

Classifier: RDP Naive Bayesian rRNA Classifier Version 2.11,  
September 2015

Taxonomical Hierarchy: RDP 16S rRNA training set 16

Query File: F13-F16 GenBank.fas

Submit Date: Wed Jul 10 07:34:42 EDT 2019

Confidence threshold (for classification to Root ONLY): 95%

Symbol +/- indicates predicted sequence orientation

2F13.1\_++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Alphaproteobacteria;100%;Rhodobacterales;100%;Rhodobacteraceae;  
100%;Roseovarius;56%  
B2F13.17++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Betaproteobacteria;100%;Burkholderiales;100%;Oxalobacteraceae;  
100%;Herbaspirillum;100%  
B2F13.18++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
BF13.18++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
BF13.20++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
BF13.25++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
BF13.28++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
B2F13.33++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
100%;Gaetbulibacter;12%  
B2F13.20++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Alphaproteobacteria;98%;SAR11;91%;Candidatus Pelagibacter;91%  
B2F13.25++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Alphaproteobacteria;100%;SAR11;100%;Candidatus Pelagibacter;  
100%  
B2F13.27++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;46%  
BF13.27++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;56%  
BF13.32++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Lucibacterium;61%  
F13.3++;Root;100%;Bacteria;100%;"Bacteroidetes";100%;Flavobacteriia;  
100%;"Flavobacteriales";100%;Flavobacteriaceae;78%;Zunongwangia;27%  
F13.31++;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
78%;Zunongwangia;27%  
2F13.7++;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;100%

2F13.8;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;55%

2F13.27;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;48%

2F13.16;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;  
100%;Vibrio;100%

B2F13.35;+;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;99%;"Flavobacteriales";99%;Flavobacteriaceae;  
78%;Kordia;17%

BF13.22;+;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
78%;Zunongwangia;27%

BF13.15;+;Root;100%;Bacteria;100%;"Bacteroidetes";  
100%;Flavobacteriia;100%;"Flavobacteriales";100%;Flavobacteriaceae;  
87%;Zunongwangia;30%

BF13.33;+;Root;100%;Bacteria;100%;"Verrucomicrobia";  
100%;Verrucomicrobiae;100%;Verrucomicrobiales;  
100%;Verrucomicrobiaceae;99%;Persicirhabdus;94%

B2F13.4;+;Root;100%;Bacteria;100%;"Verrucomicrobia";  
100%;Verrucomicrobiae;100%;Verrucomicrobiales;  
100%;Verrucomicrobiaceae;99%;Persicirhabdus;94%

B2F13.9;+;Root;100%;Bacteria;100%;"Verrucomicrobia";  
100%;Verrucomicrobiae;100%;Verrucomicrobiales;  
100%;Verrucomicrobiaceae;99%;Persicirhabdus;94%

F13.7;+;Root;100%;Bacteria;100%;"Actinobacteria";  
100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;  
100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;49%

F13.9;+;Root;100%;Bacteria;100%;"Actinobacteria";  
100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;  
100%;Propionibacterineae;100%;Propionibacteriaceae;  
100%;Propionibacterium;100%

F13.2;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;  
100%;Aliiglaciecola;78%

F13.12;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;  
100%;Aliiglaciecola;78%

BF13.35;+;Root;100%;Bacteria;100%;"Proteobacteria";  
100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;  
100%;Aliiglaciecola;78%