

## Species *Nitrosopumilus brisbanensis*

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### Etymology

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

### Nomenclatural type

[NCBI Assembly: GCA\\_038152885.1](#)<sup>TS</sup>

### Description

Based on the genome reporting standards for MAGs, the estimated completeness was 98.63%, contamination 0%, and the presence of the %S (111 bp), 16S (1,464 bp), and 23S (3,117 bp) rRNA gene and 43 tRNAs. Type genome is defined as “high-quality” draft MAG, with genome size of 1.3Mbps

### Classification

*Archaea* » *Thermoproteota* » *Nitrososphaeria* » *Nitrosopumilales* » *Nitrosopumilaceae* » *Nitrosopumilus* » *Nitrosopumilus brisbanensis*

### References

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

### Registry URL

<https://seqco.de/i:46747>

## 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)