 14 | YES | YES |
| YP_513965.1 | 2 | 14 | 13 | 12 | NO | NO |
| YP_514434.1 | 0 | 13 | 11 | 14 | NO | YES |
| YP_513610.1 | 41 | 12 | 18 | 20 | NO | YES |
| YP_513260.1 | 35 | 12 | 10 | 16 | NO | NO |
| YP_513919.1 | 17 | 12 | 11 | 12 | NO | YES |
| YP_513652.1 | 9 | 12 | 8 | 12 | NO | NO |
| YP_514069.1 | 0 | 12 | 19 | 14 | NO | NO |
| YP_513862.1 | 30 | 11 | 11 | 13 | NO | YES |
| YP_512874.1 | 19 | 11 | 11 | 10 | YES | YES |
| YP_513049.1 | 18 | 11 | 13 | 15 | YES | YES |
| YP_513747.1 | 18 | 11 | 8 | 9 | YES | YES |
| YP_514109.1 | 3 | 11 | 6 | 1 | NO | YES |
| YP_513144.1 | 0 | 11 | 19 | 19 | NO | NO |
| YP_514369.1 | 0 | 11 | 15 | 14 | YES | YES |
| YP_513551.1 | 17 | 10 | 11 | 10 | NO | NO |
| YP_513790.1 | 16 | 9 | 8 | 9 | NO | YES |
| YP_514488.1 | 7 | 9 | 5 | 10 | NO | YES |
| YP_514310.1 | 6 | 9 | 11 | 8 | NO | NO |
| YP_514129.1 | 6 | 9 | 6 | 7 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513623.1 | 3 | 9 | 16 | 12 | NO | NO |
| YP_514140.1 | 3 | 9 | 7 | 5 | NO | NO |
| YP_512961.1 | 3 | 9 | 8 | 8 | NO | NO |
| YP_514306.1 | 1 | 9 | 10 | 10 | NO | NO |
| YP_513537.1 | 1 | 9 | 7 | 7 | NO | NO |
| YP_512931.1 | 0 | 9 | 18 | 14 | NO | NO |
| YP_512973.1 | 0 | 9 | 10 | 10 | NO | NO |
| YP_513113.1 | 0 | 9 | 18 | 19 | NO | NO |
| YP_513349.1 | 0 | 9 | 9 | 11 | NO | NO |
| YP_513560.1 | 0 | 9 | 10 | 7 | NO | NO |
| YP_514354.1 | 0 | 9 | 10 | 8 | NO | NO |
| YP_513202.1 | 0 | 9 | 12 | 12 | NO | NO |
| YP_514185.1 | 0 | 9 | 18 | 15 | NO | NO |
| YP_514040.1 | 0 | 9 | 8 | 9 | NO | NO |
| YP_514107.1 | 18 | 8 | 7 | 8 | YES | YES |
| YP_514451.1 | 6 | 8 | 11 | 10 | NO | NO |
| YP_514447.1 | 5 | 8 | 14 | 7 | NO | NO |
| YP_512984.1 | 3 | 8 | 14 | 14 | NO | NO |
| YP_514250.1 | 0 | 8 | 14 | 9 | NO | NO |
| YP_514336.1 | 0 | 8 | 6 | 7 | NO | NO |
| YP_513572.1 | 0 | 8 | 8 | 5 | NO | NO |
| YP_513208.1 | 0 | 8 | 9 | 6 | NO | YES |
| YP_513322.1 | 32 | 7 | 11 | 11 | NO | YES |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513187.1 | 8 | 7 | 6 | 12 | NO | YES |
| YP_514341.1 | 2 | 7 | 7 | 7 | NO | NO |
| YP_513409.1 | 1 | 7 | 7 | 6 | NO | NO |
| YP_514524.1 | 1 | 7 | 6 | 4 | NO | NO |
| YP_513957.1 | 0 | 7 | 9 | 8 | NO | NO |
| YP_513310.1 | 4 | 6 | 7 | 9 | NO | NO |
| YP_513309.1 | 2 | 6 | 5 | 6 | NO | NO |
| YP_513875.1 | 1 | 6 | 6 | 4 | NO | YES |
| YP_514424.1 | 0 | 6 | 11 | 10 | NO | NO |
| YP_513352.1 | 0 | 6 | 15 | 13 | NO | NO |
| YP_513408.1 | 0 | 6 | 12 | 13 | NO | NO |
| YP_514276.1 | 0 | 6 | 6 | 6 | NO | NO |
| YP_512895.1 | 0 | 6 | 5 | 7 | NO | YES |
| YP_513246.1 | 0 | 6 | 8 | 8 | NO | NO |
| YP_513660.1 | 0 | 6 | 8 | 12 | NO | NO |
| YP_513029.1 | 0 | 6 | 3 | 7 | NO | YES |
| YP_513426.1 | 0 | 6 | 2 | 6 | NO | NO |
| YP_514060.1 | 0 | 6 | 6 | 6 | YES | YES |
