a "Free-living" sample associated

d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Sulfitobacter
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Caulobacterales; f__Hyphomonadaceae; g__Hyphomonas
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Alteromonadaceae; g__Alteromonas
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Oleiphilaceae; g__Marinobacter
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__TMED25; g__AG-430-B22
d__Bacteria; p__Chloroflexota; c__Dehalococcoidia; o__UBA1151; f__TMED-70; g__TMED-70
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Porticoccaceae; g__HTCC2207
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Poseidoniaceae; g__MGIIa-L1
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas_D
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales_A; f__Thalassospiraceae; g__Thalassospira
d__Bacteria; p__SAR324; c__SAR324; o__SAR324; f__NAC60-12; g__Arctic96AD-7
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Erythrobacter_A
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Alcanivoracaceae; g__Alcanivorax
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__TCS55; g__TCS55
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Poseidoniaceae; g__MGIIa-K1
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Thalassoarchaeaceae; g__MGIIb-O5
d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__TMED189; f__TMED189; g__TMED189
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__HIMB59; f__HIMB59; g__HIMB59
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter_A
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__HIMB11
d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__UBA8592; g__MedAcidi-G2A
d__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Prochlorococcus_A
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Nitrosococcales; f__Methylophagaceae; g__Methylophaga
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__TCS55; g__GCA-002701945
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__TCS55; g__TMED108
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudohongiellaceae; g__UBA9145
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Marinoscillaceae; g__MED-G16
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__MED-G14
d__Bacteria; p__Chloroflexota; c__Dehalococcoidia; o__UBA1151; f__TMED-70; g__GCA-002700125

Number of genomes

b "Less filtered" sample associated

d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__TCS55; g__TCS55
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Planktomarina
d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__TMED189; f__TMED189; g__TMED189
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__TCS55; g__UBA2126
d__Archaea; p__Crenarchaeota; c__Nitrososphaeria; o__Nitrososphaerales; f__Nitrosopumilaceae; g__Nitrosopelagicus
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Thalassoarchaeaceae; g__MGIIb-O1
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Thalassoarchaeaceae; g__Thalassarchaeum
d__Bacteria; p__Actinobacteriota; c__Acidimicrobiia; o__Microtrichales; f__MedAcidi-G1; g__UBA9410
d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Propionibacteriales; f__Nocardioidaceae; g__Nocardioides
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__AG-414-E02
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiomicrospirales; f__Thioglobaceae; g__Thioglobus
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Alcanivoracaceae; g__Alcanivorax
d__Archaea; p__Crenarchaeota; c__Nitrososphaeria; o__Nitrososphaerales; f__UBA57; g__UBA57
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__MED-G11
d__Bacteria; p__Chloroflexota; c__Dehalococcoidia; o__UBA3495; f__UBA3495; g__UBA9611
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__MED-G14
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Limnobacter
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudohongiellaceae; g__UBA9145
d__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Synechococcales; f__Cyanobiaceae; g__Prochlorococcus_A
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Pelagibacterales; f__AG-422-B15; g__AG-422-B15
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__SAR86; f__D2472; g__SAR86A
d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Verrucomicrobiales; f__Akkermansiaceae; g__Roseibacillus
d__Archaea; p__Thermoplasmatota; c__Poseidoniia; o__Poseidoniales; f__Poseidoniaceae; g__MGIIa-L1
d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Actinomycetales; f__Microbacteriaceae; g__Pontimonas
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__UBA8316
d__Bacteria; p__Marinisomatota; c__Marinisomatia; o__Marinisomatales; f__UBA2128; g__UBA2128
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Saccharospirillaceae; g__Oleibacter
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__MS024-2A
d__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Microcystaceae; g__Crocosphaera

Number of genomes