

Supplemental Table 1: List of significantly enriched transcripts in polyphosphates modulators ('Ypsi' and 'Pectin') relative to simple substrates ('Xylose' and 'NAG') models. The 'Glucanase' models were excluded from this analysis. The function 'results' from the DESeq2 package was used on the (DESeq) data object to determine enrichment. 'Polyphosphate' vs. 'SimpleSubstrate' models, where the 6 replicates for each (i.e. 3 Xylose + 3 NAG) were pooled for each comparison. Transcripts that had a significant (adjusted p-value < 0.05) log2(FoldChange) value greater than 1 or less than -1 were retained. KEGG and UniProt annotations (including taxonomic information) were then added for transcripts that had a match to one or both databases. Results are sorted by the average |log2(FoldChange)| to determine which transcripts were most consistently highly enriched (log2(FoldChange > 1) or log2(FoldChange < -1) in polyphosphates). Note: transcripts with more than one KEGG hit have only the first hit listed.

Transcript	KEGG Category	KEGG Pathway	UniProt Name	log2(FoldChange)	adjusted p-value	Enrichment	Domain	Phylum	Class	Order	Family	Genus	Species
176052_2	Cyan biosynthesis	Phenylalanine and tyrosine metabolism	4-β-glucosyl-L-phenylalanine	4.819797	1.32E-10	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
176183_1	No hits mapped out of 4 KOs		Not in UniProt	14.217541	1.01E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
176183_1	Transcription	Transcription factors	DNA-directed RNA polymerase subunit beta	14.000961	1.56E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
356336_6	No hits mapped out of 4 KOs		Not in UniProt	13.874841	1.10E-15	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
176115_7	Intracellular trafficking, assembly, and processing	Peptidases	Proteinase subtilisin-like serine protease	13.764027	5.85E-15	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
177011_7	No hits mapped out of 4 KOs		Uncharacterized protein	13.712126	2.23E-10	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
91239_1	No hits mapped out of 4 KOs		Uncharacterized protein	13.679489	2.41E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
181440_25	No hits mapped out of 4 KOs		Uncharacterized protein	13.599051	1.31E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
176122_3	Transport and binding proteins	Amino acids, peptides and amines	SAP, 5', domain-containing protein	13.579633	3.17E-10	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
347465_3	No hits mapped out of 4 KOs		Uncharacterized protein	13.508364	2.43E-12	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
180444_7	Prosthetic group, cofactors, and carriers	Folate biosynthesis	5,6,7,8-tetrahydrofolate synthase	13.461258	9.93E-10	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
180527_3	No hits mapped out of 4 KOs		Uncharacterized protein	13.427173	3.17E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
180519_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.425283	4.85E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
110372_3	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S10	13.313781	1.07E-15	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
356687_2	Translation	Translation factors	Elongation factor Tu	13.308841	2.34E-15	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
156488_4	No hits mapped out of 4 KOs		Uncharacterized protein	13.273586	2.88E-18	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
200436_3	No hits mapped out of 4 KOs		Uncharacterized protein	13.200972	1.55E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
76789_18	Transcription	Transcription factors	Cold shock protein	13.093101	6.00E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
204345_13	Carbohydrate metabolism	Citrate cycle (TCA cycle)	Citrate synthase	13.018066	1.83E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
43530_3	Transport and binding proteins	Peritrichous flagella	Peritrichous flagellin (Flagment)	13.018066	1.83E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
162482_8	No hits mapped out of 4 KOs		Uncharacterized protein	13.018066	1.83E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
413711_3	No hits mapped out of 4 KOs		Uncharacterized protein	13.018066	1.83E-16	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1074415_1	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	Protein translocase subunit SecY	13.040309	1.23E-18	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
171825_2	No hits mapped out of 4 KOs		Uncharacterized protein	13.024326	9.83E-14	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1754050_5	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S1	13.023275	8.11E-19	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
390311_7	No hits mapped out of 4 KOs		Uncharacterized protein	13.023275	8.11E-19	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
71371_7	Translation	Translation factors	Elongation factor Tu	13.023275	8.11E-19	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
781051_4	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein S16	13.023275	8.11E-19	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
300020_2	No hits mapped out of 4 KOs		Uncharacterized protein	13.023275	8.11E-19	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
107839_2	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit b6	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
813382_1	Translation	Transfer RNAs	Glutamate-tRNA ligase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1005175_3	Translation	Transfer factors	Elongation factor Tu	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1101017_2	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
160683_8	Nucleic acid metabolism	Pyrimidine metabolism	UMP decarboxylase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
712723_11	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	Phosphoenolpyruvate carboxylase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1005175_3	Translation	Transfer factors	Elongation factor Tu	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
728033_2	Amino acid metabolism	Protein synthesis and tyrosine biosynthesis	Phenylalanine hydroxylase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1056877_27	Translation	Transfer factors	Elongation factor Tu	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
202111_3	Transcription	RNA polymerase	DNA-directed RNA polymerase subunit beta	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
814524_166	Unknown function	Enzymes of unknown specificity	Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1215396_6	Carbohydrate metabolism	Protein synthesis and tyrosine biosynthesis	Phenylalanine hydroxylase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1434751_11	Defense and invasion systems	Detoxification and inactivation	β-glucuronidase	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1437966_2	Translation	Transfer factors	Elongation factor Tu	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
82106_3	Translation	Ribosomal proteins: synthesis and modification	30S ribosomal protein L2	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
168126_2	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit a6	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
701127_2	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit a6	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
107551_8	Prosthetic group, cofactors, and carriers	Iron sulfur clusters	Iron sulfur cluster assembly scaffold protein (IscU)	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
329481_1	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1010820_2	Transcription	Transcription factors	Cold shock protein (Beta-Ribn, CspA family)	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
320053_6	Transcription	Transcription factors	Cold shock protein (Beta-Ribn, CspA family)	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
181879_29	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
762901_10	Defense and invasion systems	Secreted effectors	Secreted effector	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
180721_2	Transcription	Transcription factors	DNA-directed RNA polymerase subunit beta	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
1396533_3	Nucleic acid metabolism	Cell division	Cell division protein FtsZ	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str. XT7
105449_9	No hits mapped out of 4 KOs		Uncharacterized protein	13.017874	2.38E-11	Positive	PF01093	Bacteroidetes	Chloroflexi	Chloroflexiales	Flavobacteriales	Flavobacterium	str

300973,4	Amino acid metabolism	Cytosine and methionine metabolism	5-methylthioadenosyltransferase-homocysteine methyltr	9.7782104	1.38E+18	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
1235904,1	Transcription	Transcription factors	Transcription factor G, microRNA1	9.7782104	1.38E+18	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
93029,2	Transcription	Transcription factors	RNA polymerase sigma factor R9	9.7788716	1.56E+20	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Comamonadales	Varonaceae
1802828,3	No genes mapped out of 4 KDs	Transcription factors	Molecular chaperonin subunit beta	9.7808008	3.78E+19	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
52044,5	Transcription	Transcription factors	Elongation factor Tu	9.7908857	1.28E+15	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
1708081,1	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.7948472	6.88E+14	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
20396,5	Cell motility and adhesion	Flagellar complex and associated proteins	Flagellin	9.8464121	1.12E+14	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Comamonadales	Parvomonas
1482568,1	Transport and binding proteins	Unknown substrate	Uncharacterized protein	9.8364716	1.40E+08	PolysaccharideBacteria	Vercomicrobia		Vercomicrobia bacterium
76351,1	No genes mapped out of 4 KDs	Transcription factors	3-hydroxybutyrate dehydrogenase	9.8257519	6.52E+19	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
83380,3	No genes mapped out of 4 KDs	Ribosomal proteins: synthesis and modification	Hybrid sensor histidine kinase response regulator	9.6172005	3.59E+16	PolysaccharideBacteria	BacteroidetesCytophaga	CytophagalesCytophaga	Dyadobacter sp. AR-3-6
166428,10	Transcription	Citrate cycle (TCA cycle)	Isocitrate dehydrogenase	9.8061221	2.63E+19	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
31810,2	Carbohydrate metabolism	Ribosomal proteins: synthesis and modification	Isocitrate dehydrogenase [NADP]	9.5964725	3.72E+09	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
16044,2	No genes mapped out of 4 KDs	Ribosomal proteins: synthesis and modification	Glyoxylate hydratase	9.5822801	2.07E+10	PolysaccharideBacteria	ActinobacteriaActinobacteriales	Frankiales	MotifactorMotifactor
1743114,7	No genes mapped out of 4 KDs	Ribosomal proteins: synthesis and modification	Nucleoside diphosphate containing protein	9.5544895	9.54E+09	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
195281,2	Transcription	Transcription factors	Ribosomal protein L13	9.5381145	3.47E+11	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
200678,2	Carbohydrate metabolism	Pyruvate metabolism	Pyruvate dehydrogenase E component subunit alpha	9.5375105	1.83E+07	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
124931,2	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.5077135	4.11E+11	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
102975,11	No genes mapped out of 4 KDs	Transcription factors	CD14c-like domain containing protein	9.4885107	1.84E+08	PolysaccharideBacteria	Cyanobacteria		Cyanobacteria
48382,15	Transport and binding proteins	Transcription factors	Reactive sulfation protein SpsV	9.4840037	6.93E+14	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Comamonadales	Varonaceae
