

Supplemental Table 7 List of significantly enriched transcripts in gentamycin modules (GentM) relative to all other modules (named "OtherSubstrate"). The function results from the DESeq2 package was used on the DESeq2 data object for transcriptomic data to determine enrichment patterns for "GentM" "OtherSubstrate" modules. Transcripts that had a significant Log2FCChange value greater than 1 and were significantly enriched (including taxonomic information) were then added for transcripts that had a match to one or both datasets. Results are sorted by the Log2FCChange to determine which transcripts were most consistently highly enriched (Log2FCChange > 1) or depleted (Log2FCChange < -1) in gentamycin. Note: transcripts with more than one KEGG hit have only the first hit listed.

TranscriptID	KEGG_Catagory	KEGG_Subcategory	Interfunction	Log2FCChange	adjusted_pvalue	Enrichment	Domain	Phylum	Class	Order	Family	Genus	Species
896112_3	No roles mapped out of 0 KOs		Uncharacterized protein (F fragment)	11.66160209	9.08E-24	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Gemmatimonadetes					Gemmatimonadetes bacterium HGW-Gemmatimonadetes-1
1201172_5	No roles mapped out of 0 KOs		hypothetical protein	11.22873403	1.20E-22	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Corynebacteriales	Mycobacteriaceae	Mycobacterium	Mycobacterium fragae
1318765_4	No roles mapped out of 0 KOs		T001_deg_Rec domain-containing protein	12.13894005	2.06E-17	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Corynebacteriales	Mycobacteriaceae	Mycobacterium	uncultured bacterium 20
101317_3	Transport and binding proteins		YnfM domain-containing protein	11.14413713	3.89E-16	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Corynebacteriales	Mycobacteriaceae	Mycobacterium	Mycobacterium
582015_35	No roles mapped out of 0 KOs		Phage tail measure protein, lambda family	11.16315007	3.37E-12	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Gammaproteobacteria	Enterobacteriales	Thiorhodocyclales	Thiorhodocyclaceae	Thiorhodocycla anophelis
902470_7	No roles mapped out of 0 KOs		Uncharacterized protein (F fragment)	10.80069044	8.24E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Pseudonocardiales	Pseudonocardiales	Actinobacteriaceae	Actinobacteriaceae
1405121_3	Prosthetic groups, cofactors, and carriers	Vitamin B6 metabolism	pyridoxal 5-phosphate synthase	9.58120474	5.90E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Cytophaga	Cytophagales	Cytophagaceae	Cytophaga	Cytophaga
1364448_7	No roles mapped out of 0 KOs		Nar_Xc_Umfear	10.7594441	3.33E-13	Gentamycin_Erinichthelastellato_OtherSubstrates	Nar_Xc_Umfear						
1093900_7	No roles mapped out of 0 KOs		Nar_Xc_Umfear	10.48799009	9.46E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Nar_Xc_Umfear						
997572_13	No roles mapped out of 0 KOs		Nar_Xc_Umfear	10.86214573	1.39E-12	Gentamycin_Erinichthelastellato_OtherSubstrates	Nar_Xc_Umfear						
1674053_4	No roles mapped out of 0 KOs		Uncharacterized protein (F fragment)	10.54839431	4.77E-13	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Streptomyetales	Streptomyetaceae	Streptomyces	Streptomyces sp. AC-3
1421095_1	Transport and binding proteins		peptide family protein	10.2883808	2.51E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Xanthomonas
1369240_1	No roles mapped out of 0 KOs		Nar_Xc_Umfear	10.0172573	1.91E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Nar_Xc_Umfear						
1024249_1	No roles mapped out of 1 KOs	Transcription	5'-nucleotidyl-2',3'-cyclic phosphodiesterase	9.95540291	1.45E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Cyanobacteria	Nostocales	Rivulariales	Rivulariaceae	Rivularia	Rivularia
1295762_13	Transcription	Ribosomal proteins; synthesis and modification	Uncharacterized protein 121	9.92952402	3.15E-12	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Acidobacteriales	Acidobacteriales	Acidobacteriales	RIFCPFLOWID_12_FULL_62_13
537426_6	No roles mapped out of 0 KOs		hypothetical protein	9.94939654	4.78E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Acidobacteriales	Acidobacteriales	Acidobacteriales	Acidobacteriales bacterium KES 96
1621624_9	No roles mapped out of 0 KOs		Uncharacterized protein	9.97907263	2.93E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						compost metagenome
1414789_2	No roles mapped out of 0 KOs		Uncharacterized protein	9.70825704	9.82E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Bifidobacteriales	Bifidobacteriales	Methylobacteriaceae	Methylobacteriaceae
93887_11	Transcription	Ribosomal proteins; synthesis and modification	Uncharacterized protein	9.63313647	3.72E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						compost metagenome
1294833_1	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	50S ribosomal protein L29	9.51061005	5.77E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae
1309631_3	No roles mapped out of 0 KOs		Uncharacterized protein (F fragment)	9.54601345	2.66E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Eukaryota	Arthropoda	Insecta	Phasmatodea	Bacilliales	Bacillus	Trichodesma arizonense
154689_3	No roles mapped out of 0 KOs		Lipoprotein	9.178291953	6.28E-15	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Chloroflexales	Chloroflexales	Chloroflexaceae	Chloroflexus
1331276_6	No roles mapped out of 0 KOs		HN1_U domain-containing protein	9.44132239	9.56E-13	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Micromicrobiales	Intraperiplasmic	Phycosphaera	Phycosphaera sp. S0103
412789_1	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	MCL1L29258 protein	9.440812928	9.41E-14	Gentamycin_Erinichthelastellato_OtherSubstrates	Eukaryota	Chordata	Aphellogasterales	Crocophagales	Crocophagaceae	Crocophaga	Crocophaga waltoni
1338724_4	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L28	9.40881873	9.54E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Bifidobacteriales	Idionella	Idionella	Idionella xakamensis
1232097_6	No roles mapped out of 3 KOs	Transcription	RNA polymerase subunit beta	9.391209203	5.08E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Thermoplasmales	Sulfolobales	Sulfolobales	Sulfolobales	Sulfolobales bacterium 67-14
52352_3	Transport and binding proteins	Accessory functions	Energy transducer T008	9.33479024	2.38E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Xanthomonadaceae
1291833_1	Regulatory functions	Protein interactions	Bifunctional glutamine synthetase adenyltransferase	9.28997724	1.10E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Gammaproteobacteria bacterium 12_200M_66_19
145684_7	No roles mapped out of 0 KOs		50S ribosomal protein L18 fragment	9.28098817	9.45E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadales	Xanthomonadaceae	Xanthomonadaceae bacterium
139112_7	Nucleic acid metabolism	D replication, recombination, and repair	MFN domain-containing protein	9.24968038	3.48E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales bacterium
1012146_2	No roles mapped out of 0 KOs		Two component transcriptional regulator, Lusk family	9.24821696	1.08E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						Proteobacteria bacterium
615240_3	No roles mapped out of 0 KOs		Uncharacterized protein	9.241792260	9.41E-14	Gentamycin_Erinichthelastellato_OtherSubstrates	Eukaryota	Chordata	Chordoniales	Chordoniales	Chordoniales	Batrachochytriales	Batrachochytriales dendrobatis
923605_1	Energy metabolism	Oxidative phosphorylation	F0F1 ATP synthase subunit beta (Fragment)	9.20981529	1.90E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
173522_3	Cell structure, growth, and death	Cell division	Cell division protein Flz2	9.18282281	1.52E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Gliosporiales	Gliosporiales	Gliosporiales	Gliosporiales bacterium
1862609_1	Energy metabolism	Oxidative phosphorylation	Cytochrome bo3 oxidase subunit 1 apoprotein	9.15231963	6.06E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Burkholderiales	Cupriavidaceae	Cupriavidaceae bacterium
1500227_4	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L10	9.11011691	3.87E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
594621_7	Prosthetic groups, cofactors, and carriers	In vivo sulfur clusters	GC_V2 domain-containing protein	9.054176277	1.12E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
171181_2	Carbohydrate metabolism	Starch and sucrose metabolism	Maltose-6-phosphate epimerase	9.04872614	3.71E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Propioniales	Propioniales	Propioniales	Friedmannella tuberosa
627007_5	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L23	9.04732228	9.04E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
9012288_1	Transcription	Polymerase	DNA-directed RNA polymerase subunit beta (Fragment)	9.01718155	2.41E-14	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Nitrospirales	Nitrospirales	Nitrospirales	Nitrospirales bacterium
923952_3	Energy metabolism	Oxidative phosphorylation	60S ribosomal protein (F fragment)	8.94416158	7.50E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Verrucomicrobiales	Verrucomicrobiales	Verrucomicrobiales	Verrucomicrobiales bacterium
201832_4	No roles mapped out of 0 KOs		30S ribosomal protein S19	8.94092706	6.06E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						Verrucomicrobiales bacterium
