

Species *Tantalella remota*^{Ts}

Etymology

[re.mo'ta] L. fem. adj. *remota*, remote, distant; referencing the remoteness of the locality.

Nomenclatural type

[NCBI Assembly: GCA_030765685.1](#)^{Ts}

Description

This species is the nomenclatural type for the genus *Tantalella*. The description for this species is derived from Williams et al., 2021, and supplemented with additional information. Based on genome predictions, this species is heterotrophic and encodes several proteases and peptidases to degrade proteins to amino acids. Additionally, ABC transporters for transport of simple sugars and glycoside hydrolases are encoded by the genome, along with the ability to synthesize trehalose and glycogen. Fermentation of glucose to acetyl-CoA through the EMP pathway is likely. A V-type ATPase and an Rnf complex is encoded for ATP synthesis, and an incomplete horse-shoe type TCA cycle can be reconstructed from the genome. A Group 3b [NiFe] hydrogenase has been reported for this species. All components for a Type-4a pilus and a very large ORF are present in the genome. The nomenclatural type for the species is the genome designated 3300035698_1097.

Classification

Bacteria » *Omnitrophota* » “Gorgyraia” » “Tantalellales” » “Tantalellaceae” » *Tantalella* » *Tantalella remota*^{Ts}

References

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

Registry URL

<https://seqco.de/i:33289>

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