Species *Salinivivens marinus*^{Ts}

Etymology

[ma.ri'nus] **L. masc. adj.** *marinus*, of the sea

Nomenclatural type

NCBI Assembly: GCA_038142605.1 ^{Ts}

Description

Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Cellulose and Starch). Capable of performing aerobic anoxygenic photosynthesis (pufLM), and thiosulfate oxidation (soxABCDXYZ), likely performing osmoregulation using trk1 (K+ transporter) and proXV (Glycine betaine) and inferred to be motile (fliGMN, motAB gene). Also carries genes for phosphorus uptake and regulation(pho, pst). Based on the genome reporting standards for MAGs , the estimated completeness 94.41%, contamination 0.3%, and the presence of the 5S (108 bp), 16S (1,457 bp), and 23S (2, 718bp) rRNA gene and 32 tRNAs. Type genome is defined as “high-quality” draft MAG, with genome size of 2.6 Mbps

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Salinivivens* » *Salinivivens marinus*^{Ts}

References

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

Registry URL

https://seqco.de/i:46736

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