97176_4	Intracellular trafficking, assembly, and processing	Protein interactions	50S ribosomal protein S19	8.92424047	8.81E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales bacterium
138793_1	No roles mapped out of 0 KOs		Cytochrome bc1 ubiquinol oxidase subunit 1	8.88507719	2.58E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
948872_3	No roles mapped out of 0 KOs		Uncharacterized protein	8.84849331	1.38E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales bacterium
10146007_2	No roles mapped out of 0 KOs		Cytochrome c oxidase accessory protein F4G	8.82782331	2.53E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
9720491_3	Transport and binding proteins	Protein interactions	50S ribosomal protein L23	8.81549703	9.99E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
1391919_2	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L2	8.81614873	2.07E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						Proteobacteria bacterium
187368_7	No roles mapped out of 0 KOs		PKOX class F420-dependent enzyme	8.80771022	5.70E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales bacterium AT1
1715658_3	No roles mapped out of 0 KOs		ADP superfamily phosphatase (TIGR01683) family/II	8.80620214	9.41E-14	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Chloroflexales	Chloroflexales	Chloroflexales	Chloroflexales bacterium
116657_2	Amino acid metabolism	Glycine, serine and threonine metabolism	Homoserine kinase	8.80471072	7.98E-16	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
12823_2	Transport and binding proteins	Cations and iron carrying compounds	Magnesium/cobalt efflux protein	8.80120828	2.84E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
99683_4	Carbohydrate metabolism	Arabinose sugar and nucleotide sugar metabolism	Arabinose-5-phosphate uridylyltransferase	8.79735654	9.84E-14	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
194701_4	Transcription	Ribosomal proteins; synthesis and modification	30S ribosomal protein S8	8.79170517	1.90E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
1239906_2	Defense and invasion systems	Defense and invasion systems	Gamma-cyC-like phosphatase	8.78319933	1.81E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
94925_2	Carbohydrate metabolism	Citrate cycle (TCA cycle)	Succinate-CoA ligase subunit beta (Fragment)	8.70964463	2.99E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
201832_4	No roles mapped out of 0 KOs		30S ribosomal protein S11	8.70388644	9.01E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						Verrucomicrobiales bacterium
547465_3	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	50S ribosomal protein S11	8.69420466	1.91E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales	Actinobacteriales bacterium
857039_2	No roles mapped out of 0 KOs		LyM domain protein	8.69172021	2.41E-09	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Burkholderiales	Laupriales	Laupriales mirabilis
168867_4	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L18	8.68017926	3.45E-10	Gentamycin_Erinichthelastellato_OtherSubstrates	No taxonomic annotation available						Actinobacteriales bacterium
1129114_4	Carbohydrate metabolism	Pentose and glycolysis interconversions	Phosphoenolpyruvate carboxylase	8.68407930	1.60E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
1852298_4	Nucleic acid metabolism	Ribonucleic acid metabolism	Thymidylate synthase	8.68392805	1.43E-11	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Chloroflexales	Chloroflexales	Chloroflexales	Chloroflexales bacterium
94402_6	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal protein L3	8.67157952	6.65E-08	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Chloroflexales	Chloroflexales	Chloroflexales	Chloroflexales bacterium
829565_3	No roles mapped out of 0 KOs		Uncharacterized protein	8.65905307	3.65E-06	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
1403990_2	Carbohydrate metabolism	Starch and sucrose metabolism	Peptidase S74 domain-containing protein	8.64930287	1.29E-06	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Favobacteriales	Favobacteriales	Favobacteriales	Favobacteriales bacterium
1848262_6	Nucleic acid metabolism	Transcription	Ribonucleoside diphosphate reductase	8.64915889	1.27E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Comamonadales	Comamonadaceae	Comamonadaceae	Comamonadaceae bacterium
634992_8	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Peptidyl prolyl cis-trans isomerase	8.64672136	1.87E-06	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
79124_4	No roles mapped out of 0 KOs		Uncharacterized protein	8.6262998	3.17E-07	Gentamycin_Erinichthelastellato_OtherSubstrates	Bacteria	Actinobacteria	Actinobacteriales	Burkholderiales	Comamonadales	Comamonadaceae	Comamonadaceae bacterium
102095_2													

498383_1	Nucleic acid metabolism	Pyrimidine metabolism	Ribonucleoside-diphosphate reductase	4.50349423	1.83E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_14
1202075_7	No roles mapped of 0 KOs		RNA-directed RNA polymerase III	4.077801477	1.0E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
307423_9	Amino acid metabolism	Histidine metabolism	1-(5-phosphoribosyl)-5-(5-phosphoribosyl)aminoimidate	4.46789764	0.0612932	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
109690_9	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	Alginate biosynthesis protein ALGA	4.46194848	4.99E-06	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
248454_4	Transcription	β -galactosidase	Ribitol dehydrogenase	4.45997444	5.77E-06	Getamipin_Gammaglobobacteria	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
1744530_5	No roles mapped of 0 KOs		Uncharacterized protein	4.44701725	0.0240507	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Alphaproteobacteria	Bradyrhizobium lotii
659992_5	Translation	Ribosomal protein: synthesis and modification	50S ribosomal protein L5	4.44576023	1.04E-06	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
659992_5	Nucleic acid metabolism	Replication, recombination, and repair	Replication helicase	4.43973722	0.0019351	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
54545_10	Intercellular trafficking, assembly, and processing	Chaperone protein CpnB	Chaperone protein CpnB	4.43761554	0.00665213	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
1176828_14	No roles mapped of 0 KOs		Putative RNA polymerase subunit beta'	4.43688847	0.00062404	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
990500_11	Energy metabolism	Oxidative phosphorylation	Cytochrome b ubiquinol oxidase subunit I	4.43719339	0.00768941	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
61020_6	No roles mapped of 0 KOs		Uncharacterized protein	4.43126703	1.11E-09	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
102572_2	Intercellular trafficking, assembly, and processing	Chaperone and folding factors	Chaperone protein CpnB	4.43104499	0.00243264	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	Translation	Translation factors	Translation initiation factor IF-3	4.43100143	0.00434082	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
39564_3	Translation	Ribosomal protein: synthesis and modification	30S ribosomal protein S13	4.43087043	0.02309758	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
43511_1	Amino acid metabolism	Regulatory biosynthesis	Regulatory biosynthesis protein	4.43074796	0.00214885	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
297144_2	No roles mapped of 0 KOs		Uncharacterized protein	4.43053824	1.24E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Eukaryota	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
1537272_1	No roles mapped of 0 KOs		Uncharacterized protein	4.430093958	0.00692807	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
134465_4	No roles mapped of 0 KOs		Net_In_Unref	4.43021732	0.0678378	Getamipin_Erinchellateloidei_OtherSubstrates	Net_In_Unref			
39564_3	Defense and invasion systems	Secretion systems	Type IV secretion system contractile sheath large subunit	4.43095193	0.00292158	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
39564_3	No roles mapped of 0 KOs		Histidine kinase	4.43176020	1.97E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
157907_1	Carbohydrate metabolism	Inositol phosphate metabolism	Methyltransferase-semialdehyde dehydrogenase (CoA)	4.43021851	0.00003173	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	Translation	Translation factors	Indolylglycerol phosphate dehydrogenase	4.43161376	0.00003173	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
43511_1	Amino acid metabolism	Regulatory biosynthesis	Net_In_Unref	4.43197819	0.00239784	Getamipin_Erinchellateloidei_OtherSubstrates	Net_In_Unref			
297144_2	No roles mapped of 0 KOs		YvrF family transcriptional regulator	4.43621757	1.24E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
120056_3	Transport and binding proteins	Anions	Net_In_Unref	4.43621757	0.0037984	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
703889_6	No roles mapped of 0 KOs		Uncharacterized protein	4.434544613	0.02888148	Getamipin_Erinchellateloidei_OtherSubstrates	Eukaryota	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
175069_2	Translation	Ribosomal protein: synthesis and modification	Sigma 54 modulation protein Δ S54	4.434428216	0.00514763	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
