# 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 cyle (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