102359,4	Carbohydrate metabolism	Amino acids, peptides and amines	Transcription initiation factor R-3	9.473394	3.88E+14	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
178667,6	Metabolism of other amino acids and amines	Glutamine and analogs metabolism	Rhamnulose 1-phosphate aldolase/cholesterol dehydrogenase	9.4265971	1.00E+12	PolysaccharideBacteria	BacteroidetesCytophaga	Chitinophaga	Nisslella
176041,2	Transcription	Transcription factors	Glutamate-cysteine ligase	9.4343479	6.91E+15	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Rhizobium
15922,2	Intercellular trafficking, assembly, and processing	Peptidases	Lin peptidase	9.4435162	2.20E+10	PolysaccharideBacteria	ProteobacteriaGammaproteobacteria	Sinorhizobiales	Sinorhizobium
157127,2	Transcription	Transcription factors	RNA-binding transcriptional accessory protein	9.4099323	1.18E+08	PolysaccharideBacteria	BacteroidetesChitinophaga	Chitinophagales	Chitinophaga bacterium PMP31F
103272,2	Transcription	Ribosomal proteins: synthesis and modification	Ribosomal protein S10	9.4052113	5.09E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Ohtaewalgia
84407,7	Energy metabolism	Ketogen metabolism	Ferredoxin-cytochrome b5 reductase	9.3794973	1.01E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Ohtaewalgia	Ohtaewalgia koreensis
113141,7	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	Glyceraldehyde 3-phosphate dehydrogenase	9.3621299	4.02E+12	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria		
181749,3	No genes mapped out of 4 KDs	Transcription factors	Ribosomal protein S18	9.34806	1.42E+10	PolysaccharideBacteria	ProteobacteriaGammaproteobacteria	Xanthomonadales	Xanthomonas
176420,6	Transcription	Transcription factors	Elongation factor G	9.3408873	5.03E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
114144,3	Intercellular trafficking, assembly, and processing	Chaperone and folding catalysis	Peptidyl prolyl 4G-tran isomerase	9.3388116	6.44E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
49036,3	Transcription	Transcription factors	Protein-RNA ligase	9.3172690	4.54E+18	PolysaccharideBacteria	BacteroidetesCytophaga	Chitinophaga	Oxidobacterium
6079,2	Nucleic acid metabolism	Nucleic acid metabolism	Ribose-phosphate epimerase	9.3138878	6.57E+19	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
151422,4	Intercellular trafficking, assembly, and processing	Chaperone and folding catalysis	ATP-dependent Co-protease ATP-binding subunit Cpx	9.3174245	3.78E+10	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
192981,3	Transport and binding proteins	Transcription factors	OmpA family protein	9.3138129	2.14E+10	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Comamonadales	Parvomonas
20915,4	Transport and binding proteins	Peritrichous flagella	OmpA family protein	9.3138129	2.14E+10	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Comamonadales	Parvomonas
113352,56	Intercellular trafficking, assembly, and processing	Peptidases	ATP-dependent zinc metalloprotease FtsH	9.3032045	1.11E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
102528,3	No genes mapped out of 4 KDs	Transcription factors	CD14c-like domain containing protein	9.3032045	1.11E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
145454,9	No genes mapped out of 4 KDs	Transcription factors	PAS domain 5-coil containing protein	9.2878616	9.06E+09	PolysaccharideBacteria	ProteobacteriaAlphaproteobacteria	Bradyrhizobiales	Bradyrhizobium
137031,5	No genes mapped out of 4 KDs	Transcription factors	Proteinase subunit alpha	9.2864942	4.02E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Chitinophaga	Chitinophaga
33954,8	Transcription	Transcription factors	Transcription initiation factor F-2	9.2838781	5.38E+08	PolysaccharideBacteria	Arthropoda	Insecta	Phasmodinidae
191730,3	Intercellular trafficking, assembly, and processing	Chaperone and folding catalysis	Proteinase subunit alpha	9.2838781	5.38E+08	PolysaccharideBacteria	Arthropoda	Insecta	Phasmodinidae
103977,1	No genes mapped out of 4 KDs	Chaperone and folding catalysis	60 kDa chaperonin	9.2838781	5.38E+08	PolysaccharideBacteria	Arthropoda	Insecta	Phasmodinidae
382109,9	Fatty acid and lipid metabolism	Biochemistry	Uncharacterized amino-acid ABC transporter ATP-binding subunit	9.2668848	1.24E+18	PolysaccharideBacteria	Arthropoda	Insecta	Lepidoptera
414385,5	Prosthetic groups, cofactors, and carriers	Iron sulfur clusters	Acyl carrier protein	9.2642564	1.65E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
107240,2	Signal transduction	Two-component systems	F45 assembly scaffold apponin Ucu	9.2450885	6.05E+08	PolysaccharideBacteria	Arthropoda	Insecta	Phasmodinidae
5310,2	No genes mapped out of 4 KDs	Transcription factors	Ferredoxin-cytochrome b5 reductase	9.2383173	1.01E+10	PolysaccharideBacteria	BacteroidetesCytophaga	Cytophagales	Chryseoidae
106908,4	Nucleic acid metabolism	D replication, recombination, and repair	RNA polymerase beta prime factor	9.2295726	4.27E+08	PolysaccharideBacteria	ActinobacteriaActinobacteriales	Micromonosporales	Actinoplanes
114475,14	Amino acid metabolism	Amino acids, aspartate and glutamate metabolism	Transcription factor G	9.2295726	4.27E+08	PolysaccharideBacteria	ActinobacteriaActinobacteriales	Micromonosporales	Actinoplanes
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	Burkholderia
141820,12	No genes mapped out of 4 KDs	Transcription factors	Not in_Usif	9.2075731	3.96E+17	PolysaccharideBacteria	ProteobacteriaBetaproteobacteria	Burkholderiales	

195848_3	Nucleic acid metabolism	Purine metabolism	Bi-functional purine biosynthesis protein PurH	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
382335_3	Transcription	Ribosomal proteins; synthesis and modification	Ribosomal proteins; synthesis and modification	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
28133_7	Translation	Transfer R biogenesis	Alanine-tRNA ligase	R4078654	4.97E-13	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
1337578_20	Regulatory functions	Protein interactions	Regulatory protein Inaap	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
165028_6	Translation	Transfer R biogenesis	Polynucleotide nucleotidyltransferase	R40382489	1.52E-11	Polysaccharide	Bacteroidetes	Cytophagales	Cytophagales	Chryseolaceae	Lawsontia	Lawsontia
229268_5	No files mapped out of 6 KOs	Peptidases	Uncharacterized protein	R4011184	9.74E-10	Polysaccharide	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospira	Lachnospira
162070_1	Intracellular trafficking, assembly, and processing	Ribosomal proteins; synthesis and modification	Uncharacterized protein S18	R3968174	1.0E-06	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
570287_8	Translation	Purine metabolism	Phosphoribosyltransferase	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
152908_3	Nucleic acid metabolism	Transcription factors	Transcription termination/antitermination protein NusA	R1372818	6.17E-14	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
842494_3	Transcription	Protein interactions	Protein-protein interaction regulator NusG/CP740	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
1617378_3	Intracellular trafficking, assembly, and processing	Ribosomal proteins; synthesis and modification	Citrate cyclic (TCA cycle)	R40381158	2.19E-06	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
1460317_3	Carbohydrate metabolism	Ribosomal proteins; synthesis and modification	Succinate-CoA ligase [ADP-forming] subunit beta	R13816478	3.37E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
42002_10	No files mapped out of 6 KOs	Ribosomal proteins; synthesis and modification	Probable transcriptional regulator NusG/CP740	R13816478	3.37E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
74122_40	Translation	Citrate cyclic (TCA cycle)	50S ribosomal protein L3	R14568139	8.73E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
52345_5	No files mapped out of 6 KOs	Chemotaxis	Chemotaxis protein CheV	R1393037	1.57E-08	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
1601_3	No files mapped out of 6 KOs	Translation factors	Elongation factor Tu	R1322861	1.28E-14	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
25703_1	Translation	Translation factors	Elongation factor Tu	R1322861	1.28E-14	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
111814_4	Translation	Oxidative phosphorylation	ATP synthase subunit b	R1314366	2.31E-07	Polysaccharide	Bacteroidetes	Cytophagales	Cytophagales	Chryseolaceae	Lawsontia	Lawsontia
1130999_4	Energy metabolism	No files mapped out of 6 KOs	ATP synthase subunit b	R1314366	2.31E-07	Polysaccharide	Bacteroidetes	Cytophagales	Cytophagales	Chryseolaceae	Lawsontia	Lawsontia
3643_8	No files mapped out of 6 KOs	Translation	Chemotaxis protein CheB	R1393794	1.64E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
505102_17	Signal transduction	Ribosomal proteins; synthesis and modification	Chemotaxis protein CheA	R1329681	4.15E-09	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
11202_19	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L34	R1324866	1.82E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
3244_4	Translation	Carbohydrate metabolism	Uncharacterized protein	R1324866	1.82E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
19362_2	Carbohydrate metabolism	Carbohydrate metabolism	Uncharacterized protein	R1324866	1.82E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
12102_14	No files mapped out of 6 KOs	Ribosomal proteins; synthesis and modification	Uncharacterized protein	R1324866	1.82E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
1346275_5	Transport and binding proteins	Amino acids, peptides and amines	Ethanolamine utilization protein EutP	R1320156	7.08E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
92180_5	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L6	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
54514_4	No files mapped out of 6 KOs	Ribosomal proteins; synthesis and modification	Hemix uptake protein Hmup	R1304524	9.28E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
40849_4	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L6	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
19170_2	Intracellular trafficking, assembly, and processing	Peptidases	Periplasmic enzyme endonuclease DegP-like	R1300419	4.41E-14	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
180726_7	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	Fructose 1,6-bisphosphatase class I	R1329436	7.00E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
146448_2	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L10	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
157121_2	Energy metabolism	Oxidative phosphorylation	NADH quinone oxidoreductase subunit N	R1328728	7.24E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
164112_2	Translation	Ribosomal proteins; synthesis and modification	NADH quinone oxidoreductase subunit N	R1328728	7.24E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
34868_7	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	ATP dependent Clp protease ATP-binding subunit ClpA	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
101052_3	No files mapped out of 6 KOs	Protein interactions	Intricate kinase domain-containing protein	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
83174_4	Regulatory functions	Protein interactions	Metalloprotease TMD	R1421344	1.47E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
2144_1	Translation	Transfer R biogenesis	Polynucleotide nucleotidyltransferase	R1396174	2.38E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
101713_1	No files mapped out of 6 KOs	Translation	Uncharacterized protein	R1396174	2.38E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
114893_2	No files mapped out of 6 KOs	Ribosomal proteins; synthesis and modification	PIG-1 family deacylase	R1385919	6.17E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
