**Table S4. Quantifiable identified proteins in *Escherichia coli* after exposure to 1H-BTA or its products**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Unused** | **Total** | **% Cov** | **Accession** | **Protein name** | **Gene name** | **Peptides(95%)** | **115:114\*** | **116:114** | **117:114** | **116:115** | **117:115** |
| 1 | 77.87 | 77.87 | 50.8 | P0A8V2 | DNA-directed RNA polymerase subunit beta | rpoB | 68 | 1.028 | 0.9908 | 1 | 0.9638 | 0.9728 |
| 2 | 76.74 | 76.74 | 49 | P0A8T7 | DNA-directed RNA polymerase subunit beta' | rpoC | 67 | 0.863 | 0.6607 | 0.5808 | 0.7656 | 0.6730 |
| 3 | 70.8 | 70.8 | 55.5 | P0AFG8 | Pyruvate dehydrogenase E1 component | aceE | 62 | 1.0186 | 0.8954 | 0.929 | 0.8790 | 0.9120 |
| 4 | 61.88 | 61.88 | 59.3 | P09373 | Formate acetyltransferase 1 | pflB | 61 | 1.1482 | 1.2474 | 1.0375 | 1.0864 | 0.9036 |
| 5 | 54.3 | 54.3 | 51.2 | P63284 | Chaperone protein ClpB | clpB | 48 | 1.028 | 1 | 1.0375 | 0.9728 | 1.0092 |
| 6 | 53.44 | 53.44 | 76.7 | P02925 | D-ribose-binding periplasmic protein | rbsB | 177 | 0.879 | 0.5495 | 0.1107 | 0.6251 | 0.1259 |
| 7 | 52.05 | 52.05 | 85.8 | P0CE48 | Elongation factor Tu 2 | tufB | 87 | 1.1588 | 0.879 | 1.1376 | 0.7585 | 0.9817 |
| 8 | 51.9 | 51.9 | 56.1 | P0A6M8 | Elongation factor G | fusA | 75 | 1 | 1.1376 | 1.0864 | 1.1376 | 1.0864 |
| 9 | 50.78 | 50.78 | 56 | P0A6Y8 | Chaperone protein DnaK | dnaK | 64 | 0.9376 | 0.8166 | 0.6668 | 0.8709 | 0.7112 |
| 10 | 48.91 | 48.91 | 67.2 | P0A6F5 | 60 kDa chaperonin | groL | 91 | 0.9204 | 0.9204 | 0.9376 | 1.0000 | 1.0187 |
| 11 | 48.33 | 48.33 | 54.1 | P0A9Q7 | Aldehyde-alcohol dehydrogenase | adhE | 55 | 0.9376 | 0.4529 | 0.4786 | 0.4830 | 0.5105 |
| 12 | 46.06 | 46.06 | 84.3 | P0A9B2 | Glyceraldehyde-3-phosphate dehydrogenase A | gapA | 69 | 1.2023 | 1.1588 | 1.0375 | 0.9638 | 0.8629 |
| 13 | 45.63 | 45.63 | 38.4 | P36683 | Aconitate hydratase 2 | acnB | 39 | 0.9462 | 5.1523 | 3.5318 | 5.4453 | 3.7326 |
| 14 | 45.2 | 45.51 | 43.9 | P0AFG3 | 2-oxoglutarate dehydrogenase E1 component | sucA | 50 | 1.0093 | 1.0093 | 0.9908 | 1.0000 | 0.9817 |
| 15 | 43.86 | 43.86 | 59.5 | P23843 | Periplasmic oligopeptide-binding protein | oppA | 62 | 0.9817 | 0.8551 | 0.5012 | 0.8710 | 0.5105 |
| 16 | 43.53 | 43.53 | 63 | P0ABB0 | ATP synthase subunit alpha | atpA | 52 | 0.9817 | 1 | 0.9817 | 1.0186 | 1.0000 |
| 17 | 41.39 | 41.39 | 56.3 | P0AC38 | Aspartate ammonia-lyase | aspA | 72 | 0.673 | 1 | 1.2246 | 1.4859 | 1.8196 |
| 18 | 41.09 | 41.09 | 55.8 | P0A850 | Trigger factor | tig | 38 | 0.9817 | 1 | 0.9908 | 1.0186 | 1.0093 |
| 19 | 40.59 | 40.59 | 52.9 | P13029 | Catalase-peroxidase | katG | 41 | 1.1803 | 1.3677 | 1.2359 | 1.1588 | 1.0471 |
| 20 | 39.85 | 39.85 | 38.3 | P23538 | Phosphoenolpyruvate synthase | ppsA | 35 | 0.863 | 1.1482 | 1.4454 | 1.3305 | 1.6749 |
| 21 | 39.18 | 39.18 | 40.1 | Q46811 | Uncharacterized protein YgfK | ygfK | 26 | 0.7943 | 6.1944 | 4.0179 | 7.7986 | 5.0584 |
| 22 | 38.81 | 38.81 | 42.1 | P06959 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex | aceF | 36 | 1.0471 | 0.9204 | 1 | 0.8790 | 0.9550 |
| 23 | 37.6 | 37.6 | 67.6 | P0A910 | Outer membrane protein A | ompA | 55 | 0.8395 | 0.2754 | 0.2377 | 0.3281 | 0.2831 |
| 24 | 37.33 | 37.33 | 66.7 | P0ABB4 | ATP synthase subunit beta | atpD | 57 | 0.929 | 0.8551 | 0.7798 | 0.9205 | 0.8394 |
| 25 | 37.08 | 37.08 | 68.5 | P02931 | Outer membrane protein F | ompF | 61 | 0.7379 | 1.4322 | 1.7378 | 1.9409 | 2.3551 |
| 26 | 36.59 | 36.59 | 70.1 | P0A6P9 | Enolase | eno | 48 | 1.0965 | 0.5598 | 0.6546 | 0.5105 | 0.5970 |
| 27 | 36.58 | 36.59 | 57.5 | P0A853 | Tryptophanase | tnaA | 41 | 0.8241 | 3.4995 | 2.729 | 4.2465 | 3.3115 |
| 28 | 36.39 | 36.39 | 50.5 | P0AG67 | 30S ribosomal protein S1 | rpsA | 42 | 1 | 1.0093 | 1 | 1.0093 | 1.0000 |
| 29 | 36.03 | 36.03 | 60.6 | P08200 | Isocitrate dehydrogenase [NADP] | icd | 28 | 1.0375 | 1.8535 | 1.7865 | 1.7865 | 1.7219 |
| 30 | 35.84 | 35.87 | 54.5 | P04983 | Ribose import ATP-binding protein RbsA | rbsA | 33 | 1 | 0.9908 | 0.9727 | 0.9908 | 0.9727 |
| 31 | 35.65 | 35.65 | 49.2 | P0A6Z3 | Chaperone protein HtpG | htpG | 29 | 0.912 | 1.0965 | 1.2359 | 1.2023 | 1.3552 |
| 32 | 34.05 | 34.05 | 57.3 | P15639 | Bifunctional purine biosynthesis protein PurH | purH | 23 | 1 | 1.556 | 1.4191 | 1.5560 | 1.4191 |
| 33 | 34.04 | 34.11 | 60.8 | P0A836 | Succinyl-CoA ligase [ADP-forming] subunit beta | sucC | 41 | 0.8954 | 2.9376 | 2.6546 | 3.2808 | 2.9647 |
| 34 | 33.92 | 33.92 | 76.3 | P37329 | Molybdate-binding periplasmic protein | modA | 43 | 0.9204 | 0.6194 | 0.3767 | 0.6730 | 0.4093 |
| 35 | 33.18 | 33.18 | 74.9 | P06996 | Outer membrane protein C | ompC | 66 | 0.5495 | 0.955 | 1.7378 | 1.7379 | 3.1625 |
| 36 | 32.62 | 32.62 | 44.4 | P0A9M8 | Phosphate acetyltransferase | pta | 33 | 0.52 | 0.871 | 0.8872 | 1.6750 | 1.7062 |
| 37 | 31.85 | 31.85 | 61.2 | P0A9P0 | Dihydrolipoyl dehydrogenase | lpdA | 35 | 1.1803 | 0.7379 | 0.9638 | 0.6252 | 0.8166 |
| 38 | 31.66 | 31.66 | 43.4 | P0AD61 | Pyruvate kinase I | pykF | 28 | 1.0471 | 0.5445 | 0.5546 | 0.5200 | 0.5297 |
| 39 | 30.93 | 31.1 | 51.9 | P0AC41 | Succinate dehydrogenase flavoprotein subunit | sdhA | 33 | 1.0186 | 1.0186 | 0.9908 | 1.0000 | 0.9727 |
| 40 | 30.18 | 30.27 | 38.4 | P00957 | Alanine--tRNA ligase | alaS | 26 | 0.9817 | 0.955 | 1 | 0.9728 | 1.0186 |
| 41 | 30 | 30 | 59.7 | P69908 | Glutamate decarboxylase alpha | gadA | 50 | 0.9817 | 0.955 | 0.9727 | 0.9728 | 0.9908 |
| 42 | 29.83 | 29.83 | 47.3 | P08839 | Phosphoenolpyruvate-protein phosphotransferase | ptsI | 24 | 0.8241 | 0.5152 | 0.7943 | 0.6252 | 0.9638 |
| 43 | 29.57 | 29.57 | 38.3 | P0A9M0 | Lon protease | lon | 24 | 0.8954 | 0.5495 | 0.9204 | 0.6137 | 1.0279 |
| 44 | 29.39 | 31.39 | 33.3 | P76558 | NADP-dependent malic enzyme | maeB | 36 | 1.0864 | 1.7061 | 1.3552 | 1.5704 | 1.2474 |
| 45 | 29.27 | 29.27 | 69.3 | P0A6P1 | Elongation factor Ts | tsf | 23 | 0.8166 | 1.1803 | 0.9638 | 1.4454 | 1.1803 |
| 46 | 28.91 | 28.91 | 53.4 | P0A6F3 | Glycerol kinase | glpK | 26 | 1.3062 | 2.884 | 2.6303 | 2.2079 | 2.0137 |
| 47 | 28.47 | 28.47 | 44.7 | P00363 | Fumarate reductase flavoprotein subunit | frdA | 30 | 0.8318 | 0.9376 | 0.7178 | 1.1272 | 0.8629 |
| 48 | 28.33 | 28.33 | 39.6 | P37330 | Malate synthase G | glcB | 25 | 1.0375 | 2.8576 | 2.1878 | 2.7543 | 2.1087 |
| 49 | 28.26 | 28.26 | 44.1 | P0A940 | Outer membrane protein assembly factor BamA | bamA | 22 | 1.0186 | 1.0375 | 1.0186 | 1.0186 | 1.0000 |
| 50 | 28.1 | 28.1 | 43 | P0AFG6 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex | sucB | 35 | 1 | 0.9817 | 1.0093 | 0.9817 | 1.0093 |
| 51 | 27.48 | 27.48 | 50 | P0A991 | Fructose-bisphosphate aldolase class 1 | fbaB | 28 | 1.1066 | 1.977 | 1.6144 | 1.7866 | 1.4589 |
| 52 | 27.03 | 27.03 | 50.2 | P0A8L1 | Serine--tRNA ligase | serS | 23 | 1 | 1 | 1 | 1.0000 | 1.0000 |
| 53 | 26.11 | 26.11 | 54.8 | P61889 | Malate dehydrogenase | mdh | 34 | 1.0965 | 1.888 | 1.6293 | 1.7218 | 1.4859 |
| 54 | 25.85 | 25.85 | 39.5 | P05055 | Polyribonucleotide nucleotidyltransferase | pnp | 35 | 0.9727 | 0.955 | 0.9908 | 0.9818 | 1.0186 |
| 55 | 25.24 | 25.24 | 46.7 | P65807 | Uncharacterized protein YgeY | ygeY | 24 | 0.5861 | 7.7268 | 6.368 | 13.1834 | 10.8650 |
| 56 | 25.05 | 25.05 | 40 | P21599 | Pyruvate kinase II | pykA | 20 | 0.955 | 0.929 | 0.9204 | 0.9728 | 0.9638 |
| 57 | 25.02 | 25.02 | 53 | P0C0V0 | Periplasmic serine endoprotease DegP | degP | 36 | 1.1376 | 0.8318 | 1.8197 | 0.7312 | 1.5996 |
| 58 | 25 | 25 | 41.3 | P0A799 | Phosphoglycerate kinase | pgk | 35 | 1.028 | 0.8872 | 0.7379 | 0.8630 | 0.7178 |
| 59 | 24.97 | 24.97 | 55.2 | P0A870 | Transaldolase B | talB | 33 | 0.7047 | 1.0864 | 1.2589 | 1.5416 | 1.7864 |
| 60 | 24.94 | 24.94 | 59.3 | P60422 | 50S ribosomal protein L2 | rplB | 25 | 0.9376 | 1.2023 | 0.8395 | 1.2823 | 0.8954 |
| 61 | 24.87 | 24.87 | 30.5 | P33602 | NADH-quinone oxidoreductase subunit G | nuoG | 22 | 0.9817 | 1.028 | 0.9727 | 1.0472 | 0.9908 |
| 62 | 24.68 | 24.74 | 32.7 | P00956 | Isoleucine--tRNA ligase | ileS | 19 | 0.7586 | 0.5649 | 0.6792 | 0.7447 | 0.8953 |
| 63 | 24.61 | 26.67 | 26.1 | P33195 | Glycine dehydrogenase (decarboxylating) | gcvP | 24 | 1.2246 | 2.4889 | 2.6792 | 2.0324 | 2.1878 |
| 64 | 24.52 | 24.52 | 34.4 | P23847 | Periplasmic dipeptide transport protein | dppA | 19 | 1.2134 | 1.0666 | 0.871 | 0.8790 | 0.7178 |
| 65 | 24.51 | 24.51 | 52.8 | P19926 | Glucose-1-phosphatase | agp | 32 | 0.8954 | 0.7516 | 0.5861 | 0.8394 | 0.6546 |
| 66 | 23.99 | 23.99 | 54.7 | P0A7Z4 | DNA-directed RNA polymerase subunit alpha | rpoA | 26 | 0.9638 | 0.9638 | 0.955 | 1.0000 | 0.9909 |
| 67 | 23.35 | 23.35 | 56.1 | P0AEX9 | Maltose-binding periplasmic protein | malE | 23 | 0.8954 | 0.8091 | 0.871 | 0.9036 | 0.9727 |
| 68 | 23.23 | 23.23 | 36.1 | P21513 | Ribonuclease E | rne | 22 | 1.0375 | 0.9908 | 1.0093 | 0.9550 | 0.9728 |
| 69 | 23.09 | 23.09 | 29 | P27302 | Transketolase 1 | tktA | 26 | 1.0471 | 3.4041 | 2.3121 | 3.2510 | 2.2081 |
| 70 | 23.06 | 23.06 | 41.4 | P0A7D4 | Adenylosuccinate synthetase | purA | 20 | 0.871 | 1.3183 | 1.1066 | 1.5135 | 1.2705 |
| 71 | 22.93 | 22.93 | 59.3 | P02924 | L-arabinose-binding periplasmic protein | araF | 28 | 0.9204 | 0.3436 | 0.4018 | 0.3733 | 0.4365 |
| 72 | 22.9 | 22.9 | 40.3 | P0A705 | Translation initiation factor IF-2 | infB | 16 | 0.9727 | 0.929 | 0.955 | 0.9551 | 0.9818 |
| 73 | 22.74 | 22.74 | 55.3 | P00509 | Aspartate aminotransferase | aspC | 25 | 1.1066 | 1.7378 | 1.5136 | 1.5704 | 1.3678 |
| 74 | 22.59 | 22.59 | 62.9 | P00805 | L-asparaginase 2 | ansB | 33 | 0.871 | 0.8017 | 0.7656 | 0.9204 | 0.8790 |
| 75 | 22.55 | 22.55 | 71.7 | P0AE08 | Alkyl hydroperoxide reductase subunit C | ahpC | 18 | 2.0512 | 8.8716 | 4.6559 | 4.3251 | 2.2698 |
| 76 | 22.52 | 22.52 | 59.6 | P37902 | Glutamate/aspartate periplasmic-binding protein | gltI | 31 | 1.1482 | 0.787 | 0.4875 | 0.6854 | 0.4246 |
| 77 | 22.48 | 22.48 | 43.9 | Q46803 | Uncharacterized protein YgeW | ygeW | 25 | 1.6749 | 6.4863 | 6.9823 | 3.8726 | 4.1688 |
| 78 | 22.2 | 22.2 | 33.3 | P25516 | Aconitate hydratase 1 | acnA | 18 | 0.9908 | 0.9908 | 1.0186 | 1.0000 | 1.0281 |
| 79 | 22.19 | 22.19 | 59.9 | P0AEE5 | D-galactose-binding periplasmic protein | mglB | 24 | 0.8872 | 0.413 | 0.4786 | 0.4655 | 0.5394 |
| 80 | 22.13 | 22.13 | 43 | P0A8N5 | Lysine--tRNA ligase, heat inducible | lysU | 21 | 0.9638 | 0.9638 | 1.0375 | 1.0000 | 1.0765 |
| 81 | 22.1 | 22.15 | 51.7 | P77671 | Allantoinase | allB | 18 | 1.803 | 8.8716 | 8.0168 | 4.9205 | 4.4464 |
| 82 | 22.02 | 22.02 | 92 | P0ADE6 | Uncharacterized protein YgaU | ygaU | 30 | 1.5417 | 1.4723 | 1.028 | 0.9550 | 0.6668 |
| 83 | 22.01 | 22.01 | 80.8 | P0ABT2 | DNA protection during starvation protein | dps | 30 | 1.1272 | 5.9704 | 3.2211 | 5.2967 | 2.8576 |
| 84 | 21.89 | 21.89 | 68.1 | P02413 | 50S ribosomal protein L15 | rplO | 22 | 0.8017 | 0.7656 | 0.6792 | 0.9550 | 0.8472 |
| 85 | 21.78 | 21.78 | 45 | P0AG80 | sn-glycerol-3-phosphate-binding periplasmic protein UgpB | ugpB | 14 | 1.1376 | 0.5649 | 0.5058 | 0.4966 | 0.4446 |
| 86 | 21.74 | 21.74 | 65.1 | P07014 | Succinate dehydrogenase iron-sulfur subunit | sdhB | 18 | 1.0375 | 1.028 | 1.028 | 0.9908 | 0.9908 |
| 87 | 21.55 | 21.55 | 39.9 | P0A8M3 | Threonine--tRNA ligase | thrS | 20 | 0.9376 | 0.9727 | 1.1376 | 1.0374 | 1.2133 |
| 88 | 21.54 | 23.34 | 56.4 | P0AGE9 | Succinyl-CoA ligase [ADP-forming] subunit alpha | sucD | 24 | 1.0471 | 2.884 | 1.9953 | 2.7543 | 1.9055 |
