

## Species *Makaraimicrobium thalassicum*<sup>Ts</sup>

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### Etymology

[tha.las'si.cum] Gr. fem. n. *thalassa*, the sea; Gr. neut. adj. suff. *-icum*, suffix used with the sense of pertaining to; N.L. neut. adj. *thalassicum*, of the sea

### Nomenclatural type

[NCBI Assembly: GCA\\_003644505.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Makaraimicrobium*. Estimated genome size for this species is 2 Mb. %GC content for this genome is 48.46%. No large ORF is encoded by this species. A basic acetogenic pathway for fermentation of sugars is encoded by the genome of this species. This may couple the oxidative ATP-yielding reactions of the EMP pathway, with an Rnf complex for redox balancing and a horse-shoe type TCA cycle. Of the respiratory complexes, only a respiratory F-type ATPase is encoded by this genome. Additionally, a "symbiotic" F-type ATPase and components for a Type-4 pilus is encoded by the genome. The assembly for this species was recovered from a metagenomic sediment sample from a deep-sea hydrothermal vent from Guaymas Basin, Gulf of California, Mexico, where a temperature of 10 °C has been reported. The nomenclatural type for the species is the genome GCA\_003644505.1.

### Classification

*Bacteria* » *Omnitrophota* » "Gorgyraia" » "Tantalellales" » "Tantalellaceae" » *Makaraimicrobium* » *Makaraimicrobium thalassicum*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:23710>

## References

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