131865_24	Translation	Ribosomal proteins; synthesis and modification	RNA polymerase sigma factor	R1385919	6.17E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
103390_4	Transcription	Transcription factors	RNA polymerase sigma 54 factor	R1385919	6.17E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
153448_8	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L10	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
166491_1	Translation	Translation factors	Elongation factor Tu	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
31181_1	Energy metabolism	Oxidative phosphorylation	ATP synthase epsilon chain	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
142254_5	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	Signal recognition particle receptor Ynf	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
105462_3	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	ATP dependent Clp protease ATP-binding subunit ClpA	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
161971_23	No files mapped out of 6 KOs	Non-ribosomal peptide synthetase complex F	Non-ribosomal peptide synthetase complex F	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
80428_4	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L12	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
617551_4	Ribosomal proteins; synthesis and modification	Translation factors	Translation factor L3	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
112881_1	Translation	Translation factors	Fatty acid ligase	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
140708_3	Oxygen biosynthesis and metabolism	Photosynthesis and lipopolysaccharide metabolism	Long-chain fatty acid-CoA ligase	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
120307_2	Transport and binding proteins	Chaperone and folding catalysis	Outer membrane protein OmpA	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
62893_1	Energy metabolism	NADH quinone oxidoreductase	NADH quinone oxidoreductase	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
315817_2	No files mapped out of 6 KOs	Not in UniProt	Not in UniProt	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
10977_2	No files mapped out of 6 KOs	Regulatory functions	Not in UniProt	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
66888_2	No files mapped out of 6 KOs	D interactions	Not in UniProt	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
92348_6	Nucleic acid metabolism	R degradation	RNA pyrophosphorylase	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
164211_1	Carbohydrate metabolism	Carbohydrate metabolism	beta-glucosyltransferase	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
138065_16	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein S20	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
102796_7	Amino acid metabolism	Cyclic, linear and threonine metabolism	Cyclic dihydroxyacetone (Dihydroxyacetone)	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
162767_2	Defense and invasion systems	Defense and invasion systems	Defense and invasion systems	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
184848_38	Energy metabolism	ATP synthase gamma chain	ATP synthase gamma chain	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
3218_2	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	Protein translocator subunit SecA	R1448456	7.76E-10	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
127907_5	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L6	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
107994_4	Nucleic acid metabolism	Adenosine biosynthesis	Adenosine biosynthesis	R1318783	4.11E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
116471_3	Intracellular trafficking, assembly, and processing	Peptidases	Peptidoglycan-binding protein	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
132166_14	Translation	16 S rRNA modification	RNA-directed RNA polymerase methyltransferase B	R1277878	3.27E-08	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
29175_1	Oxygen biosynthesis and metabolism	Photosynthesis	Photosynthesis	R1277878	3.27E-08	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
19320_2	Transcription	R polymerase	DNA-directed RNA polymerase subunit beta	R1253961	6.31E-14	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
61839_1	Transport and binding proteins	Cations and iron carrying compounds	Ferrous iron transport protein B	R122704	1.15E-13	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
194392_4	Amino acid metabolism	Amino acid and glutamate metabolism	Protein translocator subunit SecY	R118825	2.56E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
163736_7	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein S9	R1188448	7.93E-13	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
105276_9	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit beta	R117183	8.85E-10	Polysaccharide	Bacteroidetes	Cytophagales	Cytophagales	Chryseolaceae	Lawsontia	Lawsontia
127786_4	Transcription	Intracellular trafficking, assembly, and processing	ATP dependent zinc metalloprotease FtsH	R1039365	6.32E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
36502_1	Intracellular trafficking, assembly, and processing	Peptidases	ATP dependent zinc metalloprotease FtsH	R1039365	6.32E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
104951_17	Energy metabolism	Oxidative phosphorylation	ATP dependent Clp protease ATP-binding subunit ClpA	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
93821_1	No files mapped out of 6 KOs	Chaperone and folding catalysis	Uncharacterized protein	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
104708_3	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Uncharacterized protein	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
75477_5	No files mapped out of 6 KOs	Chaperone and folding catalysis	Uncharacterized protein	R1327433	7.44E-07	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
158448_4	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L4	R1329879	1.38E-11	Polysaccharide	Proteobacteriales	Burkholderiales	Comamonadaceae	Comamonas	Comamonas sp. B62024	
97402_2	Translation	Ribosomal proteins; synthesis and modification	50S rib									

953939_4	Transport and binding proteins	Amino acids, peptides and amines	Glutamate Aspartate periplasmic binding protein Gh1	7.6067849	3.62E+14	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
21233_3	Transition	Transfer R biogenesis	Polychlorinated naphthalene dioxygenase	7.6072789	4.4E+14	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
19381_7	Transition	Transcription factors	Cold shock protein CspC	7.6080784	4.24E+06	Polysaccharide Bacteria	Firmicutes/Bacilli	Bacillus
153770_9	Transition	Transcription factors	Floriger factor Tu	7.6092789	1.0E+07	Polysaccharide Bacteria	Firmicutes/Bacilli	Bacillus
54684_1	Transition	Transfer R biogenesis	Proline-RNA ligase	7.6094789	4.61E+13	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
108402_7	No roles mapped out of 4 KOs		Not_u__linef	7.6094883	3.88E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
91148_3	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S12	7.6098794	4.73E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
31438_1	Transition	Fatty acid and lipid metabolism	Fatty acid desaturase	7.6102386	9.58E+14	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
61764_3	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein L3	7.6103826	1.88E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Methylthio
40610_1	No roles mapped out of 4 KOs		Not_u__linef	7.6107478	4.49E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Lawsonia intracellularis
118115_5	No roles mapped out of 4 KOs		Not_u__linef	7.6107529	6.21E+11	Polysaccharide Bacteria	Chloroflexi/Chlorofleximorpha/Anaerolineae	Chloroflexus
111407_13	No roles mapped out of 4 KOs		Not_u__linef	7.6107871	4.69E+05	Polysaccharide Bacteria	Nitrospirae/Nitrospirae	Nitrospirae
8440_9	Transition	Chaperone and folding catalysis	ATP-dependent Clp protease ATP-binding subunit ClpC	7.6104749	1.79E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	
67174_1	Transition	Chaperone and folding catalysis	30S ribosomal protein L4	7.6104277	1.81E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	
71420_1	Transition	General	Polysaccharide kinase	7.6106170	1.18E+13	Polysaccharide Bacteria	Actinobacteria	Akkermansia
104668_1	Transition	Oxidative phosphorylation	Nucleoside diphosphate flavoprotein subunit	7.6105445	6.21E+14	Polysaccharide Bacteria	Actinobacteria	Akkermansia
29673_1	No roles mapped out of 4 KOs		Not_u__linef	7.6105682	1.63E+13	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
53085_2	Transition	Chaperone and folding catalysis	Uncharacterized protein	7.6104779	8.22E+11	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
14516_4	Transition	Ribosomal proteins; synthesis and modification	50S ribosomal protein L24	7.6104779	8.22E+11	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
88753_7	Transition	Chaperone and folding catalysis	Uncharacterized protein	7.6104779	1.00E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
2092_2	Transition	Oxidative phosphorylation	NADH-quinone oxidoreductase subunit B	7.6104276	1.48E+07	Polysaccharide Bacteria	Proteobacteriota/Betaproteobacteria/Burkholderia	Comamonas Varioroux
96383_2	No roles mapped out of 4 KOs		Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
57895_5	Transition	Ribosomal proteins; synthesis and modification	CAMP_b__b1_3 domain-containing protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
19363_1	No roles mapped out of 4 KOs		Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
159348_1	Transition	Transfer R biogenesis	poly(ribonucleotide uridylyltransferase)	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
55091_3	Transition	Amino acid metabolism	Valine, leucine and isoleucine metabolism	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
86490_8	Transition	Transport and binding proteins	Perin and secretin	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
43841_1	No roles mapped out of 4 KOs		Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
172332_1	Transition	Peptidases	Onp-like domain-containing protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
172332_1	Transition	Peptidases	ATP-dependent zinc metalloprotease FtsH	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
149714_7	No roles mapped out of 4 KOs		Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
78180_1	No roles mapped out of 4 KOs		Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141911_1	Transition	Peptidases	Uncharacterized protein (Fragment)	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141911_1	Transition	Peptidases	30S ribosomal protein L28	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141911_1	Transition	Peptidases	Protein HPS	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141911_1	Transition	Peptidases	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141911_1	Transition	Peptidases	30S ribosomal protein S1	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
86149_9	Transition	Nucleic acid metabolism	RNA polymerase subunit beta	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
153216_6	Transition	Fatty acid and lipid metabolism	Acyl carrier protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
9387_13	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S3	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141626_1	Transition	Carbohydrate metabolism	Acetyl-coenzyme A synthetase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
75437_2	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S9	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
99328_3	Transition	Oxidative phosphorylation	ATP synthase subunit epsilon	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
