Species *Eutrophomonas brisbanensis*[Ts]

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

Nomenclatural type
NCBI Assembly: GCA_038141705.1 [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), pyrroquinoline quinone (pqqC), nitrate uptake (NRT2), thiosulfate oxidation (sox) and sulphate assimilation (cys). There is noted absence of osmoregulation genes. Based on the genome reporting standards for MAGs , the estimated completeness 98.78%, contamination 0%, and the presence of the 16S (1,532 bp), and 23S (2, 933 bp) rRNA gene and 40 tRNAs. Type genome is defined as "high-quality" draft MAG, with one contig and genome size of 2.1 Mbps.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophomonadaceae* » *Eutrophomonas* » *Eutrophomonas brisbanensis*[Ts]

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

Registry URL
https://seqco.de/i:46738

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