Unassigned.Other.Other.Other
k__Archaea|p__Euryarchaeota|c__Halobacteria|o__Halobacteriales
k__Archaea|p__Euryarchaeota|c__Methanomicrobia|o__Methanomicrobiales
k__Archaea|p__Euryarchaeota|c__Thermoplasmatea|o__Thermoplasmatales
k__Archaea|p__Thaumarchaeota|c__Group C3|o__uncultured archaeon
k__Archaea|p__Thaumarchaeota|c__Marine Group I|o__uncultured crenarchaeote
k__Archaea|p__Thaumarchaeota|c__Marine Group I|f|g|s|
k__Archaea|p__Thaumarchaeota|c__Marine Group I|o__Unknown Order
k__Archaea|p__Thaumarchaeota|c__Marine Group I|f__uncultured archaeon|g__uncultured archaeon
k__Archaea|p__Thaumarchaeota|c__Soil Crenarchaeotic Group|f|g|s|
k__Archaea|p__Thaumarchaeota|c__Soil Crenarchaeotic Group|f|g|s__Unknown Order
k__Archaea|p__Thaumarchaeota|c__Soil Crenarchaeotic Group|f__uncultured archaeon
k__Archaea|p__Thaumarchaeota|c__Soil Crenarchaeotic Group|f|g|s__uncultured bacterium
k__Archaea|p__Thaumarchaeota|c__Soil Crenarchaeotic Group|f|g|s__uncultured crenarchaeote
k__Archaea|p__Thaumarchaeota|c__South African Gold Mine Gp 1|f|g|s|
k__Archaea|p__Thaumarchaeota|c__South African Gold Mine Gp 1|f|g|s__Unknown Order
k__Archaea|p__Thaumarchaeota|c__South African Gold Mine Gp 1|f|g|s__uncultured crenarchaeote
k__Archaea|p__Thaumarchaeota|c__terrestrial group|f__uncultured archaeon
k__Archaea|p__Thaumarchaeota|c__terrestrial group|f__uncultured crenarchaeote
k__Bacteria.Other.Other.Other
k__Bacteria|p__Acidobacteria|c__Acidobacteria.Other
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__iii1-15
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Acidobacteriales
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 11
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 12
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 13
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 17
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 18
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 2
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 20
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 25
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 4
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 5
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 6
k__Bacteria|p__Acidobacteria|c__Acidobacteria|o__Subgroup 9
k__Bacteria|p__Acidobacteria|c__Holophagae.Other
k__Bacteria|p__Acidobacteria|c__Holophagae|o__iii1-245.B16
k__Bacteria|p__Acidobacteria|c__Holophagae|o__Holophagales
k__Bacteria|p__Acidobacteria|c__Holophagae|o__Subgroup 10
k__Bacteria|p__Acidobacteria|c__Holophagae|o__Subgroup 6
k__Bacteria|p__Acidobacteria|c__Holophagae|o__Subgroup 7
k__Bacteria|p__Acidobacteria|c__Holophagae|o__TM3-58
k__Bacteria|p__Acidobacteria|c__Solibacteres.Other
k__Bacteria|p__Acidobacteria|c__Subgroup 22|o__uncultured Acidobacteria bacterium
k__Bacteria|p__Acidobacteria|c__Subgroup 22|o__uncultured bacterium
k__Bacteria|p__Acidobacteria|c__Subgroup 26|o__uncultured bacterium
k__Bacteria|p__Actinobacteria|c__Actinobacteria.Other
k__Bacteria|p__Actinobacteria|c__Acidimicrobiia|o__Acidimicrobiales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Actinomycetales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Corynebacteriales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Coriobacteriales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micromonosporales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Propionibacteriales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Pseudonocardiales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Rubrobacteriales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Streptomycetales
