

Species *Pegaeibacterium caenilacustr*^{Ts}

Etymology

[cae.ni.la.cus'tre] L. neut. n. *caenum*, mud; N.L. neut. adj. *lacustr*, of or from a lake; N.L. neut. adj. *caenilacustr*, from mud from a lake

Nomenclatural type

[NCBI Assembly: GCA_903820505.1](#)^{Ts}

Description

This species is the nomenclatural type for the genus *Pegaeibacterium*. Estimated genome sizes for the species range between 2.1 and 2.2 Mb with GC% of 54.27-54.30 %. Some components of the respiratory chain, particularly complex I and V, are encoded by genomes of this species. Cytoplasmic Group A3 [FeFe] and Group 4f [NiFe] hydrogenases are encoded by genomes of this species. As incomplete respiratory pathways are present in this species and no terminal electron acceptors are predicted from the genomes, the presence of a reversible acetyl-CoA synthetase coupled with the Group A3 [FeFe] hydrogenase may be indicative that this species is acetogenic, with respiratory complex I providing oxidized NAD⁺ and maintaining a proton gradient across the membrane, and complex V (respiratory F-type ATPase) producing ATP. Both assemblies for the species originate from freshwater sediment from Lake Alinen Mustajärvi, Finland. The nomenclatural type for the species is the genome GCA_903820505.1.

Classification

Bacteria » *Omnitrophota* » *Omnitrophia* » *Omnitrophales* » *Aquincolibacteriaceae* » *Pegaeibacterium* » *Pegaeibacterium caenilacustr*^{Ts}

References

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

Registry URL

<https://seqco.de/i:23681>

References

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