| 89 | 21.52 | 21.52 | 44.4 | P02943 | Maltoporin | lamB | 31 | 0.9036 | 1.2942 | 1.3677 | 1.4323 | 1.5136 |
| 90 | 21.36 | 21.36 | 41.8 | P0A6H5 | ATP-dependent protease ATPase subunit HslU | hslU | 19 | 1 | 0.929 | 1 | 0.9290 | 1.0000 |
| 91 | 21.16 | 21.16 | 47.2 | P45766 | Putative amino-acid ABC transporter-binding protein YhdW | yhdW | 20 | 0.8551 | 0.4571 | 0.4207 | 0.5346 | 0.4920 |
| 92 | 21.12 | 22.13 | 29.9 | P09546 | Bifunctional protein PutA | putA | 14 | 1.1272 | 3.3419 | 2.1086 | 2.9648 | 1.8707 |
| 93 | 20.98 | 20.98 | 45.8 | P31979 | NADH-quinone oxidoreductase subunit F | nuoF | 16 | 0.9638 | 0.9817 | 0.955 | 1.0186 | 0.9909 |
| 94 | 20.96 | 20.96 | 41.3 | P0A6K6 | Phosphopentomutase | deoB | 23 | 1.1272 | 0.7943 | 0.5598 | 0.7047 | 0.4966 |
| 95 | 20.83 | 20.83 | 45.3 | P16659 | Proline--tRNA ligase | proS | 20 | 1.3804 | 0.7047 | 0.8872 | 0.5105 | 0.6427 |
| 96 | 20.54 | 20.54 | 35.3 | P27550 | Acetyl-coenzyme A synthetase | acs | 20 | 0.912 | 0.7311 | 0.6486 | 0.8016 | 0.7112 |
| 97 | 20.48 | 20.48 | 38.5 | P22259 | Phosphoenolpyruvate carboxykinase [ATP] | pckA | 24 | 1.1803 | 2.6546 | 2.355 | 2.2491 | 1.9953 |
| 98 | 20.26 | 20.26 | 47.8 | P0A953 | 3-oxoacyl-[acyl-carrier-protein] synthase 1 | fabB | 18 | 0.9638 | 0.9817 | 0.9638 | 1.0186 | 1.0000 |
| 99 | 20.19 | 20.19 | 40.4 | P33599 | NADH-quinone oxidoreductase subunit C/D | nuoC | 28 | 0.9462 | 0.9462 | 0.5916 | 1.0000 | 0.6252 |
| 100 | 20.14 | 20.14 | 79.6 | P0ACF8 | DNA-binding protein H-NS | hns | 25 | 1.0093 | 0.4786 | 0.8241 | 0.4742 | 0.8165 |
| 101 | 20.13 | 20.13 | 79.7 | P0A7V0 | 30S ribosomal protein S2 | rpsB | 29 | 0.8091 | 0.929 | 1.1376 | 1.1482 | 1.4060 |
| 102 | 20.02 | 20.02 | 67.8 | P0AG55 | 50S ribosomal protein L6 | rplF | 23 | 0.879 | 0.9908 | 0.871 | 1.1272 | 0.9909 |
| 103 | 20.01 | 20.01 | 54 | P02930 | Outer membrane protein TolC | tolC | 24 | 0.9817 | 0.9817 | 0.9908 | 1.0000 | 1.0093 |
| 104 | 19.95 | 19.95 | 30.5 | P0A855 | Protein TolB | tolB | 18 | 1.1695 | 0.3162 | 0.3767 | 0.2704 | 0.3221 |
| 105 | 19.64 | 19.64 | 63.2 | P60438 | 50S ribosomal protein L3 | rplC | 20 | 0.7798 | 1.0186 | 0.8472 | 1.3062 | 1.0864 |
| 106 | 19.63 | 19.63 | 36.2 | P00579 | RNA polymerase sigma factor RpoD | rpoD | 18 | 1.0666 | 0.7516 | 0.6607 | 0.7047 | 0.6194 |
| 107 | 19.46 | 19.46 | 48.8 | P24182 | Biotin carboxylase | accC | 16 | 0.9638 | 0.955 | 0.9817 | 0.9909 | 1.0186 |
| 108 | 19.28 | 19.28 | 81.9 | P0A7R1 | 50S ribosomal protein L9 | rplI | 23 | 0.879 | 1.1169 | 0.7311 | 1.2706 | 0.8317 |
| 109 | 19.18 | 19.18 | 38.7 | P08997 | Malate synthase A | aceB | 15 | 1.0471 | 0.9817 | 0.955 | 0.9375 | 0.9120 |
| 110 | 18.76 | 18.76 | 45.8 | P0ABK5 | Cysteine synthase A | cysK | 21 | 0.7798 | 1.1066 | 1.028 | 1.4191 | 1.3183 |
| 111 | 18.75 | 18.75 | 27.7 | P0A7E5 | CTP synthase | pyrG | 17 | 0.9638 | 0.955 | 0.9817 | 0.9909 | 1.0186 |
| 112 | 18.67 | 18.86 | 35.2 | P0A9C5 | Glutamine synthetase | glnA | 15 | 1.2474 | 2.3988 | 2.9376 | 1.9230 | 2.3550 |
| 113 | 18.48 | 18.48 | 28.3 | P09152 | Respiratory nitrate reductase 1 alpha chain | narG | 16 | 0.9036 | 0.9204 | 0.9638 | 1.0186 | 1.0666 |
| 114 | 18.42 | 18.42 | 47.6 | P0A8M0 | Asparagine--tRNA ligase | asnS | 15 | 1.0666 | 0.9036 | 0.871 | 0.8472 | 0.8166 |
| 115 | 18.39 | 18.39 | 26.9 | P04825 | Aminopeptidase N | pepN | 12 | 0.8472 | 0.9638 | 1.2823 | 1.1376 | 1.5136 |
| 116 | 18.26 | 18.31 | 31.4 | P0AC33 | Fumarate hydratase class I, aerobic | fumA | 16 | 1.0093 | 4.0179 | 2.7797 | 3.9809 | 2.7541 |
| 117 | 18.22 | 18.22 | 38.7 | P00350 | 6-phosphogluconate dehydrogenase, decarboxylating | gnd | 16 | 1.028 | 1.0375 | 1 | 1.0092 | 0.9728 |
| 118 | 18.17 | 18.17 | 33 | P0ACE0 | Hydrogenase-2 large chain | hybC | 18 | 0.9462 | 0.7516 | 1.3183 | 0.7943 | 1.3933 |
| 119 | 18.01 | 18.01 | 47.2 | P0ADY1 | Peptidyl-prolyl cis-trans isomerase D | ppiD | 18 | 1.0093 | 0.929 | 1.0471 | 0.9204 | 1.0375 |
| 120 | 18 | 18 | 53.3 | P0ACJ8 | cAMP-activated global transcriptional regulator CRP | crp | 16 | 0.9638 | 1.0186 | 1.0186 | 1.0569 | 1.0569 |
| 121 | 17.73 | 17.73 | 40.4 | P31660 | 2-methylcitrate synthase | prpC | 20 | 0.9727 | 1.028 | 0.9908 | 1.0569 | 1.0186 |
| 122 | 17.4 | 17.42 | 48.2 | P0A9G6 | Isocitrate lyase | aceA | 19 | 1.0186 | 2.0893 | 1.4588 | 2.0511 | 1.4322 |
| 123 | 17.39 | 17.39 | 70.7 | P0A7W1 | 30S ribosomal protein S5 | rpsE | 31 | 1.0965 | 1.1066 | 0.7943 | 1.0092 | 0.7244 |
| 124 | 17.31 | 17.31 | 27.5 | P32176 | Formate dehydrogenase-O major subunit | fdoG | 15 | 0.9376 | 0.9204 | 0.9462 | 0.9817 | 1.0092 |
| 125 | 17.21 | 17.21 | 57.5 | P02359 | 30S ribosomal protein S7 | rpsG | 17 | 0.6982 | 0.8318 | 0.5808 | 1.1913 | 0.8319 |
| 126 | 17.19 | 17.19 | 59.3 | P0AEQ3 | Glutamine-binding periplasmic protein | glnH | 21 | 0.9036 | 0.6138 | 0.4055 | 0.6793 | 0.4488 |
| 127 | 17.09 | 17.09 | 49.3 | P37903 | Universal stress protein F | uspF | 16 | 0.9908 | 0.9908 | 1.0186 | 1.0000 | 1.0281 |
| 128 | 16.98 | 18.07 | 29.9 | P0ABJ9 | Cytochrome bd-I ubiquinol oxidase subunit 1 | cydA | 19 | 0.8872 | 0.7178 | 1.0093 | 0.8091 | 1.1376 |
| 129 | 16.8 | 16.8 | 35 | P77318 | Uncharacterized sulfatase YdeN | ydeN | 16 | 0.9376 | 0.5546 | 0.8017 | 0.5915 | 0.8551 |
| 130 | 16.75 | 16.75 | 36.7 | P75691 | Aldehyde reductase YahK | yahK | 13 | 1.0864 | 0.8241 | 0.7447 | 0.7586 | 0.6855 |
| 131 | 16.72 | 16.72 | 59.5 | P0A862 | Thiol peroxidase | tpx | 24 | 0.8872 | 1.2706 | 0.6792 | 1.4321 | 0.7656 |
| 132 | 16.62 | 16.62 | 40.8 | P08506 | D-alanyl-D-alanine carboxypeptidase DacC | dacC | 12 | 1.0186 | 0.6607 | 0.6792 | 0.6486 | 0.6668 |
| 133 | 16.31 | 16.31 | 41.5 | P0AG30 | Transcription termination factor Rho | rho | 16 | 1.0093 | 1 | 0.9908 | 0.9908 | 0.9817 |
| 134 | 16.18 | 16.18 | 47.5 | P39325 | ABC transporter periplasmic-binding protein YtfQ | ytfQ | 11 | 1.1376 | 0.6368 | 0.5598 | 0.5598 | 0.4921 |
| 135 | 16.13 | 16.13 | 48.5 | P0A8G6 | NAD(P)H dehydrogenase (quinone) | wrbA | 23 | 0.871 | 0.787 | 0.7516 | 0.9036 | 0.8629 |
| 136 | 16.12 | 16.12 | 39.8 | P39342 | Uncharacterized protein YjgR | yjgR | 13 | 1.0471 | 0.673 | 0.8166 | 0.6427 | 0.7799 |
| 137 | 16.05 | 16.05 | 61.8 | P0A7V3 | 30S ribosomal protein S3 | rpsC | 18 | 0.9817 | 0.9908 | 0.9727 | 1.0093 | 0.9908 |
| 138 | 16.02 | 16.02 | 69.4 | P0A7V8 | 30S ribosomal protein S4 | rpsD | 18 | 0.9908 | 0.9908 | 0.9727 | 1.0000 | 0.9817 |
| 139 | 16.01 | 16.01 | 52.1 | P0A7K2 | 50S ribosomal protein L7/L12 | rplL | 16 | 0.8472 | 0.871 | 1.1482 | 1.0281 | 1.3553 |
| 140 | 15.87 | 15.87 | 63.6 | P0A7J3 | 50S ribosomal protein L10 | rplJ | 15 | 0.9908 | 1.0186 | 0.9817 | 1.0281 | 0.9908 |
| 141 | 15.72 | 16.21 | 33.7 | P07813 | Leucine--tRNA ligase | leuS | 14 | 0.9638 | 1.028 | 0.9462 | 1.0666 | 0.9817 |
| 142 | 15.57 | 15.59 | 60.8 | P0A7D7 | Phosphoribosylaminoimidazole-succinocarboxamide synthase | purC | 13 | 0.9376 | 0.9376 | 0.955 | 1.0000 | 1.0186 |
| 143 | 15.41 | 15.41 | 64.2 | P60723 | 50S ribosomal protein L4 | rplD | 15 | 0.7656 | 1.0093 | 0.7112 | 1.3183 | 0.9289 |
| 144 | 15.3 | 15.3 | 34.7 | P0ABH7 | Citrate synthase | gltA | 18 | 0.955 | 2.355 | 1.7865 | 2.4660 | 1.8707 |
| 145 | 15.28 | 15.28 | 41.5 | P0AB71 | Fructose-bisphosphate aldolase class 2 | fbaA | 23 | 0.9036 | 0.4487 | 0.6546 | 0.4966 | 0.7244 |
| 146 | 15.12 | 15.12 | 55.1 | P0ABA0 | ATP synthase subunit b | atpF | 13 | 1 | 0.9638 | 0.9817 | 0.9638 | 0.9817 |
| 147 | 15.04 | 15.04 | 32.2 | P36938 | Phosphoglucomutase | pgm | 16 | 0.9376 | 0.9204 | 0.9638 | 0.9817 | 1.0279 |
| 148 | 14.84 | 17 | 51 | P0A867 | Transaldolase A | talA | 11 | 0.929 | 0.9462 | 0.9817 | 1.0185 | 1.0567 |
| 149 | 14.75 | 14.75 | 55.6 | P0A717 | Ribose-phosphate pyrophosphokinase | prs | 15 | 1.0093 | 1.0568 | 1.0375 | 1.0471 | 1.0279 |
| 150 | 14.75 | 14.75 | 35.2 | P0AB77 | 2-amino-3-ketobutyrate coenzyme A ligase | kbl | 16 | 0.9817 | 1.0186 | 1.0093 | 1.0376 | 1.0281 |
| 151 | 14.72 | 14.72 | 50.8 | P62707 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | gpmA | 19 | 1.1695 | 0.8395 | 0.6607 | 0.7178 | 0.5649 |
| 152 | 14.45 | 14.45 | 33 | P27248 | Aminomethyltransferase | gcvT | 16 | 0.9817 | 1.803 | 1.7061 | 1.8366 | 1.7379 |
| 153 | 14.23 | 14.23 | 41.7 | P0AEM9 | Cystine-binding periplasmic protein | fliY | 14 | 0.7798 | 0.6668 | 0.3664 | 0.8551 | 0.4699 |
| 154 | 14.19 | 14.19 | 32 | P37685 | Aldehyde dehydrogenase B | aldB | 11 | 1.0186 | 1 | 1.0093 | 0.9817 | 0.9909 |
| 155 | 14.12 | 14.12 | 21.2 | Q46814 | Probable hypoxanthine oxidase XdhD | xdhD | 8 | 1.7219 | 2.466 | 1.7701 | 1.4321 | 1.0280 |
| 156 | 14.09 | 16.47 | 94.5 | P68066 | Autonomous glycyl radical cofactor | grcA | 23 | 1.0568 | 4.9204 | 3.3729 | 4.6559 | 3.1916 |
| 157 | 14.02 | 14.02 | 56.9 | P0A858 | Triosephosphate isomerase | tpiA | 16 | 1.0093 | 1.0471 | 1.028 | 1.0375 | 1.0185 |
| 158 | 13.96 | 13.96 | 29 | P0A6A3 | Acetate kinase | ackA | 11 | 1.0666 | 1 | 1.0186 | 0.9376 | 0.9550 |
| 159 | 13.92 | 13.94 | 40.2 | P21889 | Aspartate--tRNA ligase | aspS | 9 | 1.0568 | 1.0666 | 0.7516 | 1.0093 | 0.7112 |
| 160 | 13.9 | 13.9 | 27 | P77737 | Oligopeptide transport ATP-binding protein OppF | oppF | 9 | 0.9638 | 1.0093 | 0.9204 | 1.0472 | 0.9550 |
| 161 | 13.66 | 13.66 | 28.5 | P39377 | Isoaspartyl dipeptidase | iadA | 10 | 1.0666 | 1.0471 | 1.0965 | 0.9817 | 1.0280 |
| 162 | 13.62 | 13.62 | 45.2 | P0AEZ3 | Septum site-determining protein MinD | minD | 14 | 1.0568 | 1.0666 | 1.0568 | 1.0093 | 1.0000 |
| 163 | 13.56 | 13.56 | 44.4 | P0A715 | 2-dehydro-3-deoxyphosphooctonate aldolase | kdsA | 8 | 0.9817 | 1.0186 | 1.0093 | 1.0376 | 1.0281 |
| 164 | 13.48 | 17.66 | 36.1 | P42632 | PFL-like enzyme TdcE | tdcE | 17 | 0.7586 | 1.5704 | 1.5704 | 2.0701 | 2.0701 |
| 165 | 13.43 | 13.43 | 55.1 | P0ABA6 | ATP synthase gamma chain | atpG | 11 | 0.9908 | 0.955 | 0.955 | 0.9639 | 0.9639 |
| 166 | 13.42 | 13.42 | 68.2 | P02358 | 30S ribosomal protein S6 | rpsF | 11 | 0.9638 | 0.9727 | 0.955 | 1.0092 | 0.9909 |
| 167 | 13.4 | 13.4 | 37.6 | P33232 | L-lactate dehydrogenase [cytochrome] | lldD | 10 | 0.9462 | 1.4191 | 1.3932 | 1.4998 | 1.4724 |
| 168 | 13.36 | 13.38 | 55.6 | P0AA10 | 50S ribosomal protein L13 | rplM | 14 | 0.8954 | 1.0471 | 0.7586 | 1.1694 | 0.8472 |
| 169 | 13.36 | 13.36 | 35.6 | P0ABP8 | Purine nucleoside phosphorylase DeoD-type | deoD | 14 | 0.8872 | 1.3677 | 1.3677 | 1.5416 | 1.5416 |
| 170 | 13.34 | 13.36 | 42.3 | P00934 | Threonine synthase | thrC | 13 | 1.0965 | 0.6918 | 1.2706 | 0.6309 | 1.1588 |
| 171 | 13.19 | 13.22 | 34.1 | P07118 | Valine--tRNA ligase | valS | 9 | 0.9908 | 1 | 1.0186 | 1.0093 | 1.0281 |
| 172 | 13.02 | 13.06 | 41.8 | P07395 | Phenylalanine--tRNA ligase beta subunit | pheT | 10 | 0.929 | 0.929 | 0.9376 | 1.0000 | 1.0093 |
| 173 | 12.77 | 12.77 | 31 | P00582 | DNA polymerase I | polA | 11 | 1.1482 | 1.0093 | 1.1169 | 0.8790 | 0.9727 |
| 174 | 12.73 | 12.73 | 52.3 | P0A6Q3 | 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase | fabA | 9 | 0.955 | 0.929 | 0.955 | 0.9728 | 1.0000 |
| 175 | 12.71 | 12.71 | 36.9 | Q46812 | Protein SsnA | ssnA | 11 | 0.6427 | 2.2699 | 2.2699 | 3.5318 | 3.5318 |
| 176 | 12.59 | 12.59 | 55 | P09551 | Lysine-arginine-ornithine-binding periplasmic protein | argT | 15 | 0.871 | 0.5598 | 0.4406 | 0.6427 | 0.5059 |
| 177 | 12.57 | 12.57 | 43.8 | P31120 | Phosphoglucosamine mutase | glmM | 11 | 0.879 | 1.1376 | 0.7586 | 1.2942 | 0.8630 |
| 178 | 12.56 | 12.56 | 27.7 | P00961 | Glycine--tRNA ligase beta subunit | glyS | 8 | 0.9727 | 1.0093 | 1.0666 | 1.0376 | 1.0965 |
