

Species *Marisalimonas marina*^{Ts}

Etymology

[ma.ri'na] L. fem. adj. *marina*, of the sea, marine

Nomenclatural type

[NCBI Assembly: GCA_038131365.1](#)^{Ts}

Description

Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin and Starch) as well as fix inorganic carbon via the Calvin cycle (*rbcLS*). Capable of nitrate (NRT2), sulphate (*ssu*) and phosphorus uptake (*pst*, *pho*) and regulation, as well as osmoregulate via multiple genes (*trkA*, *nqrF*, *mnh*, *proXV*). Could have possible motility using *motAB* and *fliGMN* genes. Based on the genome reporting standards for MAGs, the estimated completeness 91.69%, contamination 0.14%, and the presence of the 5S (109 bp), 16S (1,482 bp), and 23S (2,712 bp) rRNA gene and 32 tRNAs. Type genome is defined as “high-quality” draft MAG, with six contigs, genome size of 1.9Mbps.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Puniceispirillales* » *Marisalimonadaceae* » *Marisalimonas* » *Marisalimonas marina*^{Ts}

References

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

Registry URL

<https://seqco.de/i:46735>

References

1. Prabhu et al. (2024). Machine learning and metagenomics identifies uncharacterized taxa inferred to drive biogeochemical cycles in a subtropical hypereutrophic estuary. *ISME Communications*.
[DOI:10.1093/ismeco/ycae067](https://doi.org/10.1093/ismeco/ycae067)