

Species *Avelusimicrobium luingense*

Etymology

[lu.ing.en'se] **N.L. neut. adj.** *luingense*, of or from Luing, an island in the Inner Hebrides of Scotland, referring to the origin of the type genome from Luing cattle bred on this island

Nomenclatural type

[NCBI Assembly: GCA_900315845.1](#) ^{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 44% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium luingense*

References

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

Registry URL

<https://seqco.de/i:49137>

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)