

| Query | Comparison | Coefficient | p-Value | Taxonomic Annotation | COG Category | Description | Gene Name | EC |
|----------------|------------|-------------|---------|-----------------------|--------------|---|-----------|-------------------|
| k123_3351426_1 | 0-12 | 11.410 | < 0.001 | Clostridia | S | Flavin reductase like domain | - | - |
| k123_3689959_6 | 0-12 | 12.863 | < 0.001 | Bacilli | GM | NmrA-like family | - | - |
| k123_1682409_1 | 0-12 | 12.514 | < 0.001 | Bacilli | C | Oxidoreductase required for the transfer of electrons from pyruvate to flavodoxin | nifJ | 1.2.7.1 |
| k123_4131385_2 | 0-12 | 11.768 | < 0.001 | Bacilli | M | Domain of unknown function (DUF5011) | - | - |
| k123_3474748_6 | 0-12 | 11.248 | < 0.001 | Bacilli | E | ABC transporter substrate-binding protein | oppA | - |
| k123_2018420_1 | 0-12 | 11.126 | < 0.001 | Bacilli | G | PTS fructose transporter subunit IIC | fruA | 2.7.1.202 |
| k123_4134106_1 | 0-12 | 10.776 | < 0.001 | Bacilli | C | e3 binding domain | pdhC | 2.3.1.12 |
| k123_2451258_1 | 0-12 | 12.572 | < 0.001 | Clostridia | M | S-layer homology domain | - | - |
| k123_3683359_3 | 0-12 | 12.858 | < 0.001 | Bacilli | P | P-type ATPase | copA | 3.6.3.54 |
| k123_2018420_3 | 0-12 | 9.998 | < 0.001 | Bacilli | GKT | Transcriptional antiterminator | manR | - |
| k123_4030449_2 | 0-12 | -7.201 | < 0.001 | Gammaaproteobacteria | C | PFAM blue (type 1) copper domain protein | - | - |
| k123_1903136_2 | 0-12 | -6.769 | < 0.001 | Actinobacteria | Q | Taurine catabolism dioxygenase TauD, TfdA family | - | 1.14.11.17 |
| k123_4017556_1 | 0-12 | -6.740 | < 0.001 | Betaproteobacteria | Q | Taurine dioxygenase | - | 1.14.11.17 |
| k123_2470867_1 | 0-12 | -6.354 | < 0.001 | Actinobacteria | Q | taurine catabolism dioxygenase | tauD | 1.14.11.17 |
| k123_2231885_1 | 0-12 | -5.426 | < 0.001 | Actinobacteria | E | ABC-type branched-chain amino acid transport | - | - |
| k123_1903136_1 | 0-12 | -5.513 | < 0.001 | Actinobacteria | K | Bacterial regulatory proteins, tetR family | - | - |
| k123_3697194_1 | 0-12 | -5.446 | < 0.001 | Actinobacteria | Q | Taurine catabolism dioxygenase TauD, TfdA family | tauD | 1.14.11.17 |
| k123_4238273_1 | 0-12 | -6.106 | < 0.001 | Deltaproteobacteria | S | Part of the outer membrane protein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane | - | - |
| k123_2680211_1 | 0-12 | -5.155 | < 0.001 | Proteobacteria | Q | Multicopper oxidase | - | 1.16.3.3 |
| k123_4688925_2 | 0-12 | -6.014 | < 0.001 | Betaproteobacteria | C | D-arabinono-1,4-lactone oxidase | - | - |
| k123_785677_1 | 12-58 | 12.106 | < 0.001 | Betaproteobacteria | J | One of the primary rRNA binding proteins, it binds directly near the 3'-end of the 23S rRNA, where it nucleates assembly of the 50S subunit | rplC | - |
| k123_2456034_2 | 12-58 | 11.226 | < 0.001 | Betaproteobacteria | J | Forms part of the polypeptide exit tunnel | rplD | - |
| k123_3024550_1 | 12-58 | 10.815 | < 0.001 | Betaproteobacteria | J | This is one of the proteins that binds to the 5S RNA in the ribosome where it forms part of the central protuberance | ctc | - |
| k123_1916443_2 | 12-58 | 11.317 | < 0.001 | Betaproteobacteria | J | Binds directly to 23S ribosomal RNA and is necessary for the in vitro assembly process of the 50S ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit | rplT | - |
