

Species *Australimonas brisbanensis*^{Ts}

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_038147155.1](#)^{Ts}

Description

This is a novel group of the order and family UBA2963. Inferred to degrade Mucin, and carry genes for phosphate and phosphonate transporters. Can perform osmoregulation using *trkA* (K⁺ transporter) and multicomponent Na⁺/H⁺ transportation (*mnh*). Based on the genome reporting standards for MAGs, the estimated completeness was 98.68%, contamination 0%, and the presence of the 16S (1,472 bp), and 23S (2,898 bp) rRNA gene and 46 tRNAs. Type genome is defined as “high-quality” draft MAG, and a genome size of 1.9Mbps.

Classification

Bacteria » *Chloroflexota* » *Dehalococcoidia* » *Australimonadales* » *Australimonadaceae* » *Australimonas* » *Australimonas brisbanensis*^{Ts}

References

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

Registry URL

<https://seqco.de/i:46731>

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)