| YP_514346.1 | 0 | 6 | 5 | 8 | NO | YES |
| YP_513375.1 | 18 | 5 | 10 | 8 | NO | YES |
| YP_514221.1 | 0 | 5 | 5 | 5 | NO | NO |
| YP_513354.1 | 0 | 5 | 10 | 8 | NO | NO |
| YP_513364.1 | 0 | 5 | 9 | 4 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_512987.1 | 0 | 5 | 4 | 6 | NO | NO |
| YP_513211.1 | 0 | 5 | 7 | 5 | NO | NO |
| YP_513381.1 | 0 | 5 | 4 | 6 | NO | NO |
| YP_513890.1 | 0 | 5 | 4 | 5 | NO | NO |
| YP_513662.1 | 0 | 5 | 8 | 0 | NO | NO |
| YP_513519.1 | 0 | 5 | 6 | 3 | NO | NO |
| YP_513617.1 | 12 | 4 | 8 | 5 | NO | YES |
| YP_512875.1 | 6 | 4 | 3 | 0 | NO | YES |
| YP_513308.1 | 2 | 4 | 10 | 9 | NO | NO |
| YP_513332.1 | 0 | 4 | 3 | 4 | NO | NO |
| YP_513433.1 | 0 | 4 | 8 | 8 | NO | NO |
| YP_513288.1 | 0 | 4 | 6 | 5 | NO | NO |
| YP_512888.1 | 0 | 4 | 4 | 2 | NO | NO |
| YP_512910.1 | 0 | 4 | 4 | 4 | NO | NO |
| YP_513180.1 | 0 | 4 | 4 | 4 | NO | NO |
| YP_512982.1 | 0 | 4 | 6 | 5 | NO | NO |
| YP_513955.1 | 0 | 4 | 4 | 3 | NO | NO |
| YP_514168.1 | 0 | 4 | 6 | 4 | NO | NO |
| YP_513056.1 | 16 | 3 | 4 | 4 | NO | YES |
| YP_514174.1 | 1 | 3 | 6 | 4 | NO | NO |
| YP_513398.1 | 0 | 3 | 4 | 8 | NO | NO |
| YP_514518.1 | 0 | 3 | 4 | 10 | NO | NO |
| YP_514423.1 | 0 | 3 | 5 | 6 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513109.1 | 0 | 3 | 4 | 4 | NO | NO |
| YP_513716.1 | 0 | 3 | 2 | 5 | NO | NO |
| YP_512923.1 | 0 | 3 | 16 | 5 | NO | NO |
| YP_513117.1 | 0 | 3 | 2 | 3 | NO | NO |
| YP_514293.1 | 0 | 3 | 8 | 2 | NO | NO |
| YP_513437.1 | 0 | 3 | 11 | 6 | NO | NO |
| YP_514231.1 | 0 | 3 | 3 | 4 | NO | NO |
| YP_513413.1 | 0 | 3 | 2 | 1 | NO | NO |
| YP_512889.1 | 0 | 3 | 2 | 4 | NO | NO |
| YP_512998.1 | 0 | 3 | 10 | 7 | NO | NO |
| YP_513823.1 | 18 | 3 | 3 | 2 | NO | NO |
| YP_513977.1 | 0 | 3 | 14 | 9 | NO | NO |
| YP_514130.1 | 0 | 3 | 4 | 6 | NO | YES |
| YP_513886.1 | 0 | 3 | 3 | 5 | NO | NO |
| YP_513427.1 | 0 | 3 | 4 | 4 | NO | NO |
| YP_512975.1 | 0 | 3 | 2 | 4 | NO | NO |
| YP_513912.1 | 0 | 3 | 4 | 5 | NO | NO |
| YP_513348.1 | 0 | 3 | 0 | 4 | NO | NO |
| YP_513908.1 | 0 | 3 | 2 | 2 | NO | NO |
| YP_514514.1 | 28 | 2 | 2 | 3 | NO | YES |
| YP_513506.1 | 11 | 2 | 8 | 6 | NO | YES |
| YP_513194.1 | 6 | 2 | 14 | 16 | NO | NO |
| YP_513994.1 | 4 | 2 | 15 | 12 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513290.1 | 3 | 2 | 4 | 3 | YES | YES |
| YP_514444.1 | 2 | 2 | 3 | 2 | NO | NO |
| YP_514449.1 | 1 | 2 | 4 | 4 | NO | NO |
| YP_513550.1 | 1 | 2 | 1 | 2 | NO | NO |
| YP_513237.1 | 1 | 2 | 5 | 4 | NO | NO |
| YP_513828.1 | 0 | 2 | 2 | 4 | NO | NO |
| YP_512904.1 | 0 | 2 | 6 | 6 | NO | NO |
| YP_513742.1 | 0 | 2 | 6 | 5 | NO | YES |
| YP_513894.1 | 0 | 2 | 3 | 3 | NO | NO |
| YP_513329.1 | 0 | 2 | 4 | 5 | NO | NO |