| k123_794397_5 | 12-58 | 12.046 | < 0.001 | Betaproteobacteria | J | Ribosomal protein L17 | rplQ | - |
| k123_1010408_1 | 12-58 | 11.827 | < 0.001 | Betaproteobacteria | J | This is 1 of the proteins that binds and probably mediates the attachment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance. In the 70S ribosome it contacts protein S13 of the 30S subunit (bridge B1b), connecting the 2 subunits | rplE | - |
| k123_1115623_7 | 12-58 | 10.795 | < 0.001 | Betaproteobacteria | JKL | Belongs to the DEAD box helicase family | rhlE1 | - |
| k123_3802697_1 | 12-58 | 10.705 | < 0.001 | Betaproteobacteria | JKL | Belongs to the DEAD box helicase family | rhlE1 | - |
| k123_5130820_1 | 12-58 | 11.586 | < 0.001 | Betaproteobacteria | JKL | Belongs to the DEAD box helicase family | rhlE1 | - |
| k123_2572977_1 | 12-58 | 11.374 | < 0.001 | Betaproteobacteria | U | The central subunit of the protein translocation channel SecYEG. Consists of two halves formed by TMs 1-5 and 6-10. These two domains form a lateral gate at the front which open onto the bilayer between TMs 2 and 7, and are clamped together by SecE at the back. The channel is closed by both a pore ring composed of hydrophobic SecY residues and a short helix (helix 2A) on the extracellular side of the membrane which forms a plug. The plug probably moves laterally to allow the channel to open. The ring and the pore may move independently | secY | - |
| k123_3351426_1 | 12-58 | -10.845 | < 0.001 | Clostridia | S | Flavin reductase like domain | - | - |
| k123_3689959_6 | 12-58 | -12.298 | < 0.001 | Bacilli | GM | NmrA-like family | - | - |
| k123_4131385_2 | 12-58 | -11.203 | < 0.001 | Bacilli | M | Domain of unknown function (DUF5011) | - | - |
| k123_1682409_1 | 12-58 | -11.434 | < 0.001 | Bacilli | C | Oxidoreductase required for the transfer of electrons from pyruvate to flavodoxin | nifJ | 1.2.7.1 |
| k123_3028891_1 | 12-58 | -10.738 | < 0.001 | Clostridia | K | PFAM flavin reductase | - | - |
| k123_2018420_3 | 12-58 | -9.433 | < 0.001 | Bacilli | GKT | Transcriptional antiterminator | manR | - |
| k123_3469192_2 | 12-58 | -9.634 | < 0.001 | Clostridia | T | S-layer homology domain | - | - |
| k123_3683359_3 | 12-58 | -11.778 | < 0.001 | Bacilli | P | P-type ATPase | copA | 3.6.3.54 |
| k123_335030_2 | 12-58 | -11.417 | < 0.001 | Bacilli | C | Iron-containing alcohol dehydrogenase | adhB | 1.1.1.1,1.1.1.202 |
| k123_3012292_1 | 12-58 | -9.296 | < 0.001 | Bacilli | S | Putative neutral zinc metallopeptidase | yugP | - |
| k123_3581297_1 | 58-86 | 8.049 | < 0.001 | Fungi | - | - | - | - |
| k123_133381_1 | 58-86 | 8.362 | < 0.001 | Betaproteobacteria | C | anaerobic respiration | - | 1.7.2.6 |
| k123_3681927_1 | 58-86 | 8.474 | < 0.001 | Betaproteobacteria | C | Cytochrome C oxidase subunit II, periplasmic domain | - | 1.9.3.1 |
| k123_4461993_6 | 58-86 | 10.379 | < 0.001 | Bacteroidetes | S | Tetratricopeptide repeat protein | - | - |
| k123_1691746_1 | 58-86 | 8.748 | < 0.001 | Rhodospirillales | C | NDH-1 shuttles electrons from NADH, via FMN and iron-sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient. This subunit may bind ubiquinone | nuoH | 1.6.5.3 |
| k123_1674520_1 | 58-86 | 8.655 | < 0.001 | Alphaproteobacteria | C | Produces ATP from ADP in the presence of a proton gradient across the membrane. The alpha chain is a regulatory subunit | atpA | 3.6.3.14 |
