

Species *Pluralincolimonas frigidipaludosa*^{Ts}

Etymology

[fri.gi.di.pa.lu.do'sa] L. **masc. adj.** *frigidus*, cold; L. **fem. adj.** *paludosa*, boggy or marshy; N.L. **fem. adj.** *frigidipaludosa*, of a cold marsh or bog

Nomenclatural type

[NCBI Assembly: GCA_003141835.1](#)^{Ts}

Description

This species is the type for the genus *Pluralincolimonas*. Estimate genome size for the species is 1.6 Mb, with a %GC of 51.75 %. This species encode an ADP/ATP translocase, and respiratory complexes I and V. All components investigated for the production of a Type-4a pilus is encoded by genomes of this species, as well as a cytoplasmic Group A3 [FeFe] hydrogenase. Coupled with the Group A3 [FeFe] hydrogenase, a reversible acetyl-CoA synthetase may indicate acetogenesis in this species, through the production of acetate from acetyl-CoA by the fermentation of glucose and nucleotides. Through the use of respiratory complex I, oxidized NAD⁺ is provided and a proton gradient across the membrane is maintained, while the respiratory F-type ATPase (complex V) produces ATP. Genome data for this species originate from a permafrost sample from Stordalen Mire, Sweden, where a pH of 4.8 was reported. The nomenclatural type for the species is the genome GCA_003141835.1.

Classification

Bacteria » *Omnitrophota* » “Gorgyraia” » *Pluralincolimonadales* » *Pluralincolimonadaceae* » *Pluralincolimonas* » *Pluralincolimonas frigidipaludosa*^{Ts}

References

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

Registry URL

<https://seqco.de/i:23728>

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)