

## Species *Lloretia debesea*<sup>Ts</sup>

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### Etymology

[de.be.se'a] N.L. fem. adj. *debesea*, arbitrary name formed from the DBSE (Deep Blue Sea Enterprise)

### Nomenclatural type

[NCBI Assembly: GCA\\_963986085.1](#)<sup>Ts</sup>

### Description

This species *Lloretia debesea* sp. nov. is the type to the new genus *Lloretia* gen. nov. This genus is also the type for the new family *Lloretiaceae* fam. nov. The MAG encodes for the complete set of complexes for the oxidative electron transport phosphorylation chain, suggesting an aerobic respiration. Despite aerobic respiration, the microorganism seems to be capable of dissimilatory nitrate reduction. Predicted central carbon metabolism indicated a heterotrophic-based lifestyle, encoding all the genes for glycolysis, non-oxidative pentose phosphate pathway, pyruvate oxidation and glycogen degradation, and also including the near-complete Krebs cycle. Genes could not be detected for oxidase, catalase and lysine decarboxylase, and also those involved in motility. The MAG originates from groundwater on the island of Mallorca. The type material is strain T5.010, with a genome sequence available under ENA accession GCA\_963583845.

### Classification

*Bacteria* » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Lloretiaceae* » *Lloretia* » *Lloretia debesea*<sup>Ts</sup>

### References

Effective publication: Gago et al., 2024 [1]

### Registry URL

<https://seqco.de/i:43916>

## References

1. Gago et al. (2024). Metagenomics of two aquifers with thermal anomalies in Mallorca Island, and proposal of new uncultivated taxa named following the rules of SeqCode. *Systematic and Applied Microbiology*. [DOI:10.1016/j.syapm.2024.126506](https://doi.org/10.1016/j.syapm.2024.126506)