Query 	, C	Coefficient 11.410	p-Value < 0.001	Taxonomic Annotation Clostridia	COG Category	Description Flavin reductase like	Gene Name	EC -
	_36899596 _16824091	12.863 12.514	< 0.001 < 0.001	Bacilli Bacilli	GM C	domain NmrA-like family Oxidoreductase required for the transfer of electrons from pyruvate to	- nifJ	- 1.2.7.1
	_41313852 _34747486	11.768 11.248	< 0.001 < 0.001	Bacilli Bacilli	M E	flavodoxin Domain of unknown function (DUF5011) ABC transporter substrate-binding	- oppA	-
k123_	_20184201 _41341061	11.126 10.776	< 0.001 < 0.001	Bacilli Bacilli	G C	protein PTS fructose transporter subunit IIC e3 binding domain	fruA pdhC	2.7.1.202 2.3.1.12
k123_ k123_	_24512581 _36833593 _20184203	12.572 12.858 9.998	< 0.001 < 0.001 < 0.001	Clostridia Bacilli Bacilli	M P GKT	S-layer homology domain P-type ATPase Transcriptional antiterminator	copA manR	3.6.3.54 -
k123_	_40304492 _19031362	-7.201 -6.769	< 0.001	Gammaproteobacteria Actinobacteria	C Q	PFAM blue (type 1) copper domain protein Taurine catabolism dioxygenase TauD, TfdA family	-	1.14.11.17
k123_	_40175561 _24708671 _22318851	-6.740 -6.354 -5.426	< 0.001 < 0.001 < 0.001	Betaproteobacteria Actinobacteria Actinobacteria	Q Q E	Taurine dioxygenase taurine catabolism dioxygenase ABC-type branched-chain amino acid transport	tauD	1.14.11.17 1.14.11.17
	_19031361 _36971941	-5.513 -5.446	< 0.001 < 0.001	Actinobacteria Actinobacteria	K Q	Bacterial regulatory proteins, tetR family Taurine catabolism dioxygenase TauD, TfdA family	- tauD	1.14.11.17
k123_	_42382731	-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	-	-
	_26802111 _46889252	-5.155 -6.014	< 0.001 < 0.001	Proteobacteria Betaproteobacteria	Q C	into the outer membrane Multicopper oxidase D-arabinono-1,4- lactone oxidase	- -	1.16.3.3
k123_	_7856771	12.106	< 0.001	Betaproteobacteria	J	One of the primary rRNA binding proteins, it binds directly near the 3'-end of the 23S	rplC	-
k123_	_24560342	11.226	< 0.001	Betaproteobacteria	J	rRNA, where it nucleates assembly of the 50S subunit Forms part of the polypeptide exit tunnel	rplD	-
k123_	_30245501	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	ctc	-
k123_	_19164432	11.317	< 0.001	Betaproteobacteria	J	central protuberance Binds directly to 23S ribosomal RNA and is necessary for the in vitro assembly process of the 50S ribosomal	rplT	-
k123_	_7943975	12.046	< 0.001	Betaproteobacteria	J	subunit. It is not involved in the protein synthesizing functions of that subunit Ribosomal protein L17	$\operatorname{rpl} Q$	-
k123_	_10104081	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	${ m rplE}$	-
						ribosomal subunit, where it forms part of the central protuberance. In the 70S ribosome it contacts protein S13		
k123_	_11156237	10.795	< 0.001	Betaproteobacteria	JKL	of the 30S subunit (bridge B1b), connecting the 2 subunits Belongs to the DEAD	rhlE1	_
k123_	_38026971 _51308201	10.705 11.586	< 0.001 < 0.001	Betaproteobacteria Betaproteobacteria	JKL JKL	box helicase family Belongs to the DEAD box helicase family Belongs to the DEAD box helicase family The control subunit of	rhlE1	-
k123_	_25729771	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.	secY	-
						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		
						resides 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		