94251_1	Transition	Cell structure, growth, and death	Cell division	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
709133_2	Transition	Ribosomal proteins; synthesis and modification	Cell division	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
209754_12	Transition	Ribosomal proteins; synthesis and modification	50S ribosomal protein L14	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
102756_1	Transition	Amino acid metabolism	Alanine, aspartate and glutamate metabolism	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
170354_6	Transition	Carbohydrate metabolism	Phosphoglucomutase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141776_4	Transition	Amino acid, peptides and amines	Transfer chain amino acid ABC transporter substrate-binding protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
180801_30	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S16	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
52523_1	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S17	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
977_4	Transition	Nucleic acid metabolism	Protein RcaA	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
15570_14	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein L19	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
119200_3	Transition	Ribosomal proteins; synthesis and modification	50S ribosomal protein L5	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
92125_2	Transition	Cytosolic and methionine metabolism	Methionine synthase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
108890_5	Transition	Oxidative phosphorylation	Nucleoside diphosphate polyphosphate II	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
710384_2	Transition	Nucleic acid metabolism	Superoxide dismutase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
52645_6	Transition	Nucleic acid metabolism	Uncharacterized protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
107870_3	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S2	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
157979_2	Transition	Cell structure, growth, and death	GapM1 family protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
2656_5	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
172780_1	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein L1	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
154161_27	Transition	Ribosomal proteins; synthesis and modification	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
31448_4	Transition	Nucleic acid metabolism	Nucleoside associated protein VAP_A_124700	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
103547_9	Transition	Unknown function	Uncharacterized protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
54684_2	Transition	Energy metabolism	Carbon fixation in prokaryotes	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
192010_3	Transition	Defense and invasion systems	Cellulose and inactivation	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
165616_6	Transition	Regulation functions	Regulation functions	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
60546_1	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
30739_4	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
121782_3	Transition	Ribosomal proteins; synthesis and modification	Oxidative phosphorylation	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
20479_3	Transition	Energy metabolism	NADH-quinone oxidoreductase subunit A	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
151931_5	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S1	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
127268_5	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S13	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
108653_2	Transition	Energy metabolism	Uncharacterized protein	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
99701_3	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S14	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
128172_10	Transition	Carbohydrate metabolism	Phosphoglucomutase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
448379_11	Transition	Ribosomal proteins; synthesis and modification	30S ribosomal protein S8	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
33878_3	Transition	Carbohydrate metabolism	Maltose dehydrogenase	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
164668_8	Transition	Carbohydrate metabolism	Crizate cycle (TC4 cycle)	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
164738_2	Transition	intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
141776_4	Transition	intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
152749_2	Transition	intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
108890_5	Transition	Energy metabolism	Transfer R biogenesis	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
81121_5	Transition	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
45474_3	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
121888_2	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
151877_3	Transition	Transcription factors	Transcription factors	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
160020_4	Transition	Energy metabolism	Transcription termination/antitermination protein NusG	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
104268_16	Transition	Transcription factors	Transcription termination/antitermination protein NusA	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
98189_3	Transition	intracellular trafficking, assembly, and processing	Enzyme assembly	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
94307_1	Transition	No roles mapped out of 4 KOs	Not_u__linef	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
102426_1	Transition	Energy metabolism	Cytochrome oxidase/beta subunit 1	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroidetes/Chloroflexi/Chlorofleximorpha/Flavobacterium	Flavobacterium
9438_2	Transition	Oxidative phosphorylation	Cytochrome oxidase/beta subunit 2	7.6103911	2.10E+07	Polysaccharide Bacteria	Bacteroid	

63899.1	No roles mapped out of 4 KOs		Uncharacterized protein	68496514	8.47E-02	Polysaccharide Lyase	Streptomyces	Solanicus	Solanaceae	Capisicum	Capisicum chinense
145163.1	Energy metabolism	Oxidative phosphorylation	Iron-sulfur cluster oxidase subunit 1	68097068	1.54E-02	Polysaccharide Lyase	Proteobacter	Gammaproteobacteria	Sarcomonadaceae	Sarcomonadaceae	Sarcomonadaceae
152926.3	Translocation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L35	68873020	3.06E-08	Polysaccharide Lyase	Proteobacter	Alphaproteobacteria	Rhodospirillales	Rhodospirillales	Rhodospirillales
151774.9	Translocation	Defensin and invasion systems	Phage tail sheath protein	68427314	1.36E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Burkholderiales	Burkholderiales
33695.1	Transcription	R polymerase	DNA-directed RNA polymerase subunit beta'	64792285	2.51E-06	Polysaccharide Lyase	Bacteroidetes	Chloroflexi	Chloroflexiales	Chloroflexiales	Chloroflexiales
76122.7	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	Fructose 1,6-bisphosphate aldolase	68779126	6.03E-02	Polysaccharide Lyase	taxonomic_	annotation_	available		
13397.7	Defense and invasion systems	Detoxification and inactivation	Allyl sulfonamide lyase C	64751131	1.13E-07	Polysaccharide Lyase	taxonomic_	annotation_	available		
163320.26	No roles mapped out of 4 KOs	Transcription	Uncharacterized protein	64713689	1.88E-15	Polysaccharide Lyase	Proteobacter	Gammaproteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadales
96070.6	Translocation	Transfers R biogenesis	Phosphoenolpyruvate carboxylase C	64704123	1.44E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Comamonadales	Comamonadales	Comamonadales
122820.5	Transport and binding proteins	Cations and iron carrying compounds	Iron transporter ynfA	64700746	1.28E-14	Polysaccharide Lyase	Bacteroidetes	Flavobacteriia	Flavobacteriia	Flavobacteriia	Flavobacteriia
105214.2	Transport and binding proteins	Energy metabolism	Phosphoenolpyruvate carboxylase	64697369	4.66E-12	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Comamonadales	Comamonadales	Comamonadales
78164.4	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit alpha	64660221	1.30E-05	Polysaccharide Lyase	Arthropoda	Insecta	Phasmodata	Bacillales	Bacillales
110171.18	Energy metabolism	Oxidative phosphorylation	NADH quinone oxidoreductase subunit B	64662372	0.000200	Polysaccharide Lyase	Actinobacter	Thermoplasma	Solirubrobact	Solirubrobact	Solirubrobact
103431.4	No roles mapped out of 4 KOs	Translocation	50S ribosomal protein 18	64660814	3.03E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Comamonadales	Comamonadales	Comamonadales
20595.4	Regulatory functions	Protein interactions	Family 20 glycosyltransferase	64651385	1.05E-02	Polysaccharide Lyase	Bacteroidetes	Flavobacteriia	Marinilabidiales	Marinilabidiales	Corynebacteriales
99709.9	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysts	Uncharacterized protein	64646641	3.15E-08	Polysaccharide Lyase	taxonomic_	annotation_	available		
49461.5	No roles mapped out of 4 KOs	Translocation	Uncharacterized protein	64643963	1.14E-02	Polysaccharide Lyase	Firmicutes	Bacilli	Bacillales	Paenibacillales	Paenibacillales
164524.6	Nucleic acid metabolism	Pyrimidine metabolism	Nucleic acid metabolic byproduct release	64643129	2.25E-11	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Mutulisporales
67374.3	Transcription	R polymerase	DNA-directed RNA polymerase subunit alpha	64643424	3.62E-10	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
154510.1	No roles mapped out of 4 KOs	Translocation	Uncharacterized protein	64639709	2.37E-15	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
145510.3	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	Cytidine diphosphate dehydrogenase 1	64625786	1.06E-05	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
125564.2	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysts	Enolase	64620069	2.94E-08	Polysaccharide Lyase	Arthropoda	Insecta	Phasmodata	Bacillales	Bacillales
18179.6	Transport and binding proteins	Antions	Tricyclic transporter protein TCC	64619798	6.57E-08	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Burkholderiales	Burkholderiales
20567.3	Nucleic acid metabolism	Pyrimidine metabolism	Chaperone phosphoribosyltransferase	64618771	1.25E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
12704.3	Energy metabolism	Oxidative phosphorylation	ATP synthase subunit beta	64618647	7.03E-08	Polysaccharide Lyase	taxonomic_	annotation_	available		
164958.6	No roles mapped out of 4 KOs	Translocation	Uncharacterized protein	64618245	6.38E-13	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
164996.1	No roles mapped out of 4 KOs	Translocation	Uncharacterized protein	64618119	7.67E-07	Polysaccharide Lyase	Actinobacter	Bacteroidetes	Acidobacteriales	Acidobacteriales	Acidobacteriales
186817.8	Intracellular trafficking, assembly, and processing	Protein modification and repair	Deoxythymine synthase	64618021	4.51E-10	Polysaccharide Lyase	Arthropoda	Insecta	Phasmodata	Bacillales	Bacillales
155791.20	Cell structure, growth, and death	Spore formation and germination	SpoIV family protein	64617733	7.96E-08	Polysaccharide Lyase	Proteobacter	Hydrogenophiles	Hydrogenophiles	Hydrogenophiles	Hydrogenophiles
193299.14	No roles mapped out of 4 KOs	Translocation	50S ribosomal protein S10	64617528	1.47E-02	Polysaccharide Lyase	Arthropoda	Insecta	Phasmodata	Bacillales	Bacillales
193299.14	No roles mapped out of 4 KOs	Translocation	Uncharacterized protein	64617441	3.52E-02	Polysaccharide Lyase	Arthropoda	Insecta	Phasmodata	Bacillales	Bacillales
49022.4	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysts	Regulatory protein sigma 70 class I isozyme	64617274	1.34E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism	Pyrimidine metabolism	Thymidine reductase	64617181	1.84E-02	Polysaccharide Lyase	Proteobacter	Betaproteobacteria	Burkholderiales	Comamonadales	Comamonadales
