

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3351426_1	11.410	< 0.001	Clostridia	S	Flavin reductase like domain	-	-
k123_3689959_6	12.863	< 0.001	Bacilli	GM	NmrA-like family	-	-
k123_1682409_1	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	11.768	< 0.001	Bacilli	M	Domain of unknown function (DUF5011)	-	-
k123_3474748_6	11.248	< 0.001	Bacilli	E	ABC transporter substrate-binding protein	oppA	-
k123_2018420_1	11.126	< 0.001	Bacilli	G	PTS fructose transporter subunit IIC	fruA	2.7.1.202
k123_4134106_1	10.776	< 0.001	Bacilli	C	e3 binding domain	pdhC	2.3.1.12
k123_2451258_1	12.572	< 0.001	Clostridia	M	S-layer homology domain	-	-
k123_3683359_3	12.858	< 0.001	Bacilli	P	P-type ATPase	copA	3.6.3.54
k123_2018420_3	9.998	< 0.001	Bacilli	GKT	Transcriptional antiterminator	manR	-
k123_4030449_2	-7.201	< 0.001	Gammaproteobacteria	C	PFAM blue (type 1) copper domain protein	-	-
k123_1903136_2	-6.769	< 0.001	Actinobacteria	Q	Taurine catabolism dioxygenase Taud, TfdA family	-	1.14.11.17
k123_4017556_1	-6.740	< 0.001	Betaproteobacteria	Q	Taurine dioxygenase	-	1.14.11.17
k123_2470867_1	-6.354	< 0.001	Actinobacteria	Q	taurine catabolism dioxygenase	tauD	1.14.11.17
k123_2231885_1	-5.426	< 0.001	Actinobacteria	E	ABC-type branched-chain amino acid transport	-	-
k123_1903136_1	-5.513	< 0.001	Actinobacteria	K	Bacterial regulatory proteins, tetR family	-	-
k123_3697194_1	-5.446	< 0.001	Actinobacteria	Q	Taurine catabolism dioxygenase Taud, TfdA family	tauD	1.14.11.17
k123_4238273_1	-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	-5.155	< 0.001	Proteobacteria	Q	Multicopper oxidase	-	1.16.3.3
k123_4688925_2	-6.014	< 0.001	Betaproteobacteria	C	D-arabinono-1,4-lactone oxidase	-	-
k123_785677_1	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	11.226	< 0.001	Betaproteobacteria	J	Forms part of the polypeptide exit tunnel	rplD	-
k123_3024550_1	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	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	12.046	< 0.001	Betaproteobacteria	J	Ribosomal protein L17	rplQ	-
k123_1010408_1	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	10.795	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-
k123_3802697_1	10.705	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-
k123_5130820_1	11.586	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-
k123_2572977_1	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	-10.845	< 0.001	Clostridia	S	Flavin reductase like domain	-	-
k123_3689959_6	-12.298	< 0.001	Bacilli	GM	NmrA-like family	-	-
k123_4131385_2	-11.203	< 0.001	Bacilli	M	Domain of unknown function (DUF5011)	-	-
k123_1682409_1	-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	-10.738	< 0.001	Clostridia	K	PFAM flavin reductase	-	-
k123_2018420_3	-9.433	< 0.001	Bacilli	GKT	Transcriptional antiterminator	manR	-
k123_3469192_2	-9.634	< 0.001	Clostridia	T	S-layer homology domain	-	-
k123_3683359_3	-11.778	< 0.001	Bacilli	P	P-type ATPase	copA	3.6.3.54
k123_335030_2	-11.417	< 0.001	Bacilli	C	Iron-containing alcohol dehydrogenase	adhB	1.1.1.1,1.1.1.202
k123_3012292_1	-9.296	< 0.001	Bacilli	S	Putative neutral zinc metallopeptidase	yugP	-
k123_3581297_1	8.049	< 0.001	Fungi	-	-	-	-
k123_133381_1	8.362	< 0.001	Betaproteobacteria	C	anaerobic respiration	-	1.7.2.6
k123_3681927_1	8.474	< 0.001	Betaproteobacteria	C	Cytochrome C oxidase subunit II, periplasmic domain	-	1.9.3.1
k123_4461993_6	10.379	< 0.001	Bacteroidetes	S	Tetratricopeptide repeat protein	-	-
k123_1691746_1	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	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	8.469	< 0.001	Oceanospirillales	J	Belongs to the universal ribosomal protein uS2 family	rpsB	-
k123_788629_1	8.018	< 0.001	Bacteroidetes	PT	COGs COG3712 Fe2 -dicitrate sensor membrane component	-	-
k123_784141_1	6.602	< 0.001	Bacteroidetes	-	-	-	-
k123_2678388_2	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	-7.906	< 0.001	Bacteroidetes	-	-	-	-
