

## Species *Calypsonella navitae*<sup>Ts</sup>

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### Etymology

[na'vi.tae] L. gen. n. *navitae*, of a mariner, sailor; referring both to the marine habitat and to the Mariner deep sea vent along the Eastern Lau Spreading Center

### Nomenclatural type

[NCBI Assembly: GCA\\_035175045.1](#)<sup>Ts</sup>

### Description

The MAG belonging to this species was assembled and binned from a hydrothermal metagenome from the 'Toilet Bowl' at Mariner deep sea vent field along the Valu Fa Ridge in the Lau Basin. The genome consists of 65 contigs totaling 1,604,348 bp in length, with a GC content of 62.4%. It encodes a near-complete 16S rRNA gene (1403 bp), a partial 23S rRNA gene, and tRNA genes for all 20 standard amino acids. Analysis with CheckM2 suggests this MAG is 98.84% complete with 0.61% contamination. Phylogenomic reconstruction places this species within *Calypsonella*. Based on functional gene analysis, this lineage is likely a non-motile anaerobe that degrades protein-rich carbon sources, and it likely grows best at ~91°C.

### Classification

*Archaea* » *Thermoproteota* » *Thermoprotei* » *Acidilobales* » *Acidilobaceae* » *Calypsonella* » *Calypsonella navitae*<sup>Ts</sup>

### References

Effective publication: St. John, Reysenbach, 2024 [1]

### Registry URL

<https://seqco.de/i:32612>

## References

1. St. John, Reysenbach (2024). Genomic comparison of deep-sea hydrothermal genera related to *Aeropyrum*, *Thermoplasma* and *Calditerrivibrio*, and proposed emended description of the family Acidilobaceae. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2024.126507