

Species *Eutrophosalina marina*^{Ts}

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_038147175.1](#)^{Ts}

Description

Inferred to be marine ecotype, and can break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin, Cellulose, Sulfated polysaccharides and Starch). Also carries a polyphosphate kinase gene for polyphosphate accumulation, likely fuelling cytochrome c oxidase (coxABCD). Can perform osmoregulation using *trk1* (K⁺ transporter) and *nqrF* (Na⁺ transporter). Based on the genome reporting standards for MAGs, the estimated completeness was 96.32%, contamination 0%, and the presence of the 16S (1,522 bp), and 23S (2,775 bp) rRNA gene and 34 tRNAs. Type genome is defined as “high-quality” draft MAG, having two contigs and a genome size of 1.5Mbps.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Eutrophosalina* » *Eutrophosalina marina*^{Ts}

References

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

Registry URL

<https://seqco.de/i:46729>

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)