k123_2460567_2	-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	-6.939	< 0.001	Bacteria	-	-	-	-
k123_3353720_2	-7.036	< 0.001	Bacteroidetes	U	Preprotein translocase SecG subunit	secG	-
k123_4342821_1	-6.571	< 0.001	Bacteroidetes	CO	Redoxin	-	-
k123_680086_6	-6.695	< 0.001	Bacteroidetes	G	Sad1 / UNC-like C-terminal	-	-
k123_3687116_4	-6.677	< 0.001	Bacteroidetes	S	Belongs to the pirin family	yhhW	-
k123_349053_1	-6.992	< 0.001	Bacteroidetes	F	Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine 5'-phosphate (XMP), the first committed and rate- limiting step in the de novo synthesis of guanine nucleotides, and therefore plays an important role in the regulation of cell growth	guaB	1.1.1.205
k123_2348950_2	-6.358	< 0.001	Bacteroidetes	O	Heat shock protein	-	-
k123_1004837_2	-7.162	< 0.001	Bacteroidetes	S	Fibbrillin-like	-	-
k123_465331_1	6.832	< 0.001	Bacteroidetes	M	Pkd domain containing protein	-	-
k123_1247591_2	6.662	< 0.001	Xanthomonadales	-	-	-	-
k123_356907_3	7.008	< 0.001	Actinobacteria	I	Fatty acid desaturase	desA3_2	-
k123_1802620_3	6.775	< 0.001	Actinobacteria	S	Protein of unknown function (DUF1360)	-	-
k123_4137171_1	7.254	< 0.001	Actinobacteria	U	WD40-like Beta Propeller Repeat	-	-
k123_1449660_1	7.112	< 0.001	Actinobacteria	S	LVIVD repeat	-	-
k123_3015796_1	6.131	< 0.001	Actinobacteria	S	Tetratricopeptide repeat	-	-
k123_4469568_1	8.516	< 0.001	Gammaproteobacteria	NU	Pilin (bacterial filament)	pilA	-
k123_4013561_1	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	6.097	< 0.001	Actinobacteria	O	FKBP-type peptidyl-prolyl cis-trans isomerase	fkbB	5.2.1.8
k123_2576445_1	-7.806	< 0.001	Xanthomonadales	M	Belongs to the ompA family	mopB	-
k123_2013370_2	-7.409	< 0.001	Gammaproteobacteria	S	Protein of unknown function (DUF1471)	-	-
k123_1784040_1	-7.539	< 0.001	Clostridia	L	PFAM Reverse transcriptase (RNA-dependent)	-	-
k123_2784492_8	-7.104	< 0.001	Actinobacteria	Q	Amidohydrolase family	-	-
k123_1671881_1	-7.712	< 0.001	Bacteroidetes	P	von Willebrand factor, type A	-	-
k123_115662_2	-8.927	< 0.001	Bacilli	C	succinate dehydrogenase	sdhA	1.3.5.1,1.3.5.4
k123_2013542_1	-7.286	< 0.001	Betaproteobacteria	S	Domain of unknown function (DUF4148)	-	-
k123_784141_1	-6.401	< 0.001	Bacteroidetes	-	-	-	-
k123_126934_1	-8.876	< 0.001	Bacteroidetes	M	Belongs to the membrane fusion protein (MEP) (TC 8.A.1) family	-	-
k123_3912958_2	-7.098	< 0.001	Bacteroidetes	C	Cytochrome c oxidase	ccoG	-
k123_4347668_1	7.985	< 0.001	Archaea	-	-	-	-
k123_2010423_2	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	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	6.546	< 0.001	Acidobacteria	O	Belongs to the ClpA ClpB family	-	-
k123_461276_1	9.975	< 0.001	Bacteria	N	domain, Protein	-	-
k123_13363_1	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	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	7.640	< 0.001	Xanthomonadales	-	-	-	-
k123_4015238_2	8.717	< 0.001	Actinobacteria	U	MotA TolQ ExbB proton channel	-	-
k123_4017681_1	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	-7.066	< 0.001	Bacteroidetes	M	Pkd domain containing protein	-	-
k123_4458935_1	-7.201	< 0.001	Epsilonproteobacteria	Q	calcium- and calmodulin-responsive adenylate cyclase activity	-	-
k123_5025476_3	-8.470	< 0.001	Actinobacteria	G	phosphocarrier protein hpr	ptsH	-
k123_1114482_1	-6.397	< 0.001	Bacteroidetes	MU	Outer membrane efflux protein	-	-
k123_4360823_3	-6.013	< 0.001	Gammaproteobacteria	IQ	KR domain	-	1.1.1.159
k123_3135574_1	-7.251	< 0.001	Actinobacteria	K	transcriptional regulator (DeoR family)	fruR	-
k123_3354064_4	-6.628	< 0.001	Actinobacteria	G	Bacterial extracellular solute-binding protein	-	-
k123_2683111_1	-6.487	< 0.001	Actinobacteria	G	L-arabinose isomerase	-	5.3.1.4
k123_4463835_2	-6.188	< 0.001	Actinobacteria	K	DNA-templated transcription, initiation	-	-
k123_2915236_1	-7.060	< 0.001	Actinobacteria	M	probably involved in cell wall	-	-