153282_7	Transport and binding proteins	Oxidative phosphorylation	subunit ABC transporter gemrase subunit C/yrp	4.43438953	2.88E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Uncharacterized protein	4.43178676	0.05391482	Getamipin_Erinchellateloidei_OtherSubstrates	Eukaryota	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
400209_4	Nucleic acid metabolism	D replication, recombination, and repair	Beta sliding clamp	4.42630767	0.03860283	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
20772_2	Translation	Ribosomal protein: synthesis and modification	Ribosomal protein L7/L12	4.42715413	0.04902487	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Uncharacterized clamp	4.423490507	0.00373669	Getamipin_Erinchellateloidei_OtherSubstrates	Eukaryota	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
165594_2	No roles mapped of 0 KOs		RNA polymerase subunit β '	4.423490507	0.00373669	Getamipin_Erinchellateloidei_OtherSubstrates	Eukaryota	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
5331_3	Translation	Translation factors	Elongation factor Tu	4.43184868	0.01150318	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
153833_1	Carbohydrate metabolism	Carbohydrate metabolism	Isolate dehydrogenase (NADP)	4.431843828	0.03794923	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
61020_6	No roles mapped of 0 KOs		Isocoumarin protein PdsA	4.431813024	0.045407847	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
81350_4	Intercellular trafficking, assembly, and processing	Chaperone and folding factors	60 kDa Chaperonin	4.43088199	0.01503526	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriia bacterium RIFSPLOW22_11_FULL_65_19
107917_9	Translation	Translation factors	Type D domain-containing protein	4.432691496	0.02652615	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
61020_6	No roles mapped of 0 KOs		TP-dependent Ctp protease ATP-binding subunit Ctp	4.43071268	0.00218755	Getamipin_Erinchellateloidei_OtherSubstrates	No taxonomic annotation available			
297144_2	No roles mapped of 0 KOs		ATP-dependent Ctp protease ATP-binding subunit Ctp	4.429565225	0.03897782	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
275862_4	Transcription	Transcription factors	RNA-directed RNA polymerase subunit beta	4.43621757	0.00738025	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
990500_11	Nucleic acid metabolism	D replication, recombination, and repair	Excisionase ABC subunit A	4.427052089	5.39E-05	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Gammaglobobacteria	Gammaglobobacteria bacterium RIFSPLOW22_11_FULL_65_19
163300_5	Glycan biosynthesis and metabolism	Polysaccharide and lipopolysaccharide metabolism	Beta-hydroxybutyryl aspartyl-asparaginyl transferase	4.24640037	2.97E-07	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
657791_1	Prosthetic groups, cofactors, and carriers	Chaperone and folding factors	Chaperone protein CpnB	4.430421218	0.01388137	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	Amino acid metabolism	Ketone and methionine metabolism	S-methylthioadenosyl-asparaginyl methyltransferase	4.426389348	0.00042697	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Alphaproteobacteria	Alphaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
184016_1	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_65_19
183850_3	No roles mapped of 0 KOs		Urease	4.431992419	0.04794737	Getamipin_Erinchellateloidei_OtherSubstrates	Bacteria	Proteobacter	Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOW22_11_FULL_

168134.4	Amino acid metabolism	Cysteine and methionine metabolism	Free methionine (S)-sulfoxide reductase YebD	3.94305478	0.0122261	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
124023.7	Transcription	RNA polymerase	DNA-directed RNA polymerase subunit beta	3.9362425	0.02444084	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Chloroflexi Chloroflexi	
124142.3	No roles mapped out of 1 KOs	Polymerase	FAD-binding, 3'-domain-containing protein	3.93624061	1.28E-06	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
152001.5	Nucleic acid metabolism	Pyrimidine metabolism	Ribindocin-diphosphate reductase	3.93602858	0.03850828	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOWD_12_FUL_65_14
802629.2	Defense and invasion systems	Invasion response	Enzyme family-dependent helicase	3.9332161	0.00200141	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
381899.7	Transcription	Polymerase	DNA-directed RNA polymerase subunit beta	3.93203385	8.03E-05	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacteria	Proteobacteria bacterium
298858.25	No roles mapped out of 1 KOs	Translation factors	Mechanistic transcription protein MreE	3.93009719	2.76E-09	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Micrococci Micrococci	Actinobacteri bacterium
35414.1	No roles mapped out of 1 KOs	Arginine biosynthesis	Enzymation Factor Tu (Fragment)	3.93004313	0.00289912	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Chrysiobacteriales Chrysiobacteriales	Beta vulgaris
62399.1	No roles mapped out of 1 KOs	Secretion systems	Uncharacterized protein	3.92737744	0.02404211	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Hymenobacteriales Blastobacteriales	Blashtobacteriales sp. GI
118336.2	Transcription	R polymerase	DNA-directed RNA polymerase subunit beta'	3.92645129	0.01731535	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
160456.4	Transport and binding proteins	Unknown substrate	FuclI	3.92404978	0.00318354	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
202596.14	No roles mapped out of 1 KOs	Two-component systems	Anti-streptococcal repeat protein	3.92407985	0.01841164	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
27027.2	No roles mapped out of 1 KOs	Arginine biosynthesis	Nag_X_III	3.92134441	0.02345282	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
151515.9	Amino acid metabolism	Pyrimidine metabolism	Uncharacterized protein	3.92099228	0.00257307	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
36433.3	No roles mapped out of 1 KOs	Secretion systems	DNA-directed RNA polymerase subunit beta	3.92109193	0.00021995	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Hymenobacteriales Rhizobiales	Quailobacterium nitratifans
191791.3	Defense and invasion systems	Acquisition systems	Topin 1 secretion system contracta 3'shank large sub	3.92100563	0.04163971	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
56653.2	No roles mapped out of 1 KOs	Secretion systems	Alkaline monooxygenase alpha chain	3.92074656	0.0148662	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
293729.17	Transport and binding proteins	Amino acids, peptides and amines	ABF transporter domain-containing protein	3.92070129	0.01243879	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Bradyrhizobiales	
180552.17	No roles mapped out of 1 KOs	Two-component systems	YnfS domain-containing protein	3.91951437	0.01962838	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Acidobacteriales Acidobacteriales	Acidobacteria bacterium
106760.21	No roles mapped out of 1 KOs	Two-component systems	Uncharacterized protein	3.91850457	0.02674089	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Acidobacteriales Acidobacteriales	Acidobacteria bacterium
109826.11	Signal transduction	Polymerase	Uncharacterized protein	3.91849293	0.00231861	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Thermotogales Sulfolobales Sulfolobales	Sulfolobales bacterium
93036.7	Transcription	Ribosomal proteins: synthesis and modification	50S ribosomal L2	3.914073826	0.00271995	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Rhizobiales Hymenobacteriales Rhizobiales	Hyphomicrobium nitratifans
1248329.9	No roles mapped out of 1 KOs	Carbohydrate metabolism	Hybrid sensor histidine kinase/response regulator	3.91229859	0.01138495	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Bacteroidetes Cytophaga Cytophagales Cytophagales	Dyadobacter sp. AR-36
613136.3	Carbohydrate metabolism	Glycolysis and glyoxylate metabolism	Isolactate lyase	3.91221466	0.01047216	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales	
113185.5	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	3.91218909	0.02320838	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales	
160927.1	No roles mapped out of 1 KOs	Carbohydrate metabolism	hypothetical protein	3.911570029	0.01917997	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Methylobacteriales	Methylobacteriales bacterium
128279.2	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	3.9099904	0.0424028	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
161511.1	No roles mapped out of 1 KOs	Carbohydrate metabolism	Enzyme regulated membrane protein	3.90713143	0.00878705	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
154094.5	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	3.90728457	0.02939487	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOWD_12_FUL_62_13
101747.1	No roles mapped out of 1 KOs	Carbohydrate metabolism	Glucosyltransferase system (GTase)	3.90720264	0.02312197	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Myxococcales Myxococcales	Myxococcales bacterium 68-2
814382.2	No roles mapped out of 1 KOs	Carbohydrate metabolism	TPR_REGION domain-containing protein	3.90704905	0.03096729	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Candidatus Rubiactineta	Candidatus Rubiactineta
120382.1	No roles mapped out of 1 KOs	Unknown function	Response regulatory domain-containing protein	3.9074041512	0.03041316	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