k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Streptosporangiales
k__Bacteria|p__Actinobacteria|c__Coriobacteriia.Other
k__Bacteria|p__Actinobacteria|c__Coriobacteriia|o__Coriobacteriales
k__Bacteria|p__Actinobacteria|c__Nitriliruptoria.Other
k__Bacteria|p__Actinobacteria|c__Nitriliruptoria|o__Nitriliruptorales
k__Bacteria|p__Actinobacteria|c__OCS155.Other
k__Bacteria|p__Actinobacteria|c__OCS155|o__Actinomycetales
k__Bacteria|p__Actinobacteria|c__Thermoleophilia.Other
k__Bacteria|p__Actinobacteria|c__Thermoleophilia|o__Gaiellales
k__Bacteria|p__Armatimonadetes.Other.Other.Other
k__Bacteria|p__Armatimonadetes|c__Armatimonadia.Armatimonadia
k__Bacteria|p__Armatimonadetes|c__Armatimonadia|o__Armatimonadales
k__Bacteria|p__Armatimonadetes|c__uncultured Armatimonadetes bacterium|o__uncultured Armatimonadetes bacterium
k__Bacteria|p__Armatimonadetes|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Armatimonadetes|c__uncultured soil bacterium|o__uncultured soil bacterium
k__Bacteria|p__Armatimonadetes|c__uncultured soil bacterium|o__uncultured soil bacterium
k__Bacteria|p__BRC1.Other.Other.Other
k__Bacteria|p__BRC1|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Bacteroidetes|c__BD2-11|o__uncultured bacterium
k__Bacteria|p__Bacteroidetes|c__Bacteroidia.Other
k__Bacteria|p__Bacteroidetes|c__Bacteroidia|o__Bacteroidales
k__Bacteria|p__Bacteroidetes|c__Cytophagia.Cytophagales
k__Bacteria|p__Bacteroidetes|c__Cytophagia|o__Cytophagales
k__Bacteria|p__Bacteroidetes|c__Flavobacteriia.Flavobacteriales
k__Bacteria|p__Bacteroidetes|c__SB-5|o__uncultured bacterium
k__Bacteria|p__Bacteroidetes|c__Sphingobacteriia.Sphingobacteriales
k__Bacteria|p__Bacteroidetes|c__VC2.1 Bac22|o__Other
k__Bacteria|p__Bacteroidetes|c__VC2.1 Bac22|o__uncultured Bacteroidetes bacterium
k__Bacteria|p__Bacteroidetes|c__WCHB1-32|o__uncultured bacterium
k__Bacteria|p__Bacteroidetes|c__WCHB1-32|f__uncultured bacterium
k__Bacteria|p__Bacteroidetes|c__vadinHA17|o__uncultured bacterium
k__Bacteria|p__Candidate division BRC1.Other.Other.Other
k__Bacteria|p__Candidate division BRC1|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Candidate division BRC1|c__uncultured organism|o__uncultured organism
k__Bacteria|p__Candidate division BRC1|c__uncultured soil bacterium|o__uncultured bacterium
k__Bacteria|p__Candidate division OP11.Other.Other.Other
k__Bacteria|p__Candidate division OP11|c__uncultured Microgenomates bacterium|o__uncultured Microgenomates bacterium
k__Bacteria|p__Candidate division OP11|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Candidate division OP11|c__uncultured candidate division WS6 bacterium|o__uncultured candidate division WS6 bacterium
k__Bacteria|p__Candidate division OP3.Other.Other.Other
k__Bacteria|p__Candidate division OP3|c__uncultured Omnitrophica bacterium|o__uncultured Omnitrophica bacterium
k__Bacteria|p__Candidate division OP3|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Candidate division TM7.Other.Other.Other
k__Bacteria|p__Candidate division TM7|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Candidate division WS3.Other.Other.Other
k__Bacteria|p__Candidate division WS3|c__uncultured Lentisphaerae bacterium|o__uncultured Lentisphaerae bacterium
k__Bacteria|p__Candidate division WS3|c__uncultured Pedosphaer sp.|o__uncultured Pedosphaer sp.