| 179 | 12.41 | 12.41 | 35 | P04805 | Glutamate--tRNA ligase | gltX | 9 | 1.0471 | 1.0471 | 1.1376 | 1.0000 | 1.0864 |
| 180 | 12.25 | 12.25 | 43.4 | P11349 | Respiratory nitrate reductase 1 beta chain | narH | 7 | 1.028 | 1.0471 | 0.9462 | 1.0186 | 0.9204 |
| 181 | 12.24 | 12.24 | 57.2 | P64451 | Uncharacterized lipoprotein YdcL | ydcL | 14 | 1.1803 | 0.4246 | 0.4018 | 0.3597 | 0.3404 |
| 182 | 12.19 | 12.19 | 62.6 | P45578 | S-ribosylhomocysteine lyase | luxS | 12 | 0.871 | 0.9817 | 0.4831 | 1.1271 | 0.5546 |
| 183 | 12.17 | 14.3 | 49.6 | P33898 | Putative glyceraldehyde-3-phosphate dehydrogenase C | gapC | 14 | 1.0093 | 0.9462 | 0.9908 | 0.9375 | 0.9817 |
| 184 | 12.11 | 12.11 | 41.6 | P0A9D8 | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase | dapD | 13 | 0.871 | 1.3804 | 1.8365 | 1.5848 | 2.1085 |
| 185 | 12.09 | 12.27 | 43.9 | P0AA16 | Transcriptional regulatory protein OmpR | ompR | 9 | 0.955 | 0.6486 | 0.9817 | 0.6792 | 1.0280 |
| 186 | 12.08 | 12.08 | 27.6 | P00452 | Ribonucleoside-diphosphate reductase 1 subunit alpha | nrdA | 10 | 0.9462 | 1.2474 | 1.2023 | 1.3183 | 1.2707 |
| 187 | 12.08 | 12.08 | 43 | P45523 | FKBP-type peptidyl-prolyl cis-trans isomerase FkpA | fkpA | 12 | 1.028 | 0.929 | 0.9727 | 0.9037 | 0.9462 |
| 188 | 12.06 | 12.06 | 36.6 | P23893 | Glutamate-1-semialdehyde 2,1-aminomutase | hemL | 15 | 0.9462 | 1.0666 | 1.0186 | 1.1272 | 1.0765 |
| 189 | 12.06 | 12.06 | 15.9 | P69786 | PTS system glucose-specific EIICB component | ptsG | 9 | 1.1482 | 0.597 | 0.5754 | 0.5199 | 0.5011 |
| 190 | 12.05 | 12.53 | 52.1 | P0C018 | 50S ribosomal protein L18 | rplR | 8 | 0.9817 | 1.1695 | 0.871 | 1.1913 | 0.8872 |
| 191 | 12.05 | 12.06 | 56 | P0A7L0 | 50S ribosomal protein L1 | rplA | 26 | 1.0568 | 2.208 | 1.1588 | 2.0893 | 1.0965 |
| 192 | 12.02 | 12.02 | 78.9 | P0ACF0 | DNA-binding protein HU-alpha | hupA | 20 | 0.9727 | 1 | 1.0093 | 1.0281 | 1.0376 |
| 193 | 12 | 12 | 61.8 | P0ADY3 | 50S ribosomal protein L14 | rplN | 31 | 0.8017 | 1.3428 | 1.0864 | 1.6749 | 1.3551 |
| 194 | 12 | 12 | 27 | P77541 | Methylisocitrate lyase | prpB | 9 | 0.5546 | 2.355 | 1.5276 | 4.2463 | 2.7544 |
| 195 | 12 | 12 | 57.3 | P0C0L2 | Peroxiredoxin OsmC | osmC | 14 | 1.9055 | 0.9462 | 0.7447 | 0.4966 | 0.3908 |
| 196 | 12 | 12 | 69.6 | P68206 | UPF0337 protein YjbJ | yjbJ | 16 | 1.1376 | 0.2228 | 0.1614 | 0.1959 | 0.1419 |
| 197 | 12 | 12 | 42.8 | P0AFH8 | Osmotically-inducible protein Y | osmY | 12 | 1.2474 | 0.2858 | 0.4285 | 0.2291 | 0.3435 |
| 198 | 12 | 12 | 52.7 | P0A7R9 | 30S ribosomal protein S11 | rpsK | 19 | 0.9908 | 1 | 0.9817 | 1.0093 | 0.9908 |
| 199 | 11.85 | 11.85 | 54.9 | P0ACJ0 | Leucine-responsive regulatory protein | lrp | 8 | 0.9908 | 0.9204 | 0.9727 | 0.9289 | 0.9817 |
| 200 | 11.82 | 11.82 | 41.3 | P28635 | D-methionine-binding lipoprotein MetQ | metQ | 10 | 1.1482 | 0.7178 | 0.8241 | 0.6252 | 0.7177 |
| 201 | 11.8 | 12.09 | 26 | P00561 | Bifunctional aspartokinase/homoserine dehydrogenase 1 | thrA | 13 | 1.0568 | 1.1066 | 1.1803 | 1.0471 | 1.1169 |
| 202 | 11.8 | 11.81 | 23.7 | P77804 | Protein YdgA | ydgA | 10 | 0.9817 | 0.8872 | 0.9204 | 0.9037 | 0.9376 |
| 203 | 11.71 | 11.71 | 39.9 | P0AG82 | Phosphate-binding protein PstS | pstS | 13 | 0.9727 | 0.9727 | 0.912 | 1.0000 | 0.9376 |
| 204 | 11.71 | 11.71 | 35.7 | P37440 | Oxidoreductase UcpA | ucpA | 11 | 0.955 | 0.9727 | 1 | 1.0185 | 1.0471 |
| 205 | 11.69 | 11.69 | 86.7 | P0AF93 | Enamine/imine deaminase | ridA | 14 | 1.0965 | 1.5276 | 1.2823 | 1.3932 | 1.1694 |
| 206 | 11.61 | 12.17 | 63.8 | P0A8E7 | UPF0234 protein YajQ | yajQ | 11 | 0.9908 | 0.9817 | 0.912 | 0.9908 | 0.9205 |
| 207 | 11.53 | 11.53 | 34.3 | P26646 | Probable acrylyl-CoA reductase AcuI | acuI | 12 | 0.3436 | 1.2023 | 1.2023 | 3.4991 | 3.4991 |
| 208 | 11.52 | 11.52 | 61.5 | P0AEK2 | 3-oxoacyl-[acyl-carrier-protein] reductase FabG | fabG | 11 | 0.9462 | 1.3804 | 0.7798 | 1.4589 | 0.8241 |
| 209 | 11.51 | 11.51 | 21.5 | P07003 | Pyruvate dehydrogenase [ubiquinone] | poxB | 10 | 0.955 | 0.9462 | 0.9817 | 0.9908 | 1.0280 |
| 210 | 11.37 | 11.37 | 40.8 | P0ADV7 | Probable phospholipid-binding protein MlaC | mlaC | 9 | 0.7178 | 0.5598 | 0.673 | 0.7799 | 0.9376 |
| 211 | 11.33 | 11.33 | 44 | P30859 | Putative ABC transporter arginine-binding protein 2 | artI | 7 | 0.879 | 0.7516 | 0.4699 | 0.8551 | 0.5346 |
| 212 | 11.32 | 11.49 | 41.1 | P0A9W3 | Uncharacterized ABC transporter ATP-binding protein YjjK | ettA | 10 | 0.955 | 0.9817 | 1 | 1.0280 | 1.0471 |
| 213 | 11.31 | 11.31 | 52.5 | P0AG59 | 30S ribosomal protein S14 | rpsN | 9 | 0.871 | 0.6138 | 0.5346 | 0.7047 | 0.6138 |
| 214 | 11.3 | 11.3 | 45.4 | P0A9Q5 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta | accD | 10 | 1.4723 | 1.0186 | 1.4191 | 0.6918 | 0.9639 |
| 215 | 11.29 | 11.29 | 52.9 | P0A9Q1 | Aerobic respiration control protein ArcA | arcA | 13 | 0.863 | 0.6486 | 0.4365 | 0.7516 | 0.5058 |
| 216 | 11.25 | 11.25 | 53.3 | P0ACA3 | Stringent starvation protein A | sspA | 10 | 1.0666 | 0.9462 | 1.0471 | 0.8871 | 0.9817 |
| 217 | 11.17 | 11.17 | 24.5 | P04949 | Flagellin | fliC | 11 | 0.8017 | 0.787 | 0.5105 | 0.9817 | 0.6368 |
| 218 | 11.14 | 11.14 | 39.4 | P76108 | Putative ABC transporter periplasmic-binding protein YdcS | ydcS | 7 | 0.9376 | 0.7112 | 0.6252 | 0.7585 | 0.6668 |
| 219 | 11.12 | 11.12 | 30.8 | P0ABC7 | Modulator of FtsH protease HflK | hflK | 9 | 1.0186 | 0.7516 | 1.1695 | 0.7379 | 1.1481 |
| 220 | 11.11 | 11.11 | 53.5 | P0A7J7 | 50S ribosomal protein L11 | rplK | 11 | 0.7798 | 1.1803 | 0.9638 | 1.5136 | 1.2360 |
| 221 | 11.07 | 11.07 | 33 | P63020 | Fe/S biogenesis protein NfuA | nfuA | 7 | 0.9727 | 0.9908 | 1.0471 | 1.0186 | 1.0765 |
| 224 | 11.06 | 11.06 | 72.9 | P0A7S9 | 30S ribosomal protein S13 | rpsM | 9 | 0.871 | 0.8395 | 0.6427 | 0.9638 | 0.7379 |
| 225 | 11.02 | 11.02 | 45.3 | P0A6B7 | Cysteine desulfurase | iscS | 10 | 1.1588 | 0.9462 | 1.1272 | 0.8165 | 0.9727 |
| 226 | 10.97 | 10.97 | 34.1 | P0A796 | 6-phosphofructokinase isozyme 1 | pfkA | 7 | 1.028 | 0.4207 | 0.5012 | 0.4092 | 0.4875 |
| 227 | 10.96 | 10.96 | 34.7 | P0A786 | Aspartate carbamoyltransferase catalytic chain | pyrB | 9 | 0.8017 | 1.0093 | 1.0471 | 1.2589 | 1.3061 |
| 228 | 10.8 | 10.8 | 75.7 | P0A7R5 | 30S ribosomal protein S10 | rpsJ | 10 | 0.9727 | 1.0093 | 0.9817 | 1.0376 | 1.0093 |
| 229 | 10.72 | 10.72 | 61.4 | P0ABD3 | Bacterioferritin | bfr | 12 | 0.929 | 0.5702 | 0.7798 | 0.6138 | 0.8394 |
| 230 | 10.71 | 10.71 | 36.9 | P0A825 | Serine hydroxymethyltransferase | glyA | 7 | 0.9638 | 1.7701 | 1.9055 | 1.8366 | 1.9771 |
| 231 | 10.67 | 10.67 | 52.2 | P12758 | Uridine phosphorylase | udp | 9 | 1.0093 | 0.955 | 0.9638 | 0.9462 | 0.9549 |
| 232 | 10.63 | 10.63 | 32.8 | P08331 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase | cpdB | 11 | 0.9727 | 0.863 | 0.863 | 0.8872 | 0.8872 |
| 233 | 10.59 | 11.18 | 35.6 | P0A6L2 | 4-hydroxy-tetrahydrodipicolinate synthase | dapA | 9 | 1.0375 | 2.2284 | 2.2699 | 2.1479 | 2.1879 |
| 234 | 10.59 | 10.59 | 29.9 | P17169 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] | glmS | 7 | 0.9727 | 1 | 1.0375 | 1.0281 | 1.0666 |
| 235 | 10.57 | 10.57 | 69.2 | P69783 | Glucose-specific phosphotransferase enzyme IIA component | crr | 16 | 0.787 | 0.7943 | 0.7727 | 1.0093 | 0.9818 |
| 236 | 10.48 | 10.48 | 74.1 | P0A763 | Nucleoside diphosphate kinase | ndk | 14 | 1.0568 | 2.0512 | 1.4723 | 1.9410 | 1.3932 |
| 237 | 10.47 | 10.47 | 27.4 | P0AB89 | Adenylosuccinate lyase | purB | 8 | 1.0965 | 0.9638 | 1.028 | 0.8790 | 0.9375 |
| 238 | 10.45 | 10.45 | 36.4 | P07017 | Methyl-accepting chemotaxis protein II | tar | 11 | 0.9908 | 1.3552 | 1.3305 | 1.3678 | 1.3429 |
| 239 | 10.41 | 10.41 | 32.7 | P00962 | Glutamine--tRNA ligase | glnS | 7 | 1.0568 | 1.2706 | 1.1912 | 1.2023 | 1.1272 |
| 240 | 10.38 | 10.39 | 50.4 | P0AEK4 | Enoyl-[acyl-carrier-protein] reductase [NADH] FabI | fabI | 15 | 1.0186 | 0.9817 | 0.9908 | 0.9638 | 0.9727 |
| 241 | 10.23 | 10.23 | 77.3 | P61175 | 50S ribosomal protein L22 | rplV | 11 | 0.9727 | 1 | 0.9727 | 1.0281 | 1.0000 |
| 242 | 10.19 | 10.19 | 37.6 | P0AFF6 | Transcription termination/antitermination protein NusA | nusA | 6 | 1.0186 | 1.0186 | 1 | 1.0000 | 0.9817 |
| 243 | 10.18 | 12.67 | 18.4 | P33570 | Transketolase 2 | tktB | 9 | 1 | 0.9727 | 1.1482 | 0.9727 | 1.1482 |
| 244 | 10.15 | 10.15 | 38.9 | P0AAC0 | Universal stress protein E | uspE | 8 | 1.0471 | 0.5916 | 0.5248 | 0.5650 | 0.5012 |
| 245 | 10.05 | 10.05 | 36.1 | P0A7Z0 | Ribose-5-phosphate isomerase A | rpiA | 8 | 0.9908 | 2.466 | 2.5351 | 2.4889 | 2.5586 |
| 246 | 10.04 | 10.04 | 31 | P77674 | Gamma-aminobutyraldehyde dehydrogenase | prr | 9 | 0.7178 | 2.1086 | 1.5136 | 2.9376 | 2.1087 |
| 247 | 10.03 | 10.03 | 76.9 | P60624 | 50S ribosomal protein L24 | rplX | 8 | 0.6546 | 0.8954 | 0.5598 | 1.3679 | 0.8552 |
| 248 | 10.02 | 10.04 | 37.4 | P04982 | D-ribose pyranase | rbsD | 11 | 0.912 | 1.3183 | 1.2589 | 1.4455 | 1.3804 |
| 249 | 10.01 | 10.01 | 33.7 | P0A8F0 | Uracil phosphoribosyltransferase | upp | 9 | 0.9908 | 1.0568 | 1 | 1.0666 | 1.0093 |
| 250 | 10 | 10 | 30.9 | P21165 | Xaa-Pro dipeptidase | pepQ | 8 | 0.9817 | 1.0471 | 1.028 | 1.0666 | 1.0472 |
| 251 | 9.96 | 9.96 | 44.3 | P0AE06 | Multidrug efflux pump subunit AcrA | acrA | 12 | 0.9638 | 0.9376 | 1.1066 | 0.9728 | 1.1482 |
| 252 | 9.93 | 9.93 | 29.5 | P0A9J6 | Ribokinase | rbsK | 13 | 0.8395 | 1.7219 | 2.0137 | 2.0511 | 2.3987 |
| 253 | 9.89 | 9.9 | 62 | P68679 | 30S ribosomal protein S21 | rpsU | 7 | 0.9908 | 0.9638 | 0.9204 | 0.9727 | 0.9289 |
| 254 | 9.86 | 9.86 | 26.8 | P15034 | Xaa-Pro aminopeptidase | pepP | 6 | 1.0471 | 0.9638 | 1.0186 | 0.9204 | 0.9728 |
| 255 | 9.86 | 9.86 | 25.5 | P0AEP3 | UTP--glucose-1-phosphate uridylyltransferase | galU | 7 | 1.0666 | 0.6982 | 0.8551 | 0.6546 | 0.8017 |
| 256 | 9.84 | 9.89 | 58.1 | P0A903 | Outer membrane protein assembly factor BamC | bamC | 11 | 1.0471 | 1 | 0.9204 | 0.9550 | 0.8790 |
| 257 | 9.83 | 9.84 | 27.4 | P0A6H1 | ATP-dependent Clp protease ATP-binding subunit ClpX | clpX | 6 | 0.9817 | 0.9204 | 0.9036 | 0.9376 | 0.9204 |
| 258 | 9.81 | 9.81 | 30 | P0AGJ9 | Tyrosine--tRNA ligase | tyrS | 8 | 1 | 0.9462 | 1.0093 | 0.9462 | 1.0093 |
| 259 | 9.79 | 9.79 | 46 | P0A805 | Ribosome-recycling factor | frr | 11 | 1.0186 | 1.0093 | 1.0186 | 0.9909 | 1.0000 |
| 260 | 9.76 | 9.76 | 34.8 | P0AAI3 | ATP-dependent zinc metalloprotease FtsH | ftsH | 8 | 0.9462 | 0.9462 | 0.9727 | 1.0000 | 1.0280 |
| 261 | 9.68 | 9.68 | 69.2 | P0A7X3 | 30S ribosomal protein S9 | rpsI | 13 | 1.1803 | 1.4322 | 0.9908 | 1.2134 | 0.8394 |
| 262 | 9.65 | 9.65 | 65 | P0A6F9 | 10 kDa chaperonin | groS | 12 | 1 | 0.863 | 0.8395 | 0.8630 | 0.8395 |
| 263 | 9.57 | 9.57 | 40.1 | P0A6I0 | Cytidylate kinase | cmk | 6 | 1.0666 | 0.9462 | 1.0965 | 0.8871 | 1.0280 |
| 264 | 9.48 | 9.48 | 40.5 | P09127 | Putative uroporphyrinogen-III C-methyltransferase | hemX | 12 | 0.8166 | 0.9036 | 0.863 | 1.1065 | 1.0568 |
| 265 | 9.46 | 9.46 | 36.3 | P0AGD3 | Superoxide dismutase [Fe] | sodB | 10 | 0.8472 | 1.1376 | 1.9953 | 1.3428 | 2.3552 |
| 266 | 9.44 | 9.44 | 46.4 | P39831 | NADP-dependent 3-hydroxy acid dehydrogenase YdfG | ydfG | 6 | 1.0765 | 0.9727 | 0.9817 | 0.9036 | 0.9119 |
| 267 | 9.41 | 9.41 | 43 | P09394 | Glycerophosphoryl diester phosphodiesterase | glpQ | 8 | 1.2706 | 0.6026 | 0.912 | 0.4743 | 0.7178 |
| 268 | 9.35 | 9.35 | 48 | P0AG44 | 50S ribosomal protein L17 | rplQ | 12 | 0.8472 | 0.8241 | 0.6252 | 0.9727 | 0.7380 |