| YP_514450.1 | 0 | 2 | 2 | 4 | NO | NO |
| YP_513757.1 | 0 | 2 | 3 | 4 | NO | NO |
| YP_513355.1 | 0 | 2 | 7 | 4 | NO | NO |
| YP_514188.1 | 0 | 2 | 7 | 8 | NO | NO |
| YP_514419.1 | 0 | 2 | 4 | 4 | NO | NO |
| YP_513746.1 | 0 | 2 | 6 | 2 | NO | NO |
| YP_514074.1 | 0 | 2 | 3 | 4 | NO | NO |
| YP_513119.1 | 0 | 2 | 4 | 4 | NO | NO |
| YP_513587.1 | 0 | 2 | 2 | 4 | NO | NO |
| YP_512882.1 | 0 | 2 | 3 | 2 | NO | NO |
| YP_513646.1 | 0 | 2 | 2 | 3 | NO | NO |
| YP_513540.1 | 0 | 2 | 5 | 2 | NO | NO |
| YP_513532.1 | 0 | 1 | 5 | 6 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|-------------------------|-----------------|-----------------|-----------------|-----------------|--------------------------|---|
| YP_513376.1 | 0 | 1 | 1 | 3 | NO | NO |
| YP_514146.1 | 0 | 1 | 4 | 0 | NO | NO |
| YP_514236.1 | 0 | 1 | 3 | 1 | NO | NO |
| YP_512914.1 | 0 | 1 | 4 | 2 | NO | NO |
| YP_514242.1 | 20 | 0 | 3 | 8 | NO | YES |
| YP_514435.1 | 7 | 0 | 0 | 0 | NO | YES |
| YP_514021.1 | 3 | 0 | 0 | 0 | YES | YES |
| YP_513087.1 | 2 | 0 | 4 | 4 | NO | NO |
| YP_512970.1 | 2 | 0 | 0 | 0 | YES | YES |
| YP_513548.1 | 2 | 0 | 0 | 0 | NO | NO |
| YP_513051.1 | 2 | 0 | 0 | 0 | NO | YES |
| YP_512829.1 | 2 | 0 | 0 | 0 | NO | YES |
| YP_514352.1 | 2 | 0 | 0 | 0 | NO | YES |
| YP_514097.1 | 2 | 0 | 0 | 0 | NO | NO |
| YP_513160.1 | 1 | 0 | 0 | 0 | NO | NO |
| YP_513200.1 | 1 | 0 | 0 | 0 | NO | NO |
| YP_513344.1 | 1 | 0 | 0 | 0 | NO | NO |
| YP_513372.1 | 1 | 0 | 0 | 0 | NO | NO |
| YP_512917.1 | 1 | 0 | 0 | 0 | NO | NO |
| YP_514482.1 | 0 | 0 | 3 | 1 | NO | NO |
| YP_513195.1 | 0 | 0 | 2 | 3 | NO | NO |
| YP_514196.1 | 0 | 0 | 4 | 2 | NO | NO |
| YP_512994.1 | 0 | 0 | 4 | 4 | NO | NO |

| Accession Number | Sample A | Sample B | Sample C | Sample D | Ribosomal Protein | Reported transcription/translation complex component |
|------------------|----------|----------|----------|----------|-------------------|--|
| YP_513001.1 | 0 | 0 | 6 | 0 | NO | NO |
| YP_513711.1 | 0 | 0 | 3 | 2 | NO | NO |
| YP_513307.1 | 0 | 0 | 4 | 1 | NO | NO |
| YP_514160.1 | 0 | 0 | 2 | 3 | NO | NO |
| YP_513896.1 | 0 | 0 | 5 | 0 | NO | NO |

| | Sample A | Sample B | Sample C | Sample D | Total |
|--|---------------|---------------|---------------|---------------|---------------|
| Total spectra | 8524.0 | 5626.0 | 5879.0 | 6158.0 | 26187.0 |
| Total spectra from ribosomal proteins | 7323.0 | 3454.0 | 3401.0 | 3739.0 | 17917.0 |
| Percent spectra from ribosomal proteins | 85.91% | 61.39% | 57.85% | 60.72% | 68.42% |
| Total spectra from translation/transcription components | 8036.0 | 4081.0 | 4052.0 | 4401.0 | 20570.0 |
| Percent spectra from translation/transcription components | 94.27% | 72.54% | 68.92% | 71.47% | 78.55% |