k__Bacteria|p__Candidate division WS3|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Chlamydiae|c__Chlamydiia|o__Chlamydiales
k__Bacteria|p__Chloroflexi|c__Chloroflexia|o__Chloroflexales
k__Bacteria|p__Chloroflexi|c__Ignavibacteria|o__Ignavibacteriales
k__Bacteria|p__Chloroflexi|c__JG37-AG-4
k__Bacteria|p__Chloroflexi|c__Anaerolineae|o__Anaerolineales
k__Bacteria|p__Chloroflexi|c__Ardenticatenia|o__Ardenticatenales
k__Bacteria|p__Chloroflexi|c__Chloroflexia.Other
k__Bacteria|p__Chloroflexi|c__Caldilineae|o__Caldilineales
k__Bacteria|p__Chloroflexi|c__Chloroflexia|o__A4B07B2
k__Bacteria|p__Chloroflexi|c__Chloroflexia|o__Chloroflexales
k__Bacteria|p__Chloroflexi|c__Chloroflexia|o__Herpetosiphonales
k__Bacteria|p__Chloroflexi|c__Ktedonobacteria.Other
k__Bacteria|p__Chloroflexi|c__Ktedonobacteria|o__Ktedonobacteriales
k__Bacteria|p__Chloroflexi|c__Thermomicrobia.Other
k__Bacteria|p__Chloroflexi|c__Thermomicrobia|o__JG37-AG-4
k__Bacteria|p__Chloroflexi|c__uncultured bacterium
k__Bacteria|p__Chloroflexi|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Chloroflexi|c__uncultured soil bacterium|o__uncultured soil bacterium
k__Bacteria|p__Chloroflexi|c__uncultured soil bacterium|o__uncultured soil bacterium
k__Bacteria|p__Cyanobacteria|c__Chloroplast.Other
k__Bacteria|p__Cyanobacteria|c__Chloroplast|o__Chlorophyta
k__Bacteria|p__Cyanobacteria|c__Chloroplast|o__Streptophyta
k__Bacteria|p__Cyanobacteria|c__Gloeobacteria|o__Gloeobacterales
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria.Other
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria|o__Chroococcales
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria|o__Nostocales
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria|o__Oscillatoriales
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria|o__Pleurocapsales
k__Bacteria|p__Cyanobacteria|c__Oxyphotobacteria|o__Synechococcales
k__Bacteria|p__Deferribacteres|c__Deferribacteres.Deferribacteres
k__Bacteria|p__Deferribacteres|c__Deferribacteres|o__Deferribacteres
k__Bacteria|p__Deinococcus-Thermus|c__Deinococci|o__JG37-AG-4
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__SPAM33
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__Elusimicrobiales
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__Lineage 1a
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__Lineage 1b
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__Lineage 2
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__Lineage 4
k__Bacteria|p__Elusimicrobia|c__Elusimicrobia|o__MVP-88
k__Bacteria|p__Fibrobacteres|c__Fibrobacteria|o__Fibrobacterales
k__Bacteria|p__Firmicutes|c__Bacilli.Other
k__Bacteria|p__Firmicutes|c__Bacilli|o__A-15
k__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales
k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales
k__Bacteria|p__Firmicutes|c__Bacilli|o__Turicibacterales
k__Bacteria|p__Firmicutes|c__Clostridia.Other
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales
k__Bacteria|p__Firmicutes|c__Clostridia|o__Halanaerobiales
k__Bacteria|p__Firmicutes|c__Clostridia|o__Thermoanaerobacterales
k__Bacteria|p__Firmicutes|c__Erysipelotrichia|o__Erysipelotrichales
k__Bacteria|p__Firmicutes|c__Negativicutes|o__Selenomonadales
k__Bacteria|p__Firmicutes|c__Tissierellia.Other
k__Bacteria|p__Firmicutes|c__ORM2|o__uncultured Clostridiales bacterium
k__Bacteria|p__Firmicutes|c__ORM2|o__uncultured Firmicutes bacterium
k__Bacteria|p__Firmicutes|c__ORM2|o__uncultured bacterium
k__Bacteria|p__Firmicutes|c__ORM2|o__uncultured organism
k__Bacteria|p__Fusobacteria|c__Fusobacteriia.Other
k__Bacteria|p__Fusobacteria|c__Fusobacteriia|o__Fusobacteriales
k__Bacteria|p__Gemmatimonadetes|c__Gemmatimonadetes.ATB25-2a0C1 terrestrial group
k__Bacteria|p__Gemmatimonadetes|c__Gemmatimonadetes.ATB25-2a0C2 terrestrial group
k__Bacteria|p__Gemmatimonadetes|c__Gemmatimonadetes|o__Gemmatimonadales
k__Bacteria|p__Gemmatimonadetes|c__Gemmatimonadetes.S0134 terrestrial group
k__Bacteria|p__Lentisphaerae|c__Lentisphaeria|o__Lentisphaerales
k__Bacteria|p__Lentisphaerae|c__ZB050|o__uncultured bacterium
k__Bacteria|p__Lentisphaerae|c__MB-A-2011|o__uncultured bacterium
k__Bacteria|p__Lentisphaerae|c__OPB35|o__uncultured bacterium
k__Bacteria|p__Lentisphaerae|c__WCHB1-41|o__uncultured bacterium
