

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3586165_1	4.699	0	Thermodesulfobacteria	NU	Type II secretion system (T2SS), protein E, N-terminal domain	-	-
k123_5240316_1	3.444	0	Planctomycetes	S	TIGRFAM type VI secretion protein, VC_A0111 family	-	-
k123_4233415_1	4.708	0	Bacteria	-	-	-	-
k123_5247798_1	4.101	0	Bacteria	CO	amine dehydrogenase activity	-	-
k123_1022852_1	3.340	0	Deltaproteobacteria	K	ROS/MUCR transcriptional regulator protein	-	-
k123_4454813_1	4.159	0	Bacteria	D	protein conserved in cyanobacteria	-	-
k123_3793442_4	4.229	0	Actinobacteria	G	pfkB family carbohydrate kinase	kdgK	2.7.1.45
k123_3567914_2	3.910	0	Acidobacteria	-	-	-	-
k123_3575243_1	3.586	0	Bacteroidetes	S	Protein of unknown function (DUF1501)	-	-
k123_1456133_1	3.496	0	Actinobacteria	U	TadE-like protein	-	-
k123_1678879_1	3.364	0	Actinobacteria	K	DNA binding	-	-
k123_1448646_1	4.154	0	Alphaproteobacteria	S	Type VI secretion system effector, Hcp	-	-
k123_2582928_1	3.665	0	Cyanobacteria	T	Signal Transduction Histidine Kinase	-	-
k123_4454279_1	4.115	0	Acidobacteria	S	Type VI secretion system effector, Hcp	-	-
k123_2804786_1	4.518	0	Gammaproteobacteria	T	Domain present in phytochromes and cGMP-specific phosphodiesterases.	-	-
k123_4681706_1	-3.333	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_2129273_1	-3.939	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_2784358_1	-4.226	0	Fungi	O	Heat shock protein	HSP82	-
k123_2453574_1	-3.251	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_2580989_1	-3.034	0	Fungi	O	MreB/Mbl protein	SSA2	-
k123_784972_1	-3.361	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_5131902_2	-3.945	0	Bacteria	N	domain, Protein	-	3.2.1.81,3.2.1.97
k123_1897324_1	-2.804	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_1007534_1	-3.669	0	Actinobacteria	C	Ferredoxin	fdxA	-
k123_1119824_1	-3.191	0	Actinobacteria	O	Heat shock 70 kDa protein	dnaK	-
k123_3696373_1	-2.768	0	Actinobacteria	O	Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions	groL2	-
k123_3023451_1	-5.388	0	Fungi	O	Hsp90 protein	HSP82	-
k123_1018246_1	-2.400	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_4142344_1	-3.376	0	Fungi	O	Hsp90 protein	HSP82	-
k123_3914888_1	-3.146	0	Actinobacteria	G	Phosphoketolase	-	4.1.2.22,4.1.2.9