Species *Allorhodoferax lacus*

Etymology

[la'cus] **L. gen. n.** *lacus*, of a lake, referring to the habitat from which the type strain was isolated.

Nomenclatural type

NCBI Assembly: GCA_965194635.1 Ts

Reference Strain

Strain scJ0038966: ZE-M1

Description

Type strain is *Allorhodoferax lacus* ZE-M1 (GCA_965194635.1), isolated from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. ZE-M1 has a genome size of 3.7 Mbp with a genomic GC content of 60.1%, contains 6 rRNA genes and 46 tRNAs. The genome is a high-quality draft consisting of 2 contigs. Genes for flagellar and pilus assembly were annotated. Pathways for cyanate and urea degradation, glycolate and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Curvibacter* sp. AEP1-3 (GCF_002163715.1), with an average amino acid identity of 86.2% and average nucleotide identity of 81.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Rhodoferax_C; s__.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Allorhodoferax* » *Allorhodoferax lacus*

References

Effective publication: Salcher et al., 2025 [1]

Registry URL

https://seqco.de/i:48720

References

1. Salcher et al. (2025). Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature Communications*. DOI:10.1038/s41467-025-63266-9