185153.4	Nucleic acid metabolism										

122879.2	No roles mapped out of 4 KOs		122879.2	No roles mapped out of 4 KOs	Unconjugated protein
128263.2	No roles mapped out of 4 KOs		128263.2	No roles mapped out of 4 KOs	Unconjugated protein
64021.6	Transport and binding proteins	Unconjugated substrate	64021.6	Transport and binding proteins	Unconjugated substrate
1012775.3	No roles mapped out of 4 KOs		1012775.3	No roles mapped out of 4 KOs	Unconjugated protein
124657.3	No roles mapped out of 4 KOs		124657.3	No roles mapped out of 4 KOs	Unconjugated protein
90306.4	Transport and binding proteins		90306.4	Transport and binding proteins	
1151776.1	No roles mapped out of 4 KOs		1151776.1	No roles mapped out of 4 KOs	Unconjugated protein
85233.2	No roles mapped out of 4 KOs		85233.2	No roles mapped out of 4 KOs	Unconjugated protein
96483.1	Catabolic reactions		96483.1	Catabolic reactions	
76247.7	Intracellular trafficking, assembly, and processing		76247.7	Intracellular trafficking, assembly, and processing	
782342.1	No roles mapped out of 4 KOs		782342.1	No roles mapped out of 4 KOs	Unconjugated protein
120280.3	No roles mapped out of 4 KOs		120280.3	No roles mapped out of 4 KOs	Unconjugated protein
102002.2	Prosthetic groups, cofactors, and carriers		102002.2	Prosthetic groups, cofactors, and carriers	
79792.1	Transcription		79792.1	Transcription	
12672.2	No roles mapped out of 4 KOs		12672.2	No roles mapped out of 4 KOs	Unconjugated protein
134046.3	No roles mapped out of 4 KOs		134046.3	No roles mapped out of 4 KOs	Unconjugated protein
31185.5	No roles mapped out of 4 KOs		31185.5	No roles mapped out of 4 KOs	Unconjugated protein
154489.1	Nucleic acid metabolism		154489.1	Nucleic acid metabolism	
36417.3	Catabolic reactions		36417.3	Catabolic reactions	
156787.1	Cell motility and adherence		156787.1	Cell motility and adherence	
102683.0	Amnio acid metabolism		102683.0	Amnio acid metabolism	
17037.1	Transcription		17037.1	Transcription	
79059.15	No roles mapped out of 4 KOs		79059.15	No roles mapped out of 4 KOs	Unconjugated protein
82313.2	Intracellular trafficking, assembly, and processing		82313.2	Intracellular trafficking, assembly, and processing	
79892.2	No roles mapped out of 4 KOs		79892.2	No roles mapped out of 4 KOs	Unconjugated protein
614862.1	Nucleic acid metabolism		614862.1	Nucleic acid metabolism	
116401.5	Carbohydrate metabolism		116401.5	Carbohydrate metabolism	
705.1	No roles mapped out of 4 KOs		705.1	No roles mapped out of 4 KOs	Unconjugated protein
290220.3	No roles mapped out of 4 KOs		290220.3	No roles mapped out of 4 KOs	Unconjugated protein
120175.2	No roles mapped out of 4 KOs		120175.2	No roles mapped out of 4 KOs	Unconjugated protein
48142.2	Translation		48142.2	Translation	
53329.2	Intracellular trafficking, assembly, and processing		53329.2	Intracellular trafficking, assembly, and processing	
170977.2	No roles mapped out of 4 KOs		170977.2	No roles mapped out of 4 KOs	Unconjugated protein
76027.1	No roles mapped out of 4 KOs		76027.1	No roles mapped out of 4 KOs	Unconjugated protein
41007.4	No roles mapped out of 4 KOs		41007.4	No roles mapped out of 4 KOs	Unconjugated protein
1271751.17	Transport and binding proteins	Amnio acids, peptides and amines	1271751.17	Transport and binding proteins	Amnio acids, peptides and amines
157619.16	No roles mapped out of 4 KOs		157619.16	No roles mapped out of 4 KOs	Unconjugated protein
164346.1	Translation		164346.1	Translation	
82358.4	Carbohydrate metabolism		82358.4	Carbohydrate metabolism	
121719.1	No roles mapped out of 4 KOs		121719.1	No roles mapped out of 4 KOs	Unconjugated protein
123279.5	Amnio acid metabolism		123279.5	Amnio acid metabolism	
162677.1	Intracellular trafficking, assembly, and processing		162677.1	Intracellular trafficking, assembly, and processing	
15179.9	Transport and binding proteins		15179.9	Transport and binding proteins	
824828.3	Nucleic acid metabolism		824828.3	Nucleic acid metabolism	
48477.2	No roles mapped out of 4 KOs		48477.2	No roles mapped out of 4 KOs	Unconjugated protein
1133640.7	Transport and binding proteins	Protein export, secretion, and sorting	1133640.7	Transport and binding proteins	Protein export, secretion, and sorting
65068.7	Fatty acid and lipid metabolism		65068.7	Fatty acid and lipid metabolism	
36188.4	No roles mapped out of 4 KOs		36188.4	No roles mapped out of 4 KOs	Unconjugated protein
14132.1	Translocation		14132.1	Translocation	
159494.5	No roles mapped out of 4 KOs		159494.5	No roles mapped out of 4 KOs	Unconjugated protein
102678.1	No roles mapped out of 4 KOs		102678.1	No roles mapped out of 4 KOs	Unconjugated protein
133435.1	Cell motility and adherence		133435.1	Cell motility and adherence	
6777.1	Transcription		6777.1	Transcription	
174747.6	Carbohydrate metabolism		174747.6	Carbohydrate metabolism	
64332.2	Carbohydrate metabolism		64332.2	Carbohydrate metabolism	
94658.1	No roles mapped out of 4 KOs		94658.1	No roles mapped out of 4 KOs	Unconjugated protein
182179.1	Nucleic acid metabolism		182179.1	Nucleic acid metabolism	
102099.5	Nucleic acid metabolism		102099.5	Nucleic acid metabolism	
121796.3	No roles mapped out of 4 KOs		121796.3	No roles mapped out of 4 KOs	Unconjugated protein
174830.5	No roles mapped out of 4 KOs		174830.5	No roles mapped out of 4 KOs	Unconjugated protein
11073.2	Transcription		11073.2	Transcription	
129663.1	Nucleic acid metabolism		129663.1	Nucleic acid metabolism	
61431.12	No roles mapped out of 4 KOs		61431.12	No roles mapped out of 4 KOs	Unconjugated protein
50256.14	No roles mapped out of 4 KOs		50256.14	No roles mapped out of 4 KOs	Unconjugated protein
81849.6	No roles mapped out of 4 KOs		81849.6	No roles mapped out of 4 KOs	Unconjugated protein
11100.1	Transcription		11100.1	Transcription	
113172.4	Energy metabolism		113172.4	Energy metabolism	
1026176.8	Energy metabolism		1026176.8	Energy metabolism	
1005414.13	Nucleic acid metabolism		1005414.13	Nucleic acid metabolism	
41026.1	Nucleic acid metabolism		41026.1	Nucleic acid metabolism	
103133.1	Transport and binding proteins		103133.1	Transport and binding proteins	
60270.1	Oxygen biochemistry		60270.1	Oxygen biochemistry	
150011.5	Nucleic acid metabolism		150011.5	Nucleic acid metabolism	
174631.4	No roles mapped out of 4 KOs		174631.4	No roles mapped out of 4 KOs	Unconjugated protein
174052.7	No roles mapped out of 4 KOs		174052.7	No roles mapped out of 4 KOs	Unconjugated protein
79531.3	Defense and invasion systems		79531.3	Defense and invasion systems	
69987.2	Translocation		69987.2	Translocation	
129342.6	Amnio acid metabolism		129342.6	Amnio acid metabolism	
146140.5	No roles mapped out of 4 KOs		146140.5	No roles mapped out of 4 KOs	Unconjugated protein
102102.1	No roles mapped out of 4 KOs		102102.1	No roles mapped out of 4 KOs	Unconjugated protein
1102432.1	No roles mapped out of 4 KOs		1102432.1	No roles mapped out of 4 KOs	Unconjugated protein
95261.1	Amnio acid metabolism		95261.1	Amnio acid metabolism	
72039.1	Transport and binding proteins		72039.1	Transport and binding proteins	
7107.6	Energy metabolism		7107.6	Energy metabolism	
60300.1	Transport and binding proteins		60300.1	Transport and binding proteins	
26191.1	No roles mapped out of 4 KOs		26191.1	No roles mapped out of 4 KOs	Unconjugated protein
118340.1	No roles mapped out of 4 KOs		118340.1	No roles mapped out of 4 KOs	Unconjugated protein
513458.4	No roles mapped out of 4 KOs		513458.4	No roles mapped out of 4 KOs	Unconjugated protein
901276.9	No roles mapped out of 4 KOs		901276.9	No roles mapped out of 4 KOs	Unconjugated protein
118340.1	No roles mapped out of 4 KOs		118340.1	No roles mapped out of 4 KOs	Unconjugated protein
184514.4	Energy metabolism		184514.4	Energy metabolism	
116198.5	Transport and binding proteins		116198.5	Transport and binding proteins	
924346.1	Regulatory factors		924346.1	Regulatory factors	
33427.1	Amnio acid metabolism		33427.1	Amnio acid metabolism	
80463.1	Carbohydrates, organic alcohols, and acids		80463.1	Carbohydrates, organic alcohols, and acids	
149898.5	No roles mapped out of 4 KOs		149898.5	No roles mapped out of 4 KOs	Unconjugated protein
149599.4	No roles mapped out of 4 KOs		149599.4	No roles mapped out of 4 KOs	Unconjugated protein
156379.16	Prosthetic groups, cofactors, and carriers		156379.16	Prosthetic groups, cofactors, and carriers	
117662.1	Nucleic acid metabolism		117662.1	Nucleic acid metabolism	
262257.5	No roles mapped out of 4 KOs		262257.5	No roles mapped out of 4 KOs	Unconjugated protein
170492.3	Energy metabolism		170492.3	Energy metabolism	
26796.1	No roles mapped out of 4 KOs		26796.1	No roles mapped out of 4 KOs	Unconjugated protein
115414.1	Carbohydrate metabolism		115414.1	Carbohydrate metabolism	
113211.5	Amnio acids, peptides and amines		113211.5	Amnio acids, peptides and amines	
951418.1	No roles mapped out of 4 KOs		951418.1	No roles mapped out of 4 KOs	Unconjugated protein
1129121.5	Transport and binding proteins		1129121.5	Transport and binding proteins	
40078.4	Intracellular trafficking, assembly, and processing		40078.4	Intracellular trafficking, assembly, and processing	
182729.7	No roles mapped out of 4 KOs		182729.7	No roles mapped out of 4 KOs	Unconjugated protein
184448.7	No roles mapped out of 4 KOs		184448.7	No roles mapped out of 4 KOs	Unconjugated protein
164385.6	No roles mapped out of 4 KOs		164385.6	No roles mapped out of 4 KOs	Unconjugated protein
1194862.127	Prosthetic groups, cofactors, and carriers		1194862.127	Prosthetic groups, cofactors, and carriers	
156436.4	Translation		156436.4	Translation	
102102.1	Signal transduction		102102.1	Signal transduction	
137292.1	No roles mapped out of 4 KOs		137292.1	No roles mapped out of 4 KOs	Unconjugated protein
170160.2	Carbohydrate metabolism		170160.2	Carbohydrate metabolism	
132721.4	Amnio acid metabolism		132721.4	Amnio acid metabolism	
180577.1	No roles mapped out of 4 KOs		180577.1	No roles mapped out of 4 KOs	Unconjugated protein
115384.12	Intracellular trafficking, assembly, and processing		115384.12	Intracellular trafficking, assembly, and processing	
114630.6	Defense and invasion systems		114630.6	Defense and invasion systems	
102002.2	Prosthetic groups, cofactors, and carriers		102002.2	Prosthetic groups, cofactors, and carriers	
89219.4	Regulatory factors		89219.4	Regulatory factors	
114791.3	No roles mapped out of 4 KOs		114791.3	No roles mapped out of 4 KOs	Unconjugated protein
805147.4	Nucleic acid metabolism		805147.4	Nucleic acid metabolism	
89021.1	No roles mapped out of 4 KOs		89021.1	No roles mapped out of 4 KOs	Unconjugated protein
116700.2	Signal transduction		116700.2	Signal transduction	
758144.4	Defense and invasion systems		758144.4	Defense and invasion systems	
1542179.5	Transcription		1542179.5	Transcription	
1156363.4	No roles mapped out of 4 KOs		1156363.4	No roles mapped out of 4 KOs	Unconjugated protein
1203536.1	Carbohydrate metabolism		1203536.1	Carbohydrate metabolism	
171929.2	Translocation		171929.2	Translocation	
644.2	Transcription		644.2	Transcription	
102002.2	Prosthetic groups, cofactors, and carriers		102002.2	Prosthetic groups, cofactors, and carriers	
154773.3	No roles mapped out of 4 KOs		154773.3	No roles mapped out of 4 KOs	Unconjugated protein
104288.2	Transport and binding proteins		104288.2	Transport and binding proteins	
82091.4	Carbohydrate metabolism		82091.4	Carbohydrate metabolism	
140237.4	No roles mapped out of 4 KOs		140237.4	No roles mapped out of 4 KOs	Unconjugated protein
6638.1	No roles mapped out of 4 KOs		6638.1	No roles mapped out of 4 KOs	Unconjugated protein
60683.1	Amnio acid metabolism		60683.1	Amnio acid metabolism	
100294.4	Transport and binding proteins		100294.4	Transport and binding proteins	
88960.7	Energy metabolism		88960.7	Energy metabolism	