| 269 | 9.31 | 9.31 | 28.1 | P0AES6 | DNA gyrase subunit B | gyrB | 5 | 1 | 0.9908 | 1 | 0.9908 | 1.0000 |
| 270 | 9.3 | 9.3 | 53.3 | P0A707 | Translation initiation factor IF-3 | infC | 10 | 0.9204 | 0.9727 | 0.9204 | 1.0568 | 1.0000 |
| 271 | 9.29 | 9.3 | 23 | P21499 | Ribonuclease R | rnr | 6 | 0.9376 | 0.9727 | 0.929 | 1.0374 | 0.9908 |
| 272 | 9.26 | 9.26 | 70.6 | P69441 | Adenylate kinase | adk | 10 | 1.2246 | 1.3804 | 1.4997 | 1.1272 | 1.2246 |
| 273 | 9.26 | 9.26 | 60.9 | P76402 | UPF0339 protein YegP | yegP | 10 | 0.929 | 0.3631 | 0.4169 | 0.3909 | 0.4488 |
| 274 | 9.21 | 9.21 | 33.7 | P27306 | Soluble pyridine nucleotide transhydrogenase | sthA | 9 | 0.8954 | 1.3677 | 1.3677 | 1.5275 | 1.5275 |
| 275 | 9.12 | 9.13 | 42 | P25553 | Lactaldehyde dehydrogenase | aldA | 9 | 0.9908 | 0.8872 | 0.929 | 0.8954 | 0.9376 |
| 276 | 9.05 | 9.08 | 26.6 | P0AES4 | DNA gyrase subunit A | gyrA | 6 | 1.0765 | 1 | 1.1376 | 0.9289 | 1.0568 |
| 277 | 8.93 | 8.93 | 36.3 | P0A9X4 | Rod shape-determining protein MreB | mreB | 9 | 1 | 0.9638 | 0.9727 | 0.9638 | 0.9727 |
| 278 | 8.87 | 8.87 | 23.7 | P15288 | Cytosol non-specific dipeptidase | pepD | 8 | 0.9908 | 0.8318 | 1.0666 | 0.8395 | 1.0765 |
| 279 | 8.83 | 8.83 | 41.9 | P0A993 | Fructose-1,6-bisphosphatase class 1 | fbp | 6 | 0.9638 | 1.1912 | 1.1272 | 1.2359 | 1.1695 |
| 280 | 8.83 | 8.83 | 35.3 | P0A912 | Peptidoglycan-associated lipoprotein | pal | 9 | 1.2023 | 1.5136 | 2.3335 | 1.2589 | 1.9409 |
| 281 | 8.82 | 8.82 | 57.4 | P0A7K6 | 50S ribosomal protein L19 | rplS | 10 | 0.9817 | 1.0186 | 1.0186 | 1.0376 | 1.0376 |
| 282 | 8.78 | 8.78 | 60.5 | P0ACE7 | HIT-like protein HinT | hinT | 7 | 1.1272 | 1.0568 | 1.2942 | 0.9375 | 1.1482 |
| 283 | 8.77 | 8.77 | 15.3 | P63235 | Probable glutamate/gamma-aminobutyrate antiporter | gadC | 9 | 1 | 1 | 1 | 1.0000 | 1.0000 |
| 284 | 8.73 | 8.73 | 22.6 | P28304 | Quinone oxidoreductase 1 | qorA | 6 | 0.9727 | 0.9727 | 0.955 | 1.0000 | 0.9818 |
| 285 | 8.64 | 8.64 | 23.1 | P39173 | Putative glucose-6-phosphate 1-epimerase | yeaD | 7 | 0.9638 | 1.028 | 1.0093 | 1.0666 | 1.0472 |
| 286 | 8.62 | 8.62 | 26.2 | P33136 | Glucans biosynthesis protein G | mdoG | 7 | 1.0186 | 0.9036 | 0.9908 | 0.8871 | 0.9727 |
| 287 | 8.61 | 8.61 | 72 | P0ADW3 | Inner membrane protein YhcB | yhcB | 9 | 1.0093 | 1.0765 | 0.9727 | 1.0666 | 0.9637 |
| 288 | 8.6 | 8.6 | 21.3 | P0A6T1 | Glucose-6-phosphate isomerase | pgi | 6 | 1.0093 | 0.929 | 0.912 | 0.9204 | 0.9036 |
| 289 | 8.57 | 8.57 | 37.7 | P77161 | 2-hydroxy-3-oxopropionate reductase | glxR | 6 | 1.3428 | 2.2491 | 2.0512 | 1.6749 | 1.5276 |
| 290 | 8.57 | 8.57 | 48.4 | P25894 | Metalloprotease LoiP | loiP | 7 | 0.879 | 0.8318 | 0.863 | 0.9463 | 0.9818 |
| 291 | 8.56 | 8.56 | 36.7 | P0ABZ6 | Chaperone SurA | surA | 8 | 1.1272 | 1.0093 | 1.0471 | 0.8954 | 0.9289 |
| 292 | 8.53 | 8.53 | 66 | P68919 | 50S ribosomal protein L25 | rplY | 10 | 0.7112 | 1 | 0.7798 | 1.4061 | 1.0965 |
| 293 | 8.47 | 8.47 | 27.8 | P21179 | Catalase HPII | katE | 7 | 0.9638 | 1.0186 | 0.955 | 1.0569 | 0.9909 |
| 294 | 8.4 | 8.4 | 36.3 | P60906 | Histidine--tRNA ligase | hisS | 8 | 1.0965 | 1.1803 | 1.1588 | 1.0764 | 1.0568 |
| 295 | 8.4 | 8.4 | 26.6 | P0A9A6 | Cell division protein FtsZ | ftsZ | 9 | 1.3932 | 2.1281 | 1.803 | 1.5275 | 1.2941 |
| 296 | 8.36 | 8.36 | 29.3 | P04079 | GMP synthase [glutamine-hydrolyzing] | guaA | 9 | 0.8395 | 0.955 | 1.0568 | 1.1376 | 1.2588 |
| 297 | 8.29 | 8.36 | 33 | P0AEB2 | D-alanyl-D-alanine carboxypeptidase DacA | dacA | 4 | 1.0965 | 0.9462 | 0.9727 | 0.8629 | 0.8871 |
| 298 | 8.25 | 8.25 | 51.6 | P76177 | Protein YdgH | ydgH | 10 | 0.9817 | 0.929 | 0.7178 | 0.9463 | 0.7312 |
| 299 | 8.24 | 8.24 | 32.6 | P37095 | Peptidase B | pepB | 8 | 1.0765 | 1.2359 | 0.9908 | 1.1481 | 0.9204 |
| 300 | 8.22 | 8.24 | 20.3 | P0A7A7 | Glycerol-3-phosphate acyltransferase | plsB | 6 | 0.9462 | 0.9908 | 1.0375 | 1.0471 | 1.0965 |
| 301 | 8.19 | 8.19 | 43.5 | P0ABA4 | ATP synthase subunit delta | atpH | 7 | 0.8551 | 0.7798 | 0.6368 | 0.9119 | 0.7447 |
| 302 | 8.17 | 8.17 | 41 | P67910 | ADP-L-glycero-D-manno-heptose-6-epimerase | hldD | 10 | 1.0666 | 0.7798 | 0.6792 | 0.7311 | 0.6368 |
| 303 | 8.17 | 8.17 | 31.6 | P18843 | NH(3)-dependent NAD(+) synthetase | nadE | 7 | 0.9908 | 0.9376 | 1.0093 | 0.9463 | 1.0187 |
| 304 | 8.15 | 8.18 | 29.9 | P00490 | Maltodextrin phosphorylase | malP | 6 | 1.1066 | 0.9817 | 1.0186 | 0.8871 | 0.9205 |
| 305 | 8.12 | 8.12 | 28.2 | P0AFK9 | Spermidine/putrescine-binding periplasmic protein | potD | 10 | 1.1588 | 1.6749 | 1.2359 | 1.4454 | 1.0665 |
| 306 | 8.09 | 8.09 | 31.1 | P77774 | Outer membrane protein assembly factor BamB | bamB | 11 | 0.9462 | 0.9638 | 0.9727 | 1.0186 | 1.0280 |
| 307 | 8.08 | 8.09 | 40.3 | P07004 | Gamma-glutamyl phosphate reductase | proA | 9 | 0.7656 | 0.8954 | 0.8872 | 1.1695 | 1.1588 |
| 308 | 8.06 | 8.06 | 30.3 | P37648 | Protein YhjJ | yhjJ | 8 | 1.2823 | 1.1482 | 1.2246 | 0.8954 | 0.9550 |
| 309 | 8.06 | 8.06 | 58.1 | P62399 | 50S ribosomal protein L5 | rplE | 8 | 1.028 | 1.2023 | 1.0765 | 1.1696 | 1.0472 |
| 310 | 8.05 | 8.05 | 32.9 | P0AEZ9 | Molybdenum cofactor biosynthesis protein B | moaB | 8 | 1.0375 | 0.4831 | 0.413 | 0.4656 | 0.3981 |
| 311 | 8.04 | 8.04 | 18 | P10408 | Protein translocase subunit SecA | secA | 5 | 1.0965 | 0.9727 | 1.2474 | 0.8871 | 1.1376 |
| 312 | 8.04 | 8.04 | 60.9 | P0AEU7 | Chaperone protein Skp | skp | 16 | 0.7047 | 0.4246 | 0.6138 | 0.6025 | 0.8710 |
| 313 | 8.03 | 8.03 | 56.5 | P64596 | Uncharacterized protein YraP | yraP | 9 | 1.028 | 1 | 0.9817 | 0.9728 | 0.9550 |
| 314 | 8.02 | 8.02 | 45.1 | P0AC47 | Fumarate reductase iron-sulfur subunit | frdB | 6 | 1.2134 | 0.5808 | 1.0864 | 0.4787 | 0.8953 |
| 315 | 8.01 | 8.02 | 32.5 | P76145 | Trans-aconitate 2-methyltransferase | tam | 6 | 1.0666 | 1.0568 | 0.929 | 0.9908 | 0.8710 |
| 316 | 8.01 | 8.01 | 45 | P75818 | Uncharacterized lipoprotein YbjP | ybjP | 8 | 1.0093 | 0.871 | 0.955 | 0.8630 | 0.9462 |
| 317 | 8.01 | 8.01 | 62.6 | P75694 | Uncharacterized protein YahO | yahO | 11 | 0.7178 | 0.092 | 0.1754 | 0.1282 | 0.2444 |
| 318 | 8.01 | 8.01 | 46.5 | P0AG86 | Protein-export protein SecB | secB | 7 | 0.9638 | 1.0186 | 1 | 1.0569 | 1.0376 |
| 319 | 8.01 | 8.01 | 41.7 | P0ABD8 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase | accB | 9 | 0.9462 | 0.929 | 0.955 | 0.9818 | 1.0093 |
| 320 | 8 | 8 | 52.5 | P0AFG0 | Transcription termination/antitermination protein NusG | nusG | 7 | 1.0093 | 0.7112 | 0.955 | 0.7046 | 0.9462 |
| 321 | 8 | 8 | 37.3 | P0ADC1 | LPS-assembly lipoprotein LptE | lptE | 7 | 1.0666 | 0.8091 | 0.9376 | 0.7586 | 0.8791 |
| 322 | 8 | 8 | 42.5 | P0A915 | Outer membrane protein W | ompW | 8 | 0.929 | 0.863 | 1.1169 | 0.9290 | 1.2023 |
| 323 | 8 | 8 | 29.3 | P0AAB6 | UTP--glucose-1-phosphate uridylyltransferase | galF | 10 | 1.0568 | 0.7516 | 0.5808 | 0.7112 | 0.5496 |
| 324 | 8 | 8 | 25.5 | P21367 | Uncharacterized protein YcaC | ycaC | 5 | 0.9817 | 0.9638 | 0.9638 | 0.9818 | 0.9818 |
| 325 | 8 | 8 | 55.5 | P0ADX7 | Uncharacterized protein YhhA | yhhA | 5 | 0.9908 | 0.0497 | 0.2911 | 0.0502 | 0.2938 |
| 326 | 7.91 | 7.95 | 25 | P24171 | Peptidyl-dipeptidase dcp | dcp | 5 | 1.0375 | 1.1169 | 0.9908 | 1.0765 | 0.9550 |
| 327 | 7.87 | 7.87 | 32.6 | P29745 | Peptidase T | pepT | 6 | 0.9638 | 0.9908 | 0.955 | 1.0280 | 0.9909 |
| 328 | 7.84 | 7.87 | 31.8 | P30147 | Hydroxypyruvate isomerase | hyi | 6 | 1.028 | 1.1803 | 1.0666 | 1.1482 | 1.0375 |
| 329 | 7.84 | 7.84 | 37.7 | P0AFC7 | NADH-quinone oxidoreductase subunit B | nuoB | 7 | 1.0471 | 1.0765 | 1 | 1.0281 | 0.9550 |
| 330 | 7.82 | 7.82 | 31.3 | P0AFK0 | Protein PmbA | pmbA | 7 | 0.8954 | 0.9727 | 1 | 1.0863 | 1.1168 |
| 331 | 7.82 | 7.82 | 35.8 | P0A998 | Ferritin-1 | ftnA | 6 | 1.0375 | 1.7378 | 1.7061 | 1.6750 | 1.6444 |
| 332 | 7.8 | 8.04 | 44.7 | P0AC59 | Glutaredoxin-2 | grxB | 6 | 1.0186 | 1.0186 | 0.9908 | 1.0000 | 0.9727 |
| 333 | 7.8 | 7.8 | 38.7 | P39177 | Universal stress protein G | uspG | 9 | 1.1482 | 1.9588 | 1.4588 | 1.7060 | 1.2705 |
| 334 | 7.78 | 7.78 | 65.3 | P0A7T7 | 30S ribosomal protein S18 | rpsR | 7 | 0.863 | 1.4997 | 1.1066 | 1.7378 | 1.2823 |
| 335 | 7.76 | 7.77 | 22 | P06612 | DNA topoisomerase 1 | topA | 4 | 0.9204 | 0.929 | 1.0568 | 1.0093 | 1.1482 |
| 336 | 7.7 | 8.08 | 27.6 | P0ACY3 | Uncharacterized protein YeaG | yeaG | 7 | 1.0864 | 1.1588 | 1.1272 | 1.0666 | 1.0376 |
| 337 | 7.65 | 7.65 | 28.6 | P66899 | Diaminopropionate ammonia-lyase | ygeX | 7 | 0.6252 | 2.8576 | 2.2284 | 4.5707 | 3.5643 |
| 338 | 7.64 | 7.65 | 16.5 | P26616 | NAD-dependent malic enzyme | maeA | 5 | 0.5598 | 0.7311 | 0.5916 | 1.3060 | 1.0568 |
| 339 | 7.53 | 7.53 | 24.8 | P0A9Q9 | Aspartate-semialdehyde dehydrogenase | asd | 5 | 1.1803 | 1.2823 | 1.2023 | 1.0864 | 1.0186 |
| 340 | 7.48 | 7.48 | 14.8 | P76440 | NAD-dependent dihydropyrimidine dehydrogenase subunit PreT | preT | 7 | 1.406 | 4.2462 | 2.3335 | 3.0201 | 1.6597 |
| 341 | 7.44 | 7.44 | 41.4 | Q46800 | Xanthine dehydrogenase FAD-binding subunit | xdhB | 9 | 0.9817 | 1.0965 | 1.1272 | 1.1169 | 1.1482 |
| 342 | 7.44 | 7.44 | 51.1 | P0A6Y1 | Integration host factor subunit beta | ihfB | 5 | 0.8241 | 0.3467 | 0.4875 | 0.4207 | 0.5916 |
| 343 | 7.39 | 7.39 | 31.5 | P77243 | 2-methylcitrate dehydratase | prpD | 7 | 1.0568 | 3.3729 | 2.0137 | 3.1916 | 1.9055 |
| 344 | 7.38 | 10.8 | 38.9 | P0AEU0 | Histidine-binding periplasmic protein | hisJ | 10 | 1.0471 | 0.9204 | 0.7178 | 0.8790 | 0.6855 |
| 345 | 7.33 | 7.33 | 55.4 | P0A7W7 | 30S ribosomal protein S8 | rpsH | 10 | 1.0471 | 1.0093 | 1.0864 | 0.9639 | 1.0375 |
| 346 | 7.32 | 7.32 | 35.3 | P0A6X3 | RNA-binding protein Hfq | hfq | 9 | 0.8472 | 1 | 0.8091 | 1.1804 | 0.9550 |
| 347 | 7.27 | 7.27 | 33 | Q46799 | Xanthine dehydrogenase molybdenum-binding subunit | xdhA | 9 | 0.8241 | 1.6144 | 1.4723 | 1.9590 | 1.7866 |
| 348 | 7.26 | 17.87 | 42.8 | P0A8N3 | Lysine--tRNA ligase | lysS | 20 | 1.3062 | 1.5417 | 0.787 | 1.1803 | 0.6025 |
| 349 | 7.22 | 7.22 | 24.7 | P0AET8 | 7-alpha-hydroxysteroid dehydrogenase | hdhA | 5 | 0.9908 | 1.2134 | 1.2134 | 1.2247 | 1.2247 |
| 350 | 7.22 | 7.22 | 55.3 | P0AG48 | 50S ribosomal protein L21 | rplU | 7 | 0.7311 | 1.1803 | 0.8241 | 1.6144 | 1.1272 |
| 351 | 7.2 | 9.07 | 23.8 | P24183 | Formate dehydrogenase, nitrate-inducible, major subunit | fdnG | 9 | 0.6194 | 0.5445 | 0.4571 | 0.8791 | 0.7380 |
| 352 | 7.18 | 9.44 | 29.6 | P0AAG8 | Galactose/methyl galactoside import ATP-binding protein MglA | mglA | 6 | 1 | 0.9462 | 1.028 | 0.9462 | 1.0280 |
| 353 | 7.17 | 7.17 | 36.6 | P0A955 | KHG/KDPG aldolase | eda | 6 | 0.8954 | 0.9638 | 1 | 1.0764 | 1.1168 |
| 354 | 7.1 | 7.15 | 35.4 | P0A7G6 | Protein RecA | recA | 8 | 0.8091 | 0.929 | 0.7727 | 1.1482 | 0.9550 |
| 355 | 7.1 | 7.1 | 26.9 | P32132 | GTP-binding protein TypA/BipA | typA | 6 | 0.8241 | 1.1482 | 1.1803 | 1.3933 | 1.4322 |
| 356 | 7.06 | 7.07 | 23.5 | P07913 | L-threonine 3-dehydrogenase | tdh | 6 | 0.9908 | 1.0186 | 1.0965 | 1.0281 | 1.1067 |
| 357 | 7.02 | 7.04 | 32.1 | P23917 | Fructokinase | mak | 5 | 0.929 | 0.912 | 0.9817 | 0.9817 | 1.0567 |
| 358 | 6.92 | 6.92 | 23.5 | P07001 | NAD(P) transhydrogenase subunit alpha | pntA | 7 | 1.028 | 1.0965 | 1.0765 | 1.0666 | 1.0472 |
| 359 | 6.9 | 6.9 | 73.9 | P0A9Y6 | Cold shock-like protein CspC | cspC | 10 | 0.6982 | 1.556 | 0.8872 | 2.2286 | 1.2707 |
| 360 | 6.83 | 6.83 | 33.5 | P09372 | Protein GrpE | grpE | 7 | 0.9817 | 0.955 | 1.0093 | 0.9728 | 1.0281 |
