

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

Taxonomical Hierarchy: RDP 16S rRNA training set 16

Query File: F5-F8 GenBank.fas

Submit Date: Wed Jul 10 07:31:13 EDT 2019

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

Symbol +/- indicates predicted sequence orientation

F5.2_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Lucibacterium;66%
F5.4_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;47%
F5.19_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;57%
F5.20_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;48%
F5.1_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Lucibacterium;64%
F5.24_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;54%
F5.6_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Lucibacterium;52%
F5.11_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;63%
F5.12_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;48%
F5.15_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;94%
F5.29_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Lucibacterium;64%
F5.31_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Lucibacterium;74%
F5.10_++;Root;100%;Bacteria;100%;"Proteobacteria";
100%;Gammaproteobacteria;100%;"Vibrionales";100%;Vibrionaceae;
100%;Vibrio;63%
F5.16_++;Root;100%;Bacteria;100%;"Actinobacteria";
100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;
100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;51%
F5.21_++;Root;100%;Bacteria;100%;"Actinobacteria";
100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;
100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;49%
F5.28_++;Root;100%;Bacteria;100%;"Actinobacteria";

100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;
 100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;58%
 F5.9_++;Root;100%;Bacteria;100%;"Actinobacteria";
 100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;
 100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;67%
 F5.30_++;Root;100%;Bacteria;100%;"Actinobacteria";
 100%;Actinobacteria;100%;Actinobacteridae;100%;Actinomycetales;
 100%;Micrococcineae;100%;Microbacteriaceae;100%;Rhodoluna;49%
 F5.3_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;Rhodobacterales;100%;Rhodobacteraceae;
 100%;Roseovarius;56%
 F5.17_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;Rhodobacterales;100%;Rhodobacteraceae;
 100%;Roseovarius;54%
 F5.25_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;Rhodobacterales;100%;Rhodobacteraceae;
 100%;Roseovarius;57%
 F5.14_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;Rhodobacterales;100%;Rhodobacteraceae;
 100%;Roseovarius;59%
 F5.18_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;SAR11;100%;Candidatus Pelagibacter;
 100%
 F5.26_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;SAR11;100%;Candidatus Pelagibacter;
 100%
 F5.22_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Alphaproteobacteria;100%;SAR11;100%;Candidatus Pelagibacter;
 100%
 F5.7_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;
 100%;Aliiglaciecola;78%
 F5.8_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;
 100%;Aliiglaciecola;78%
 F5.23_++;Root;100%;Bacteria;100%;"Proteobacteria";
 100%;Gammaproteobacteria;100%;Alteromonadales;100%;Alteromonadaceae;
 100%;Aliiglaciecola;78%
 F5.5_++;Root;100%;Bacteria;100%;"Bacteroidetes";100%;Flavobacteriia;
 99%;"Flavobacteriales";99%;Flavobacteriaceae;99%;Aureicoccus;34%
 F5.32_++;Root;100%;Bacteria;100%;"Bacteroidetes";100%;Flavobacteriia;
 99%;"Flavobacteriales";99%;Flavobacteriaceae;99%;Aureicoccus;34%