

Family *Fervidibacteraceae*

Etymology

[Fer.vi.di.bac.ter.a'ce.ae] N.L. masc. n. *Fervidibacter*, referring to the type genus *Fervidibacter*; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Fervidibacteraceae*, the *Fervidibacter* family

Nomenclatural type

Genus *Fervidibacter*

Description

Most members of the family are aerobic, with both the high-affinity and low-affinity terminal oxidases present in the genomes. All members are likely polysaccharide-degrading with numerous carbohydrate-active enzymes encoded by genomes of the family. GC content in the family range between 49% and 59%. The oxidative pentose phosphate pathway and the tricarboxylic acid cycle are complete for the family.

Classification

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

References

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

Registry URL

<https://seqco.de/i:44090>

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](https://doi.org/10.1038/s41467-024-53784-3)