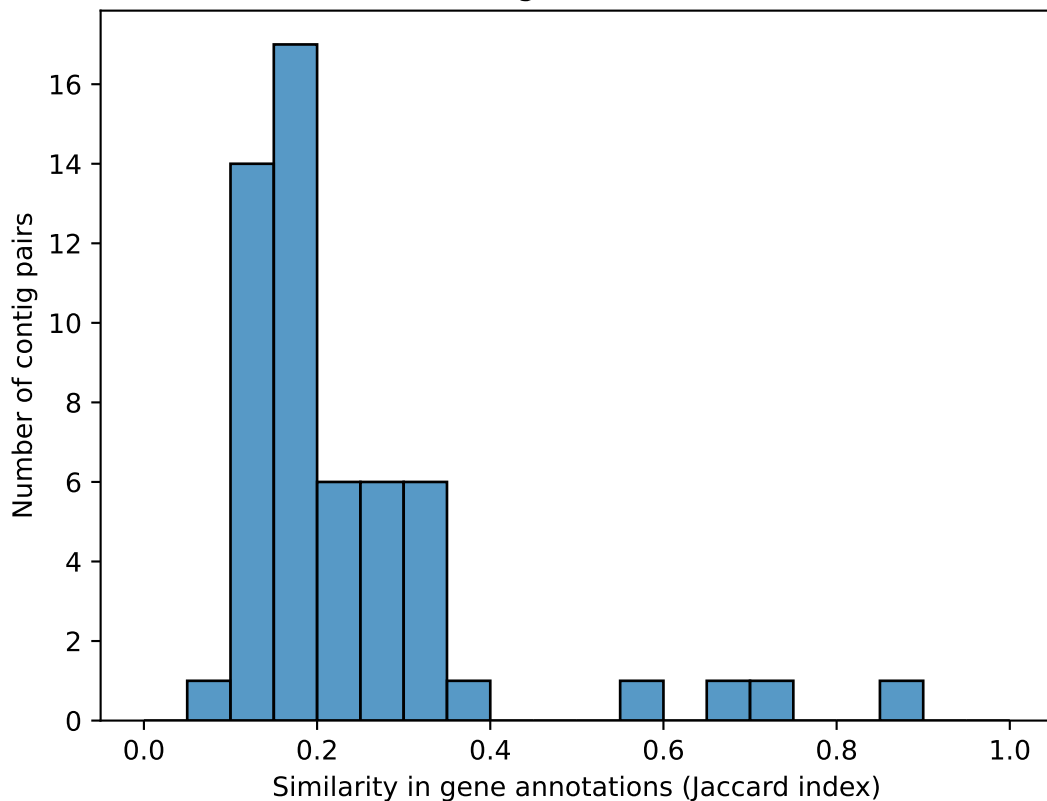
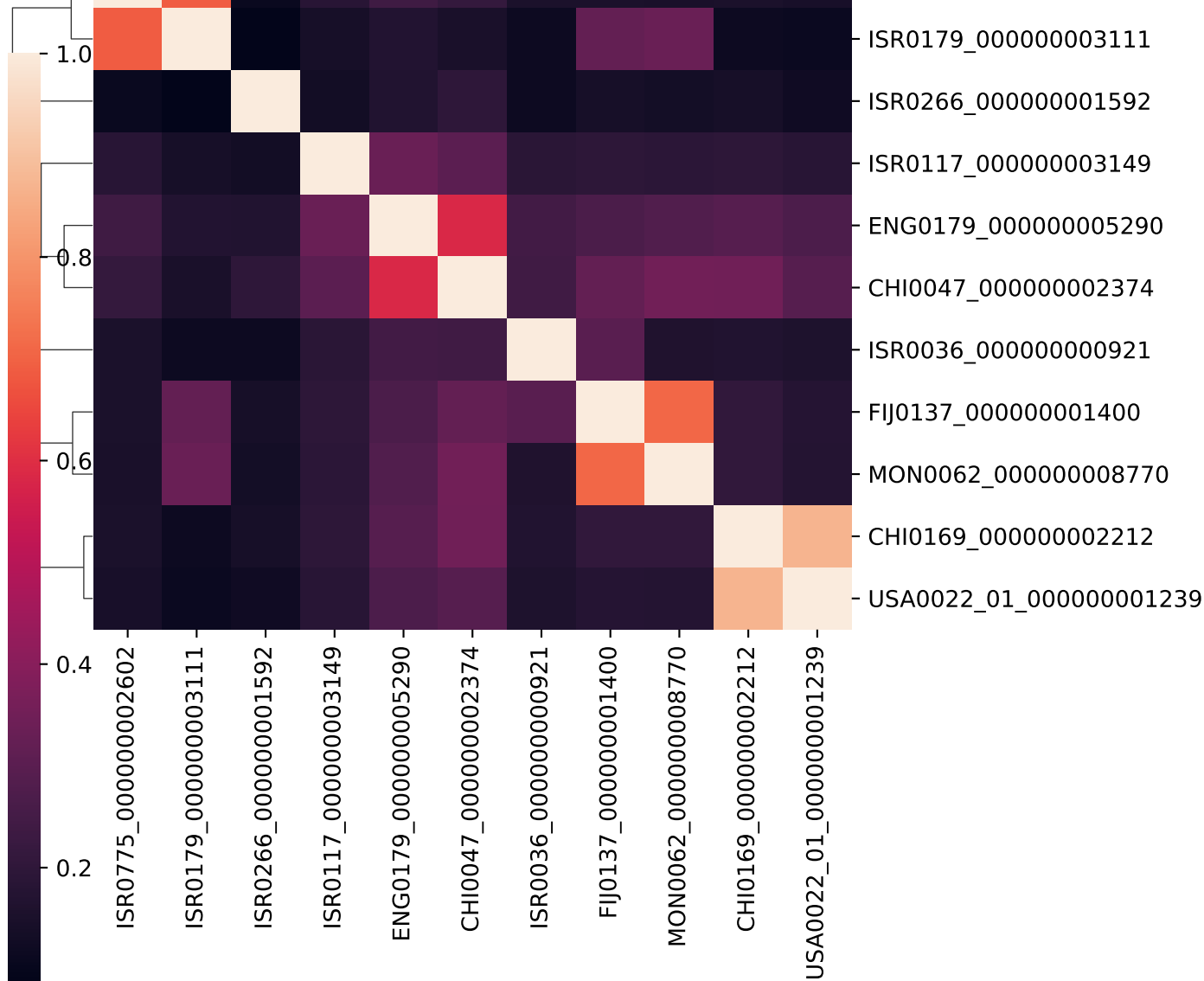
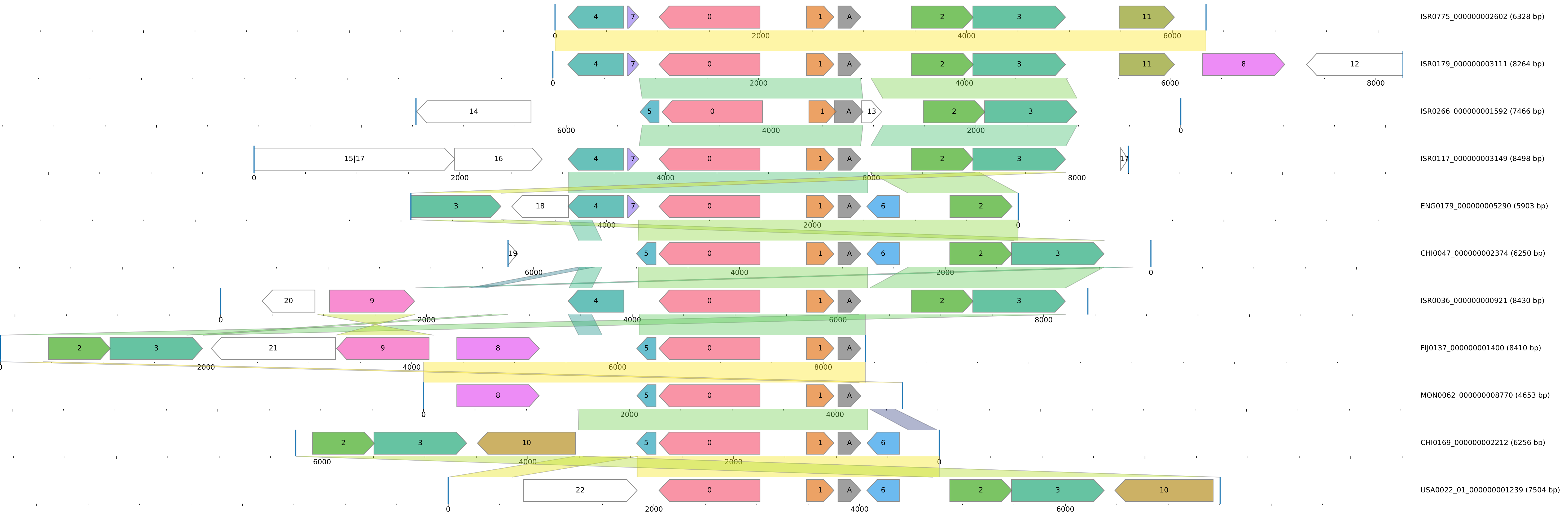
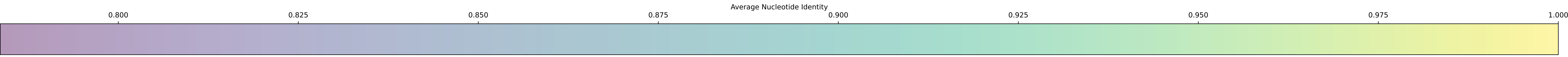


Contig similarities



Similarity in gene annotations (Jaccard index)





accession	card	representative contigs	COG_2014_FUNCTION	COG_2020_FUNCTION	COG_2020_PATHWAY	KEGG_Module	KOfam	Pfam_v32	mmseqs	resfam
A	COG4115	11	----	COG4115:Toxin_component_of_the_Txe-Axe_toxin-antitoxin_module_Txe/YoeB_family	COG20_4115:Toxin_component_of_the_Txe-Axe_toxin-antitoxin_module_Txe/YoeB_family_(PDB:2A6Q)	----	----	K19158:toxin_YoeB_[EC:3.1.-.-]	PF06769.14:YoeB-like_toxin_of_bacterial_type_II_toxin-antitoxin_system PF05016.15:PartE_toxin_of_type_II_toxin-antitoxin_system_parDE	mmseqs_40_18476509 mmseqs_5_21692046 mmseqs_20_49264533 mmseqs_25_18981569 mmseqs_30_33353384 mmseqs_30_49637121 mmseqs_40_50030072 mmseqs_5_38866086
0	COG5527	11	----	COG5527:Protein_involved_in_initiation_of_plasmid_replication	COG20_5527:Protein_involved_in_initiation_of_plasmid_replication_(PDB:2Z9O)	----	----	PF01051.21:Initiator_Replication_protein	mmseqs_25_318285	----
1	mmseqs_5_46990681	11	----			----	----		mmseqs_5_46990681	----
2	mmseqs_5_318210	10	----			----	----		mmseqs_5_318210	----
3	mmseqs_5_318209	10	----			----	----		mmseqs_5_318209	----
4	mmseqs_5_318283	5	----			----	----		mmseqs_5_318283	----
5	mmseqs_5_318284	5	----			----	----		mmseqs_5_318284	----
6	mmseqs_5_318270	4	----			----	----		mmseqs_5_318270	----
