

D_0_Archaea;D_1_Thaumarchaeota;D_2_Soil Crenarchaeotic Group(SCG)

D_0_Bacteria;D_1_Acidobacteria;D_2_Blastocatellia

D_0_Bacteria;D_1_Acidobacteria;D_2_Holophagae

D_0_Bacteria;D_1_Acidobacteria;D_2_Solibacteres

D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 17

D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 22

D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 5

D_0_Bacteria;D_1_Acidobacteria;D_2_Subgroup 6

D_0_Bacteria;D_1_Acidobacteria;Other

D_0_Bacteria;D_1_Actinobacteria;D_2_Acidimicrobiia

D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria

D_0_Bacteria;D_1_Actinobacteria;D_2_Coriobacteriia

D_0_Bacteria;D_1_Actinobacteria;D_2_MB-A2-108

D_0_Bacteria;D_1_Actinobacteria;D_2_Nitriliruptoria

D_0_Bacteria;D_1_Actinobacteria;D_2_OPB41

D_0_Bacteria;D_1_Actinobacteria;D_2_Rubrobacteria

D_0_Bacteria;D_1_Actinobacteria;D_2_TakashiAC-B11

D_0_Bacteria;D_1_Actinobacteria;D_2_Thermoleophilia

D_0_Bacteria;D_1_Actinobacteria;Other

D_0_Bacteria;D_1_Armatimonadetes;D_2_Armatimonadia

D_0_Bacteria;D_1_Armatimonadetes;D_2_Fimbriimonadia

D_0_Bacteria;D_1_Armatimonadetes;D_2_uncultured

D_0_Bacteria;D_1_BRC1;D_2_uncultured bacterium

D_0_Bacteria;D_1_BRC1;Other

D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes BD2-2

D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidetes Incertae Sedis

D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia

D_0_Bacteria;D_1_Bacteroidetes;D_2_Cytophagia

D_0_Bacteria;D_1_Bacteroidetes;D_2_Flavobacteriia

D_0_Bacteria;D_1_Bacteroidetes;D_2_Sphingobacteriia

D_0_Bacteria;D_1_Chlamydiae;D_2_Chlamydiae

D_0_Bacteria;D_1_Chlorobi;D_2_Chlorobia

D_0_Bacteria;D_1_Chloroflexi;D_2_Anaerolineae

D_0_Bacteria;D_1_Chloroflexi;D_2_Ardenticatenia

D_0_Bacteria;D_1_Chloroflexi;D_2_Caldilineae

D_0_Bacteria;D_1_Chloroflexi;D_2_Chloroflexi Incertae Sedis

D_0_Bacteria;D_1_Chloroflexi;D_2_Chloroflexia

D_0_Bacteria;D_1_Chloroflexi;D_2_Gitt-GS-136

D_0_Bacteria;D_1_Chloroflexi;D_2_JG30-KF-CM66

D_0_Bacteria;D_1_Chloroflexi;D_2_JG37-AG-4

D_0_Bacteria;D_1_Chloroflexi;D_2_KD4-96

D_0_Bacteria;D_1_Chloroflexi;D_2_Ktedonobacteria

D_0_Bacteria;D_1_Chloroflexi;D_2_NLS2-31

D_0_Bacteria;D_1_Chloroflexi;D_2_P2-11E

D_0_Bacteria;D_1_Chloroflexi;D_2_S085

D_0_Bacteria;D_1_Chloroflexi;D_2_SAR202 clade

D_0_Bacteria;D_1_Chloroflexi;D_2_TK10

D_0_Bacteria;D_1_Chloroflexi;D_2_Thermomicrobia

D_0_Bacteria;D_1_Chloroflexi;Other

D_0_Bacteria;D_1_Cyanobacteria;D_2_Chloroplast

D_0_Bacteria;D_1_Cyanobacteria;D_2_Cyanobacteria

D_0_Bacteria;D_1_Cyanobacteria;D_2_Melainabacteria

D_0_Bacteria;D_1_Deinococcus-Thermus;D_2_Deinococci

D_0_Bacteria;D_1_Elusimicrobia;D_2_Elusimicrobia

D_0_Bacteria;D_1_FBP;D_2_uncultured bacterium

D_0_Bacteria;D_1_Fibrobacteres;D_2_Fibrobacteria

D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli

D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia

D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia

D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes

D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacteriia

D_0_Bacteria;D_1_Gemmatimonadetes;D_2_BD2-11 terrestrial group

D_0_Bacteria;D_1_Gemmatimonadetes;D_2_Gemmatimonadetes

D_0_Bacteria;D_1_Gemmatimonadetes;D_2_Longimicrobia

D_0_Bacteria;D_1_Gemmatimonadetes;D_2_S0134 terrestrial group

D_0_Bacteria;D_1_Hydrogenedentes;D_2_uncultured bacterium

D_0_Bacteria;D_1_Nitrospirae;D_2_Nitrospira

D_0_Bacteria;D_1_Planctomycetes;D_2_Phycisphaerae

D_0_Bacteria;D_1_Planctomycetes;D_2_Planctomycetacia

D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria

D_0_Bacteria;D_1_Proteobacteria;D_2_Betaproteobacteria

D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria

D_0_Bacteria;D_1_Proteobacteria;D_2_Epsilonproteobacteria

D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria

D_0_Bacteria;D_1_Proteobacteria;D_2_JTB23

D_0_Bacteria;D_1_Proteobacteria;D_2_SPOTSOC00m83

D_0_Bacteria;D_1_Proteobacteria;Other

D_0_Bacteria;D_1_SBR1093;Other

D_0_Bacteria;D_1_SR1 (Absconditabacteria);Ambiguous_taxa

D_0_Bacteria;D_1_SR1 (Absconditabacteria);D_2_uncultured bacterium

D_0_Bacteria;D_1_Saccharibacteria;D_2_uncultured bacterium

D_0_Bacteria;D_1_Saccharibacteria;Other

D_0_Bacteria;D_1_Spirochaetae;D_2_Spirochaetes

D_0_Bacteria;D_1_Synergistetes;D_2_Synergistia

D_0_Bacteria;D_1_TM6 (Dependentiae);Other

D_0_Bacteria;D_1_Tectomicrobia;D_2_Tectomicrobia Incertae Sedis

D_0_Bacteria;D_1_Tectomicrobia;D_2_uncultured bacterium

D_0_Bacteria;D_1_Verrucomicrobia;D_2_OPB35 soil group

D_0_Bacteria;D_1_Verrucomicrobia;D_2_Opitutae

D_0_Bacteria;D_1_Verrucomicrobia;D_2_Spartobacteria

D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobiae

D_0_Bacteria;Other;Other

Unassigned;Other;Other