k__Bacteria|p__NPL-UPA2.Other.Other.Other
k__Bacteria|p__NPL-UPA2|c__uncultured Omnitrophica bacterium|o__uncultured Omnitrophica bacterium
k__Bacteria|p__NPL-UPA2|c__uncultured Verrucomicrobia bacterium|o__uncultured Verrucomicrobia bacterium
k__Bacteria|p__NPL-UPA2|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__Nitrospinae|c__Nitrospinia|o__Nitrospinales
k__Bacteria|p__Planctomycetes|c__BD7-11|o__Other
k__Bacteria|p__Planctomycetes|c__BD7-11|o__uncultured bacterium
k__Bacteria|p__Planctomycetes|c__OM190|o__uncultured planctomycete
k__Bacteria|p__Planctomycetes|c__OM190|o__Other
k__Bacteria|p__Planctomycetes|c__ORM3|o__uncultured bacterium
k__Bacteria|p__Planctomycetes|c__ORM3|o__uncultured planctomycete
k__Bacteria|p__Planctomycetes|c__ORM3|o__uncultured planctomycete
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__CCM11a
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__Gemmata group
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__Phycisphaerales
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__Pla1 lineage
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__Other
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__S15-B06
k__Bacteria|p__Planctomycetes|c__Phycisphaerae|o__WD2101 soil group
k__Bacteria|p__Planctomycetes|c__Planctomycetes.Other
k__Bacteria|p__Planctomycetes|c__Pla1 lineage.Other
k__Bacteria|p__Planctomycetes|c__Pla1 lineage|o__uncultured bacterium
k__Bacteria|p__Planctomycetes|c__Pla3 lineage.Other
k__Bacteria|p__Planctomycetes|c__Pla3 lineage|o__uncultured bacterium
k__Bacteria|p__Planctomycetes|c__Pla3 lineage|o__uncultured planctomycete
k__Bacteria|p__Planctomycetes|c__Pla4 lineage|o__Pla4lineage|f__Pla4lineage
k__Bacteria|p__Planctomycetes|c__vadinHA49|o__Other
k__Bacteria|p__Planctomycetes|c__vadinHA49|o__uncultured bacterium
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Caulobacterales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Emcibacteraceae
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Hyphomicrobiales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Kiloniellales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Kordiimonadales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhodospirillales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rickettsiales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sneathiellales
k__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sphingomonadales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__B1-T85
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Burkholderiales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Methylophilales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Hydrogenophilales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Methylophilales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Nitrosomonadales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Nitrosomonadales
k__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Rhodocyclales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__TA18-25
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__ICT N117
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Other
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__GR-1A4A9
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Bdellovibrionales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Desulfobacterales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Desulfobacteriales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Desulfovibrionales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Myxococcales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Syntrophobacterales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__SR-MT3-90
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Syntrophobacterales
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__SM1D1 (SedimentPlume group B)
k__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__D1-D028-T07-29
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Syntrophobacterales
k__Bacteria|p__Proteobacteria|c__Zoo-1B-5|o__uncultured bacterium
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__JdFD