| k123_4907595_1 | 58-86 | 8.469 | < 0.001 | Oceanospirillales | J | Belongs to the universal ribosomal protein uS2 family | rpsB | - |
| k123_788629_1 | 58-86 | 8.018 | < 0.001 | Bacteroidetes | PT | COGs COG3712 Fe2 -dicitrate sensor membrane component | - | - |
| k123_784141_1 | 58-86 | 6.602 | < 0.001 | Bacteroidetes | - | - | - | - |
| k123_2678388_2 | 58-86 | 7.966 | < 0.001 | Betaproteobacteria | C | Subunits I and II form the functional core of the enzyme complex. Electrons originating in cytochrome c are transferred via heme a and Cu(A) to the binuclear center formed by heme a3 and Cu(B) | coxB | 1.9.3.1 |
| k123_903075_1 | 58-86 | -7.906 | < 0.001 | Bacteroidetes | - | - | - | - |
| k123_2460567_2 | 58-86 | -7.060 | < 0.001 | Bacteroidetes | S | Functions as a peptidoglycan terminase that cleaves nascent peptidoglycan strands endolytically to terminate their elongation | mltG | - |
| k123_680086_2 | 58-86 | -6.939 | < 0.001 | Bacteria | - | - | - | - |
| k123_3353720_2 | 58-86 | -7.036 | < 0.001 | Bacteroidetes | U | Preprotein translocase SecG subunit | secG | - |
| k123_4342821_1 | 58-86 | -6.571 | < 0.001 | Bacteroidetes | CO | Redoxin | - | - |
| k123_680086_6 | 58-86 | -6.695 | < 0.001 | Bacteroidetes | G | Sad1 / UNC-like C-terminal | - | - |
| k123_3687116_4 | 58-86 | -6.677 | < 0.001 | Bacteroidetes | S | Belongs to the pirin family | yhhW | - |
| k123_349053_1 | 58-86 | -6.992 | < 0.001 | Bacteroidetes | F | Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine | guaB | 1.1.1.205 |
| k123_2348950_2 | 58-86 | -6.358 | < 0.001 | Bacteroidetes | O | Heat shock protein | - | - |
| k123_1004837_2 | 58-86 | -7.162 | < 0.001 | Bacteroidetes | S | Fimbrillin-like | - | - |
| k123_465331_1 | 86-168 | 6.832 | < 0.001 | Bacteroidetes | M | Pkd domain containing protein | - | - |
| k123_1247591_2 | 86-168 | 6.662 | < 0.001 | Xanthomonadales | - | - | - | - |
| k123_356907_3 | 86-168 | 7.008 | < 0.001 | Actinobacteria | I | Fatty acid desaturase | desA3_2 | - |
| k123_1802620_3 | 86-168 | 6.775 | < 0.001 | Actinobacteria | S | Protein of unknown function (DUF1360) | - | - |
| k123_4137171_1 | 86-168 | 7.254 | < 0.001 | Actinobacteria | U | WD40-like Beta Propeller Repeat | - | - |
| k123_1449660_1 | 86-168 | 7.112 | < 0.001 | Actinobacteria | S | LVIYD repeat | - | - |
| k123_3015796_1 | 86-168 | 6.131 | < 0.001 | Actinobacteria | S | Tetratricopeptide repeat | - | - |
| k123_4469568_1 | 86-168 | 8.516 | < 0.001 | Gammaaproteobacteria | NU | Pilin (bacterial filament) | pilA | - |
| k123_4013561_1 | 86-168 | 6.723 | < 0.001 | Xanthomonadales | N | Required for morphogenesis and for the elongation of the flagellar filament by facilitating polymerization of the flagellin monomers at the tip of growing filament. Forms a capping structure, which prevents flagellin subunits (transported through the central channel of the flagellum) from leaking out without polymerization at the distal end | fliD | - |
| k123_4136401_2 | 86-168 | 6.097 | < 0.001 | Actinobacteria | O | FKBP-type peptidyl-prolyl cis-trans isomerase | fkfB | 5.2.1.8 |
| k123_2576445_1 | 86-168 | -7.806 | < 0.001 | Xanthomonadales | M | Belongs to the ompA family | mopB | - |
