

Species *Aelusimicrobium faecicola*

Etymology

[fae.ci'co.la] **L. fem. n.** *faex*, dregs; **L. fem. n. suff.** *-cola*, inhabitant; **N.L. fem. n.** *faecicola*, inhabitant of feces

Nomenclatural type

[NCBI Assembly: GCA_021636085.1](https://ncbi.nlm.nih.gov/assembly/GCA_021636085.1) ^{Ts}

Description

The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 50% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Aelusimicrobium » *Aelusimicrobium faecicola*

References

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

Registry URL

<https://seqco.de/i:49146>

References

1. Mies et al. (2025). Comparative genomics of Elusimicrobiaceae (phylum Elusimicrobiota) and description of the isolates *Elusimicrobium simillimum* sp. nov., *Elusimicrobium posterum* sp. nov., and *Parelusimicrobium proximum* gen. nov. sp. nov. *Systematic and Applied Microbiology*. [DOI:10.1016/j.syapm.2025.126606](https://doi.org/10.1016/j.syapm.2025.126606)