

## Species *Velaminicoccus archaeovor*<sup>Ts</sup>

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### Etymology

[ar.chae.o.vo'rus] Gr. **masc. adj.** *archaios*, ancient; L. **v. voro**, to eat, to devour; N.L. **masc. adj.** *archaeovor*, archaea (ancient microorganisms) devouring

### Nomenclatural type

[INSDC Nucleotide: CP019384.1](#)<sup>Ts</sup>

### Description

The species is represented by the phylotype and strain LiM and its genome (GenBank number [CP019384](#)). The genome of 1.97 Mb has a GC content of 52.9%. OP3 LiM was highly enriched in a limonene-degrading methanogenic enrichment culture. Cells are coccoid. They are ultramicrobacteria 0.2 µm in diameter and occur free living and attached to other microorganisms. The bacterium is maintained in slowly growing *Methanosaeta*-rich methanogenic enrichment cultures in freshwater medium with low concentrations of limonene as the carbon source at 28°C. It can be visualized by the FISH probe OP3-565.

### Classification

*Bacteria* » *Omnitrophota* » “*Velamenicoccia*” » “*Velamenicoccales*” » “*Velamenicoccaceae*” » *Velaminicoccus* » *Velaminicoccus archaeovor*<sup>Ts</sup>

### References

Effective publication: Kizina et al., 2022 [1]

### Registry URL

<https://seqco.de/i:23450>

## References

1. Kizina et al. (2022). *Methanosaeta* and “*Candidatus Velaminicoccus archaeovor*”. *Applied and Environmental Microbiology*. [DOI:10.1128/aem.02407-21](https://doi.org/10.1128/aem.02407-21)