

Species *Zapsychnus exili*^{TS}

Etymology

[ex.i'l.i] L. gen. n. *exili*, of an exile, refugee; referring to the isolation of Ace Lake, cut off from the Southern Ocean.

Nomenclatural type

[NCBI Assembly: GCA_030765585.1](#)^{TS}

Description

This species is the nomenclatural type for the genus *Zapsychnus*. The estimated genome size is 2.1 Mb. Based on the description in Williams et al., 2021, an incomplete horse-shoe type TCA cycle is encoded by this genome, and this species is predicted to be heterotrophic. Glucose is predicted to be fermented through the EMP pathway. A Group 3d [NiFe] hydrogenase is predicted from the genome, and a V-type ATPase, respiratory F-type ATPase and Rnf complex for ATP synthesis is present. A reversible acetyl-CoA synthetase may be indicative of acetogenesis in this species. A conductive pilin is also encoded by the genome. All genes for a tight-adherence complex (Tad) and Type-4a pilus are present in the genome. The nomenclatural type for the species is the genome 3300035698_1555, recovered from metagenomic sampling and sequencing of Ace Lake, Antarctica.

Classification

Bacteria » *Omnitrophota* » “Velamenicoccia” » “Zapsychnales” » “Zapsychnaceae” » *Zapsychnus* » *Zapsychnus exili*^{TS}

References

Effective publication: Williams et al., 2021 [1]

Registry URL

<https://seqco.de/i:33302>

References

1. Williams et al. (2021). Shedding Light on Microbial “Dark Matter”: Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. *Frontiers in Microbiology*. DOI:10.3389/fmicb.2021.741077