

Species *Eutrophobius brisbanensis*^{Ts}

Etymology

[bris.ban.en'sis] N.L. masc. adj. *brisbanensis*, of or belonging to Brisbane

Nomenclatural type

[NCBI Assembly: GCA_038131795.1](#)^{Ts}

Description

Inferred to break down a Chitin and Cellulose as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Likely performing sulfate assimilation (cys), polyphosphate accumulation (ppk1) and osmoregulation (trkA, nqrF, mnh). Based on the genome reporting standards for MAGs, the estimated completeness was 98.24%, contamination 0.88%, and the presence of the 5S (110bp), 16S (1.540 bp), and 23S (2,877 bp) rRNA gene and 46 tRNAs. Type genome is defined as “high-quality” draft MAG, with genome size of 2.7Mbps.

Classification

Bacteria » *Pseudomonadota* » *Gammaproteobacteria* » *Eutrophobiales* » *Eutrophobiaceae* » *Eutrophobius* » *Eutrophobius brisbanensis*^{Ts}

References

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

Registry URL

<https://seqco.de/i:46746>

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)