

Species *Fredricksoniimonas borealis*

Etymology

[bo.re.a'lis] L. fem. adj. *borealis*, pertaining to the North, boreal

Nomenclatural type

[NCBI Assembly: GCA_903901225.1](#)^{TS}

Description

In addition to characteristics provided for the genus, the estimated genome size for members of this species is 2.2-2.4 Mb with a GC content of 54.57-55.10 %. Genes associated with respiratory complexes, specifically complex I, II, III and V, and cytochrome bd ubiquinol are encoded by genomes of this species. A Group A3 [FeFe] hydrogenase is encoded by this species. A reversible acetyl-CoA synthetase may be indicative of acetate utilization, and/or acetogenesis coupled with the Group A3 [FeFe] hydrogenase. All genes required for the production of a Type-4a pilus and the tight-adherence complex are encoded by the genomes of the species, as well as very large ORFs. All assemblies originate from methane-rich freshwater lakes in Finland. The type for the species is the genome GCA_903901225.1.

Classification

Bacteria » *Omnitrophota* » “Velamenicoccia” » “Zapsychrales” » *Fredricksoniimonadaceae* » *Fredricksoniimonas* » *Fredricksoniimonas borealis*

References

Effective publication: Seymour et al., 2023 [1]

Registry URL

<https://seqco.de/i:23756>

References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. [DOI:10.1038/s41564-022-01319-1](https://doi.org/10.1038/s41564-022-01319-1)