

Species *Pelagilacustribacter hypolimneticus*^{Ts}

Etymology

[hy.po.lim.ne'ti.cus] **G.** *hypo*, below, under; **N.L. neut. adj.** *limneticus*, of a lake; **N.L. masc. adj.** *hypolimneticus*, referring to the deep zone of lakes, the hypolimnion

Nomenclatural type

[NCBI Assembly: GCA_965235125.1](https://ncbi.nlm.nih.gov/assembly/GCA_965235125.1)^{Ts}

Description

Type genome is *Pelagilacustribacter hypolimneticus* TrH-25oct19-165 (GCA_965235125.1), a metagenome-assembled genome (MAG) assembled from 150 m depth from Traunsee, Austria (date: 2019-10-25). TrH-25oct19-165 has a genome size of 1 Mbp with a genomic GC content of 29.2% and contains 19 tRNAs. The genome is of high quality, consisting of 87 contigs, with a completeness of 93.4%, contamination of 4.8% and strain heterogeneity of 20% as assessed with checkM. The metagenome was assembled with megahit from short-read sequencing (Illumina NovaSeq). The closest cultivated relative is *Cosmipelagibacter malulaniensis* HIMB058 (GCA_000419545.1), with an average amino acid identity of 58.8% and average nucleotide identity of 68.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__SYDM01; s__SYDM01 sp005801485.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagilacustribacter* » *Pelagilacustribacter hypolimneticus*^{Ts}

References

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

Registry URL

<https://seqco.de/i:49885>

References

1. Fernandes et al. (2025). Ecophysiology and global dispersal of the freshwater SAR11-IIIb genus *Fontibacterium*. *Nature Microbiology*. [DOI:10.1038/s41564-025-02091-8](https://doi.org/10.1038/s41564-025-02091-8)