7	mmseqs_5_318207	4	----			----	----		mmseqs_5_318207	----
8	ErmF	3	ErmF	COG0030:16S_rRNA_A1518_and_A1519_N6-dimethyltransferase_RsmA/KsgA/DIM1_(may_also_have_DNA_glycosylase/AP_lyase_activity)	COG20_0030:16S_rRNA_A1518_and_A1519_N6-dimethyltransferase_RsmA/KsgA/DIM1_(may_also_have_DNA_glycosylase/AP_lyase_activity)_(RsmA)_(PDB:1QYR)	COG20PATH_16S_rRNA_modification:16S_rRNA_modification	----	K00561:23S_rRNA_(adenine-N6)-dimethyltransferase_[EC:2.1.1.184]	PF00398.20:Ribosomal_RNA_adenine_dimethylase PF13649.6:Methyltransferase_domain	mmseqs_20_44854716 mmseqs_20_46213925 mmseqs_30_45717258 mmseqs_5_42569366 mmseqs_5_46613503
9	COG3293	2	----	COG3293	COG20_3293:Transposase	----	----	K07492:putative_transposase	PF13340.6:Putative_transposase_of_IS4/5_family_(DUF4096) PF13359.6:DDE_superfamily_endonuclease PF13586.6:Transposase_ODE_domain	mmseqs_20_34977557 mmseqs_20_40694593 mmseqs_20_49962670 mmseqs_25_35004774 mmseqs_25_38015274 mmseqs_50_44008419 mmseqs_5_38637922 mmseqs_5_49377341 mmseqs_25_46237899
10	COG2367	2	----	COG2367:Beta-lactamase_class_A	COG20_2367:Beta-lactamase_class_A_(PenP)_(PDB:6W34)	----	M00627:beta-Lactam_resistance_Bla_system	K17836:beta-lactamase_class_A_[EC:3.5.2.6]	PF00144.24:Beta-lactamase PF13354.6:Beta-lactamase_enzyme_family	mmseqs_20_27807555 mmseqs_20_45597049 mmseqs_25_17672097 mmseqs_25_50144613 mmseqs_25_50168160 mmseqs_30_28098525 mmseqs_30_28463173 mmseqs_30_45820968 mmseqs_40_49500529 mmseqs_5_27807555 mmseqs_5_40934773