1314328.3	Unknown function	General	Enzyme, oxidase domain-containing protein	3.90712014	2.4E-12	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
752170.1	Nucleic acid metabolism	Purine metabolism	RhA polymerase	3.90706248	0.03444717	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Rubrobacteri Rubrobacteri Rubrobacteri	Rubrobacteri bacterium
125246.9	Transcription	Transcription factors	DNA polymerase sigma factor RpoD (Fragment)	3.906830051	0.00118487	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria	Betaproteobacteria bacterium RIFSPLOWD_12_61_14
119430.1	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	3.90681844	0.01189176	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Rhizobiales Rhizobiales	Rhizobiales bacterium
54577.2	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	GalT domain-containing protein	3.90483265	0.03446226	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Methylobacteriales	Methylobacteriales bacterium
120822.3	Energy metabolism	Protein interactions	Enzyme, oxidase subunit, subunit II	3.90479209	0.02733683	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	No taxonomic annotation available	
158082.3	Regulatory factors	Protein interactions	GalT domain-containing protein	3.904487813	0.03494219	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Chloroflexi Chloroflexi	
110617.1	No roles mapped out of 1 KOs	Arginine biosynthesis	Transglutaminase-like protein	3.90443212	0.03800805	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
84079.1	Amino acid metabolism	Purine metabolism	Adenylosuccinylase	3.903719377	0.01468307	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
154409.11	Nucleic acid metabolism	Purine metabolism	Phosphoribosylformylglycinamide cyclo-ligase	3.902846451	0.030071737	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Verrucomicrobia Verrucomicrobia	Verrucomicrobia bacterium
159030.6	No roles mapped out of 1 KOs	Polymerase	Uncharacterized protein	3.90252269	0.01786089	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri	uncharacterized bacterium
46243.2	Transcription	Polymerase	DNA-directed RNA polymerase subunit beta	3.90215871	0.02472638	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales	Rhizobiales bacterium
1515839.1	No roles mapped out of 1 KOs	Protein export, secretion, and sorting	DNA binding response regulator	3.900886154	0.00204246	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
161129.5	Transport and binding proteins	Calos and iron carrying compounds	NarX/NarJ antiporter subunit	3.90064549	0.04630801	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Micrococci Micrococci	Arthrobaacter sp. 9C14
168275.1	Amino acid metabolism	Histidine metabolism	Indoxylglyoxylate phosphate dehydratase	3.90055669	0.02795886	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales	
102544.13	Nucleic acid metabolism	Replication, recombination, and repair	Topoisomerase II	3.900279492	0.01962838	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Rhizobiales Rhizobiales	Oxibacteriales bacterium
565819.7	No roles mapped out of 1 KOs	Carbohydrate metabolism	Response regulator receiver domain-containing protein	3.900258191	1.15E-07	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
116922.2	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	2.99934324	0.03868163	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Rhizobiales	Rhizobiales bacterium
100566.7	No roles mapped out of 1 KOs	Carbohydrate metabolism	TPR_2ncrym_C domain-containing protein	2.99871349	0.04518897	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri	
167191.9	Defense and invasion systems	Detoxification and inactivation	Allyl hydroperoxide reductase protein F	2.98978018	0.04148683	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
151827.2	No roles mapped out of 1 KOs	Detoxification and inactivation	Uncharacterized protein	2.988127787	0.02052074	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
120054.2	No roles mapped out of 1 KOs	Carbohydrate metabolism	Beta-lactamase	2.97936225	0.03581582	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Genmatimae Genmatimae Genmatimae Genmatimae	Genmatimae bacterium
22059.9	No roles mapped out of 1 KOs	Energy metabolism	Dfd450 domain-containing protein	2.962879711	0.03141382	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Methylobacteriales	Methylobacteriales bacterium
89362.1	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit alpha	2.95413864	0.04877766	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Rhizobiales	Rhizobiales bacterium
96484.1	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	Putative UDP-glucose-hexose 1-phosphate uridylyltransferase	2.94879927	0.03476023	Gefamiprin_Erinchocelatato_OtherSubstrates	Archaea	Thaumarchaeota Thaumarchaeota	
96370.8	Transport and binding proteins	Amino acids, peptides and amines	Leucine/isoleucine/valine transporter subunit ATP-B	2.94011241	0.04940534	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria	uncharacterized Actinobacteri bacterium
47428.2	Signal transduction	Phosphotransferase system (PTS)	Phosphotransferase system (PTS) phosphotransferase	2.93747482	3.24E-08	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri	Actinobacteri bacterium
931781.5	Fatty acid and lipid metabolism	Bioynthesis	Carbamoyl phosphate synthetase	2.93402431	0.03048039	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
119211.2	Transcription	General	Uncharacterized protein	2.93144572	0.000171437	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
278227.9	No roles mapped out of 2 KOs	Pestigallin metabolism	D-Alanine-D-alanine ligase	2.916217853	0.04371155	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Sphingomonas Sphingomonas	Sphingomonas sp. T127-24
110795.1	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit alpha	2.903445420	0.02795886	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Rhizobiales Rhizobiales	Rhizobiales bacterium
62284.5	Prosthetic groups, cofactors, and carriers	Nicotinate and nicotinamide metabolism	NAD(P) transhydrogenase subunit beta	2.89363483	0.01109197	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
99331.1	Transport and binding proteins	Amino acids, peptides and amines	Peptide ABC transporter substrate-binding protein	2.88744245	0.01939282	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Firmicutes Clostridia	Clostridia bacterium
127852.2	Transcription	Ribosomal proteins: synthesis and modification	60S ribosomal protein S16	2.88691249	0.01977976	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Bacteroidetes Bacteroidetes	Bacteroidetes bacterium
154953.3	No roles mapped out of 1 KOs	Prosthetic groups, cofactors, and carriers	Uncharacterized protein	2.886790021	0.04725064	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
159059.1	Transcription	Gene-duplication	GenA domain-containing protein	2.886749615	0.00213267	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
142928.2	Amino acid metabolism	Phenylalanine metabolism	D-alanine oxidohydrogenase	2.873727074	0.00317929	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
301362.1	No roles mapped out of 1 KOs	Ribosomal proteins: synthesis and modification	Rpl138 domain-containing protein	2.865724485	0.00892824	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
124209.3	Transcription	Transcription factors	60S ribosomal protein L3	2.849627837	0.04203886	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Flavobacteriales Flavobacteriales	Flavobacteriales bacterium
143882.4	No roles mapped out of 1 KOs	Transcription	Flavin, Reduct domain-containing protein	2.84423312	1.26E-08	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
161139.3	Nucleic acid metabolism	Oxidative phosphorylation, and repair	Chromosomal replication initiator protein DnaX	2.837848309	0.04963838	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacter Actinobacteri Streptomyces Streptomyces	
742320.5	Carbohydrate metabolism	Carbohydrate metabolism	Ribose ABC transporter, periplasmic-rose-binding p	2.829217942	0.01127764	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonas	
143129.1	No roles mapped out of 1 KOs	Cytosolic (TCA) cycle	Uncharacterized protein	2.82864079	0.00972887	Gefamiprin_Erinchocelatato_OtherSubstrates	Eukaryota	Arthropoda Branchiopoda Diplostroa Diplostroa	Diplostroa magna
65009.7	Carbohydrate metabolism	Cytosolic (TCA) cycle	Phosphotransferase system (PTS) phosphotransferase I	2.818357601	0.03285623	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Rhizobiales Rhizobiales	Rhizobiales bacterium
64021.6	Transport and binding proteins	Unknown substrate	ABC 2-type transporter	2.81801205	0.04379608	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Actinobacteri	Actinobacteri bacterium
110795.1	No roles mapped out of 1 KOs	Carbohydrate metabolism	Uncharacterized protein	2.80941309	0.01793171	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
90274.2	Carbohydrate metabolism	Carbohydrate and folding catalysis	Phosphoglucomutase	2.807020328	2.7E-09	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available		
93705.1	Carbohydrate metabolism	Glycolysis/Gluconeogenesis	PCQ-dependent dehydrogenase, methanol/ethanol f	2.797232626	0.00648187	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales Comamonadaceae	
93146.9	Carbohydrate metabolism	Glycolysis/Gluconeogenesis	Enolase	2.79696334	0.01287878	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales Comamonadaceae	Comamonadaceae bacterium
