**Figure 1.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Acinetobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 2.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Aequorivita* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 3.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Alcanivorax* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 4a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Algoriphagus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 4b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Algoriphagus* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 5.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Aliivibrio* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 6a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Alkalihalobacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 6b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Alkalihalobacillus* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 7.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Aquimarina* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 8.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Arenibacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 9.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Arenicella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10c.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10d.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10e.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 10f.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bacillus* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 11.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bizionia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 12.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Bowmanella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 13a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Brachybacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 13b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Brachybacterium* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 14.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Brevibacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 15.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Castellaniella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 16a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Chromohalobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 16b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Chromohalobacter* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 17.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Clavibacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 18.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Cobetia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 19.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Corynebacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 20.** Phylogenetic tree based on the genetic distance1 of the 26S rDNA sequences of the *Cystofilobasidium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 21.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Dietzia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 22.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Exiguobacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 23.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Feifantangia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 24.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Fictibacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 25.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Flaviramulus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 26.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Francisella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 27.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Gordonia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 28a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Halomonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 28b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Halomonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 28c.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Halomonas* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 29.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Hoeflea* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 30a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Idiomarina* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 30b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Idiomarina* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 31.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Janibacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 32a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Labrenzia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 32b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Labrenzia* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 33.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Lacinutrix* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 34a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Leisingera* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 34b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Leisingera* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 35.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Limimaricola* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 36.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Loktanella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 37.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Marinobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 38.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Marivivens* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 39.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Mesobacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 40.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Micrococcus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 41.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Mycolicibacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 42.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Neptunomonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 43.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Nesterenkonia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 44.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Nocardioides* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 45.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Novosphingobium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 46.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Oceanobacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 47.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Paenibacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 48.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Paenisporosarcina* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 49a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Paracoccus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 49b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Paracoccus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 50.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Paraglaciecola* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 51.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Parasphingorhabdus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 52.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pelagicola* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 53.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Peribacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 54.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Phaeobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 55a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Photobacterium* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 55b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Photobacterium* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 56.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Planococcus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 57.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudidiomarina* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 58a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudoalteromonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 58b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudoalteromonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 58c.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudoalteromonas* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 59.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudomonas* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 60.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudorhodobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 61.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Pseudovibrio* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 62.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Psychrobacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 63a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Qipengyuania* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 63b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Qipengyuania* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 64.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Rheinheimera* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 65.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Rhodococcus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 66.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Roseivirga* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 67.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Ruegeria* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 68a.** Phylogenetic tree based on the genetic distance1 of the 26S rDNA sequences of the *Saccharomyces* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 68b.** Phylogenetic tree based on the genetic distance1 of the 26S rDNA sequences of the *Saccharomyces* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 69.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Salegentibacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 70a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Salinicola* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 70b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Salinicola* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 71.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Salinisphaera* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 72.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Serratia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 73a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Shewanella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 73b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Shewanella* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 74.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Sporosarcina* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 75a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Staphylococcus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 75b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Staphylococcus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 76.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Stappia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 77.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Sufflavibacter* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 78.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Tenacibaculum* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 79.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Thalassobacillus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 80.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Thalassospira* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 81a.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Vibrio* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 81b.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Vibrio* isolates compared to the sequence of the type strains available in the “Blast” database. Individual analysis of short sequences.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 82.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Vicingus* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 83.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Yoonia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.

**Figure 84.** Phylogenetic tree based on the genetic distance1 of the 16S rDNA sequences of the *Zobellia* isolates compared to the sequence of the type strains available in the “Blast” database.

**Distance**

1 Evolutionary distance between sequences based on similarity in the aligned region. The bar indicates 0.2% sequence divergence.