

Species *Salivita marina*^{Ts}

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_038144425.1](#)^{Ts}

Description

Inferred to break down a wide range of organic carbon substrates (Chitin, Mucin, Xylan, Cellulose and Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Encodes genes for nitrate uptake (NRT2), thiosulfate oxidation (soxABCDXYZ), sulphate assimilation (cys), phosphorus uptake and regulation (pho, pst), polyphosphate kinase and phosphatase (ppa). Can perform osmoregulation (trkA, nqrF, nhaC) and is possibly motile (fliGMN, motAB). Based on the genome reporting standards for MAGs, the estimated completeness was 91.02%, contamination 1.36%, and the presence of the 5S (110bp), 16S (1,532 bp), and 23S (2,880 bp) rRNA gene and 42 tRNAs. Type genome is defined as “high-quality” draft MAG, with genome size of 3.3Mbps.

Classification

Bacteria » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Salivitaceae* » *Salivita* » *Salivita marina*^{Ts}

References

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

Registry URL

<https://seqco.de/i:46742>

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)