11	COG0262	2	----	COG0262:Dihydrofolate_reductase	COG20_0262:Dihydrofolate_reductase_(FolA)_(PDB:1DDR)	COG20PATH_Folate_biosynthesis:Folate_biosynthesis	----	----	PF00186.19 PF01872.17:RibD_C-terminal_domain	mmseqs_20_18371528 mmseqs_20_28690327 mmseqs_20_35561040 mmseqs_20_40981152 mmseqs_20_46036020 mmseqs_20_47039986 mmseqs_20_50109747 mmseqs_20_507442 mmseqs_25_18690724 mmseqs_25_27809843 mmseqs_25_33762828 mmseqs_25_34224826 mmseqs_25_41658507 mmseqs_25_843930 mmseqs_30_34418893 mmseqs_30_38588413 mmseqs_30_38787878 mmseqs_30_40287828 mmseqs_30_44338752 mmseqs_30_47439118 mmseqs_30_48853272 mmseqs_40_25053080 mmseqs_40_33507810 mmseqs_40_43317101 mmseqs_40_44996468 mmseqs_40_47589658 mmseqs_40_7279357 mmseqs_50_42231614 mmseqs_50_45825785 mmseqs_5_34213475 mmseqs_5_38588413 mmseqs_5_39284910 mmseqs_5_42992153 mmseqs_5_43837334 mmseqs_5_47251912 mmseqs_5_50030374 mmseqs_5_50053062
12	COG0654	1	tetX	COG0654:2-polyphenyl-6-methoxyphenol_hydroxylase_and_related_FAD-dependent_oxidoreductases	COG20_0654:2-polyphenyl-6-methoxyphenol_hydroxylase_and_related_FAD-dependent_oxidoreductases_(UbiH)_(PDB:1BF3)	COG20PATH_Ubiquinone_biosynthesis:Ubiquinone_biosynthesis	----	K18221:tetracycline_11a-monoxygenase_tetracycline_resistance_protein_[EC:1.14.13.231]	PF01494.19:FAD_binding_domain	mmseqs_5_40919492
13	PF05534.12	1	----	----	----	----	----	----	PF05534.12:HicB_family	----