184742.3	Nucleic acid metabolism	Replication, recombination, and repair	ATPase, gamma system A	2.79255131	0.00199976	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
171813.2	Cell structure, growth, and death	Spore formation and germination	SporeA family protein	2.771494226	0.00068085	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria Rhizobiales	Rhizobiales bacterium
160099.7	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	Uncharacterized protein	2.771262123	0.00328029	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Gammaproteobacteria Pseudomonas Pseudomonadaceae	
80225.11	Transcription	Transcription factors	RNA polymerase sigma factor RpoD	2.771146663	0.006627446	Gefamiprin_Erinchocelatato_OtherSubstrates	Bacteria	Proteobacter Alphaproteobacteria Rhizobiales Bradyrhizobiales	Bradyrhizobiales bacterium
157318.3	No roles mapped out of 1 KOs	Arginine biosynthesis	Antimicrotransferrase	2.769379966	3.12E-05	Gefamiprin_Erinchocelatato_OtherSubstrates	No taxonomic annotation available</		

494343_4	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S9	2.115007707	012969113	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1612780_1	Translation	Transfer f biogenesis	30S ribosomal protein S10	2.115344010	012969113	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Chryseolinea	Chryseolinea	flava	
193870_3	Nucleic acid metabolism	Pyrimidine	CTP synthase	2.150508709	012721759	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium ADuB18425	
1304266_6	Transcription	ATP-dependent RNA helicase DhsA	ATP-dependent RNA helicase DhsA	2.142046262	013035727	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
931051_47	Energy metabolism	Oxidative phosphorylation	Adenosine c dehydrogenase 1	2.138813930	010331768	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes						
1042830_10	Transport and binding proteins	High-affinity choline transport protein	High-affinity choline transport protein	2.115736505	010308114	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
101297_1	No roles mapped out of 0 KOs	Uncharacterized protein	Uncharacterized protein	2.115736505	010308114	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
212329_2	Prosthetic groups, cofactors, and carriers	Coenzyme M	Coenzyme M	2.139522294	010942458	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Chryseolinea	Nitrosopira	Nitrosopira	Nitrosopira	Candidatus Nitrosopira gagensis
367274_4	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein L4	2.12284832	012312079	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1184045_3	No roles mapped out of 0 KOs	Uncharacterized protein	Uncharacterized protein	2.12284832	012312079	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
122273_7	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein L1	2.121476759	010780695	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
1110355_5	Intracellular trafficking, assembly, and processing	Chaperone and folding catalyst	Chaperone protein DnaK	2.112123965	010904953	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
140291_1	Nucleic acid metabolism	DNA replication, recombination, and repair	DNA replication, recombination, and repair	2.110291418	012245112	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
1668731_4	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein S12	2.107181133	010274721	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
205679_5	Carbohydrate metabolism	Ribonucleotide dehydrogenase	Ribonucleotide dehydrogenase	2.080827076	010802778	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
110472_49	Transport and binding proteins	Interactin subunit	Interactin subunit	2.084442295	0106442295	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Archea	Archaeota	Thaumarchaeota	Thaumarchaeota	Basilliales	Bacillus	
1513701_4	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein S10	2.088182628	010674728	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
897925_3	Intracellular trafficking, assembly, and processing	Intracellular trafficking, assembly, and processing	NDH9-dependent metalloprotease PstH	2.081493937	010431013	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
151144_3	Carbohydrate metabolism	Pyruvate metabolism	Acetyltransferase component of pyruvate dehydrogenase	2.087919154	010808993	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
192960_3	Translation	Ribosomal proteins: synthesis and modification	Ribosomal protein L4	2.078332004	010844839	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
329483_1	No roles mapped out of 0 KOs	Uncharacterized protein	Glyoxal oxidase-like protein	2.076100808	010426189	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Betaproteobacteria	Nitrospirillum	Nitrospirillum	Nitrospirillum	Nv12	
951292_1	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S9	2.067446075	010571813	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Chryseolinea	Chryseolinea	flava	
193183_2	Prosthetic groups, cofactors, and carriers	Polyphosphorylation	Putative metal chaperone Y1C	2.067446075	010571813	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
897198_1	No roles mapped out of 1 KOs	Chaperone and folding catalyst	Carboxon starvation protein A	2.058486463	010393795	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
1154207_22	Intracellular trafficking, assembly, and processing	Intracellular trafficking, assembly, and processing	NADH-dependent betaine aldehyde dehydrogenase	2.057044149	010224064	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
180031_6	Amino acid metabolism	Glycine, serine and threonine metabolism	Transketolase	2.055404997	010369791	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Ohtaekawa	Koreans	
1413190_2	Carbohydrate metabolism	NAD(P) dependent alcohol dehydrogenase	NAD(P) dependent alcohol dehydrogenase	2.051401214	010369791	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Ohtaekawa	Koreans	
1624440_2	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	Glyoxal synthase large subunit	2.041409239	2.51E-08	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Chryseolinea	Chryseolinea	flava	
104478_3	Cell structure, growth, and death	Cell division	Cell division protein FtsK	2.040261031	010720078	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1045661_11	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein L11	2.040261031	010720078	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
106796_3	Cell structure, growth, and death	Two-component systems	DUF2807 domain-containing protein	2.031160996	011133824	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1420096_3	Amino acid metabolism	Chaperone and folding catalyst	Chaperone protein DnaK	2.031160996	011133824	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
601348_5	Intracellular trafficking, assembly, and processing	Protein modification and repair	Agoniprotein N acetyltransferase	2.024945645	010254171	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium ADuB18037	
929729_3	Intracellular trafficking, assembly, and processing	Translation factors	Elongation factor G	2.024404641	010762005	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
104236_4	No roles mapped out of 0 KOs	Uncharacterized protein	Genomic endonuclease (Fragment)	2.020879055	010624041	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
549790_7	Intracellular trafficking, assembly, and processing	Chaperone and folding catalyst	60 kDa chaperonin	2.010358942	010872543	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
104274_19	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein L1A	2.007411725	010428762	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
1448802_10	Glycan biosynthesis and metabolism	UDP-N-acetylglucosamine 6-epimerase	UDP-N-acetylglucosamine 6-epimerase	2.007411725	010428762	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1130999_4	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit beta	1.996239586	010451338	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
127812_2	Transcription	DNA-directed RNA polymerase subunit beta'	DNA-directed RNA polymerase subunit beta'	1.992398807	010378007	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
100650_16	Amino acid metabolism	Histidine metabolism	Forminimidylglyoxylate deiminase	1.981126213	010761106	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonas	Pseudomonas	Pseudomonas	putida	
104022_2	Amino acid metabolism	Valine, leucine and isoleucine metabolism	Threonine dehydratase	1.979317766	010473194	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
160023_1	Energy metabolism	DNA replication, recombination, and repair	DNA-directed RNA polymerase subunit beta'	1.975281214	010204048	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
160202_2	Transcription	DNA replication, recombination, and repair	DNA-directed RNA polymerase subunit beta'	1.975281214	010204048	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
43384_8	Intracellular trafficking, assembly, and processing	Chaperone and folding catalyst	Chaperone protein Hsc70	1.974736151	010808044	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
104210_3	Unknown function	ATPase	ATPase	1.969361316	010902186	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Firmicutes	Clostridia	Clostridiales	Petropococcus	Candidatus Candidatus Desulfurococcus	sp.	
