

## Genus *Fervidibacter*

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### Etymology

[Fer.vi.di.bac'ter] L. masc. adj. *fervidus*, hot, steaming; N.L. masc. n. *bacter*, a rod; N.L. masc. n. *Fervidibacter*, a hot rod

### Nomenclatural type

Species *Fervidibacter sacchari*<sup>Ts</sup>

### Description

Genomes belonging to the genus have been recovered from metagenomic sequence data from thermal environments in Antarctica, Canada, China, Japan, and USA. GC content within the genus range between 49% to 59%. Phylogenomic congruence and relative evolutionary divergence along with ANI and AAI values support designation of this group as a genus. ANI values among species in the genus are below species delineation guidelines. Available genome data support members of the genus largely being aerobic or microaerophilic, with subunits of both the high-affinity and low-affinity terminal oxidases encoded within the genus. Numerous glycoside hydrolases are encoded by species in the genus, supporting a likely saccharolytic lifestyle for members of the genus.

### Classification

*Bacteria* » *Armatimonadota* » *Fervidibacteria* » *Fervidibacterales* » *Fervidibacteraceae* » *Fervidibacter*

### References

Effective publication: Nou et al., 2024 [1]  
Assigned taxonomically: Rinke et al., 2013 [2]

### Registry URL

<https://seqco.de/i:32166>

## References

1. Nou et al. (2024). Genome-guided isolation of the hyperthermophilic aerobic *Fervidibacter sacchari* reveals conserved polysaccharide metabolism in the Armatimonadota. *Nature Communications*. DOI:10.1038/s41467-024-53784-3
2. Rinke et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*. DOI:10.1038/nature12352