| 361 | 6.81 | 6.81 | 23.3 | P15640 | Phosphoribosylamine--glycine ligase | purD | 5 | 0.9204 | 1.0093 | 0.9462 | 1.0966 | 1.0280 |
| 362 | 6.81 | 6.81 | 25.5 | P0ABQ2 | 2-hydroxy-3-oxopropionate reductase | garR | 8 | 0.6982 | 1.888 | 1.1376 | 2.7041 | 1.6293 |
| 363 | 6.76 | 6.76 | 54.6 | P0AET2 | Acid stress chaperone HdeB | hdeB | 15 | 0.9204 | 0.5702 | 0.8241 | 0.6195 | 0.8954 |
| 364 | 6.68 | 6.68 | 44.2 | P0AFR4 | Uncharacterized protein YciO | yciO | 4 | 1.1912 | 0.9638 | 0.9204 | 0.8091 | 0.7727 |
| 365 | 6.6 | 6.61 | 62.4 | P0AA25 | Thioredoxin-1 | trxA | 7 | 1.0186 | 1.2246 | 1.1695 | 1.2022 | 1.1481 |
| 366 | 6.6 | 6.6 | 27.5 | P0A917 | Outer membrane protein X | ompX | 5 | 0.8551 | 0.8241 | 1.0666 | 0.9637 | 1.2473 |
| 367 | 6.58 | 6.58 | 33.4 | P0AES2 | Glucarate dehydratase | gudD | 6 | 1.1695 | 1.3183 | 0.9638 | 1.1272 | 0.8241 |
| 368 | 6.56 | 6.56 | 35.8 | P0ABU2 | Ribosome-binding ATPase YchF | ychF | 5 | 1.0666 | 1.1482 | 1.2023 | 1.0765 | 1.1272 |
| 369 | 6.55 | 6.59 | 34.4 | P0ACF4 | DNA-binding protein HU-beta | hupB | 6 | 0.787 | 0.871 | 0.6607 | 1.1067 | 0.8395 |
| 370 | 6.54 | 6.55 | 68 | P0A7F3 | Aspartate carbamoyltransferase regulatory chain | pyrI | 9 | 1.0965 | 1.406 | 1.1482 | 1.2823 | 1.0472 |
| 371 | 6.53 | 6.53 | 42.1 | P23869 | Peptidyl-prolyl cis-trans isomerase B | ppiB | 9 | 0.955 | 1.2823 | 1.1272 | 1.3427 | 1.1803 |
| 372 | 6.48 | 6.48 | 25.2 | P76576 | UPF0070 protein YfgM | yfgM | 3 | 1.0568 | 0.9376 | 1.0375 | 0.8872 | 0.9817 |
| 373 | 6.47 | 6.47 | 42.7 | P0AD59 | Inhibitor of vertebrate lysozyme | ivy | 5 | 0.8395 | 0.3837 | 0.863 | 0.4571 | 1.0280 |
| 374 | 6.42 | 6.45 | 27.8 | P0A9C3 | Aldose 1-epimerase | galM | 4 | 1 | 1.0864 | 1.0568 | 1.0864 | 1.0568 |
| 375 | 6.4 | 6.4 | 41.1 | P76268 | Transcriptional regulator KdgR | kdgR | 5 | 1.0093 | 0.929 | 0.9817 | 0.9204 | 0.9727 |
| 376 | 6.38 | 6.38 | 33.2 | P0ABC3 | Modulator of FtsH protease HflC | hflC | 7 | 0.9817 | 0.9638 | 0.9204 | 0.9818 | 0.9376 |
| 377 | 6.34 | 6.34 | 29.6 | P0A6U8 | Glycogen synthase | glgA | 7 | 1.6293 | 0.6855 | 0.912 | 0.4207 | 0.5597 |
| 378 | 6.34 | 6.34 | 29.2 | P31142 | 3-mercaptopyruvate sulfurtransferase | sseA | 7 | 1.0093 | 1.0965 | 0.9908 | 1.0864 | 0.9817 |
| 379 | 6.33 | 6.33 | 20.1 | P0A6J5 | D-amino acid dehydrogenase small subunit | dadA | 7 | 0.955 | 0.9908 | 1.1066 | 1.0375 | 1.1587 |
| 380 | 6.3 | 6.3 | 46.6 | P0A7L3 | 50S ribosomal protein L20 | rplT | 8 | 0.9908 | 1.1482 | 0.7311 | 1.1589 | 0.7379 |
| 381 | 6.27 | 6.27 | 32 | P0AAI9 | Malonyl CoA-acyl carrier protein transacylase | fabD | 10 | 0.9817 | 1.0666 | 1.028 | 1.0865 | 1.0472 |
| 382 | 6.26 | 6.26 | 22.2 | P42588 | Putrescine aminotransferase | patA | 4 | 1.0186 | 0.7379 | 0.7727 | 0.7244 | 0.7586 |
| 383 | 6.22 | 6.22 | 37.9 | P00448 | Superoxide dismutase [Mn] | sodA | 4 | 0.9036 | 0.8551 | 0.6918 | 0.9463 | 0.7656 |
| 384 | 6.22 | 6.22 | 56.5 | P0AC69 | Glutaredoxin-4 | grxD | 7 | 1.3183 | 3.5318 | 2.1281 | 2.6791 | 1.6143 |
| 385 | 6.21 | 6.21 | 18.9 | P31554 | LPS-assembly protein LptD | lptD | 6 | 1.0864 | 0.9727 | 0.9727 | 0.8953 | 0.8953 |
| 386 | 6.2 | 6.29 | 25.5 | P52643 | D-lactate dehydrogenase | ldhA | 4 | 0.9462 | 0.912 | 0.9376 | 0.9639 | 0.9909 |
| 387 | 6.19 | 6.19 | 21.8 | P15254 | Phosphoribosylformylglycinamidine synthase | purL | 5 | 0.955 | 1.1272 | 1.0375 | 1.1803 | 1.0864 |
| 388 | 6.19 | 6.19 | 41.5 | P0ADK0 | Uncharacterized protein YiaF | yiaF | 7 | 0.8318 | 0.912 | 0.9638 | 1.0964 | 1.1587 |
| 389 | 6.17 | 6.17 | 18.8 | P76113 | NADPH-dependent curcumin reductase | curA | 6 | 0.929 | 1.0568 | 0.9727 | 1.1376 | 1.0470 |
| 390 | 6.16 | 6.16 | 25.1 | P13482 | Periplasmic trehalase | treA | 6 | 1.0765 | 1 | 0.9204 | 0.9289 | 0.8550 |
| 391 | 6.16 | 6.16 | 62.6 | P0A800 | DNA-directed RNA polymerase subunit omega | rpoZ | 10 | 0.9817 | 0.9376 | 0.9036 | 0.9551 | 0.9204 |
| 392 | 6.14 | 6.14 | 29 | P0AC02 | Outer membrane protein assembly factor BamD | bamD | 5 | 1.2359 | 1.3183 | 1.3932 | 1.0667 | 1.1273 |
| 393 | 6.12 | 6.12 | 30.1 | P22255 | 3'(2'),5'-bisphosphate nucleotidase CysQ | cysQ | 7 | 0.7516 | 0.5495 | 0.4365 | 0.7311 | 0.5808 |
| 394 | 6.1 | 6.1 | 55.1 | P0AE52 | Putative peroxiredoxin bcp | bcp | 6 | 0.7798 | 0.3221 | 1.2474 | 0.4131 | 1.5996 |
| 395 | 6.08 | 6.08 | 24.3 | P68767 | Cytosol aminopeptidase | pepA | 3 | 0.929 | 1.0471 | 1.0666 | 1.1271 | 1.1481 |
| 396 | 6.05 | 6.06 | 32.9 | P0A6E4 | Argininosuccinate synthase | argG | 4 | 1.0864 | 1.2589 | 1.028 | 1.1588 | 0.9462 |
| 397 | 6.05 | 6.05 | 40 | P0AES9 | Acid stress chaperone HdeA | hdeA | 5 | 0.7943 | 0.6486 | 0.6368 | 0.8166 | 0.8017 |
| 398 | 6.04 | 6.04 | 18.3 | P46130 | Putative acyl-CoA thioester hydrolase YbhC | ybhC | 4 | 1 | 0.9462 | 0.929 | 0.9462 | 0.9290 |
| 399 | 6.03 | 6.03 | 23.8 | P30850 | Exoribonuclease 2 | rnb | 3 | 0.912 | 1.0186 | 0.787 | 1.1169 | 0.8629 |
| 400 | 6.03 | 6.03 | 50.8 | P0ACY1 | Putative NAD(P)H nitroreductase YdjA | ydjA | 4 | 0.6026 | 0.2938 | 0.9817 | 0.4876 | 1.6291 |
| 401 | 6.03 | 6.03 | 38.7 | P0A905 | Outer membrane lipoprotein SlyB | slyB | 13 | 0.9817 | 0.3565 | 0.7178 | 0.3631 | 0.7312 |
| 402 | 6.02 | 6.02 | 10.6 | P0ABI8 | Cytochrome bo(3) ubiquinol oxidase subunit 1 | cyoB | 4 | 1.1066 | 0.6855 | 1.4588 | 0.6195 | 1.3183 |
| 403 | 6.01 | 6.11 | 59.7 | P77695 | Protein GnsB | gnsB | 3 | 0.871 | 0.8395 | 0.8872 | 0.9638 | 1.0186 |
| 404 | 6.01 | 6.01 | 41.4 | P61316 | Outer-membrane lipoprotein carrier protein | lolA | 5 | 1.2942 | 1.1376 | 1.1482 | 0.8790 | 0.8872 |
| 405 | 6.01 | 6.01 | 37.5 | P0ADB1 | Osmotically-inducible lipoprotein E | osmE | 8 | 0.863 | 0.413 | 0.5012 | 0.4786 | 0.5808 |
| 406 | 6 | 6.9 | 63.8 | P0A972 | Cold shock-like protein CspE | cspE | 9 | 1.2942 | 1.5276 | 1.0864 | 1.1803 | 0.8394 |
| 407 | 6 | 6 | 71.7 | P0A6X7 | Integration host factor subunit alpha | ihfA | 9 | 0.9462 | 0.3908 | 0.4699 | 0.4130 | 0.4966 |
| 408 | 6 | 6 | 64.2 | P0AF36 | Cell division protein ZapB | zapB | 4 | 1.028 | 1.0375 | 1.0186 | 1.0092 | 0.9909 |
| 409 | 6 | 6 | 50.6 | P0A7U7 | 30S ribosomal protein S20 | rpsT | 9 | 0.871 | 0.6792 | 0.8472 | 0.7798 | 0.9727 |
| 410 | 6 | 6 | 31.5 | P0A7S3 | 30S ribosomal protein S12 | rpsL | 6 | 0.7178 | 1.1169 | 0.787 | 1.5560 | 1.0964 |
| 411 | 6 | 6 | 46.5 | P0ACX3 | Putative monooxygenase YdhR | ydhR | 7 | 0.9638 | 1.028 | 0.9462 | 1.0666 | 0.9817 |
| 412 | 6 | 6 | 82.7 | P0AB14 | Uncharacterized protein YccJ | yccJ | 8 | 0.7727 | 0.673 | 0.4656 | 0.8710 | 0.6026 |
| 413 | 6 | 6 | 29.8 | P0ADU2 | Probable quinol monooxygenase YgiN | ygiN | 6 | 0.9376 | 0.8954 | 0.9638 | 0.9550 | 1.0279 |
| 414 | 6 | 6 | 50 | P25738 | Acidic protein MsyB | msyB | 4 | 0.8241 | 0.9908 | 1 | 1.2023 | 1.2134 |
| 415 | 6 | 6 | 63.3 | P0AF70 | Uncharacterized protein YjeI | yjeI | 9 | 0.955 | 0.9908 | 0.912 | 1.0375 | 0.9550 |
| 416 | 6 | 6 | 26.9 | P0AA91 | Uncharacterized lipoprotein YeaY | yeaY | 6 | 1.2474 | 0.3597 | 1.2134 | 0.2884 | 0.9727 |
| 417 | 6 | 6 | 33.3 | P0A6A8 | Acyl carrier protein | acpP | 11 | 0.8551 | 0.5152 | 1.0765 | 0.6025 | 1.2589 |
| 418 | 5.96 | 6 | 19.3 | P0A8R0 | Regulator of ribonuclease activity A | rraA | 4 | 0.955 | 1.0666 | 1.0186 | 1.1169 | 1.0666 |
| 419 | 5.92 | 5.92 | 54.6 | P0AFW2 | Ribosome modulation factor | rmf | 3 | 0.7727 | 0.4656 | 0.7311 | 0.6026 | 0.9462 |
| 420 | 5.91 | 5.91 | 21.7 | P23830 | CDP-diacylglycerol--serine O-phosphatidyltransferase | pssA | 4 | 0.9638 | 0.9462 | 0.912 | 0.9817 | 0.9463 |
| 421 | 5.89 | 5.89 | 15.4 | P64557 | Uncharacterized protein YgfM | ygfM | 5 | 2.2699 | 2.5823 | 3.8726 | 1.1376 | 1.7061 |
| 422 | 5.87 | 5.87 | 19.6 | P00550 | PTS system mannitol-specific EIICBA component | mtlA | 10 | 1.2589 | 0.4487 | 0.7311 | 0.3564 | 0.5807 |
| 423 | 5.74 | 5.75 | 77.8 | P0A7M6 | 50S ribosomal protein L29 | rpmC | 6 | 0.9727 | 1.0375 | 1.028 | 1.0666 | 1.0569 |
| 424 | 5.72 | 5.72 | 78.6 | P0A7M9 | 50S ribosomal protein L31 | rpmE | 9 | 1.0864 | 0.52 | 0.6668 | 0.4786 | 0.6138 |
| 425 | 5.7 | 8.27 | 23.4 | P0AG90 | Protein translocase subunit SecD | secD | 6 | 1 | 0.955 | 0.955 | 0.9550 | 0.9550 |
| 426 | 5.7 | 5.7 | 19.7 | P37194 | Outer membrane protein slp | slp | 9 | 0.9908 | 0.955 | 0.9727 | 0.9639 | 0.9817 |
| 427 | 5.67 | 5.67 | 29.9 | P0A9D2 | Glutathione S-transferase GstA | gstA | 5 | 0.9376 | 1.028 | 0.9908 | 1.0964 | 1.0567 |
| 428 | 5.66 | 5.66 | 52.5 | P64581 | Uncharacterized protein YqjD | yqjD | 7 | 0.9376 | 0.6486 | 0.5754 | 0.6918 | 0.6137 |
| 429 | 5.64 | 7.82 | 60.5 | P0AGL2 | Putative reactive intermediate deaminase TdcF | tdcF | 6 | 0.7586 | 0.787 | 1.1376 | 1.0374 | 1.4996 |
| 430 | 5.62 | 5.62 | 12.6 | P00959 | Methionine--tRNA ligase | metG | 4 | 0.8954 | 1.2359 | 0.9462 | 1.3803 | 1.0567 |
| 431 | 5.62 | 5.62 | 12.3 | P16095 | L-serine dehydratase 1 | sdaA | 5 | 1.0375 | 0.9376 | 1.0568 | 0.9037 | 1.0186 |
| 432 | 5.57 | 5.57 | 39.6 | P0A877 | Tryptophan synthase alpha chain | trpA | 4 | 1.0568 | 1.0471 | 0.8872 | 0.9908 | 0.8395 |
| 433 | 5.56 | 5.56 | 33.7 | P68187 | Maltose/maltodextrin import ATP-binding protein MalK | malK | 5 | 1.3183 | 0.8318 | 1.2023 | 0.6310 | 0.9120 |
| 434 | 5.55 | 5.56 | 72 | P0A7T3 | 30S ribosomal protein S16 | rpsP | 6 | 1.028 | 1.0765 | 1.028 | 1.0472 | 1.0000 |
| 435 | 5.52 | 5.52 | 22.3 | P76027 | Oligopeptide transport ATP-binding protein OppD | oppD | 5 | 1.0965 | 1.0186 | 1.2023 | 0.9290 | 1.0965 |
| 436 | 5.5 | 5.5 | 33.1 | P0AFD1 | NADH-quinone oxidoreductase subunit E | nuoE | 4 | 1.0568 | 1.1169 | 1.0186 | 1.0569 | 0.9639 |
| 437 | 5.47 | 5.47 | 22.4 | P06149 | D-lactate dehydrogenase | dld | 6 | 0.9638 | 1.028 | 0.955 | 1.0666 | 0.9909 |
| 438 | 5.46 | 5.46 | 23.3 | P31658 | Molecular chaperone Hsp31 and glyoxalase 3 | hchA | 8 | 1.0186 | 1.1376 | 1.1272 | 1.1168 | 1.1066 |
| 439 | 5.44 | 5.46 | 44.8 | Q46868 | Uncharacterized protein YqiC | yqiC | 3 | 0.9376 | 0.9462 | 1.0568 | 1.0092 | 1.1271 |
| 440 | 5.4 | 5.4 | 43.3 | P0AEQ1 | Protein GlcG | glcG | 5 | 1 | 1.0568 | 1.028 | 1.0568 | 1.0280 |
| 441 | 5.39 | 5.39 | 26.9 | P31663 | Pantothenate synthetase | panC | 3 | 1.0666 | 0.929 | 1.0765 | 0.8710 | 1.0093 |
| 442 | 5.35 | 5.35 | 54.9 | P0A8W8 | UPF0304 protein YfbU | yfbU | 4 | 1.0186 | 1.0093 | 0.9204 | 0.9909 | 0.9036 |
| 443 | 5.35 | 5.35 | 38 | P0A9P4 | Thioredoxin reductase | trxB | 7 | 0.9376 | 1.0765 | 0.9036 | 1.1481 | 0.9637 |
| 444 | 5.32 | 5.32 | 17 | P41409 | Pyrimidine-specific ribonucleoside hydrolase RihA | rihA | 4 | 0.955 | 0.9376 | 1.1066 | 0.9818 | 1.1587 |
| 445 | 5.3 | 5.3 | 47.1 | P0A6L0 | Deoxyribose-phosphate aldolase | deoC | 5 | 1.0666 | 0.6026 | 0.871 | 0.5650 | 0.8166 |
| 446 | 5.29 | 5.29 | 21.5 | P0ADG7 | Inosine-5'-monophosphate dehydrogenase | guaB | 5 | 1.1376 | 1.0666 | 0.9376 | 0.9376 | 0.8242 |
| 447 | 5.26 | 5.26 | 36.4 | P0ABS1 | RNA polymerase-binding transcription factor DksA | dksA | 5 | 1.0666 | 2.3768 | 2.0137 | 2.2284 | 1.8880 |
| 448 | 5.25 | 5.28 | 27 | P13035 | Aerobic glycerol-3-phosphate dehydrogenase | glpD | 5 | 0.7311 | 1.6444 | 1.9055 | 2.2492 | 2.6063 |
| 449 | 5.24 | 5.24 | 17.1 | P0ABU5 | Enhancing lycopene biosynthesis protein 2 | elbB | 4 | 0.955 | 2.5351 | 1.6144 | 2.6546 | 1.6905 |
| 450 | 5.2 | 5.2 | 32.7 | P00960 | Glycine--tRNA ligase alpha subunit | glyQ | 4 | 1.0093 | 1.2246 | 1.0864 | 1.2133 | 1.0764 |
| 451 | 5.13 | 5.14 | 20.2 | P0A6R0 | 3-oxoacyl-[acyl-carrier-protein] synthase 3 | fabH | 4 | 0.9727 | 1.0965 | 0.9727 | 1.1273 | 1.0000 |