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Aeromonadales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Alteromonadales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__BD7-8 marine group
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__CB-BH6
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Chromatiales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__E2
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Enterobacteriales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Gammaproteobacteria Incertae Sedis
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__KI89A clade
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Legionellales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Methylococcales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__NB30
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Pasteurellales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Pseudomonadales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Salinisphaerales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Sua007
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Thiotrichales
k__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales
k__Bacteria|p__Proteobacteria|c__PB23|o__uncultured bacterium
k__Bacteria|p__Proteobacteria|c__Zetaproteobacteria.Other
k__Bacteria|p__Proteobacteria|c__Mariprofundus ferrooxydans PV-1|o__uncultured bacterium
k__Bacteria|p__Proteobacteria|c__Zetaproteobacteria|o__Mariprofundales
k__Bacteria|p__Proteobacteria|c__Zetaproteobacteria|o__SAR202 clade|f__Other
k__Bacteria|p__Proteobacteria|c__Zetaproteobacteria|o__SAR202 clade|f__uncultured bacterium
k__Bacteria|p__Proteobacteria|c__Zetaproteobacteria|o__Zetaproteobacteria Incertae Sedis
k__Bacteria|p__Saccharibacteria|c__Saccharibacteria.Other
k__Bacteria|p__TM6.Other.Other.Other
k__Bacteria|p__TM6|c__Other
k__Bacteria|p__TM6|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__TM6|c__uncultured candidate division TM6 bacterium|o__uncultured candidate division TM6 bacterium
k__Bacteria|p__Tenericutes|c__Mollicutes.Other
k__Bacteria|p__Tenericutes|c__Mollicutes|o__Acholeplasmatales
k__Bacteria|p__Tenericutes|c__Mollicutes|o__Entomoplasmatales
k__Bacteria|p__Tenericutes|c__Mollicutes|o__Haloplasmatales
k__Bacteria|p__Tenericutes|c__Mollicutes|o__Mycoplasmatales
k__Bacteria|p__Thermotogae|c__Thermotogae|o__Thermotogales
k__Bacteria|p__Verrucomicrobia.Other.Other
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__Other
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__Unknown Order
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__uncultured Opitutae bacterium EU417
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__uncultured Opitutae bacterium
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__uncultured Verrucomicrobia bacterium
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__uncultured Verrucomicrobia subdivision 3 bacterium
k__Bacteria|p__Verrucomicrobia|c__OPB35 soil group|o__uncultured bacterium
k__Bacteria|p__Verrucomicrobia|c__Opitutae.Other.Other.Other
k__Bacteria|p__Verrucomicrobia|c__Opitutae|o__uncultured bacterium
k__Bacteria|p__Verrucomicrobia|c__Opitutae|o__Opitutales
k__Bacteria|p__Verrucomicrobia|c__Opitutae|o__Puniceicoccales
k__Bacteria|p__Verrucomicrobia|c__Opitutae|o__vadinHA64
k__Bacteria|p__Verrucomicrobia|c__S-BQ-57 soil group|o|f|s|
k__Bacteria|p__Verrucomicrobia|c__S-BQ-57 soil group|o__uncultured Verrucomicrobia bacterium
k__Bacteria|p__Verrucomicrobia|c__S-BQ-57 soil group|o__uncultured bacterium
k__Bacteria|p__Verrucomicrobia|c__Spartobacteria.Other
k__Bacteria|p__Verrucomicrobia|c__Spartobacteria|o__Chthoniobacterales
k__Bacteria|p__Verrucomicrobia|c__Spartobacteria|o__Unknown Order
k__Bacteria|p__Verrucomicrobia|c__Verrucomicrobiae.Verrucomicrobiae
k__Bacteria|p__Verrucomicrobia|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__WD272|c__Other|o__Other
k__Bacteria|p__WD272|c__uncultured Candidatus Saccharibacteria sp.|o__uncultured Candidatus Saccharibacteria sp.
k__Bacteria|p__WCHB1-60|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__WD272|c__uncultured candidate division WS3 bacterium|o__uncultured bacterium
k__Bacteria|p__WD272|c__uncultured bacterium|o__uncultured bacterium
k__Bacteria|p__WD272|c__uncultured cyanobacterium|o__uncultured cyanobacterium