

Family *Fausingibacteraceae*

Etymology

[fau.sin.gi.bac.te.ra'ce.ae] **N.L. masc.** *Fausingibacter*, the type genus of the family; **L. fem. pl. suff.** *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Fausingibacteraceae*, the *Fausingibacter* family

Nomenclatural type

Genus *Fausingibacter*

Description

Family established on the basis of phylogenomic comparisons to GTDB R226. Formerly known as family JAHFUA01 in GTDB R226. The description of the family is the same as for its type species *Fausingibacter adiacens*.

Classification

Bacteria » *Acidobacteriota* » *Terriglobia* » *Terriglobales* » *Fausingibacteraceae*

References

Effective publication: Sereika et al., 2025 [1]

Registry URL

<https://seqco.de/i:53820>

References

1. Sereika et al. (2025). Genome-resolved long-read sequencing expands known microbial diversity across terrestrial habitats. *Nature Microbiology*. [DOI:10.1038/s41564-025-02062-z](https://doi.org/10.1038/s41564-025-02062-z)