| 452 | 5.13 | 5.13 | 59.4 | P62768 | UPF0325 protein YaeH | yaeH | 5 | 1.0375 | 1.1803 | 1.0568 | 1.1376 | 1.0186 |
| 453 | 5.08 | 5.76 | 16.1 | P0ACB7 | Protein HemY | hemY | 6 | 1.1803 | 0.787 | 0.787 | 0.6668 | 0.6668 |
| 454 | 5.04 | 5.05 | 25.1 | P0A9K3 | PhoH-like protein | ybeZ | 4 | 1.1376 | 1.3183 | 1.0471 | 1.1588 | 0.9204 |
| 455 | 5.01 | 5.02 | 29.2 | P39099 | Periplasmic pH-dependent serine endoprotease DegQ | degQ | 4 | 0.9908 | 0.9036 | 0.9204 | 0.9120 | 0.9289 |
| 456 | 5 | 5.01 | 32 | P0AFP6 | Putative GTP cyclohydrolase 1 type 2 | ybgI | 4 | 0.9908 | 1 | 1.0864 | 1.0093 | 1.0965 |
| 457 | 5 | 5 | 81.4 | P0AG51 | 50S ribosomal protein L30 | rpmD | 8 | 1.0093 | 1 | 1.0471 | 0.9908 | 1.0375 |
| 458 | 4.95 | 4.95 | 34.8 | P0AC53 | Glucose-6-phosphate 1-dehydrogenase | zwf | 5 | 1.0666 | 0.9376 | 0.9376 | 0.8791 | 0.8791 |
| 459 | 4.95 | 4.95 | 47.6 | P0AG63 | 30S ribosomal protein S17 | rpsQ | 4 | 1.0093 | 1.0471 | 1.0186 | 1.0375 | 1.0092 |
| 460 | 4.89 | 4.89 | 27.3 | P0ADZ7 | UPF0092 membrane protein YajC | yajC | 8 | 0.9817 | 1.0471 | 1.0375 | 1.0666 | 1.0568 |
| 461 | 4.86 | 4.86 | 22.2 | P77395 | Uncharacterized protein YbbN | ybbN | 4 | 1.1588 | 0.7727 | 0.3162 | 0.6668 | 0.2729 |
| 462 | 4.85 | 4.85 | 15.8 | P0AC86 | Glycogen phosphorylase | glgP | 6 | 0.9638 | 1.1803 | 0.9462 | 1.2246 | 0.9817 |
| 463 | 4.81 | 4.81 | 19.7 | P00909 | Tryptophan biosynthesis protein TrpCF | trpC | 4 | 1.3183 | 0.6918 | 0.5702 | 0.5248 | 0.4325 |
| 464 | 4.75 | 4.75 | 29.7 | P76142 | Autoinducer 2-binding protein LsrB | lsrB | 10 | 1.028 | 1.0471 | 0.9036 | 1.0186 | 0.8790 |
| 465 | 4.74 | 4.74 | 52 | P0ADZ0 | 50S ribosomal protein L23 | rplW | 5 | 0.9817 | 1.0471 | 0.9376 | 1.0666 | 0.9551 |
| 466 | 4.72 | 4.72 | 17.7 | P00864 | Phosphoenolpyruvate carboxylase | ppc | 4 | 0.9638 | 0.5808 | 0.8551 | 0.6026 | 0.8872 |
| 467 | 4.7 | 4.7 | 52.6 | P64503 | Uncharacterized protein YebV | yebV | 5 | 1.0568 | 0.6486 | 0.7447 | 0.6137 | 0.7047 |
| 468 | 4.67 | 4.67 | 20.8 | P08312 | Phenylalanine--tRNA ligase alpha subunit | pheS | 4 | 0.8318 | 0.7586 | 0.5546 | 0.9120 | 0.6667 |
| 469 | 4.66 | 4.68 | 31.3 | P63224 | Phosphoheptose isomerase | gmhA | 5 | 1 | 1.1066 | 1.0375 | 1.1066 | 1.0375 |
| 470 | 4.59 | 4.59 | 68 | P0A7M2 | 50S ribosomal protein L28 | rpmB | 4 | 0.879 | 1.5849 | 1.0965 | 1.8031 | 1.2474 |
| 471 | 4.57 | 4.57 | 13.1 | P25714 | Membrane protein insertase YidC | yidC | 5 | 1.1066 | 1.1169 | 1.0568 | 1.0093 | 0.9550 |
| 472 | 4.54 | 4.54 | 39.3 | P11875 | Arginine--tRNA ligase | argS | 4 | 0.9204 | 0.929 | 0.955 | 1.0093 | 1.0376 |
| 473 | 4.49 | 4.49 | 21.3 | P0A6G7 | ATP-dependent Clp protease proteolytic subunit | clpP | 5 | 0.863 | 0.8872 | 0.8872 | 1.0280 | 1.0280 |
| 474 | 4.46 | 4.46 | 11.9 | P37637 | Multidrug resistance protein MdtF | mdtF | 3 | 1.3932 | 1.3062 | 1.3062 | 0.9376 | 0.9376 |
| 475 | 4.46 | 4.46 | 26 | P31133 | Putrescine-binding periplasmic protein | potF | 5 | 0.9727 | 0.6607 | 0.7379 | 0.6792 | 0.7586 |
| 476 | 4.46 | 4.46 | 22.6 | P0A759 | Glucosamine-6-phosphate deaminase | nagB | 8 | 1.0666 | 0.9817 | 1.0864 | 0.9204 | 1.0186 |
| 477 | 4.43 | 4.43 | 42.1 | P37636 | Multidrug resistance protein MdtE | mdtE | 6 | 1.4322 | 1.1588 | 1.3804 | 0.8091 | 0.9638 |
| 478 | 4.42 | 4.42 | 24.5 | P40120 | Glucans biosynthesis protein D | mdoD | 4 | 0.8395 | 1.0666 | 0.9817 | 1.2705 | 1.1694 |
| 479 | 4.4 | 4.4 | 26.7 | P27434 | Cytoskeleton protein RodZ | rodZ | 5 | 0.929 | 0.7586 | 0.8472 | 0.8166 | 0.9119 |
| 480 | 4.4 | 4.4 | 39.3 | P0ADT8 | Uncharacterized protein YgiM | ygiM | 4 | 1.1376 | 1.028 | 0.8395 | 0.9037 | 0.7380 |
| 481 | 4.39 | 4.39 | 34.6 | P76537 | Uncharacterized protein YfeY | yfeY | 3 | 1.2706 | 0.9204 | 0.9204 | 0.7244 | 0.7244 |
| 482 | 4.32 | 4.32 | 40.1 | P0ABD5 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | accA | 4 | 0.8017 | 0.8241 | 0.8551 | 1.0279 | 1.0666 |
| 483 | 4.31 | 4.32 | 30 | P00895 | Anthranilate synthase component 1 | trpE | 5 | 1.1376 | 0.871 | 0.871 | 0.7656 | 0.7656 |
| 484 | 4.31 | 4.31 | 30.9 | P07650 | Thymidine phosphorylase | deoA | 6 | 1.1272 | 0.9638 | 1.0186 | 0.8550 | 0.9037 |
| 485 | 4.25 | 4.25 | 31.2 | Q46808 | Uncharacterized protein YqeB | yqeB | 6 | 0.9727 | 1.6596 | 1.3305 | 1.7062 | 1.3678 |
| 486 | 4.25 | 4.25 | 18.6 | P77348 | Periplasmic murein peptide-binding protein | mppA | 6 | 1.1376 | 1.2359 | 1.1169 | 1.0864 | 0.9818 |
| 487 | 4.23 | 4.23 | 19 | P52697 | 6-phosphogluconolactonase | pgl | 3 | 0.912 | 1 | 0.9462 | 1.0965 | 1.0375 |
| 488 | 4.22 | 4.22 | 19 | P60651 | Agmatinase | speB | 4 | 0.912 | 0.8241 | 0.912 | 0.9036 | 1.0000 |
| 489 | 4.21 | 4.21 | 22.3 | P69924 | Ribonucleoside-diphosphate reductase 1 subunit beta | nrdB | 6 | 0.9204 | 0.9462 | 0.955 | 1.0280 | 1.0376 |
| 490 | 4.19 | 4.19 | 32.4 | P0A7A9 | Inorganic pyrophosphatase | ppa | 7 | 0.9817 | 1.0093 | 0.9727 | 1.0281 | 0.9908 |
| 491 | 4.17 | 4.18 | 15.7 | P03841 | Maltose operon periplasmic protein | malM | 2 | 1.1066 | 0.8472 | 1.028 | 0.7656 | 0.9290 |
| 492 | 4.17 | 4.17 | 35.9 | P0A744 | Peptide methionine sulfoxide reductase MsrA | msrA | 5 | 0.879 | 0.7586 | 0.871 | 0.8630 | 0.9909 |
| 493 | 4.16 | 4.16 | 46.9 | P61320 | Outer-membrane lipoprotein LolB | lolB | 3 | 1.1169 | 0.9817 | 1.1588 | 0.8790 | 1.0375 |
| 494 | 4.16 | 4.16 | 14.8 | P10384 | Long-chain fatty acid transport protein | fadL | 4 | 1.5417 | 0.912 | 1.4997 | 0.5916 | 0.9728 |
| 495 | 4.15 | 4.15 | 57.7 | P0AA04 | Phosphocarrier protein HPr | ptsH | 5 | 0.9727 | 0.9727 | 1 | 1.0000 | 1.0281 |
| 496 | 4.1 | 4.1 | 17.6 | P0AG16 | Amidophosphoribosyltransferase | purF | 3 | 1.1695 | 1.2823 | 1.1912 | 1.0965 | 1.0186 |
| 497 | 4.08 | 4.08 | 21.1 | P0ABF6 | Cytidine deaminase | cdd | 3 | 0.9036 | 0.955 | 0.929 | 1.0569 | 1.0281 |
| 498 | 4.07 | 4.07 | 25.1 | Q46857 | 2,5-diketo-D-gluconic acid reductase A | dkgA | 3 | 1.0471 | 0.8472 | 0.9036 | 0.8091 | 0.8630 |
| 499 | 4.07 | 4.07 | 24 | P0ACP1 | Catabolite repressor/activator | cra | 3 | 1.0765 | 0.9817 | 0.9376 | 0.9119 | 0.8710 |
| 500 | 4.06 | 4.07 | 20.2 | P0A6V1 | Glucose-1-phosphate adenylyltransferase | glgC | 7 | 1 | 0.955 | 0.929 | 0.9550 | 0.9290 |
| 501 | 4.06 | 4.06 | 33.9 | P46853 | Uncharacterized oxidoreductase YhhX | yhhX | 4 | 0.7727 | 0.9462 | 0.912 | 1.2245 | 1.1803 |
| 502 | 4.06 | 4.06 | 23.6 | P77775 | Epimerase family protein YfcH | yfcH | 4 | 1.0568 | 0.4831 | 0.6026 | 0.4571 | 0.5702 |
| 503 | 4.05 | 4.05 | 26.8 | P0A8J8 | ATP-dependent RNA helicase RhlB | rhlB | 3 | 0.8472 | 1.0186 | 0.9908 | 1.2023 | 1.1695 |
| 504 | 4.05 | 4.05 | 25.9 | P60716 | Lipoyl synthase | lipA | 3 | 1.1376 | 1.3062 | 1.0666 | 1.1482 | 0.9376 |
| 505 | 4.04 | 4.04 | 27.4 | P0A6P5 | GTPase Der | der | 3 | 1.0093 | 1.0186 | 1.1272 | 1.0092 | 1.1168 |
| 506 | 4.04 | 4.04 | 32 | P77581 | Succinylornithine transaminase | astC | 4 | 0.8472 | 0.929 | 0.9036 | 1.0966 | 1.0666 |
| 507 | 4.03 | 4.03 | 34.1 | P0AEG4 | Thiol:disulfide interchange protein DsbA | dsbA | 3 | 1.0471 | 0.9908 | 0.879 | 0.9462 | 0.8395 |
| 508 | 4.02 | 4.02 | 37.8 | P0A9A9 | Ferric uptake regulation protein | fur | 5 | 0.929 | 0.9376 | 0.9376 | 1.0093 | 1.0093 |
| 509 | 4.02 | 4.02 | 23.2 | P0AE22 | Class B acid phosphatase | aphA | 3 | 1.028 | 0.8872 | 0.7311 | 0.8630 | 0.7112 |
| 510 | 4.02 | 4.02 | 68.1 | Q2M7R5 | Uncharacterized protein YibT | yibT | 4 | 1.0186 | 0.955 | 0.9204 | 0.9376 | 0.9036 |
| 511 | 4.01 | 4.04 | 4.2 | P0ABN5 | Anaerobic C4-dicarboxylate transporter DcuA | dcuA | 3 | 0.912 | 0.9462 | 0.9462 | 1.0375 | 1.0375 |
| 512 | 4.01 | 4.03 | 11.3 | P10121 | Signal recognition particle receptor FtsY | ftsY | 3 | 1.0186 | 1 | 0.8318 | 0.9817 | 0.8166 |
| 513 | 4.01 | 4.02 | 23.6 | P39406 | Ribosomal RNA small subunit methyltransferase C | rsmC | 3 | 1.1169 | 0.9727 | 0.8954 | 0.8709 | 0.8017 |
| 514 | 4.01 | 4.01 | 25.2 | P11557 | Protein DamX | damX | 3 | 0.787 | 0.879 | 1.4588 | 1.1169 | 1.8536 |
| 515 | 4.01 | 4.01 | 17.8 | P0A9T0 | D-3-phosphoglycerate dehydrogenase | serA | 2 | 1.0765 | 1.1912 | 1.0765 | 1.1065 | 1.0000 |
| 516 | 4.01 | 4.01 | 52.3 | P0A8B5 | Nucleoid-associated protein YbaB | ybaB | 3 | 0.912 | 0.8954 | 0.912 | 0.9818 | 1.0000 |
| 517 | 4.01 | 4.01 | 23.5 | P0AB38 | Penicillin-binding protein activator LpoB | lpoB | 5 | 1.0568 | 1.1482 | 1.2134 | 1.0865 | 1.1482 |
| 518 | 4.01 | 4.01 | 60 | P0AAZ7 | UPF0434 protein YcaR | ycaR | 4 | 1.1482 | 1.0568 | 0.912 | 0.9204 | 0.7943 |
| 519 | 4.01 | 4.01 | 37.4 | P0AC62 | Glutaredoxin-3 | grxC | 6 | 1.0093 | 0.9204 | 0.9204 | 0.9119 | 0.9119 |
| 520 | 4 | 4.01 | 44.1 | P0ADY7 | 50S ribosomal protein L16 | rplP | 9 | 0.9817 | 0.9727 | 0.9638 | 0.9908 | 0.9818 |
| 521 | 4 | 4.01 | 19.1 | P0AAI5 | 3-oxoacyl-[acyl-carrier-protein] synthase 2 | fabF | 4 | 0.879 | 0.7379 | 0.6918 | 0.8395 | 0.7870 |
| 522 | 4 | 4 | 24.4 | P0A8A0 | Probable transcriptional regulatory protein YebC | yebC | 3 | 0.631 | 0.929 | 1.2246 | 1.4723 | 1.9407 |
| 523 | 4 | 4 | 21.2 | P0ACA7 | Glutathione S-transferase GstB | gstB | 2 | 1.1376 | 1.0965 | 1.1272 | 0.9639 | 0.9909 |
| 524 | 4 | 4 | 54 | P0AD49 | Ribosome-associated inhibitor A | raiA | 3 | 0.8872 | 1.0093 | 0.8551 | 1.1376 | 0.9638 |
| 525 | 4 | 4 | 48.7 | P69776 | Major outer membrane lipoprotein Lpp | lpp | 10 | 0.4169 | 0.6918 | 1.4859 | 1.6594 | 3.5642 |
| 526 | 4 | 4 | 43.3 | P69411 | Outer membrane lipoprotein RcsF | rcsF | 2 | 1.0471 | 0.6792 | 1.556 | 0.6486 | 1.4860 |
| 527 | 4 | 4 | 23 | P0AGE0 | Single-stranded DNA-binding protein | ssb | 6 | 0.9638 | 1.1066 | 1.1066 | 1.1482 | 1.1482 |
| 528 | 4 | 4 | 14.6 | P0A927 | Nucleoside-specific channel-forming protein tsx | tsx | 3 | 1 | 0.879 | 0.9036 | 0.8790 | 0.9036 |
| 529 | 4 | 4 | 29.3 | P0A784 | Oligoribonuclease | orn | 2 | 0.9817 | 0.8017 | 1.2023 | 0.8166 | 1.2247 |
| 530 | 4 | 4 | 23.3 | P0AC19 | D-erythro-7,8-dihydroneopterin triphosphate epimerase | folX | 2 | 0.879 | 2.5119 | 2.1281 | 2.8577 | 2.4210 |
| 531 | 4 | 4 | 38.9 | P69222 | Translation initiation factor IF-1 | infA | 3 | 0.955 | 0.7047 | 1.2134 | 0.7379 | 1.2706 |
| 532 | 4 | 4 | 14.7 | P0AFL3 | Peptidyl-prolyl cis-trans isomerase A | ppiA | 2 | 0.955 | 1 | 0.9204 | 1.0471 | 0.9638 |
| 533 | 4 | 4 | 12.8 | P0AAA1 | Inner membrane protein YagU | yagU | 2 | 0.787 | 0.7656 | 0.7516 | 0.9728 | 0.9550 |
| 534 | 3.91 | 3.91 | 31.1 | P0A9L3 | FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase | fklB | 4 | 1.1912 | 1.2589 | 1.1376 | 1.0568 | 0.9550 |
| 535 | 3.88 | 3.88 | 12.1 | P0ABK2 | Cytochrome bd-I ubiquinol oxidase subunit 2 | cydB | 6 | 0.6368 | 0.7244 | 1.2134 | 1.1376 | 1.9055 |
| 536 | 3.84 | 3.84 | 32 | P76143 | Uncharacterized aldolase LsrF | lsrF | 5 | 0.9638 | 1.0765 | 0.9204 | 1.1169 | 0.9550 |
| 537 | 3.81 | 4.33 | 31.1 | P63417 | Uncharacterized N-acetyltransferase YhbS | yhbS | 2 | 0.879 | 0.929 | 1.0093 | 1.0569 | 1.1482 |
| 538 | 3.81 | 3.9 | 20.2 | P0AFI2 | DNA topoisomerase 4 subunit A | parC | 3 | 1.5417 | 1.2474 | 1.4859 | 0.8091 | 0.9638 |
| 539 | 3.81 | 3.81 | 17.3 | P31677 | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] | otsA | 3 | 0.9376 | 1 | 1.2246 | 1.0666 | 1.3061 |
| 540 | 3.81 | 3.81 | 26.5 | P0A6Q6 | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | fabZ | 4 | 0.6855 | 0.9376 | 1.2706 | 1.3678 | 1.8535 |
| 541 | 3.79 | 3.79 | 25.5 | P0AAJ3 | Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit | fdnH | 3 | 0.7586 | 0.787 | 0.8166 | 1.0374 | 1.0765 |
| 542 | 3.78 | 4.93 | 21.1 | P0ADA3 | Murein hydrolase activator NlpD | nlpD | 5 | 1.0093 | 1.0186 | 1.1376 | 1.0092 | 1.1271 |