102549.4	Signal transduction		102549.4	Signal transduction	
6619.2	Energy metabolism		6619.2	Energy metabolism	
120175.2	Unconjugated protein		120175.2	Unconjugated protein	
68728.5	Cell motility and adherence		68728.5	Cell motility and adherence	
154712.1	Transport and binding proteins		154712.1	Transport and binding proteins	
137321.4	Transport and binding proteins		137321.4	Transport and binding proteins	
1416236.3	Carbohydrate metabolism		1416236.3	Carbohydrate metabolism	
15231.5	Transcription		15231.5	Transcription	
118627.2	Amnio acid metabolism		118627.2	Amnio acid metabolism	
75896.2	Signal transduction		75896.2	Signal transduction	
1178121.2	Transcription		1178121.2	Transcription	
65130.1	No roles mapped out of 4 KOs		65130.1	No roles mapped out of 4 KOs	Unconjugated protein
2362.9	Nucleic acid metabolism		2362.9	Nucleic acid metabolism	
39113.4	Carbohydrate metabolism		39113.4	Carbohydrate metabolism	
110900.1	Cell motility and adherence		110900.1	Cell motility and adherence	
86391.3	Transport and binding proteins		86391.3	Transport and binding proteins	
140237.4	No roles mapped out of 4 KOs		140237.4	No roles mapped out of 4 KOs	Unconjugated protein
56037.1	Translation		56037.1	Translation	
18889.3	Transport and binding proteins		18889.3	Transport and binding proteins	
102027.2	Transport and binding proteins		102027.2	Transport and binding proteins	
117023.2	Transport and binding proteins		117023.2	Transport and binding proteins	
25022.4	No roles mapped out of 4 KOs		25022.4	No roles mapped out of 4 KOs	Unconjugated protein
1164173.3	No roles mapped out of 4 KOs		1164173.3	No roles mapped out of 4 KOs	Unconjugated protein
101930.2	Signal transduction		101930.2	Signal transduction	
88378.9	No roles mapped out of 4 KOs		88378.9	No roles mapped out of 4 KOs	Unconjugated protein
20633.4	Carbohydrate metabolism		20633.4	Carbohydrate metabolism	
139352.5	Nucleic acid metabolism		139352.5	Nucleic acid metabolism	
162150.15	Nucleic acid metabolism		162150.15	Nucleic acid metabolism	
148447.1	No roles mapped out of 4 KOs		148447.1	No roles mapped out of 4 KOs	Unconjugated protein
63407.1	Transport and binding proteins		63407.1	Transport and binding proteins	
82091.4	Carbohydrate metabolism		82091.4	Carbohydrate metabolism	
54307.0	Carbohydrate metabolism		54307.0	Carbohydrate metabolism	
31887.4	Signal transduction		31887.4	Signal transduction	
69480.20	Amnio acid metabolism		69480.20	Amnio acid metabolism	
102102.1	Translocation		102102.1	Translocation	
21327.5	No roles mapped out of 4 KOs		21327.5	No roles mapped out of 4 KOs	Unconjugated protein
83000.9	No roles mapped out of 4 KOs		83000.9	No roles mapped out of 4 KOs	Unconjugated protein
86043.4	Transport and binding proteins		86043.4	Transport and binding proteins	
2952.4	Transport and binding proteins		2952.4	Transport and binding proteins	
144902.9	Transport and binding proteins		144902.9	Transport and binding proteins	
101930.2	Signal transduction		101930.2	Signal transduction	
141892.1	No roles mapped out of 4 KOs		141892.1	No roles mapped out of 4 KOs	Unconjugated protein
151691.3	Nucleic acid metabolism		151691.3	Nucleic acid metabolism	
3262.9	Nucleic acid metabolism		3262.9	Nucleic acid metabolism	
140383.7	Energy metabolism		140383.7	Energy metabolism	
117023.2	Transport and binding proteins		117023.2	Transport and binding proteins	
348249.15	No roles mapped out of 4 KOs		348249.15	No roles mapped out of 4 KOs	Unconjugated protein
116330.36	No roles mapped out of 4 KOs		116330.36	No roles mapped out of 4 KOs	Unconjugated protein
34720836.6	Unconjugated protein		34720836.6	Unconjugated protein	
34720837.1	Unconjugated protein		34720837.1	Unconjugated protein	
34720838.2	Unconjugated protein		34720838.2	Unconjugated protein	
34720839.3	Unconjugated protein		34720839.3	Unconjugated protein	
34720840.4	Unconjugated protein		34720840.4	Unconjugated protein	
34720841.5	Unconjugated protein		34720841.5	Unconjugated protein	
34720842.6	Unconjugated protein		34720842.6	Unconjugated protein	
34720843.7	Unconjugated protein		34720843.7	Unconjugated protein	
34720844.8	Unconjugated protein		34720844.8	Unconjugated protein	
34720845.9	Unconjugated protein		34720845.9	Unconjugated protein	
34720846.0	Unconjugated protein		34720846.0	Unconjugated protein	
34720847.1	Unconjugated protein		34720847.1	Unconjugated protein	
34720848.2	Unconjugated protein		34720848.2	Unconjugated protein	
34720849.3	Unconjugated protein		34720849.3	Unconjugated protein	
34720850.4	Unconjugated protein		34720850.4	Unconjugated protein	

759370_2	Signal transduction	Taxis	Chemotaxis	20699991	0.006537	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
759370_1	Tropism and chemotaxis metabolism	General degradation	Chemical synthesis	21059154	0.001088	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
103167_12	Transport and binding proteins	Amino acids, peptides and amines	Periplasmic chaperone and Csa synthase	21051787	0.023607	Polysaccharide	taxonomic annotation available	
23835_3	Nucleic acid metabolism	RNA and DNA repair	RecA and RecBCDE	21051788	0.007386	Polysaccharide	taxonomic annotation available	
28330_2	Transport and binding proteins	Amino acids, peptides and amines	Metabolic protein tyrosinase	20482792	0.040774	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
298112_4	No roles mapped out of 4 KOs		HTF/R32 domain-containing protein	20474544	0.010393	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
118706_4	Nucleic acid metabolism	D replication, recombination, and repair	21020847	0.007781	Polysaccharide	taxonomic annotation available		
103167_14	Transport and binding proteins	RNA and DNA repair	UtrA	20210392	0.001868	Polysaccharide	taxonomic annotation available	
119325_5	Transport and binding proteins	Chaperone and folding catalysis	UgtC	19030846	0.005774	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
144847_6	Cell structure, growth, and death	Bacterial nucleoid protein H1 alpha subunit	Hsp90	19811415	0.024074	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
144702_5	No roles mapped out of 4 KOs	Highly-affinity branched-chain amino acid transporter ATP-binding protein	High-affinity branched-chain amino acid transporter ATP-binding protein	19784789	0.015778	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
174005_4	Intracellular trafficking, assembly, and processing	Peptidases	Proteinase K	19746749	0.021166	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
154886_3	Intracellular trafficking, assembly, and processing	Peptidases	D-alanyl-D-alanine amidase	19704484	0.007280	Polysaccharide	taxonomic annotation available	
174194_3	No roles mapped out of 4 KOs	Sigma 54 dependent transcriptional regulator	Sigma 54 dependent transcriptional regulator	19129424	0.009798	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
523126_12	No roles mapped out of 4 KOs	Endonuclease/phosphatase domain-containing protein	Endonuclease/phosphatase domain-containing protein	19000627	0.044610	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
183243_1	No roles mapped out of 4 KOs	RNA 5'-triphosphatase	RNA 5'-triphosphatase	19008168	0.004203	Polysaccharide	taxonomic annotation available	
541307_5	No roles mapped out of 4 KOs	Prosthetic group, cofactors, and carriers	3-hydroxy-ACP reductase	19081541	0.024909	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
851519_3	Cofactor metabolism	Pyruvate and thioester metabolism	ClaA	18937476	0.011709	Polysaccharide	taxonomic annotation available	
183033_4	Transport and binding proteins	Proteinase K	Proteinase K	18382147	0.015443	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
123222_4	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	ABC transporter domain-containing protein	18320779	0.005168	Polysaccharide	taxonomic annotation available	
183428_5	Fatty acid and lipid metabolism	Biochemistry of unsaturated fatty acids	Chaperone SurA	18378184	0.027514	Polysaccharide	taxonomic annotation available	
1757370_3	Transport and binding proteins	Amino acids, peptides and amines	L-carnitine dehydrogenase	18295804	0.015188	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
150127_1	Translocation	RNA and ribase modification	OpaC domain-containing protein	18496898	0.006176	Polysaccharide	taxonomic annotation available	
154407_4	Transport and binding proteins	RNA and ribase modification	RNA(AC) RNA(UC)-C5'-methyltransferase	17999457	0.018898	Polysaccharide	taxonomic annotation available	
154206_4	No roles mapped out of 4 KOs	Amino acids, peptides and amines	L-lysine-binding periplasmic protein	17959233	0.002601	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
823384_3	Transport and binding proteins	Amino acids, peptides and amines	Proton motive force transducer	17848452	0.010788	Polysaccharide	taxonomic annotation available	
46086_8	Transport and binding proteins	Amino acids, peptides and amines	ABC transporter domain-containing protein	17805781	0.020072	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
79572_9	Cell motility and chemotaxis	Flagellar complex and associated proteins	High-affinity branched-chain amino acid transporter ATP-binding protein	17761306	0.002468	Polysaccharide	taxonomic annotation available	
102702_9	No roles mapped out of 4 KOs	Polysaccharide and lipopolysaccharide metabolism	Transcriptional regulator MntA	17424857	0.012631	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
98177_2	No roles mapped out of 4 KOs	RNA and ribase modification	Uncharacterized protein T	17422812	0.044702	Polysaccharide	taxonomic annotation available	
2354_4	Transport and binding proteins	Amino acids	Uncharacterized protein T	17426207	0.041911	Polysaccharide	taxonomic annotation available	
70198_4	No roles mapped out of 4 KOs	RNA polymerase	DNA polymerase	17294243	0.021371	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
80092_3	Cell motility and chemotaxis	Flagellar complex and associated proteins	Flagellar motor stator protein	17131926	0.048901	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
119312_1	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	Arabinose import ATP-binding protein AraG	17154723	0.004897	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
103167_11	No roles mapped out of 4 KOs	RNA and DNA repair	PhcA	17152447	0.015897	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
154206_2	Signal transduction	Taxis	Chemotaxis proteins	16992921	0.030926	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
759843_3	Translocation	Ribosomal proteins: synthesis and modification	S05 ribosomal protein L2	16926394	0.032840	Polysaccharide	Proteobacterium: Betaproteobacteria: Burkholderia	Burkholderia
150127_3	No roles mapped out of 4 KOs	Transcriptional regulation	Transcriptional regulator, LysR family	16888858	0.043668	Polysaccharide	taxonomic annotation available	
40366_3	Transport and binding proteins	Amino acids, peptides and amines	Periplasmic chaperone and Csa synthase	16829793	0.021772	Polysaccharide	taxonomic annotation available	
154206_2	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	L-lysine-binding periplasmic protein	16743761	0.003183	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
150127_1	No roles mapped out of 4 KOs	Amino acids, peptides and amines	UtrA	16691415	0.009808	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
162665_5	Transport and binding proteins	Amino acids, peptides and amines	UtrA	16468941	0.015763	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
85391_3	Transport and binding proteins	Taxis	Chemotaxis proteins	16468941	0.015763	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
145125_1	No roles mapped out of 4 KOs	Amino acids, peptides and amines	GlnK	16468939	0.009454	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
169141_4	No roles mapped out of 4 KOs	ATP-dependent helixase	Uncharacterized protein T	16415329	0.045165	Polysaccharide	taxonomic annotation available	