| k123_2013370_2 | 86-168 | -7.409 | < 0.001 | Gammaaproteobacteria | S | Protein of unknown function (DUF1471) | - | - |
| k123_1784040_1 | 86-168 | -7.539 | < 0.001 | Clostridia | L | PFAM Reverse transcriptase (RNA-dependent DNA polymerase) | - | - |
| k123_2784492_8 | 86-168 | -7.104 | < 0.001 | Actinobacteria | Q | Amidohydrolase family | - | - |
| k123_1671881_1 | 86-168 | -7.712 | < 0.001 | Bacteroidetes | P | von Willebrand factor, type A | - | - |
| k123_115662_2 | 86-168 | -8.927 | < 0.001 | Bacilli | C | succinate dehydrogenase | sdhA | 1.3.5.1,1.3.5.4 |
| k123_2013542_1 | 86-168 | -7.286 | < 0.001 | Betaproteobacteria | S | Domain of unknown function (DUF4148) | - | - |
| k123_784141_1 | 86-168 | -6.401 | < 0.001 | Bacteroidetes | - | - | - | - |
| k123_126934_1 | 86-168 | -8.876 | < 0.001 | Bacteroidetes | M | Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family | - | - |
| k123_3912958_2 | 86-168 | -7.098 | < 0.001 | Bacteroidetes | C | cytochrome c oxidase | ccoG | - |
| k123_4347668_1 | 168-376 | 7.985 | < 0.001 | Archaea | - | - | - | - |
| k123_2010423_2 | 168-376 | 8.457 | < 0.001 | Acidobacteria | J | Forms part of the ribosomal stalk, playing a central role in the interaction of the ribosome with GTP-bound translation factors | rplJ | - |
| k123_4021403_1 | 168-376 | 6.597 | < 0.001 | Acidobacteria | O | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions | groL | - |
| k123_2899693_1 | 168-376 | 6.546 | < 0.001 | Acidobacteria | O | Belongs to the ClpA ClpB family | - | - |
| k123_461276_1 | 168-376 | 9.975 | < 0.001 | Bacteria | N | domain, Protein | - | - |
| k123_13363_1 | 168-376 | 6.773 | < 0.001 | Acidobacteria | O | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions | groL | - |
| k123_3585893_1 | 168-376 | 6.944 | < 0.001 | Acidobacteria | K | DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates | rpoC | 2.7.7.6 |
| k123_3020221_1 | 168-376 | 7.640 | < 0.001 | Xanthomonadales | - | - | - | - |
| k123_4015238_2 | 168-376 | 8.717 | < 0.001 | Acidobacteria | U | MotA TolQ ExbB | - | - |
| k123_4017681_1 | 168-376 | 8.220 | < 0.001 | Acidobacteria | J | Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation | rpsC | - |
| k123_465331_1 | 168-376 | -7.066 | < 0.001 | Bacteroidetes | M | Pkd domain containing protein | - | - |
| k123_4458935_1 | 168-376 | -7.201 | < 0.001 | Epsilonproteobacteria | Q | calcium- and calmodulin-responsive adenylate cyclase activity | - | - |
| k123_5025476_3 | 168-376 | -8.470 | < 0.001 | Actinobacteria | G | phosphocarrier protein hpr | ptsH | - |
| k123_1114482_1 | 168-376 | -6.397 | < 0.001 | Bacteroidetes | MU | Outer membrane efflux protein | - | - |
| k123_4360823_3 | 168-376 | -6.013 | < 0.001 | Gammaaproteobacteria | IQ | KR domain | - | 1.1.1.159 |
| k123_3135574_1 | 168-376 | -7.251 | < 0.001 | Actinobacteria | K | transcriptional regulator (DeoR family) | fruR | - |
| k123_3354064_4 | 168-376 | -6.628 | < 0.001 | Actinobacteria | G | Bacterial extracellular solute-binding protein | - | - |
| k123_2683111_1 | 168-376 | -6.487 | < 0.001 | Actinobacteria | G | L-arabinose isomerase | - | 5.3.1.4 |
| k123_4463835_2 | 168-376 | -6.188 | < 0.001 | Actinobacteria | K | DNA-templated transcription, initiation | - | - |
| k123_2915236_1 | 168-376 | -7.060 | < 0.001 | Actinobacteria | M | probably involved in cell wall | - | - |