| 543 | 3.77 | 3.77 | 19.5 | P37744 | Glucose-1-phosphate thymidylyltransferase 1 | rfbA | 3 | 1 | 0.9638 | 0.8954 | 0.9638 | 0.8954 |
| 544 | 3.77 | 3.77 | 23.9 | P0AB52 | Protein YchN | ychN | 2 | 1.1695 | 1.0864 | 1.2823 | 0.9289 | 1.0965 |
| 545 | 3.72 | 3.72 | 28.7 | P0A6T9 | Glycine cleavage system H protein | gcvH | 2 | 0.955 | 1.0568 | 1 | 1.1066 | 1.0471 |
| 546 | 3.72 | 3.72 | 19.2 | P0A6N4 | Elongation factor P | efp | 3 | 0.9376 | 0.9638 | 0.879 | 1.0279 | 0.9375 |
| 547 | 3.68 | 3.68 | 5.8 | P15078 | Carbon starvation protein A | cstA | 3 | 1.0765 | 1.0375 | 1.3552 | 0.9638 | 1.2589 |
| 548 | 3.66 | 4.42 | 19.7 | P0A6W9 | Glutamate--cysteine ligase | gshA | 3 | 0.7178 | 0.9036 | 1.0765 | 1.2588 | 1.4997 |
| 549 | 3.64 | 3.64 | 48.6 | P0ADQ7 | Uncharacterized protein YgaM | ygaM | 3 | 0.8872 | 0.7244 | 0.5395 | 0.8165 | 0.6081 |
| 550 | 3.61 | 3.61 | 15.2 | P0AB67 | NAD(P) transhydrogenase subunit beta | pntB | 3 | 1.0375 | 1 | 1.028 | 0.9639 | 0.9908 |
| 551 | 3.59 | 3.59 | 30.7 | P0ACC7 | Bifunctional protein GlmU | glmU | 5 | 1.1169 | 1.0186 | 0.9638 | 0.9120 | 0.8629 |
| 552 | 3.55 | 3.55 | 22.7 | P0AGD7 | Signal recognition particle protein | ffh | 2 | 1.1272 | 0.9908 | 0.8091 | 0.8790 | 0.7178 |
| 553 | 3.55 | 3.55 | 56.4 | P0A7N9 | 50S ribosomal protein L33 | rpmG | 3 | 1 | 0.9727 | 0.9908 | 0.9727 | 0.9908 |
| 554 | 3.51 | 3.51 | 15.8 | P52647 | Probable pyruvate-flavodoxin oxidoreductase | ydbK | 2 | 1.0186 | 0.7311 | 0.4055 | 0.7177 | 0.3981 |
| 555 | 3.51 | 3.51 | 40.9 | P0A734 | Cell division topological specificity factor | minE | 3 | 0.8551 | 0.955 | 0.9204 | 1.1168 | 1.0764 |
| 556 | 3.49 | 3.49 | 21.1 | P0A8K1 | Phosphatidylserine decarboxylase proenzyme | psd | 2 | 0.8472 | 1.2474 | 0.787 | 1.4724 | 0.9289 |
| 557 | 3.49 | 3.49 | 16.1 | P33362 | Putative osmoprotectant uptake system substrate-binding protein OsmF | yehZ | 2 | 1.1272 | 0.8872 | 0.7943 | 0.7871 | 0.7047 |
| 558 | 3.48 | 3.52 | 38.3 | P0AFM6 | Phage shock protein A | pspA | 4 | 1.1482 | 0.6252 | 1.5136 | 0.5445 | 1.3182 |
| 559 | 3.44 | 3.44 | 19.4 | Q46851 | L-glyceraldehyde 3-phosphate reductase | gpr | 2 | 1.0568 | 1.0471 | 1.1376 | 0.9908 | 1.0765 |
| 560 | 3.41 | 3.41 | 22.5 | P37051 | Formyltetrahydrofolate deformylase | purU | 3 | 1.0186 | 1.0965 | 0.9817 | 1.0765 | 0.9638 |
| 561 | 3.4 | 3.4 | 19.4 | P0A9K9 | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD | slyD | 2 | 0.6486 | 0.7798 | 0.7244 | 1.2023 | 1.1169 |
| 562 | 3.39 | 3.39 | 21.2 | P25526 | Succinate-semialdehyde dehydrogenase [NADP(+)] GabD | gabD | 2 | 1.0471 | 1.5417 | 1.5276 | 1.4724 | 1.4589 |
| 563 | 3.36 | 3.36 | 24.5 | P75745 | Uncharacterized protein YbgK | ybgK | 2 | 0.863 | 1.2942 | 0.9376 | 1.4997 | 1.0864 |
| 564 | 3.31 | 3.31 | 45.8 | P0A901 | Outer membrane lipoprotein Blc | blc | 5 | 1.0186 | 0.879 | 0.9036 | 0.8629 | 0.8871 |
| 565 | 3.26 | 3.26 | 38.3 | P76193 | Probable L,D-transpeptidase YnhG | ynhG | 7 | 0.8551 | 0.5546 | 0.5546 | 0.6486 | 0.6486 |
| 566 | 3.24 | 3.24 | 22.1 | P77717 | Uncharacterized lipoprotein YbaY | ybaY | 2 | 0.8954 | 0.6982 | 0.6252 | 0.7798 | 0.6982 |
| 567 | 3.22 | 5.74 | 44.9 | P0ADZ4 | 30S ribosomal protein S15 | rpsO | 3 | 0.9908 | 1.028 | 1.028 | 1.0375 | 1.0375 |
| 568 | 3.19 | 3.19 | 31.9 | P39384 | Uncharacterized protein YjiM | yjiM | 4 | 1.4723 | 2.9107 | 1.7061 | 1.9770 | 1.1588 |
| 569 | 3.17 | 3.18 | 32.2 | P0A9M5 | Xanthine phosphoribosyltransferase | gpt | 3 | 1.1169 | 1.0864 | 1.1376 | 0.9727 | 1.0185 |
| 570 | 3.17 | 3.17 | 16.6 | P25889 | NAD-dependent dihydropyrimidine dehydrogenase subunit PreA | preA | 2 | 0.5598 | 1.0864 | 0.673 | 1.9407 | 1.2022 |
| 571 | 3.14 | 3.14 | 16.7 | P77735 | Uncharacterized oxidoreductase YajO | yajO | 2 | 0.8954 | 1.0864 | 1.028 | 1.2133 | 1.1481 |
| 572 | 3.14 | 3.14 | 34.6 | P76002 | Inhibitor of g-type lysozyme | pliG | 2 | 0.9204 | 0.8395 | 0.955 | 0.9121 | 1.0376 |
| 573 | 3.12 | 3.12 | 25.8 | P0A729 | Maf-like protein YceF | yceF | 3 | 1.0864 | 0.955 | 1.1066 | 0.8791 | 1.0186 |
| 574 | 3.11 | 3.11 | 40.2 | P0A7U3 | 30S ribosomal protein S19 | rpsS | 5 | 0.9462 | 0.9817 | 0.9462 | 1.0375 | 1.0000 |
| 575 | 3.09 | 3.09 | 25.6 | P0AB80 | Branched-chain-amino-acid aminotransferase | ilvE | 2 | 1.0375 | 1.0471 | 1.1912 | 1.0093 | 1.1481 |
| 576 | 3.06 | 3.06 | 15.4 | P76594 | Uncharacterized protein YfiQ | pka | 4 | 1.0765 | 1.4454 | 1.406 | 1.3427 | 1.3061 |
| 577 | 3.06 | 3.06 | 13.9 | P13024 | Protein FdhE | fdhE | 2 | 0.8091 | 0.8872 | 0.871 | 1.0965 | 1.0765 |
| 578 | 3.03 | 3.03 | 27.9 | P0AFC3 | NADH-quinone oxidoreductase subunit A | nuoA | 3 | 1.1376 | 1.0093 | 1.0375 | 0.8872 | 0.9120 |
| 579 | 3.02 | 3.02 | 20.2 | P0A9J8 | P-protein | pheA | 2 | 0.9204 | 1.0093 | 1.0666 | 1.0966 | 1.1588 |
| 580 | 3.02 | 3.02 | 17.5 | P75874 | Uncharacterized protein YccU | yccU | 3 | 1.1376 | 0.879 | 0.8472 | 0.7727 | 0.7447 |
| 581 | 3.01 | 3.01 | 16.8 | P0AG27 | Uncharacterized protein YibN | yibN | 3 | 1.3804 | 1.7701 | 1.3677 | 1.2823 | 0.9908 |
| 582 | 3 | 3 | 23.5 | P0AAJ8 | Hydrogenase-2 operon protein HybA | hybA | 3 | 1.0093 | 0.955 | 0.929 | 0.9462 | 0.9204 |
| 583 | 2.97 | 2.97 | 30 | P66948 | TPR repeat-containing protein YfgC | bepA | 4 | 0.6026 | 0.7656 | 0.597 | 1.2705 | 0.9907 |
| 584 | 2.96 | 2.96 | 28.8 | P30177 | Uncharacterized protein YbiB | ybiB | 4 | 1.2134 | 1.0471 | 1.1066 | 0.8629 | 0.9120 |
| 585 | 2.95 | 2.96 | 43 | P62620 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | ispG | 4 | 1.6444 | 0.6792 | 0.5649 | 0.4130 | 0.3435 |
| 586 | 2.94 | 2.94 | 49.5 | P0AEH5 | Protein ElaB | elaB | 5 | 1.0568 | 0.8241 | 0.8318 | 0.7798 | 0.7871 |
| 587 | 2.9 | 2.9 | 37.4 | P0A9N4 | Pyruvate formate-lyase 1-activating enzyme | pflA | 3 | 1.0471 | 0.9204 | 0.9376 | 0.8790 | 0.8954 |
| 588 | 2.89 | 2.89 | 27.2 | P0AE88 | Transcriptional regulatory protein CpxR | cpxR | 2 | 1.1066 | 0.9462 | 1.1066 | 0.8551 | 1.0000 |
| 589 | 2.84 | 2.84 | 32.3 | P23721 | Phosphoserine aminotransferase | serC | 3 | 0.9908 | 1.4997 | 1.4859 | 1.5136 | 1.4997 |
| 590 | 2.83 | 2.85 | 26.1 | P21507 | ATP-dependent RNA helicase SrmB | srmB | 4 | 0.929 | 1 | 1.0186 | 1.0764 | 1.0964 |
| 591 | 2.77 | 2.77 | 70.6 | P0A7L8 | 50S ribosomal protein L27 | rpmA | 3 | 0.8091 | 0.9036 | 0.5702 | 1.1168 | 0.7047 |
| 592 | 2.76 | 2.76 | 24.7 | P76316 | D-cysteine desulfhydrase | dcyD | 3 | 1.0864 | 0.863 | 0.9204 | 0.7944 | 0.8472 |
| 593 | 2.76 | 2.76 | 19.1 | P08178 | Phosphoribosylformylglycinamidine cyclo-ligase | purM | 4 | 1.2474 | 1.0186 | 1.0093 | 0.8166 | 0.8091 |
| 594 | 2.73 | 2.73 | 19.7 | P37645 | Uncharacterized protein YhjG | yhjG | 3 | 0.9817 | 0.8091 | 0.7447 | 0.8242 | 0.7586 |
| 595 | 2.73 | 2.73 | 29.6 | P16700 | Thiosulfate-binding protein | cysP | 3 | 0.8472 | 0.7178 | 0.7244 | 0.8473 | 0.8551 |
| 596 | 2.69 | 2.69 | 31.2 | P0AF18 | N-acetylglucosamine-6-phosphate deacetylase | nagA | 5 | 1.1376 | 1.1272 | 1.1272 | 0.9909 | 0.9909 |
| 597 | 2.69 | 2.69 | 32.8 | P0ACQ4 | Hydrogen peroxide-inducible genes activator | oxyR | 3 | 0.912 | 1.1066 | 1.1169 | 1.2134 | 1.2247 |
| 598 | 2.66 | 2.66 | 28.4 | P0ABU0 | 1,4-Dihydroxy-2-naphthoyl-CoA synthase | menB | 3 | 1.8535 | 3.1333 | 1.977 | 1.6905 | 1.0666 |
| 599 | 2.64 | 2.64 | 35.6 | P23882 | Methionyl-tRNA formyltransferase | fmt | 2 | 0.8017 | 1.3804 | 1.1803 | 1.7218 | 1.4722 |
| 600 | 2.6 | 2.6 | 18 | P04425 | Glutathione synthetase | gshB | 3 | 1.0093 | 1.2706 | 1.1376 | 1.2589 | 1.1271 |
| 601 | 2.6 | 2.6 | 23.4 | P0AFX4 | Regulator of sigma D | rsd | 2 | 1 | 1.0965 | 1.1803 | 1.0965 | 1.1803 |
| 602 | 2.57 | 2.57 | 30.7 | P06999 | 6-phosphofructokinase isozyme 2 | pfkB | 4 | 1.1066 | 1.0568 | 0.8872 | 0.9550 | 0.8017 |
| 603 | 2.54 | 2.54 | 30.8 | P25539 | Riboflavin biosynthesis protein RibD | ribD | 3 | 0.4875 | 0.52 | 0.4875 | 1.0667 | 1.0000 |
| 604 | 2.51 | 2.51 | 36.2 | P0AFU8 | Riboflavin synthase | ribC | 4 | 0.9638 | 1.3305 | 0.9638 | 1.3805 | 1.0000 |
| 605 | 2.49 | 3.27 | 17 | P33363 | Periplasmic beta-glucosidase | bglX | 3 | 1 | 0.9908 | 1.1066 | 0.9908 | 1.1066 |
| 606 | 2.49 | 2.49 | 29.3 | P76034 | Uncharacterized HTH-type transcriptional regulator YciT | yciT | 2 | 1.1169 | 1.0765 | 1.0666 | 0.9638 | 0.9550 |
| 607 | 2.48 | 2.49 | 7.8 | P02916 | Maltose transport system permease protein MalF | malF | 2 | 1.1588 | 0.8872 | 1.2023 | 0.7656 | 1.0375 |
| 608 | 2.48 | 2.49 | 19.8 | P0A7J0 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | ribB | 6 | 1.2823 | 1.1169 | 0.879 | 0.8710 | 0.6855 |
| 609 | 2.47 | 2.49 | 26.3 | P10346 | Glutamine transport ATP-binding protein GlnQ | glnQ | 6 | 0.9908 | 1 | 1.0568 | 1.0093 | 1.0666 |
| 610 | 2.44 | 2.44 | 27.5 | P23839 | UPF0701 protein YicC | yicC | 3 | 1.1912 | 1.0965 | 1.1272 | 0.9205 | 0.9463 |
| 611 | 2.41 | 2.41 | 18.6 | P42599 | Uncharacterized oxidoreductase YgjR | ygjR | 2 | 1.7701 | 0.52 | 1.0765 | 0.2938 | 0.6082 |
| 612 | 2.4 | 2.4 | 36.8 | P0AEE1 | Protein DcrB | dcrB | 5 | 0.8472 | 0.8395 | 1 | 0.9909 | 1.1804 |
| 613 | 2.36 | 2.36 | 12.1 | P37652 | Cyclic di-GMP-binding protein | bcsB | 2 | 1.1482 | 1.0765 | 1.0186 | 0.9376 | 0.8871 |
| 614 | 2.34 | 2.34 | 21.9 | Q46807 | Carbamate kinase-like protein YqeA | yqeA | 2 | 1.028 | 1.3305 | 1.3305 | 1.2943 | 1.2943 |
| 615 | 2.34 | 2.34 | 27 | P0A7B5 | Glutamate 5-kinase | proB | 3 | 1.0375 | 1.0186 | 0.9376 | 0.9818 | 0.9037 |
| 616 | 2.33 | 2.36 | 21 | P45395 | Arabinose 5-phosphate isomerase KdsD | kdsD | 4 | 1.0965 | 0.6668 | 0.9036 | 0.6081 | 0.8241 |
| 617 | 2.32 | 4.28 | 36.6 | P0ADS6 | Uncharacterized protein YggE | yggE | 6 | 1.0093 | 0.8872 | 0.8872 | 0.8790 | 0.8790 |
| 618 | 2.32 | 2.32 | 23.1 | P0A794 | Pyridoxine 5'-phosphate synthase | pdxJ | 1 | 0.7586 | 0.8954 | 0.8472 | 1.1803 | 1.1168 |
| 619 | 2.31 | 2.33 | 49.2 | P69913 | Carbon storage regulator | csrA | 3 | 0.9817 | 1.0093 | 0.9462 | 1.0281 | 0.9638 |
| 620 | 2.3 | 2.3 | 25.1 | P0A8G3 | Uronate isomerase | uxaC | 3 | 0.912 | 1.0093 | 1 | 1.1067 | 1.0965 |
| 621 | 2.28 | 2.44 | 19.9 | P45464 | Penicillin-binding protein activator LpoA | lpoA | 1 | 0.4742 | 0.7656 | 0.7727 | 1.6145 | 1.6295 |
| 622 | 2.28 | 2.28 | 12.8 | P08390 | USG-1 protein | usg | 3 | 1.1912 | 1.2134 | 0.9204 | 1.0186 | 0.7727 |
| 623 | 2.27 | 2.27 | 32.4 | P0AGG4 | Thioredoxin-2 | trxC | 2 | 1.1588 | 0.4529 | 1.2706 | 0.3908 | 1.0965 |
| 624 | 2.26 | 2.28 | 17.7 | P60785 | Elongation factor 4 | lepA | 3 | 1.1376 | 0.9204 | 0.9376 | 0.8091 | 0.8242 |
| 625 | 2.26 | 2.26 | 39.1 | P0A7P5 | 50S ribosomal protein L34 | rpmH | 2 | 0.9462 | 0.9638 | 0.912 | 1.0186 | 0.9639 |
| 626 | 2.25 | 2.25 | 15.1 | P76187 | Oxidoreductase YdhF | ydhF | 3 | 0.871 | 0.863 | 0.8166 | 0.9908 | 0.9375 |
| 627 | 2.23 | 2.23 | 22.3 | P0ADR8 | LOG family protein YgdH | ygdH | 3 | 0.8241 | 0.8551 | 1 | 1.0376 | 1.2134 |
| 628 | 2.23 | 2.23 | 17.5 | P77552 | Uncharacterized protein YdhQ | ydhQ | 1 | 0.9376 | 0.912 | 0.912 | 0.9727 | 0.9727 |
| 629 | 2.22 | 2.23 | 19.5 | P0ABQ4 | Dihydrofolate reductase | folA | 3 | 1.0471 | 1.2474 | 1.0093 | 1.1913 | 0.9639 |
| 630 | 2.19 | 2.36 | 15.3 | P0AE12 | AMP nucleosidase | amn | 1 | 0.929 | 1.1803 | 1.1912 | 1.2705 | 1.2822 |
| 631 | 2.18 | 2.18 | 33.7 | P33221 | Phosphoribosylglycinamide formyltransferase 2 | purT | 2 | 1.028 | 1.1912 | 1.1272 | 1.1588 | 1.0965 |
| 632 | 2.18 | 2.18 | 24.9 | P37387 | D-xylose-binding periplasmic protein | xylF | 2 | 0.8954 | 0.8395 | 0.929 | 0.9376 | 1.0375 |