151302_20	Carbohydrate metabolism	Pyruvate metabolism	ATP-dependent helixase HspA	16311864	0.002840	Polysaccharide	taxonomic annotation available	
97448_3	Signal transduction	Taxis	HspA protein	16251571	0.024903	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
150127_1	No roles mapped out of 4 KOs	Chemotaxis proteins	Chemotaxis proteins	16156448	0.021405	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
150127_1	No roles mapped out of 4 KOs	Prosthetic group, cofactors, and carriers	Prosthetic group, cofactors, and carriers	16152389	0.004387	Polysaccharide	taxonomic annotation available	
150127_1	No roles mapped out of 4 KOs	Carboxylate metabolism	D-carboxylate-acyl coenzyme D	16156305	0.002447	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
150127_1	No roles mapped out of 4 KOs	Oxidoreductase, zinc-binding protein	Oxidoreductase, zinc-binding protein	16151817	0.018902	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
42815_4	Amino acid metabolism	Citric acid cycle	Malic enzyme 1-phosphatase isoenzyme	16143478	0.048094	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
116564_2	Signal transduction	General	KaC	16143478	0.048094	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
823384_3	Energy metabolism	General	1,5-dioxynucleoside	16143478	0.048094	Polysaccharide	Proteobacterium: Gammaproteobacteria: Pseudomonas	Pseudomonas
104022_9	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	beta-D-glucosyl-2-epimerase	15299352	0.008862	Polysaccharide	taxonomic annotation available	
156269_5	Transport and binding proteins	Amino acids, peptides and amines	Alginate biosynthesis protein AlgA	15210205	0.003813	Polysaccharide	taxonomic annotation available	
183428_5	Transport and binding proteins	Cationic and non-cationic proteases	YnfH YnfJ YnfK YnfL YnfM YnfN YnfO YnfP YnfQ YnfR YnfS YnfT YnfU YnfV YnfW YnfX YnfY YnfZ Ynf1 Ynf2 Ynf3 Ynf4 Ynf5 Ynf6 Ynf7 Ynf8 Ynf9 Ynf10 Ynf11 Ynf12 Ynf13 Ynf14 Ynf15 Ynf16 Ynf17 Ynf18 Ynf19 Ynf20 Ynf21 Ynf22 Ynf23 Ynf24 Ynf25 Ynf26 Ynf27 Ynf28 Ynf29 Ynf30 Ynf31 Ynf32 Ynf33 Ynf34 Ynf35 Ynf36 Ynf37 Ynf38 Ynf39 Ynf40 Ynf41 Ynf42 Ynf43 Ynf44 Ynf45 Ynf46 Ynf47 Ynf48 Ynf49 Ynf50 Ynf51 Ynf52 Ynf53 Ynf54 Ynf55 Ynf56 Ynf57 Ynf58 Ynf59 Ynf60 Ynf61 Ynf62 Ynf63 Ynf64 Ynf65 Ynf66 Ynf67 Ynf68 Ynf69 Ynf70 Ynf71 Ynf72 Ynf73 Ynf74 Ynf75 Ynf76 Ynf77 Ynf78 Ynf79 Ynf80 Ynf81 Ynf82 Ynf83 Ynf84 Ynf85 Ynf86 Ynf87 Ynf88 Ynf89 Ynf90 Ynf91 Ynf92 Ynf93 Ynf94 Ynf95 Ynf96 Ynf97 Ynf98 Ynf99 Ynf100 Ynf101 Ynf102 Ynf103 Ynf104 Ynf105 Ynf106 Ynf107 Ynf108 Ynf109 Ynf110 Ynf111 Ynf112 Ynf113 Ynf114 Ynf115 Ynf116 Ynf117 Ynf118 Ynf119 Ynf120 Ynf121 Ynf122 Ynf123 Ynf124 Ynf125 Ynf126 Ynf127 Ynf128 Ynf129 Ynf130 Ynf131 Ynf132 Ynf133 Ynf134 Ynf135 Ynf136 Ynf137 Ynf138 Ynf139 Ynf140 Ynf141 Ynf142 Ynf143 Ynf144 Ynf145 Ynf146 Ynf147 Ynf148 Ynf149 Ynf150 Ynf151 Ynf152 Ynf153 Ynf154 Ynf155 Ynf156 Ynf157 Ynf158 Ynf159 Ynf160 Ynf161 Ynf162 Ynf163 Ynf164 Ynf165 Ynf166 Ynf167 Ynf168 Ynf169 Ynf170 Ynf171 Ynf172 Ynf173 Ynf174 Ynf175 Ynf176 Ynf177 Ynf178 Ynf179 Ynf180 Ynf181 Ynf182 Ynf183 Ynf184 Ynf185 Ynf186 Ynf187 Ynf188 Ynf189 Ynf190 Ynf191 Ynf192 Ynf193 Ynf194 Ynf195 Ynf196 Ynf197 Ynf198 Ynf199 Ynf200 Ynf201 Ynf202 Ynf203 Ynf204 Ynf205 Ynf206 Ynf207 Ynf208 Ynf209 Ynf210 Ynf211 Ynf212 Ynf213 Ynf214 Ynf215 Ynf216 Ynf217 Ynf218 Ynf219 Ynf220 Ynf221 Ynf222 Ynf223 Ynf224 Ynf225 Ynf226 Ynf227 Ynf228 Ynf229 Ynf230 Ynf231 Ynf232 Ynf233 Ynf234 Ynf235 Ynf236 Ynf237 Ynf238 Ynf239 Ynf240 Ynf241 Ynf242 Ynf243 Ynf244 Ynf245 Ynf246 Ynf247 Ynf248 Ynf249 Ynf250 Ynf251 Ynf252 Ynf253 Ynf254 Ynf255 Ynf256 Ynf257 Ynf258 Ynf259 Ynf260 Ynf261 Ynf262 Ynf263 Ynf264 Ynf265 Ynf266 Ynf267 Ynf268 Ynf269 Ynf270 Ynf271 Ynf272 Ynf273 Ynf274 Ynf275 Ynf276 Ynf277 Ynf278 Ynf279 Ynf280 Ynf281 Ynf282 Ynf283 Ynf284 Ynf285 Ynf286 Ynf287 Ynf288 Ynf289 Ynf290 Ynf291 Ynf292 Ynf293 Ynf294 Ynf295 Ynf296 Ynf297 Ynf298 Ynf299 Ynf300 Ynf301 Ynf302 Ynf303 Ynf304 Ynf305 Ynf306 Ynf307 Ynf308 Ynf309 Ynf310 Ynf311 Ynf312 Ynf313 Ynf314 Ynf315 Ynf316 Ynf317 Ynf318 Ynf319 Ynf320 Ynf321 Ynf322 Ynf323 Ynf324 Ynf325 Ynf326 Ynf327 Ynf328 Ynf329 Ynf330 Ynf331 Ynf332 Ynf333 Ynf334 Ynf335 Ynf336 Ynf337 Ynf338 Ynf339 Ynf340 Ynf341 Ynf342 Ynf343 Ynf344 Ynf345 Ynf346 Ynf347 Ynf348 Ynf349 Ynf350 Ynf351 Ynf352 Ynf353 Ynf354 Ynf355 Ynf356 Ynf357 Ynf358 Ynf359 Ynf360 Ynf361 Ynf362 Ynf363 Ynf364 Ynf365 Ynf366 Ynf367 Ynf368 Ynf369 Ynf370 Ynf371 Ynf372 Ynf373 Ynf374 Ynf375 Ynf376 Ynf377 Ynf378 Ynf379 Ynf380 Ynf381 Ynf382 Ynf383 Ynf384 Ynf385 Ynf386 Ynf387 Ynf388 Ynf389 Ynf390 Ynf391 Ynf392 Ynf393 Ynf394 Ynf395 Ynf396 Ynf397 Ynf398 Ynf399 Ynf400 Ynf401 Ynf402 Ynf403 Ynf404 Ynf405 Ynf406 Ynf407 Ynf408 Ynf409 Ynf410 Ynf411 Ynf412 Ynf413 Ynf414 Ynf415 Ynf416 Ynf417 Ynf418 Ynf419 Ynf420 Ynf421 Ynf422 Ynf423 Ynf424 Ynf425 Ynf426 Ynf427 Ynf428 Ynf429 Ynf430 Ynf431 Ynf432 Ynf433 Ynf434 Ynf435 Ynf436 Ynf437 Ynf438 Ynf439 Ynf440 Ynf441 Ynf442 Ynf443 Ynf444 Ynf445 Ynf446 Ynf447 Ynf448 Ynf449 Ynf450 Ynf451 Ynf452 Ynf453 Ynf454 Ynf455 Ynf456 Ynf457 Ynf458 Ynf459 Ynf460 Ynf461 Ynf462 Ynf463 Ynf464 Ynf465 Ynf466 Ynf467 Ynf468 Ynf469 Ynf470 Ynf471 Ynf472 Ynf473 Ynf474 Ynf475 Ynf476 Ynf477 Ynf478 Ynf479 Ynf480 Ynf481 Ynf482 Ynf483 Ynf484 Ynf485 Ynf486 Ynf487 Ynf488 Ynf489 Ynf490 Ynf491 Ynf492 Ynf493 Ynf494 Ynf495 Ynf496 Ynf497 Ynf498 Ynf499 Ynf500 Ynf501 Ynf502 Ynf503 Ynf504 Ynf505 Ynf506 Ynf507 Ynf508 Ynf509 Ynf510 Ynf511 Ynf512 Ynf513 Ynf514 Ynf515 Ynf516 Ynf517 Ynf518 Ynf519 Ynf520 Ynf521 Ynf522 Ynf523 Ynf524 Ynf525 Ynf526 Ynf527 Ynf528 Ynf529 Ynf530 Ynf531 Ynf532 Ynf533 Ynf534 Ynf535 Ynf536 Ynf537 Ynf538 Ynf539 Ynf540 Ynf541 Ynf542 Ynf543 Ynf544 Ynf545 Ynf546 Ynf547 Ynf548 Ynf549 Ynf550 Ynf551 Ynf552 Ynf553 Ynf554 Ynf555 Ynf556 Ynf557 Ynf558 Ynf559 Ynf560 Ynf561 Ynf562 Ynf563 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79023.2	Energy metabolism	Carbon fixation in prokaryotes	Biotin carboxylase	-1.336719	0.047254	Polysaccharide	taxonomic_annotation_available	
82092.5	Transport and binding proteins	Cofactor and prosthetic group	Neur. exporter protein 8	-1.348834	0.056186	Polysaccharide	taxonomic_annotation_available	
105475.2	Transport and binding proteins	Amino acids, peptides and amines	RFB domain-containing protein	-1.358983	0.011899	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
77623.2	Carbohydrate metabolism	Carbohydrate and glycoconjugate metabolism	Carbohydrate transferase subunit alpha	-1.360547	0.018052	Polysaccharide	taxonomic_annotation_available	
79535.2	Regulatory functions	Small molecule interactions	Ribonucleic binding ATPase YnfP	-1.364688	0.051185	Polysaccharide/No taxonomic_annotation_available		
114899.4	No roles mapped out of 4 IDs		Seleconitrin	-1.362678	0.014769	Polysaccharide/No taxonomic_annotation_available		
146098.4	No roles mapped out of 4 IDs	Nonribosomal biodegradation and metabolism	Hydroxymethylglutaryl reductase	-1.395232	0.012482	Polysaccharide/No taxonomic_annotation_available		
134355.2	No roles mapped out of 4 IDs		Uncharacterized protein	-1.393977	0.045077	Polysaccharide/No taxonomic_annotation_available		
49209.2	No roles mapped out of 4 IDs		Uncharacterized protein	-1.393441	0.015143	Polysaccharide/Pseudomonas/Pseudomonas/daede	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas/daede	
114464.2	No roles mapped out of 4 IDs		Cytochrome c oxidase accessory protein CooG	-1.399308	0.024607	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
131404.3	Transcription	Ribosomal proteins; synthesis and modification	50S ribosomal subunit L3	-1.393441	0.015143	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	Betaproteobacteria bacterium RF/CF/POW02_12_Full_01_58
176570.8	Transcription	RN polymerase	DNA-directed RNA polymerase subunit beta	-1.404365	0.025078	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	Proteobacteria bacterium
43409.1	Carbohydrate metabolism	Nucleoside phosphate metabolism	Inositol phosphatase (Fragment)	-1.421236	0.024874	Polysaccharide/Bacteria	Proteobacterium/Betaproteobacteria/Oxalacetabacterium/Oxalacetabacterium bacterium	Oxalacetabacterium bacterium
169183.1	Fatty acid and lipid metabolism	Glycerol and glycerophospholipid metabolism	Glycerophospholipid diester phosphotransferase	-1.412121	0.017821	Polysaccharide/No taxonomic_annotation_available		
32188.2	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L5	-1.421236	0.011428	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	Gammaproteobacteria bacterium
113187.5	Prosthetic groups, cofactors, and carriers	Carbon and/or nitrogen fixation	Formyltransferase/Asparaginase	-1.423632	0.012482	Polysaccharide/No taxonomic_annotation_available		
111913.1	Carbohydrate metabolism	Glycolysis / gluconeogenesis	Oxydihydroxy-3-phosphoglyceraldehyde	-1.437354	0.020678	Polysaccharide/No taxonomic_annotation_available		
145719.3	Energy metabolism	Electron transport	ETF domain-containing protein	-1.447375	0.011282	Polysaccharide/No taxonomic_annotation_available		
56668.5	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Ferredoxin-NADP reductase	-1.455847	0.012146	Polysaccharide/No taxonomic_annotation_available		
134298.2	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein L13	-1.445747	0.021754	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
72546.2	Prosthetic groups, cofactors, and carriers	Ubiquitin and other targeted protein modifications	Ubc1 domain-containing protein	-1.466786	0.015103	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
70374.17	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Bacterioferritin	-1.463829	0.012426	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
180186.8	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Thioaldehyde interchange protein	-1.469047	0.001676	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas sp. MF48E3	
72461.16	Intracellular trafficking, assembly, and processing	Proteases	Sho zinc aminopeptidase	-1.479251	0.002789	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	Proteobacteria bacterium
104908.11	Intracellular trafficking, assembly, and processing	Ribosomal proteins; synthesis and modification	30S ribosomal protein S19	-1.504809	0.012782	Polysaccharide/No taxonomic_annotation_available		
149077.4	Transport and binding proteins	Unkown substrate	AEC transporter ATP-binding protein	-1.507349	0.023042	Polysaccharide/No taxonomic_annotation_available		
84087.2	Amino acid metabolism	Cysteine, serine and threonine metabolism	Thioamino acid transferase	-1.510485	0.002803	Polysaccharide/No taxonomic_annotation_available		
24737.4	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	beta-D-glucosyltransferase	-1.515749	0.002297	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
97447.4	Translation	Ribosomal proteins; synthesis and modification	Ribosomal subunit interface protein	-1.523401	0.022452	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
19444.3	Translation	Ribosomal proteins; synthesis and modification	Ribosome-binding factor A	-1.525777	0.002644	Polysaccharide/No taxonomic_annotation_available		
17053.1	Regulatory functions	Intracellular Trafficking Type Tpx	Intracellular Trafficking Type Tpx	-1.531146	0.002994	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	Synidactylocastrum Synidactylocastrum
118300.3	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	10S chaperone	-1.545474	0.021981	Polysaccharide/No taxonomic_annotation_available		
82134.1	No roles mapped out of 4 IDs		Not in Unifast	-1.553816	0.042701	Polysaccharide/No taxonomic_annotation_available		
61508.1	Regulatory functions	General	Translational GTPase TpxA	-1.564213	0.019228	Polysaccharide/Bacteria	Planctomycetes bacterium	Planctomycetes bacterium
61508.2	Regulatory functions	General	Translational GTPase TpxA	-1.564213	0.019228	Polysaccharide/Bacteria	Planctomycetes bacterium	Planctomycetes bacterium