k123_ k123_	_33514261 _36899596 _41313852	-10.845 -12.298 -11.203	< 0.001 < 0.001 < 0.001	Clostridia Bacilli Bacilli	S GM M	Flavin reductase like domain NmrA-like family Domain of unknown function (DUF5011)	-	1 2 7 1
	_16824091 _30288911	-11.434 -10.738	< 0.001 < 0.001	Bacilli Clostridia	C	Oxidoreductase required for the transfer of electrons from pyruvate to flavodoxin PFAM flavin reductase	nifJ -	1.2.7.1
k123_ k123_		-9.433 -9.634 -11.778	< 0.001 < 0.001 < 0.001	Bacilli Clostridia Bacilli	GKT T P	Transcriptional antiterminator S-layer homology domain P-type ATPase	manR - copA	- - 3.6.3.54
k123_ k123_	_335030_2 _3012292_1 _3581297_1	-11.417 -9.296 8.049	< 0.001 < 0.001 < 0.001	Bacilli Bacilli Fungi	C S	Iron-containing alcohol dehydrogenase Putative neutral zinc metallopeptidase	adhB yugP -	1.1.1.1,1.1.202
k123_ k123_	_133381_1 _3681927_1 _4461993_6	8.362 8.474 10.379	< 0.001 < 0.001 < 0.001	Betaproteobacteria Betaproteobacteria Bacteroidetes	C C	anaerobic respiration Cytochrome C oxidase subunit II, periplasmic domain Tetratricopeptide	-	1.7.2.6 1.9.3.1
k123_	_16917461	8.748	< 0.001	Rhodospirillales	С	repeat protein NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the	nuoH	1.6.5.3
						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		
k123_	_16745201	8.655	< 0.001	Alphaproteobacteria	С	gradient. This subunit may bind ubiquinone Produces ATP from ADP in the presence of a proton gradient	atpA	3.6.3.14
k123_	_49075951	8.469	< 0.001	Oceanospirillales	J	across the membrane. The alpha chain is a regulatory subunit Belongs to the universal ribosomal protein uS2 family	rpsB	-
k123_	_7886291 _7841411 _26783882	8.018 6.602 7.966	< 0.001 < 0.001 < 0.001	Bacteroidetes Bacteroidetes Betaproteobacteria	PT - C	COGs COG3712 Fe2 -dicitrate sensor membrane component - Subunits I and II form	- - coxB	- - 1.9.3.1
						the functional core of the enzyme complex. Electrons originating in cytochrome c are transferred via heme a and Cu(A) to the		
	_9030751 _24605672	-7.906 -7.060	< 0.001 < 0.001	Bacteroidetes Bacteroidetes	- S	binuclear center formed by heme a3 and Cu(B) - Functions as a	- mltG	-
M120_			0.001	Basterolastes		peptidoglycan terminase that cleaves nascent peptidoglycan strands endolytically to terminate their	mvo	
k123_ k123_	_6800862 _33537202 _43428211	-6.939 -7.036 -6.571	< 0.001 < 0.001 < 0.001	Bacteria Bacteroidetes Bacteroidetes	- U CO	elongation - Preprotein translocase SecG subunit Redoxin	- secG -	- -
k123_	_6800866 _36871164 _3490531	-6.695 -6.677 -6.992	< 0.001 < 0.001 < 0.001	Bacteroidetes Bacteroidetes	G S F	Sad1 / UNC-like C-terminal Belongs to the pirin family Catalyzes the	- yhhW guaB	- - 1.1.1.205
						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		
k123_	_2348950_2 _1004837_2 _465331_1	-6.358 -7.162 6.832	< 0.001 < 0.001 < 0.001	Bacteroidetes Bacteroidetes	O S M	regulation of cell growth Heat shock protein Fimbrillin-like Pkd domain	- -	-
k123_ k123_ k123_	_1247591_2 _356907_3 _1802620_3 _4137171_1	6.662 7.008 6.775 7.254	< 0.001 < 0.001 < 0.001 < 0.001	Xanthomonadales Actinobacteria Actinobacteria	I S U	containing protein Fatty acid desaturase Protein of unknown function (DUF1360) WD40-like Beta	- desA3_2 -	-
