

Species *Polynucleobacter hahnii*

Etymology

[hah.ni'i] **L. masc. gen. n.** *hahnii*, of Hahn, named after the scientist Martin W. Hahn, who isolated and described many species of the genus *Polynucleobacter*.

Nomenclatural type

[NCBI Assembly: GCA_965234415.1](#) ^{Ts}

Reference Strain

[Strain sc|0038961](#): ZE-4

Description

Type strain is *Polynucleobacter hahnii* ZE-4 (GCA_965234415.1), isolated from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. ZE-4 has a genome size of 2.3 Mbp with a genomic GC content of 43.7%, contains 3 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). No genes for flagellar assembly and chemotaxis were annotated. Pathways for nitrate reduction, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Polynucleobacter* sp. IMCC 30228 (GCF_021395205.1), with an average amino acid identity of 86.6% and average nucleotide identity of 82.8%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Polynucleobacter; s__Polynucleobacter sp903944725.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Polynucleobacter* » *Polynucleobacter hahnii*

References

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

Registry URL

<https://seqco.de/i:48716>

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](https://doi.org/10.1038/s41467-025-63266-9)