68050.5	Transport and binding proteins	Unkown substrate	ATC transporter domain-containing protein	-1.581594	0.021654	Polysaccharide/No taxonomic_annotation_available		
35713.4	Transcription	Transcription factors	RNA polymerase sigma factor RpoD	-1.582286	0.021227	Polysaccharide/Bacteria	Proteobacterium/Betaproteobacteria/Pseudomonas/Pseudomonas	Betaproteobacteria bacterium
149889.2	Signal transduction	Signal transduction	Signal-dependent DNA-binding response regulator	-1.585873	0.017012	Polysaccharide/No taxonomic_annotation_available		
150629.3	No roles mapped out of 4 IDs		Purine sugar transport protein	-1.595489	0.009275	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
93242.4	Nucleic acid metabolism	DNA degradation	ATP-dependent RNA helicase BsdA	-1.618989	0.004707	Polysaccharide/No taxonomic_annotation_available		
107778.12	No roles mapped out of 4 IDs		Bacterial regulatory Helix-turn-helix, YnfR family protein	-1.618989	0.011808	Polysaccharide/No taxonomic_annotation_available		
170165.2	Fatty acid and lipid metabolism	Fatty acid degradation	3-ketolactyl-CoA thioesterase	-1.617588	0.038742	Polysaccharide/No taxonomic_annotation_available		
182922.4	Defense and invasion systems	Defensin and/or insectivore	Methionine	-1.622696	0.020384	Polysaccharide/No taxonomic_annotation_available		
48719.2	Transport and binding proteins	Amino acids, peptides and amines	Cytochrome c oxidase subunit I	-1.627472	0.025951	Polysaccharide/No taxonomic_annotation_available		
56278.9	Amino acid metabolism	Cysteine, serine and threonine metabolism	homoserine kinase	-1.639725	0.002147	Polysaccharide/No taxonomic_annotation_available		
113506.9	Amino acid metabolism	Cysteine, serine and threonine metabolism	50S ribosomal protein L15	-1.643148	0.001970	Polysaccharide/No taxonomic_annotation_available		
42429.3	Translation	Ribosomal proteins; synthesis and modification	NS-carbamoylornithinase ribonucleotide mutase	-1.646077	0.027039	Polysaccharide/No taxonomic_annotation_available		
45404.3	Nucleic acid metabolism	Purine metabolism	Cytosine methyltransferase	-1.646077	0.027039	Polysaccharide/No taxonomic_annotation_available		
145719.3	Intracellular trafficking, assembly, and processing	Protein export, secretion, and sorting	NS-carbamoylornithinase ribonucleotide mutase	-1.646077	0.027039	Polysaccharide/No taxonomic_annotation_available		
31849.8	No roles mapped out of 4 IDs		60S chaperone	-1.663724	0.029932	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	Betaproteobacteria bacterium RF/CF/POW02_12_Full_08_20
175116.1	Fatty acid and lipid metabolism	Chaperone and folding catalysis	Fatty acid oxidation complex subunit alpha	-1.668812	0.017682	Polysaccharide/No taxonomic_annotation_available		
77023.10	No roles mapped out of 4 IDs		TraM domain-containing protein	-1.696917	0.009146	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
82700.4	Intracellular trafficking, assembly, and processing	Proteases	Oxyphosphatase	-1.705555	0.013881	Polysaccharide/No taxonomic_annotation_available		
77182.2	Carbohydrate metabolism	Butanediol metabolism	3-hydroxyacyl-CoA thioesterase	-1.709892	0.032745	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
109629.3	No roles mapped out of 4 IDs		Uncharacterized protein	-1.713778	0.004024	Polysaccharide/No taxonomic_annotation_available		
80705.2	Intracellular trafficking, assembly, and processing	Proteases	Oxyphosphatase	-1.732725	0.009365	Polysaccharide/No taxonomic_annotation_available		
139837.9	Carbohydrate metabolism	Protein phosphate pathway	Ribulose-phosphate 3-epimerase	-1.738719	0.021454	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	compost metagenome
144711.1	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Chaperone ATP-binding protein	-1.738719	0.021454	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
118693.8	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	Glucose ABC transporter, ATP-binding subunit	-1.745206	0.049263	Polysaccharide/No taxonomic_annotation_available		
102738.23	No roles mapped out of 4 IDs		Uncharacterized protein	-1.752409	0.025942	Polysaccharide/No taxonomic_annotation_available		
51741.5	No roles mapped out of 4 IDs		Uncharacterized protein	-1.764784	0.002188	Polysaccharide/No taxonomic_annotation_available		
24744.8	No roles mapped out of 4 IDs		Two component transcriptional regulator, winged helix family member	-1.767815	0.002793	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	compost metagenome
170296.1	Transport and binding proteins	Transport and binding proteins	Zinc-dependent carboxylase large subunit	-1.778077	0.016061	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
49338.3	Carbohydrate metabolism	Biopolymer metabolism	2-Oxyglutarate carboxylase large subunit	-1.790818	9.26E-05	Polysaccharide/No taxonomic_annotation_available		
60900.1	Translation	Ribosomal proteins; synthesis and modification	50S ribosomal protein S17	-1.797173	0.017144	Polysaccharide/No taxonomic_annotation_available		
170287.2	Energy metabolism	Oxidative phosphorylation	Cytochrome c oxidase subunit 1 homolog, bacteroid	-1.811236	0.002002	Polysaccharide/No taxonomic_annotation_available		
162411.1	Intracellular trafficking, assembly, and processing	Ribosomal proteins; synthesis and modification	60S chaperone	-1.821873	0.014857	Polysaccharide/No taxonomic_annotation_available		
121610.10	Nucleic acid metabolism	Purine metabolism	Carbamate kinase	-1.844406	0.022874	Polysaccharide/No taxonomic_annotation_available		
30466.3	Amino acid metabolism	Arginine and proline metabolism	Pyridoxal-5-carboxylate reductase	-1.838715	0.001444	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
79145.1	Intracellular trafficking, assembly, and processing	Protein modification and repair	Protein deformylase	-1.868165	0.011282	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
109447.17	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	10S chaperone	-1.871718	0.011282	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
100161.4	No roles mapped out of 4 IDs		Phage terminase, small subunit	-1.878812	0.011102	Polysaccharide/No taxonomic_annotation_available		
140594.3	Carbohydrate metabolism	Citrate cycle (TCA cycle)	Citrate synthase	-1.879813	0.032313	Polysaccharide/Bacteria	Proteobacterium/Alphaproteobacteria/Sphingomonas/Erythrobacter/Croceosulfon	
180937.2	Nonribosomal biodegradation and metabolism	Nonribosomal biodegradation and metabolism	NS-carbamoylornithinase ribonucleotide mutase	-1.894149	0.002033	Polysaccharide/Bacteria	Proteobacterium/Betaproteobacteria/Pseudomonas/daede	
56217.8	Intracellular trafficking, assembly, and processing	Proteases	Lon protease	-1.903516	0.019344	Polysaccharide/No taxonomic_annotation_available		
134362.1	Regulatory functions	Small molecule interactions	Histidine kinase (Fragment)	-1.924077	0.003074	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas sp. HMW931	
102158.2	Nonribosomal biodegradation and metabolism	Ribonucleic acid degradation	Ferredoxin-NADP reductase	-1.938666	0.016566	Polysaccharide/No taxonomic_annotation_available		
169888.5	Intracellular trafficking, assembly, and processing	Proteins and protein interactions	Carboxylphosphoryl-in-oxidase	-1.940811	0.001726	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas/daede	
109447.17	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Protein GroEL	-1.951437	0.001726	Polysaccharide/No taxonomic_annotation_available		
118799.1	Energy metabolism	Oxidative phosphorylation	NADH-quinone oxidoreductase subunit F	-1.954998	0.035527	Polysaccharide/Bacteria	Actinobacteria/Thermoplasma/Solirubrobacterales	Solirubrobacterales bacterium 67-14
102738.23	Intracellular trafficking, assembly, and processing	Defensin and/or insectivore	Proteinase inhibitor	-1.951437	0.001726	Polysaccharide/No taxonomic_annotation_available		
1288.6	Defense and invasion systems	Defensin and/or insectivore	Allyl hydroperoxide reductase subunit B	-1.958465	0.035863	Polysaccharide/No taxonomic_annotation_available		
680270.8	Energy metabolism	Sulfur metabolism	Sulfite adenylyltransferase subunit 2	-1.959854	0.020390	Polysaccharide/No taxonomic_annotation_available		
102158.2	Energy metabolism	Oxidative phosphorylation	Cytochrome c oxidase, hcb-type, subunit 4	-1.960294	0.012615	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas	
149447.17	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis	Sulfhydryltransferase beta chain	-1.961848	0.000743	Polysaccharide/No taxonomic_annotation_available		
56217.8	Intracellular trafficking, assembly, and processing	Proteases	Lon protease	-1.970759	2.14E-07	Polysaccharide/No taxonomic_annotation_available		
60112.6	Regulatory functions	D interactions	Proteinase inhibitor	-1.972074	0.001897	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/Pseudomonas sp. ES3-13	
144610.13	No roles mapped out of 4 IDs		Phage	-1.992903	0.007801	Polysaccharide/No taxonomic_annotation_available		
1128603.1	Transport and binding proteins	Carbohydrates, organic alcohols, and acids	AEC transmembrane type-1 domain-containing protein	-1.950206	0.044077	Polysaccharide/No taxonomic_annotation_available		
144134.1	No roles mapped out of 4 IDs		Uncharacterized protein	-1.983136	0.021805	Polysaccharide/Bacteria	Bacteroidetes bacterium	Bacteroidetes bacterium
90462.1	Transport and binding proteins	Protein and protein interactions	Tooth-dependent copper receptor	-1.984478	0.025160	Polysaccharide/Bacteria	Proteobacterium/Gammaproteobacteria/Pseudomonas/daede	
39781.6	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Chaperone protein Hsp60	-1.920907	0.009262	Polysaccharide/No taxonomic_annotation_available		
1288.6	Defense and invasion systems	Defensin and/or insectivore	Allyl hydroperoxide reductase E	-1.123538	0.019613	Polysaccharide/No taxonomic_annotation_available		
42936.1	No roles mapped out of 4 IDs		Uncharacterized protein	-1.123538	0.019613	Polysaccharide/No taxonomic_annotation_available		
71857.3	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Chaperone protein Dsb	-1.123538	0.019613	Polysaccharide/Bacteria	Actinobacteria	Actinobacteria bacterium
1288.6	Defense and invasion systems	Defensin and/or insectivore	Allyl hydroperoxide reductase E	-1.123538	0.019613	Polysaccharide/No taxonomic_annotation_available		
70241.6	Carbohydrate metabolism	Chaperone and folding catalysis	Bacterioferritin	-1.143246	0.041167	Polysaccharide/No taxonomic_annotation_available		
77090.1	Carbohydrate metabolism	Biopolymer metabolism	3-ketolactyl-CoA thioesterase	-1.146149	0.008707	Polysaccharide/No taxonomic_annotation_available		
170141.2	Fatty acid and lipid metabolism	Biopolymer metabolism	Fatty acid oxidation complex subunit alpha	-1.161291	0.011299	Polysaccharide/No taxonomic_annotation_available		
168129.1	No roles mapped out of 4 IDs		Not in Unifast	-1.161291	0.011299	Polysaccharide/No taxonomic_annotation_available		
90218.20	No roles mapped out of 4 IDs		Prothymine II formyltransferase 2	-1.167209	0.008047	Polysaccharide/No taxonomic_annotation_available		
103008.0	No roles mapped out of 4 IDs		PAO3	-1.172327	0.002000	Polysaccharide/No taxonomic_annotation_available		
170287.2	Energy metabolism	Oxidative phosphorylation	Cytochrome c oxidase, hcb-type, subunit 1	-1.187192	0.027676	Polysaccharide/No taxonomic_annotation_available		
102158.2	Nucleic acid metabolism	Purine metabolism	Sensor protein PhoQ	-1.197366	0.006207	Polysaccharide/No taxonomic_annotation_available		
24744.8	No roles mapped out of 4 IDs		Sulfite adenylyltransferase subunit 2	-1.204865	0.012110	Polysaccharide/No taxonomic_annotation_available		
52051.9	Energy metabolism	Oxidative phosphorylation	NADH-quinone oxidoreductase subunit A	-1.204865	0.012110	Polysaccharide/No taxonomic_annotation_available		
102158.2	Intracellular trafficking, assembly, and processing	Chaperone and folding catalysis	Chaperone protein Hsp60	-1.212278	0.002713	Polysaccharide/Bacteria	Chloroflexi	Chloroflexi bacterium