

Species *Proruminimicrobium quisquiliarum*^{TS}

Etymology

[quis.qui.li.a.'rum] L. **gen. pl. n.** *quisquiliarum*, from waste, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_018433245.1](#)^{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 35.1 mol% and the estimated genome size is 2.0 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Proruminimicrobium* » *Proruminimicrobium quisquiliarum*^{TS}

References

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

Registry URL

<https://seqco.de/i:32940>

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