100431_3	Signal transduction	Phosphate regulator sensor protein PhoK	Phosphate regulator sensor protein PhoK	1.968233719	010209490	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
427466_2	Energy metabolism	DNA replication, recombination, and repair	DNA-directed RNA polymerase subunit beta'	1.967235938	010251718	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
24096_3	No roles mapped out of 0 KOs	Uncharacterized protein	DUF4157 domain-containing protein	1.957795242	010403989	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
36077_17	Nucleic acid metabolism	DNA replication, recombination, and repair	PrnA	1.954936055	010398545	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
551409_1	No roles mapped out of 0 KOs	Uncharacterized protein	PrnA	1.951432529	010398545	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1711813_9	Translation	Ribosomal proteins: synthesis and modification	50S ribosomal protein L4	1.951081771	010370749	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
897176_1	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S8	1.951788319	010212480	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
1172805_6	Prosthetic groups, cofactors, and carriers	Ribosomal proteins: synthesis and modification	50S ribosomal protein L12	1.950162224	010381163	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
131882_1	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S1	1.944873355	010302083	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
102458_24	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit beta	1.932494969	010378007	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
1114160_4	Nucleic acid metabolism	Purine metabolism	Adenosine phosphoribosyltransferase	1.927544549	010880417	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
61774_10	Defense and invasion systems	Detoxification and inactivation	Allyl hydroxylase reductase subunit C11e protein	1.924639446	010391226	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
191725_2	Nucleic acid metabolism	Purine metabolism	5-methyltetrahydrofolate glycinamide synthase	1.921420033	010454602	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonas	Pseudomonas	Pseudomonas	putida	
185030_4	Energy metabolism	Oxidative phosphorylation	ATP synthase gamma chain	1.917919233	010133843	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
206331_8	Fatty acid and lipid metabolism	Bioisoprenylation	3-hydroxyacyl-CoA synthase	1.916413213	010008406	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
62545_14	Amino acid metabolism	Proteinase, alanine, tyrosine and tryptophan biosynthesis	Proteinase, alanine, tyrosine and tryptophan biosynthesis	1.915090614	010508171	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
198970_14	Intracellular trafficking, assembly, and processing	Chaperone and folding catalyst	60 kDa chaperonin	1.909779384	010099719	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes					Bacteroidetes bacterium	
724616_9	No roles mapped out of 0 KOs	Uncharacterized protein	Uncharacterized protein	1.906604422	010409289	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonas	Pseudomonas	Pseudomonas	putida	
124807_3	No roles mapped out of 1 KOs	Uncharacterized protein	MuK-like ATPase	1.902621449	010436495	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
103977_5	Transport and binding proteins	Anions	DUF320 domain-containing protein	1.905442091	010741704	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
74275_4	Nucleic acid metabolism	DNA replication, recombination, and repair	Type II DNA topoisomerase subunit B	1.894797968	010483280	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Bacteroidetes	Cytophaga	Cytophaga	Ohtaekawa	Ohtaekawa	Koreans	
141412_1	Translation	Translation factors	Elongation factor Tu	1.89388041	010614982	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Nevskiales	Sinobacter	Sinobacter	Sinobacter	
189925_2	No roles mapped out of 0 KOs	Uncharacterized protein	Senescence-associated protein	1.893247211	010112248	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Nevskiales	Sinobacter	Sinobacter	Sinobacter	
1070825_12	Defense and invasion systems	Secreted factors	Flagellin and cobalt efflux protein CnC	1.888888888	010391226	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Proteobacteria	Gammaproteobacteria	Nevskiales	Sinobacter	Sinobacter	Sinobacter	
345006_6	Energy metabolism	Iron transport	Formate dehydrogenase	1.8869291	010006434	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Chloroflexi					Chloroflexi bacterium	
177626_8	Translation	Translation factors	Initiation factor 1	1.885083188	010483280	Getamipin_Erwinchaelelatio_OtherSubstrates	Bacteria	Chloroflexi					Chloroflexi bacterium	
726510_4	Prosthetic groups, cofactors, and carriers	Ubiquitin and other terpenoid-quinone biosynthesis	3-oxoacyl-CoA synthase	1.878019687	010420455	Getamipin_Erwinchaelelatio_OtherSubstrates	No taxonomic annotation available							
597668_1	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	Glutamate synthase large subunit beta	1.874182442	010805848	Getamipin_Erwinchaele								

1023687_2	No roles mapped of 0 KOs		Murein D-endopeptidase MepM/ murein hydrolase	1.42928044	040477423	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1024162_1	Amino acid metabolism	Glycine, serine and threonine metabolism	2-phosphoglycerate 2-epimerase	1.42928212	040477424	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1026028_1	Cell motility and adherence	Flagella complex and associated proteins	Flagellar hook protein FlgE	1.43774078	040431797	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1027763_9	Nucleic acid metabolism	Replication, recombination, and repair	DNA topoisomerase I	1.439263786	040476724	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1029391_1	Transcription	RNA polymerase	RNA polymerase polymerase subunit beta'	1.44128101	040208366	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Actinobacteria Chloroflexi Chloroflexales Chloroflexaceae Chloroflexus Chloroflexus segnis	
1031130_3	Energy metabolism	Oxidative phosphorylation	Succinate dehydrogenase iron-sulfur subunit	1.44862555	040784080	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1032071_3	Energy metabolism	Oxidative phosphorylation	NADH:quinone oxidoreductase subunit F	1.449911217	040896449	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1032083_1	Transcription	RNA polymerase, synthesis and modification	S1 RNA polymerase (Fragment)	1.450292093	042242788	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1034440_2	No roles mapped of 0 KOs		Energy-dependent translocase protein ETTA	1.456077447	040564915	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1034450_1	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	Citrate synthase (NADH) large chain	1.456424047	040321773	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1034541_1	Energy metabolism	Oxidative phosphorylation	Cytochrome b	1.488913902	040300497	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1034550_1	No roles mapped of 0 KOs		Uncharacterized protein	1.490265825	040474026	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1034593_1	No roles mapped of 0 KOs		Iron reductase (DMAN/TAB) family NADH:FAD:NAD	1.51197863	04048027	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1034613_5	Translation	Transfer R biogenesis	Phenylalanine-tRNA ligase beta subunit	1.52049116	040289335	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Actinobacteria Micromonospora Micromonospora Krausella Krausella chromomera	
1034643_3	Transcription	Transfer R biogenesis	Ribonuclease P2	1.53308424	040204727	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1034785_1	No roles mapped of 0 KOs		HTF-type toxin-domain-containing protein	1.54278785	04039067	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1040244_4	Defense and invasion systems	Detoxification and inactivation	Anticoagulant_AhpC/75A family	1.538599224	040387787	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1040293_1	Cell structure, growth, and death	Division	Citrate synthase cooperator CsdB	1.54156113	040231738	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1043612_2	Unknown function	General	Putative phosphoenolpyruvate synthase regulatory protein	1.55324421	040423957	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1051596_4	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	Protein-export protein SecB	1.564603791	040267982	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1052935_16	No roles mapped of 0 KOs		Polysaccharide/lysine-granule-associated protein	1.570701007	040389794	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1059272_6	Glycan biosynthesis and metabolism	Peptidoglycan metabolism	Membrane-bound lytic murein transglycosylase D	1.57606335	040262888	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1062495_2	Signal transduction	Phosphotransferase system (PTS)	Phosphotransferase system phosphotransferase	1.576515068	040892021	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1118380_2	Carbohydrate metabolism	Glycolysis/ Gluconeogenesis	Phosphoenolpyruvate carboxylase (ATP)	1.576619713	040452458	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
128966_1	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	Glutamate synthase, large subunit, N term	1.580710264	040394726	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
129627_19	Prosthetic groups, cofactors, and carriers	Iron-sulfur clusters	F437 biogenesis protein WfsA	1.584844054	040265937	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
106627_21	Amino acid metabolism	Cysteine and methionine metabolism	Methionine synthase	1.58743357	040139045	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
101664_5	No roles mapped of 0 KOs		NAD-specific pyruvate dehydrogenase	1.600998756	040308323	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
101693_16	No roles mapped of 0 KOs		Iron-sulfur/oxalothionin-granule-associated protein	1.612002475	040482174	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
