

## Species *Ruminimicrobium bovinum*<sup>Ts</sup>

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### Etymology

[bo.vi'num] L. neut. adj. *bovinum*, of or belonging to cattle, referring to the isolation source

### Nomenclatural type

[NCBI Assembly: GCA\\_900316875.1](#)<sup>Ts</sup>

### 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 31.0 mol% and the estimated genome size is 1.9 Mbp.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobium* » *Ruminimicrobium bovinum*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:32932>

## References

1. Mies et al. (2024). Genome reduction and horizontal gene transfer in the evolution of Endomicrobia—rise and fall of an intracellular symbiosis with termite gut flagellates. *mBio*. DOI:10.1128/mbio.00826-24