

D_0_Archaea;D_1_Euryarchaeota;D_2_Halobacteria;D_3_Halobacteriales
 D_0_Archaea;D_1_Nanohaloarchaeota;D_2_uncultured archaeon;D_3_uncultured archaeon
 D_0_Archaea;D_1_Nanohaloarchaeota;D_2_uncultured haloarchaeon;D_3_uncultured haloarchaeon
 D_0_Archaea;D_1_Nanohaloarchaeota;Other;Other
 D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG);D_3_uncultured archaeon
 D_0_Bacteria;D_1_Acidobacteria;D_2_Acidobacteria;D_3_Acidobacteriales
 D_0_Bacteria;D_1_Acidobacteria;D_2_Acidobacteria;D_3_Subgroup 3
 D_0_Bacteria;D_1_Acidobacteria;D_2_Acidobacteria;D_3_Subgroup 4
 D_0_Bacteria;D_1_Actinobacteria;D_2_Acidimicrobiia;D_3_Acidimicrobiales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Actinomycetales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Corynebacteriales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Frankiales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Kineosporiales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Propionibacteriales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Pseudonocardiales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Nitrliruptoria;D_3_Euzebyales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Rubrobacteria;D_3_Rubrobacterales
 D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia;D_3_Solirubrobacterales
 D_0_Bacteria;D_1_Armatimonadetes;D_2_Armatimonadia;D_3_Armatimonadales
 D_0_Bacteria;D_1_Armatimonadetes;D_2_uncultured bacterium;D_3_uncultured bacterium
 D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales
 D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia;D_3_Cytophagales
 D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia;D_3_Order II
 D_0_Bacteria;D_1_Bacteroidetes;D_2_Flavobacteriia;D_3_Flavobacteriales
 D_0_Bacteria;D_1_Bacteroidetes;D_2_Sphingobacteriia;D_3_Sphingobacteriales
 D_0_Bacteria;D_1_Chloroflexi;D_2_Ardenticatenia;D_3_Ardenticatenales
 D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria;D_3_C0119
 D_0_Bacteria;D_1_Chloroflexi;D_2_Thermomicrobia;D_3_JG30-KF-CM45
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured Chlorophyta
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured bacterium
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured eukaryote
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;D_3_uncultured organism
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast;Other
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionI
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionII
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionIII
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_SubsectionIV
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;D_3_uncultured
 D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria;Other
 D_0_Bacteria;D_1_Deinococcus-Thermus;D_2_Deinococci;D_3_Deinococcales
 D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales
 D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales
 D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales
 D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacteriia;D_3_Fusobacteriales
 D_0_Bacteria;D_1_Gemmatimonadetes;D_2_Gemmatimonadetes;D_3_AT425-EubC11 terrestrial group
 D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae;D_3_Phycisphaerales
 D_0_Bacteria;D_1_Planctomycetes;D_2_Planctomycetacia;D_3_Planctomycetales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Caulobacteriales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhizobiales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodobacterales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Sphingomonadales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Burkholderiales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria;D_3_Neisseriales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfuromonadales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Myxococcales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Alteromonadales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Chromatiales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Oceanospirillales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pasteurellales
 D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales
 D_0_Bacteria;D_1_TM6;D_2_uncultured bacterium;D_3_uncultured bacterium
 D_0_Bacteria;D_1_Verrucomicrobia;D_2_Spartobacteria;D_3_Chthoniobacteriales
 Unassigned;Other;Other;Other