103901_6	Nucleic acid metabolism	Purine metabolism	Bifunctional (P)idipyr synthetase III and guanosine F	1.616821209	040101781	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
104443_9	Intracellular trafficking, assembly, and processing	Chromosome and folding factors	ATP-dependent Clp protease ATP-binding subunit ClpB	1.619397272	040424678	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
104457_1	Intracellular trafficking, assembly, and processing	Chromosome and folding factors	ATP-dependent Clp protease ATP-binding subunit ClpX	1.622719616	040383718	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
106805_2	Carbohydrate metabolism	General	Glucan biosynthesis protein G3	1.627513617	040007448	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
103002_1	Unknown function	General	PEP2323 protein PEP_1475	1.630950506	040309107	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
103302_6	Translation	Transfer factors	Elongation factor Ts	1.639207313	040074351	Getafamin	Deplete/Related/OtherSubstrates	Eukaryota	Arthropoda Insecta Phasmatodea Bacillales Bacillus	
105763_1	Unknown function	Enzymes of unknown specificity	Cadmoxytransferase	1.644620207	040774107	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Insecta	
106075_3	Glycan biosynthesis and metabolism	Glycan biosynthesis and metabolism	N-acetylmannosyl 6-epimerase D-glucuronate-2,6-d	1.639302025	040308323	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
106886_14	Energy metabolism	Oxidative phosphorylation	CB3-type cytochrome c oxidase subunit	1.66147176	040147238	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
101001_4	Nucleic acid metabolism	Reproduction	Ribonuclease R	1.670406813	040139304	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
102932_2	Signal transduction	Two-component systems	Response regulator C	1.67436397	04047204	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
104421_1	No roles mapped of 0 KOs		methanol:nicotinamide N channel	1.711740347	040662053	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
102786_3	Amino acid metabolism	Lysine biosynthesis	2-hydroxy-2-thiopyridine synthase	1.712766195	040398188	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
75108_3	Carbohydrate metabolism	Starch and sucrose metabolism	Alpha-1,4-glycan phosphorylase	1.719798117	040386053	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1031760_4	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	Ugopeptin	1.723579713	040540032	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1032070_2	Cell motility and adherence	Surface structures and assembly platforms	Response regulator GsaA	1.740261829	040882765	Getafamin	Deplete/Related/OtherSubstrates	No taxonomic annotation available		
1032763_6	Cell structure, growth, and death	Chromosome and associated proteins	ParB domain-containing protein	1.742536246	040540131	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1037026_3	Defense and invasion systems	Protein, prosthetic group, membrane repair	Pyridoxal methionine sulfide reductase NrdA	1.744862211	040130484	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1040125_3	Glycan biosynthesis and metabolism	Peptidoglycan metabolism	N-acetylglucosaminyl 1,4-beta-D-glucosyltransferase	1.749397267	040487265	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1051731_2	Transcription	Transcription factors	RNA polymerase-binding transcription factor DNA	1.760446244	040430384	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1040131_4	Cell motility and adherence	Surface structures and assembly platforms	Flagellin	1.76053925	040403884	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1042748_6	Intracellular trafficking, assembly, and processing	Chaperone and folding factors	ATP-dependent Clp protease ATP-binding subunit ClpC	1.762370797	040663577	Getafamin	Deplete/Related/OtherSubstrates	Eukaryota	Arthropoda Insecta Phasmatodea Bacillales Bacillus	
1056892_1	Transcription	Energy metabolism	RNA polymerase-associated protein RPA	1.764101987	040424024	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
105199_9	Energy metabolism	Oxidative phosphorylation	Cytochrome b	1.76621087	040482174	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
102555_4	Glycan biosynthesis and metabolism	Peptidoglycan metabolism	Penicillin-binding protein 1A	1.787288489	040622320	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae
107229_2	Transcription	Ribosomal proteins: synthesis and modification	50S ribosomal protein L9	1.799739403	040106887	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Gemmatimonadetes bacterium	
1068962_2	Nucleic acid metabolism	Replication, recombination, and repair	DNA topoisomerase II	1.800646161	040187458	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
107894_3	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit alpha	1.815512623	040404845	Getafamin	Deplete/Related/OtherSubstrates	Eukaryota	Arthropoda Insecta Phasmatodea Bacillales Bacillus	
1012213_5	Intracellular trafficking, assembly, and processing	Peptides	Stable cellulosomal glucanase	1.816279255	040132748	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
438479_1	No roles mapped of 0 KOs		Uncharacterized conserved protein YJL1, contains Glyc	1.824418458	040488984	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
428416_1	Nucleic acid metabolism	Replication, recombination, and repair	DNA gyrase subunit A	1.838779331	040452496	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
107116_1	Transcription	Transfer R biogenesis	Phenylalanyl-tRNA synthetase (His) amidotransferase: Gamma	1.83920447	040483275	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1036624_2	Transport and binding proteins	Regulatory functions	GT-binding protein YnfP/YnfM	1.841610335	040488884	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1032654_24	Transport and binding proteins	Regulatory functions	Unknown subunit	1.844172029	040186725	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	Acidobacteria	
104004_1	Carbohydrate metabolism	Glycolysis/ Gluconeogenesis	Adipate kinase (TCA cycle)	1.845219011	040173777	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
103197_1	No roles mapped of 0 KOs		HFH-type transcriptional regulator FhuH	1.846487939	040300617	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
104004_1	Regulatory functions	General	HTF-type toxin-domain-containing protein	1.846879178	040484738	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
103195_3	Amino acid metabolism	Glycine, serine and threonine metabolism	Glycine cleavage system H protein	1.871727527	040453217	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1040270_3	Intracellular trafficking, assembly, and processing	Protein modification and repair	Signal peptidase	1.871979775	04051252	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
103768_2	Defense and invasion systems	Detoxification and inactivation	Enzyme	1.87238959	040143467	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
106201_2	Fatty acid and lipid metabolism	Fatty acid degradation	Long-chain fatty-acyl-CoA ligase	1.877956179	040306729	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1081121_2	Transcription	Fatty acid metabolism	Valine-tRNA ligase	1.891141286	040129786	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1079158_2	Defense and invasion systems	Defense and invasion systems	Vancomycin 8-phosphate acyltransferase	1.894319788	040398188	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1080538_6	No roles mapped of 0 KOs		Glycyltransferase	1.910728926	040424374	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Bacteroidetes	
1120002_19	Transport and binding proteins	Surface structures and assembly platforms	Flagellin	1.912691085	040403884	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1034521_2	Unknown function	General	Decarboxylase family protein	1.927737084	040274730	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1101073_6	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S19	1.938991324	040229955	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Firmicutes Bacilli Bacillales Bacillales	
1084316_6	No roles mapped of 0 KOs		Link domain-containing protein	1.943481872	040454187	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1032763_6	Cell structure, growth, and death	Chromosome and associated proteins	AAA_11 domain-containing protein	1.956028829	040434266	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1041763_3	Glycan biosynthesis and metabolism	Polysaccharide and lipopolysaccharide metabolism	OTF-4-dehydroformyltransferase	1.959746729	040028077	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1103044_4	Regulatory functions	Regulatory functions	Protein motor switch protein FliG	1.960227254	040473724	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1081203_3	Fatty acid and lipid metabolism	Bioisoprenoids	Malonyl-CoA-acyl carrier protein transacylase	1.966337329	040474723	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1051518_14	No roles mapped of 0 KOs		Uncharacterized protein	1.966731541	040209124	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1040641_1	Intracellular trafficking, assembly, and processing	Peptides	DsC	1.972454889	0401763106	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
106839_4	No roles mapped of 0 KOs		Nrd_X_in_Vnrf	1.973141981	040187736	Getafamin	Deplete/Related/OtherSubstrates	Nrd_X_in_Vnrf		
1041737_10	Defense and invasion systems	Detoxification and inactivation	OTF-4-dehydroformyltransferase	1.979961487	040187736	Getafamin	Deplete/Related/OtherSubstrates	Bacter	Acidobacteria Thaumarchaeota Solirubrobacterales Solirubrobacterales bacterium URH00059	
1085041_5	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	GABT	1.997614864	040348805	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1038462_2	Transcription	Transcription factors	Transcription termination/antitermination protein Nts	1.998223396	04011388	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Chloroflexi Thermoanaerobacteriales Sphaerobacterales Sphaerobacterales Sphaerobacterales Sphaerobacterales bacterium	
