

Genus *Fausingibacter*

Etymology

[fau.sin.gi.bac'ter] **Danish n.** *Fausing*, Danish parish; **N.L. masc. n.** *bacter*, a rod; **N.L. masc. n.** *Fausingibacter*, Microbe named after the Danish parish of Fausing, near which the genome of the type species was recovered.

Nomenclatural type

Species *Fausingibacter adiacens*^{TS}

Description

Genus established on the basis of phylogenomic comparisons to GTDB R226 and 16S rRNA classifications to Silva 138.2. Formerly known as genus JAHFUA01 in GTDB R226. The description of the genus is the same as for its type species *Fausingibacter adiacens*.

Classification

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

References

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

Registry URL

<https://seqco.de/i:53800>

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