Species *Eutrophovita brisbanensis*[Ts]

Etymology

[bris.ba.nen'sis] **N.L. fem. adj.** *brisbanensis*, of or belonging to Brisbane

Nomenclatural type

NCBI Assembly: GCA_038147395.1 [Ts]

Description

Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Cellulose and Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Encodes genes for urea uptake and degradation (ureABC, urtABCDE), phosphorus uptake and regulation (pho, pst), polyphosphate kinase (ppk1), pyrroquinoline quinone (pqqC), thiosulfate oxidation (sox) and sulphate assimilation (cys). Based on the genome reporting standards for MAGs , the estimated completeness 92.77%, contamination 0.61%, and the presence of the 16S (1,532 bp), and 23S (2,933 bp) rRNA gene and 37 tRNAs. Type genome is defined as "high-quality" draft MAG,with genome size of 2.1 Mbps.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophovitaceae* » *Eutrophovita* » *Eutrophovita brisbanensis*[Ts]

References

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

Registry URL

https://seqco.de/i:46740

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