1038462_2	Transcription	Transcription factors	Transcription factors	1.998223396	04011388	Getafamin	Deplete/Related/OtherSubstrates	OtherSubstrates	No taxonomic annotation available	
1038462_2	Transcription	Transcription factors	Channel protein TolC	1.999000928	040388388	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1038462_2	Transcription	Transcription factors	Phosphoenolpyruvate carboxylase	1.999000928	040388388	Getafamin	Deplete/Related/OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomonas Pseudomonadaceae	
1038462_2										

846831_4	No roles mapped out of 0 KOs	Sensor protein Zra5	3.158883265	0.02260184	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
426866_4	Transport and binding proteins	USP-N-acetylmuramoyl-L-peptide-D-alanyl-D-alain	-3.17283804	0.02913208	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
173023_1	Carbohydrate metabolism	Phosphoenolpyruvate carboxylase	-3.17678234	0.02918807	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1272649_6	Regulatory functions	GlnR	-3.199807567	0.03211296	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1380875_6	Glycan biosynthesis and metabolism	Regioepithecium	-3.20028875	0.02752846	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
914104_8	Unknown function	Alpha-2-macroglobulin family protein	-3.20770485	0.0425371	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
1817386_2	Translation	Ribosomal RNA large subunit methyltransferase F	-3.211284917	0.02628093	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1854475_1	Nucleic acid metabolism	ATP-dependent helicase, putative	-3.22245675	0.02020713	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
964204_4	Carbohydrate metabolism	Phosphoenolpyruvate carboxylase (Fragment)	-3.232468618	0.02543345	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
40231_5	Nucleic acid metabolism	GTP phosphohydrolase, (Pip)Gpp synthetase I / Gua	-3.23662526	0.03704748	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
622824_1	Amino acid metabolism	Lysine degradation	-3.24102578	0.02343842	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
180033_2	Transport and binding proteins	Substrate binding region of ABC-type glycine betaine	-3.24188577	0.04254107	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
1317020_7	Transport and binding proteins	Unknown substrate	-3.245182028	0.03971731	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1741964_3	No roles mapped out of 1 KOs	Sigma 54 dependent transcriptional regulator	-3.259840756	0.03876374	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
1465964_1	Transport and binding proteins	OmcC	-3.271849417	0.02027548	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	
705374_10	Defense and invasion systems	Pointin and secretin	-3.27286441	0.04464663	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1831351_1	Cell structure, growth, and death	Detoxification and inactivation	-3.278444546	0.01854071	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
486024_3	Amino acid metabolism	Cell division	-3.28223272	0.01583406	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1204954_4	Prosthetic groups, cofactors, and carriers	Phenylalanine, tyrosine and tryptophan biosynthesis	-3.311317144	0.016538609	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
104792_3	Nucleic acid metabolism	Thymidine metabolism	-3.350452	0.0324002	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1356573_9	Metabolism of other amino acids and amines	Oxalium metabolism	-3.35817035	0.020025281	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
892368_3	No roles mapped out of 0 KOs	Pimeloyl-ACP methyl ester carboxylesterase	-3.375286231	0.035217737	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
1713183_9	Intracellular trafficking, assembly, and processing	Heat shock protein 15	-3.400460906	0.04868289	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
525336_5	Carbohydrate metabolism	Starch and sucrose metabolism	-3.41514102	0.049105132	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
209456_5	Cell motility and adherence	TZSP_E domain-containing protein	-3.42072072	0.031627099	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1632462_8	No roles mapped out of 0 KOs	Nuc_in_Uinref	-3.455269148	0.020035339	Gentamycin_DepleteRelativeTo_OtherSubstrates	Nuc_in_Uinref	
100336_2	No roles mapped out of 1 KOs	NTF Family protein RsaA	-3.479380167	0.025178194	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
43261_1	Cell motility and adherence	Flgk	-3.483748542	0.02229915	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
250222_5	Carbohydrate metabolism	6-phosphogluconate dehydrogenase, decarboxylating	-3.488212599	0.01604946	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
722750_18	Transcription	Regulator of nucleoside diphosphate kinase	-3.50958794	0.010130049	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
1342427_9	Transport and binding proteins	Zinc transporter	-3.512209963	0.011284868	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
705374_11	Transport and binding proteins	ABC transporter domain-containing protein	-3.53689006	0.030781017	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
1177983_1	Transport and binding proteins	Periplasmic dipptide transport protein	-3.570226037	0.01031811	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1126172_2	No roles mapped out of 0 KOs	circulantly permuted type 2 ATP-grp protein	-3.57157226	0.017072316	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
799293_13	Glycan biosynthesis and metabolism	Lipid 4 deacylase	-3.601340642	0.02722638	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
1247813_6	Amino acid metabolism	Aminotransferase (Fragment)	-3.607174763	0.000215509	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Deltaproteobacteria
910538_4	Regulatory functions	Bifunctional uridylyltransferase/uridylyl-removing enz	-3.620545556	0.02943804	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
902817_4	Energy metabolism	NADH:quione oxidoreductase subunit G	-3.65140804	0.011619786	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
280474_5	Transport and binding proteins	OpaK domain-containing protein	-3.654124846	0.018913384	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
154121_13	Amino acid metabolism	Ambrosinate phosphoribosyltransferase	-3.65931176	0.027574897	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacteria
904622_24	No roles mapped out of 0 KOs	Signal transduction histidine kinase	-3.664652398	0.023438462	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
554328_4	Energy metabolism	Thiosulfate sulftransferase, rhodanese	-3.669730107	0.011332332	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
126446_5	Terpenoids and polyketides metabolism	Ditranz,polycis-undecaprenyl-diphosphate synthase (I	-3.707168913	0.005020721	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
567378_8	Signal transduction	Chemotaxis protein	-3.72734428	0.01741892	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
347665_3	No roles mapped out of 0 KOs	Uncharacterized protein	-3.77906263	0.03818384	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Betaproteobacteria
1246446_6	Translation	Uncharacterized protein	-3.781173134	0.0071338	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
419369_1	Terpenoids and polyketides metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthas	-3.827964016	0.0071338	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1184465_6	Carbohydrate metabolism	Alpha-1,4-glucan:maltose-3-phosphate maltoyltransf	-3.871776044	0.02490917	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
1280533_5	Regulatory functions	Acetolactate synthase 3 regulatory subunit	-3.878102777	0.016490291	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	
247444_9	Transport and binding proteins	Omp_B3orf domain-containing protein	-3.898124955	0.024293117	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
44057_3	Signal transduction	OmpB-like domain-containing protein	-3.91022641	0.01048511	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonadaceae
260776_8	Energy metabolism	Cytochrome c domain-containing protein	-3.94159424	0.026191942	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
810515_3	Energy metabolism	Fumarate reductase flavoprotein subunit	-3.96213936	0.02941937	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Actinobacter Actinobacter Streptomyces Thermomonas Actinobacilli Actinobacilla Heredia
852023_2	Transport and binding proteins	SBP_bac_5 domain-containing protein	-3.97599567	2.18E-05	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Candidatus Rokubacteria
121895_6	No roles mapped out of 0 KOs	SucP/RagA Family TorB-linked outer membrane prot	-4.091162582	0.026136884	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Candidatus Rokubacteria
391218_14	Translation	35S (ribosomal protein S11	-4.158512663	0.032026446	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Bacteroidetes
899225_2	Nucleic acid metabolism	DntI	-4.188245151	0.049421335	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
18149920_2	No roles mapped out of 0 KOs	Uncharacterized protein	-4.19380851	0.029326523	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Actinobacter Actinobacter Corynebacter Corynebacter Corynebacterium Jellekium
1742062_5	Carbohydrate metabolism	Glyoxylis / Gluconogenesis	-4.210212784	0.01493854	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
1742062_5	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	-4.274920643	0.024384955	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
826564_1	No roles mapped out of 0 KOs	hypothetical protein	-4.274740772	0.02502073	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Proteobacter Gammaprotei Pseudomona Pseudomonas
1509965_5	Transport and binding proteins	Arginine/ornithine ABC transporter, periplasmic argir	-4.369200599	0.02448094	Gentamycin_DepleteRelativeTo_OtherSubstrates	No_taxonomic_annotation_available	
204346_3	No roles mapped out of 0 KOs	Beta-lactamase domain-containing protein	-4.424838014	0.026236978	Gentamycin_DepleteRelativeTo_OtherSubstrates	Bacteria	Chloroflex
							Chloroflex bacterium 54-19