| 633 | 2.18 | 2.18 | 22.4 | P27250 | Aldehyde reductase Ahr | ahr | 2 | 0.9817 | 1.0093 | 0.955 | 1.0281 | 0.9728 |
| 634 | 2.17 | 2.18 | 40.8 | P16681 | Protein PhnB | phnB | 2 | 1.0568 | 0.6855 | 1.0765 | 0.6487 | 1.0186 |
| 635 | 2.17 | 2.17 | 32.8 | P0AAG3 | Glutamate/aspartate transport ATP-binding protein GltL | gltL | 1 | 0.9727 | 0.9204 | 0.9908 | 0.9462 | 1.0186 |
| 636 | 2.15 | 2.15 | 36 | P20605 | Probable adenosine monophosphate-protein transferase fic | fic | 3 | 1.1169 | 1.0093 | 1.028 | 0.9037 | 0.9204 |
| 637 | 2.14 | 2.14 | 22.6 | P76658 | Bifunctional protein HldE | hldE | 4 | 0.955 | 1.2023 | 1.2023 | 1.2590 | 1.2590 |
| 638 | 2.12 | 2.12 | 28.8 | P0AEG6 | Thiol:disulfide interchange protein DsbC | dsbC | 2 | 1.0765 | 1.0186 | 1.0965 | 0.9462 | 1.0186 |
| 639 | 2.11 | 2.11 | 53.9 | P0A8P3 | Probable Fe(2+)-trafficking protein | yggX | 3 | 1.1695 | 0.9908 | 0.9817 | 0.8472 | 0.8394 |
| 640 | 2.1 | 2.1 | 22.3 | P0A9S1 | Lactaldehyde reductase | fucO | 4 | 0.7047 | 1.3183 | 1.3183 | 1.8707 | 1.8707 |
| 641 | 2.1 | 2.1 | 22.9 | P0A9S5 | Glycerol dehydrogenase | gldA | 2 | 1.0471 | 1.1066 | 0.9817 | 1.0568 | 0.9375 |
| 642 | 2.08 | 2.08 | 23.4 | P0A8C1 | UPF0145 protein YbjQ | ybjQ | 2 | 1.1912 | 0.4786 | 1.0471 | 0.4018 | 0.8790 |
| 643 | 2.07 | 2.07 | 20 | P06715 | Glutathione reductase | gor | 2 | 1.0666 | 1.1169 | 0.597 | 1.0472 | 0.5597 |
| 644 | 2.06 | 2.07 | 26.8 | P06983 | Porphobilinogen deaminase | hemC | 2 | 0.8091 | 0.9908 | 0.8954 | 1.2246 | 1.1067 |
| 645 | 2.06 | 2.07 | 20 | P0A6N8 | Elongation factor P-like protein | yeiP | 1 | 0.863 | 1.2942 | 0.9908 | 1.4997 | 1.1481 |
| 646 | 2.05 | 2.06 | 15.5 | P77748 | Uncharacterized protein YdiJ | ydiJ | 1 | 0.9817 | 1.2134 | 1.0666 | 1.2360 | 1.0865 |
| 647 | 2.05 | 2.05 | 25.1 | Q46829 | 6-phospho-beta-glucosidase BglA | bglA | 1 | 1.0864 | 1.1588 | 1.1272 | 1.0666 | 1.0376 |
| 648 | 2.05 | 2.05 | 15.9 | P0A817 | S-adenosylmethionine synthase | metK | 2 | 1.4997 | 1.5136 | 1.6144 | 1.0093 | 1.0765 |
| 649 | 2.05 | 2.05 | 28.5 | P0A8W2 | Transcriptional regulator SlyA | slyA | 3 | 1.1169 | 1.0864 | 1 | 0.9727 | 0.8953 |
| 650 | 2.04 | 2.04 | 35.9 | P0ACD4 | NifU-like protein | iscU | 1 | 0.6486 | 0.912 | 1.0965 | 1.4061 | 1.6906 |
| 651 | 2.03 | 2.03 | 27 | P0ADE8 | tRNA-modifying protein YgfZ | ygfZ | 3 | 0.9817 | 1.1588 | 1.0375 | 1.1804 | 1.0568 |
| 652 | 2.03 | 2.03 | 37 | P0AFY8 | Negative modulator of initiation of replication | seqA | 1 | 1.0666 | 1 | 1.0568 | 0.9376 | 0.9908 |
| 653 | 2.03 | 2.03 | 25.2 | P0A8Q0 | Fumarate reductase subunit C | frdC | 1 | 0.955 | 0.863 | 0.955 | 0.9037 | 1.0000 |
| 654 | 2.03 | 2.03 | 12.1 | P17443 | UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | murG | 2 | 0.7943 | 0.8954 | 0.912 | 1.1273 | 1.1482 |
| 655 | 2.02 | 4.04 | 17.5 | P17952 | UDP-N-acetylmuramate--L-alanine ligase | murC | 3 | 1.0864 | 0.8472 | 0.8872 | 0.7798 | 0.8166 |
| 656 | 2.02 | 2.02 | 38.8 | P0AAT9 | Uncharacterized protein YbeL | ybeL | 2 | 1.1066 | 1.0765 | 1.2589 | 0.9728 | 1.1376 |
| 657 | 2.02 | 2.02 | 15.2 | P0ACI0 | Right origin-binding protein | rob | 1 | 1.0666 | 0.7112 | 1.1482 | 0.6668 | 1.0765 |
| 658 | 2.01 | 2.66 | 15.1 | P00946 | Mannose-6-phosphate isomerase | manA | 3 | 1.3552 | 1 | 2.2284 | 0.7379 | 1.6443 |
| 659 | 2.01 | 2.07 | 21.2 | P17115 | Arabinose 5-phosphate isomerase GutQ | gutQ | 1 | 1.1376 | 1.0186 | 1.1169 | 0.8954 | 0.9818 |
| 660 | 2.01 | 2.06 | 20.7 | P75915 | Chaperone protein YcdY | ycdY | 2 | 0.9036 | 0.912 | 0.863 | 1.0093 | 0.9551 |
| 661 | 2.01 | 2.02 | 12.1 | P0AAA9 | Zinc resistance-associated protein | zraP | 2 | 1.9055 | 1.2134 | 3.9084 | 0.6368 | 2.0511 |
| 662 | 2.01 | 2.01 | 19.4 | P35340 | Alkyl hydroperoxide reductase subunit F | ahpF | 1 | 1.2246 | 1.1376 | 1.1272 | 0.9290 | 0.9205 |
| 663 | 2.01 | 2.01 | 27.8 | P75914 | Probable phosphatase YcdX | ycdX | 1 | 0.1754 | 1.9231 | 1.1169 | 10.9641 | 6.3677 |
| 664 | 2.01 | 2.01 | 19.5 | P0AF03 | Molybdopterin adenylyltransferase | mog | 3 | 0.7727 | 1.0093 | 0.8166 | 1.3062 | 1.0568 |
| 665 | 2.01 | 2.01 | 10.8 | P77213 | Carboxylate-amine ligase YbdK | ybdK | 2 | 0.8395 | 1.2823 | 1.1912 | 1.5275 | 1.4189 |
| 666 | 2.01 | 2.01 | 10.2 | P37666 | Glyoxylate/hydroxypyruvate reductase B | ghrB | 2 | 1.0666 | 1.3552 | 1.2589 | 1.2706 | 1.1803 |
| 667 | 2.01 | 2.01 | 9.6 | P36767 | Recombination-associated protein RdgC | rdgC | 1 | 0.7656 | 0.8091 | 0.8017 | 1.0568 | 1.0472 |
| 668 | 2.01 | 2.01 | 13.5 | P61714 | 6,7-dimethyl-8-ribityllumazine synthase | ribE | 4 | 1.1066 | 1.0765 | 0.9462 | 0.9728 | 0.8551 |
| 669 | 2.01 | 2.01 | 30.4 | P36560 | Acid shock protein | asr | 4 | 0.3342 | 0.0964 | 2.4889 | 0.2885 | 7.4473 |
| 670 | 2.01 | 2.01 | 13.3 | P0AFZ3 | Stringent starvation protein B | sspB | 2 | 1.0666 | 1.1588 | 0.8091 | 1.0864 | 0.7586 |
| 671 | 2.01 | 2.01 | 8 | P31057 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | panB | 2 | 1.1803 | 1.0568 | 1.2589 | 0.8954 | 1.0666 |
| 672 | 2 | 27.91 | 58.4 | P69910 | Glutamate decarboxylase beta | gadB | 50 | 0.9036 | 0.7586 | 0.6855 | 0.8395 | 0.7586 |
| 673 | 2 | 4.02 | 13.2 | P30744 | L-serine dehydratase 2 | sdaB | 2 | 1.5849 | 1.1695 | 1.3677 | 0.7379 | 0.8630 |
| 674 | 2 | 2.26 | 14.6 | P07639 | 3-dehydroquinate synthase | aroB | 1 | 1.0864 | 1.1376 | 0.9204 | 1.0471 | 0.8472 |
| 675 | 2 | 2.08 | 13.2 | P00547 | Homoserine kinase | thrB | 1 | 0.8472 | 1.3552 | 0.8551 | 1.5996 | 1.0093 |
| 676 | 2 | 2.04 | 7.3 | P0AEP7 | Glyoxylate carboligase | gcl | 1 | 1 | 1.5276 | 1.2706 | 1.5276 | 1.2706 |
| 677 | 2 | 2.01 | 41.7 | P0ADK8 | Uncharacterized protein YibL | yibL | 1 | 0.9036 | 0.8872 | 0.9817 | 0.9819 | 1.0864 |
| 678 | 2 | 2 | 19.3 | P23909 | DNA mismatch repair protein MutS | mutS | 1 | 1.0375 | 0.7447 | 1.556 | 0.7178 | 1.4998 |
| 679 | 2 | 2 | 14.3 | P0A6Z1 | Chaperone protein HscA | hscA | 1 | 0.9376 | 1.028 | 1.556 | 1.0964 | 1.6596 |
| 680 | 2 | 2 | 21.5 | P75957 | Lipoprotein-releasing system ATP-binding protein LolD | lolD | 1 | 0.4169 | 0.6607 | 0.6792 | 1.5848 | 1.6292 |
| 681 | 2 | 2 | 18.4 | P06720 | Alpha-galactosidase | melA | 1 | 1.0965 | 1.2589 | 0.929 | 1.1481 | 0.8472 |
| 682 | 2 | 2 | 25.1 | P0AB24 | Iron uptake system component EfeO | efeO | 1 | 0.6081 | 0.9727 | 0.955 | 1.5996 | 1.5705 |
| 683 | 2 | 2 | 12.1 | P0ABH0 | Cell division protein FtsA | ftsA | 1 | 1.1912 | 0.9638 | 1.1272 | 0.8091 | 0.9463 |
| 684 | 2 | 2 | 33.1 | P0A7G2 | Ribosome-binding factor A | rbfA | 2 | 1.0093 | 0.8166 | 0.7311 | 0.8091 | 0.7244 |
| 685 | 2 | 2 | 26.8 | P64604 | Probable phospholipid ABC transporter-binding protein MlaD | mlaD | 2 | 1.556 | 0.9204 | 1.2474 | 0.5915 | 0.8017 |
| 686 | 2 | 2 | 11.2 | P0A6S7 | Glycerol-3-phosphate dehydrogenase [NAD(P)+] | gpsA | 1 | 1.0186 | 0.9204 | 1.2359 | 0.9036 | 1.2133 |
| 687 | 2 | 2 | 22.8 | P65367 | Uncharacterized protein YqcA | yqcA | 1 | 0.9727 | 0.9204 | 0.863 | 0.9462 | 0.8872 |
| 688 | 2 | 2 | 16.9 | P63177 | 23S rRNA (guanosine-2'-O-)-methyltransferase RlmB | rlmB | 1 | 1.3428 | 1.0666 | 1.1169 | 0.7943 | 0.8318 |
| 689 | 2 | 2 | 14.2 | P39310 | Uncharacterized protein YtfB | ytfB | 1 | 0.9036 | 0.6026 | 0.9204 | 0.6669 | 1.0186 |
| 690 | 2 | 2 | 18.2 | P32162 | UPF0381 protein YiiS | yiiS | 1 | 1.2706 | 1.0765 | 1.028 | 0.8472 | 0.8091 |
| 691 | 2 | 2 | 16.3 | P17117 | Oxygen-insensitive NADPH nitroreductase | nfsA | 1 | 0.8954 | 0.912 | 0.929 | 1.0185 | 1.0375 |
| 692 | 2 | 2 | 22.4 | P0AF12 | 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase | mtnN | 2 | 0.8551 | 0.9376 | 0.8318 | 1.0965 | 0.9728 |
| 693 | 2 | 2 | 14.7 | P0A8T1 | Ribosomal protein L11 methyltransferase | prmA | 2 | 1.7701 | 1.0568 | 1.3932 | 0.5970 | 0.7871 |
| 694 | 2 | 2 | 20 | P0A832 | SsrA-binding protein | smpB | 1 | 1.2359 | 1.3305 | 1.1272 | 1.0765 | 0.9120 |
| 695 | 2 | 2 | 13.7 | P45955 | Uncharacterized protein YbgF | cpoB | 1 | 0.5395 | 0.7379 | 0.597 | 1.3677 | 1.1066 |
| 696 | 2 | 2 | 22.4 | P22186 | Protein MraZ | mraZ | 2 | 0.5495 | 0.7244 | 0.7727 | 1.3183 | 1.4062 |
| 697 | 2 | 2 | 10.8 | P0AFH2 | Oligopeptide transport system permease protein OppB | oppB | 1 | 0.9817 | 1.0568 | 1.1376 | 1.0765 | 1.1588 |
| 698 | 2 | 2 | 38.3 | P0AD33 | UPF0381 protein YfcZ | yfcZ | 2 | 1.0666 | 1.0864 | 1.0568 | 1.0186 | 0.9908 |
| 699 | 2 | 2 | 14.5 | P0A908 | MltA-interacting protein | mipA | 2 | 0.9462 | 1.3062 | 1.556 | 1.3805 | 1.6445 |
| 700 | 2 | 2 | 12.5 | P0A7B8 | ATP-dependent protease subunit HslV | hslV | 3 | 0.9376 | 1.1588 | 1.0666 | 1.2359 | 1.1376 |
| 701 | 2 | 2 | 9.4 | P00963 | Aspartate--ammonia ligase | asnA | 1 | 1.0864 | 1.6144 | 1.6144 | 1.4860 | 1.4860 |
| 702 | 2 | 2 | 17.6 | P38521 | Uncharacterized protein YggL | yggL | 1 | 1.3183 | 1.3677 | 1.5417 | 1.0375 | 1.1695 |
| 703 | 2 | 2 | 19.4 | P0AB55 | Protein YciI | yciI | 1 | 1.0765 | 1.2134 | 1.0864 | 1.1272 | 1.0092 |
| 704 | 2 | 2 | 6.2 | P0A9F3 | HTH-type transcriptional regulator CysB | cysB | 1 | 0.8318 | 0.9462 | 0.8241 | 1.1375 | 0.9907 |
| 705 | 2 | 2 | 27.7 | P0A7Q1 | 50S ribosomal protein L35 | rpmI | 2 | 0.9727 | 0.9727 | 0.9204 | 1.0000 | 0.9462 |
| 706 | 2 | 2 | 13.5 | P0A790 | Aspartate 1-decarboxylase | panD | 2 | 0.8395 | 0.9462 | 0.8241 | 1.1271 | 0.9817 |
| 707 | 2 | 2 | 11.4 | P68699 | ATP synthase subunit c | atpE | 2 | 0.7379 | 0.7798 | 1.1169 | 1.0568 | 1.5136 |
| 708 | 2 | 2 | 8.5 | P0AF50 | Uncharacterized protein YjbR | yjbR | 2 | 0.8954 | 0.955 | 0.9462 | 1.0666 | 1.0567 |
| 709 | 2 | 2 | 39.6 | P0ADB7 | Entericidin B | ecnB | 6 | 0.787 | 0.2606 | 0.182 | 0.3311 | 0.2313 |
| 710 | 2 | 2 | 17.7 | P0A937 | Outer membrane protein assembly factor BamE | bamE | 3 | 0.6194 | 0.5649 | 0.6546 | 0.9120 | 1.0568 |
| 711 | 2 | 2 | 13.6 | P09996 | Uncharacterized protein YidB | yidB | 1 | 1.1695 | 0.6138 | 0.7586 | 0.5248 | 0.6487 |
| 712 | 77.87 | 77.87 | 50.8 | P0A8V2 | DNA-directed RNA polymerase subunit beta | rpoB | 68 | 115:114 | 116:114 | 117:114 | 116:115 | 117:115 |
| 713 | 76.74 | 76.74 | 49 | P0A8T7 | DNA-directed RNA polymerase subunit beta' | rpoC | 67 | 1.028 | 0.9908 | 1 | 0.9638 | 0.9728 |
| 714 | 70.8 | 70.8 | 55.5 | P0AFG8 | Pyruvate dehydrogenase E1 component | aceE | 62 | 0.863 | 0.6607 | 0.5808 | 0.7656 | 0.6730 |
| 715 | 61.88 | 61.88 | 59.3 | P09373 | Formate acetyltransferase 1 | pflB | 61 | 1.0186 | 0.8954 | 0.929 | 0.8790 | 0.9120 |
| 716 | 54.3 | 54.3 | 51.2 | P63284 | Chaperone protein ClpB | clpB | 48 | 1.1482 | 1.2474 | 1.0375 | 1.0864 | 0.9036 |
| 717 | 53.44 | 53.44 | 76.7 | P02925 | D-ribose-binding periplasmic protein | rbsB | 177 | 1.028 | 1 | 1.0375 | 0.9728 | 1.0092 |
| 718 | 52.05 | 52.05 | 85.8 | P0CE48 | Elongation factor Tu 2 | tufB | 87 | 0.879 | 0.5495 | 0.1107 | 0.6251 | 0.1259 |
| 719 | 51.9 | 51.9 | 56.1 | P0A6M8 | Elongation factor G | fusA | 75 | 1.1588 | 0.879 | 1.1376 | 0.7585 | 0.9817 |
| 720 | 50.78 | 50.78 | 56 | P0A6Y8 | Chaperone protein DnaK | dnaK | 64 | 1 | 1.1376 | 1.0864 | 1.1376 | 1.0864 |
| 721 | 48.91 | 48.91 | 67.2 | P0A6F5 | 60 kDa chaperonin | groL | 91 | 0.9376 | 0.8166 | 0.6668 | 0.8709 | 0.7112 |
| 722 | 48.33 | 48.33 | 54.1 | P0A9Q7 | Aldehyde-alcohol dehydrogenase | adhE | 55 | 0.9204 | 0.9204 | 0.9376 | 1.0000 | 1.0187 |

**\*114, 115, 116, 117 stand for the proteins extracted from *Escherichia coli* after exposure to medium solution, medium solution with 1 mg L-1 TBA, medium solution with TBA intermediates produced in UV/H2O2 treatment and medium solution with TBA intermediates produced in UV/ TiO2 treatment, respectively.**