14	COG20_2826	1	----	COG2826:Transposase_and_inactivated_derivatives_IS30_family	COG20_2826:Transposase_and_inactivated_derivatives_IS30_family_(Tra8)	----	----	K07482:transposase_IS30_family	PF00665.26:Integrase_core_domain PF13384.6:Homeodomain-like_domain PF13518.6:Helix-turn-helix_domain PF13565.6 PF13936.6	mmseqs_20_1138328 mmseqs_20_26217732 mmseqs_20_34118053 mmseqs_20_39611311 mmseqs_20_41768490 mmseqs_20_840957 mmseqs_25_21769472 mmseqs_25_34826290 mmseqs_25_39378629 mmseqs_25_48777609 mmseqs_25_49092157 mmseqs_25_7253592 mmseqs_25_840957 mmseqs_30_1407520 mmseqs_30_1438561 mmseqs_30_19137885 mmseqs_30_1978401 mmseqs_30_21409397 mmseqs_30_33758598 mmseqs_40_1407520 mmseqs_40_42923361 mmseqs_40_48230206 mmseqs_40_48311530 mmseqs_5_40324800 mmseqs_5_40577760 mmseqs_5_44855065 mmseqs_5_47474719 mmseqs_5_524682
15	COG0480	1	tetQ	COG0480:Translation_elongation_factor_EF-G_a_GTPase	COG20_0480:Translation_elongation_factor_EF-G_a_GTPase_(FusA)_(PDB:1DAR)	COG20PATH_Translation_factors:Translation_factors	----	K18220:ribosomal_protection_tetracycline_resistance_protein	PF00009.27:Elongation_factor_Tu_GTP_binding_domain PF00679.24:Elongation_factor_G_C-terminus PF01926.23:50S_ribosome-binding_GTPase PF03764.18:Elongation_factor_G_domain_IV PF14492.6:Elongation_Factor_G_domain_II	mmseqs_20_28126948 mmseqs_25_18427017 mmseqs_25_44750995 mmseqs_30_35557096 mmseqs_30_49901209 mmseqs_5_34986014 mmseqs_5_36995716