k123_ k123_	_14496601 _30157961	7.112 6.131	< 0.001 < 0.001	Actinobacteria Actinobacteria	U S S NU	Propeller Repeat LVIVD repeat Tetratricopeptide repeat	- - pil∆	-
	_44695681 _40135611	8.516 6.723	< 0.001 < 0.001	Gammaproteobacteria Xanthomonadales	NU N	Pilin (bacterial filament) Required for morphogenesis and for the elongation of the flagellar filament by	pilA fliD	-
						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		
k123_	_41364012	6.097	< 0.001	Actinobacteria	O	leaking out without polymerization at the distal end FKBP-type peptidyl-prolyl	fkbB	5.2.1.8
k123_	_25764451 _20133702	-7.806 -7.409	< 0.001 < 0.001	Xanthomonadales Gammaproteobacteria Clostridia	M S	cis-trans isomerase Belongs to the ompA family Protein of unknown function (DUF1471)	mopB -	- -
k123_	_17840401 _27844928	-7.539 -7.104	< 0.001	Clostridia Actinobacteria	L Q	PFAM Reverse transcriptase (RNA-dependent DNA polymerase) Amidohydrolase family	-	-
k123_	_16718811 _1156622 _20135421	-7.712 -8.927 -7.286	< 0.001 < 0.001 < 0.001	Bacilli Betaproteobacteria	P C S	von Willebrand factor, type A succinate dehydrogenase Domain of unknown	- sdhA	- 1.3.5.1,1.3.5.4 -
k123_		-6.401 -8.876	< 0.001 < 0.001 < 0.001	Bacteroidetes Bacteroidetes	- M	function (DUF4148) - Belongs to the membrane fusion protein (MFP) (TC	- -	- -
k123_	_39129582 _43476681 _20104232	-7.098 7.985 8.457	< 0.001 < 0.001 < 0.001	Bacteroidetes Archaea Acidobacteria	C - J	8.A.1) family cytochrome c oxidase Forms part of the ribosomal stalk, playing a central role	ccoG - rplJ	- - -
k123	_40214031	6.597	< 0.001	Acidobacteria	O	playing a central role in the interaction of the ribosome with GTP-bound translation factors Prevents misfolding	groL	-
u	<u>.</u> .	(1	1			and promotes the refolding and proper assembly of unfolded polypeptides generated under stress		
k123_	_28996931 _4612761 _133631	6.546 9.975 6.773	< 0.001 < 0.001 < 0.001	Acidobacteria Bacteria Acidobacteria	O N O	conditions Belongs to the ClpA ClpB family domain, Protein Prevents misfolding	- groL	- -
						and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions		
k123_	_35858931	6.944	< 0.001	Acidobacteria	K	conditions DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside	rpoC	2.7.7.6
	_30202211 _40152382	7.640 8.717	< 0.001 < 0.001	Xanthomonadales Acidobacteria	- U	the four ribonucleoside triphosphates as substrates - MotA TolQ ExbB proton channel	- -	- -
k123_	_40176811	8.220	< 0.001	Acidobacteria	J	Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for	rpsC	-
	_4653311 _44589351	-7.066 -7.201	< 0.001 < 0.001	Bacteroidetes Epsilonproteobacteria	M Q	translation Pkd domain containing protein calcium- and calmodulin-responsive	-	-
	_50254763 _11144821	-8.470 -6.397	< 0.001 < 0.001	Actinobacteria Bacteroidetes	G MU	adenylate cyclase activity phosphocarrier protein hpr Outer membrane	ptsH -	-
k123_ k123_	_43608233 _31355741	-6.013 -7.251	< 0.001 < 0.001	Gammaproteobacteria Actinobacteria	IQ K	efflux protein KR domain transcriptional regulator (DeoR family)	- fruR	1.1.1.159
k123_	_33540644 _26831111 _44638352	-6.628 -6.487 -6.188	< 0.001 < 0.001 < 0.001	Actinobacteria Actinobacteria Actinobacteria	G G K	Bacterial extracellular solute-binding protein L-arabinose isomerase DNA-templated transcription,	- - -	5.3.1.4 -
k193	_29152361	-7.060	< 0.001	Actinobacteria	M	initiation probably involved in cell wall	-	-