16	COG0745	1	----	COG0745:DNA-binding_response_regulator_OmpR_family_contains_REC_and_winged-helix_(WHTH)_domain COG2205:K+-sensing_histidine_kinase_KdpD	COG20_0642:Signal_transduction_histidine_kinase_(BaeS)_(PDB:1JOY) COG20_0745:DNA-binding_response_regulator_OmpR_family_contains_REC_and_winged-helix_(WHTH)_domain (OmpR)_(PDB:1XHF)	----	----	----	mmseqs_5_47009178	----
17	PF00009.27	1	tetQ	----	----	----	----	----	PF00009.27:Elongation_factor_Tu_GTP_binding_domain	----
18	COG20_1878	1	----	----	COG20_1878:Kynurenine_formamidase_(PDB:1R61)	----	----	----	PF04199.13:Putative_cyclase	mmseqs_25_50083259 mmseqs_30_23802849 mmseqs_5_17195676
19	COG0449	1	----	phosphate_synthetase_contains_amidotransferase_and_phosphosugar_isomerase_domains	COG20_0449:Glucosamine_6-phosphate_synthetase_contains_amidotransferase_and_phosphosugar_isomerase_domains_(GlmS)_(PDB:2J6H)	----	----	----	----	----
20	COG20_3467	1	----	phosphate_synthetase_contains_amidotransferase_and_phosphosugar_isomerase_domains	COG20_3467:Nitroimidazole_reductase_NimA_or_a_related_FMN-containing_flavoprotein_pyridoxamine_5'-phosphate_oxidase_superfamily_(NimA)_(PDB:1W3O)	----	----	K07005:uncharacterized_protein	PF01243.20:Pyridoxamine_5'-phosphate_oxidase PF12900.7	mmseqs_20_1328259 mmseqs_20_49041351 mmseqs_20_50167537 mmseqs_25_2154152 mmseqs_25_35834072 mmseqs_30_18420707 mmseqs_30_24320293 mmseqs_30_35834072 mmseqs_30_36798477 mmseqs_30_49971783 mmseqs_40_28722058 mmseqs_40_36448212
21	PF05593.14	1	----	----	----	----	----	----	PF05593.14:RHS_Repeat	----
22	COG3385	1	----	COG3385:IS4_transposase	----	----	----	----	PF01609.21	mmseqs_20_6885918 mmseqs_25_6885918 mmseqs_5_44925341