

Family *Velaminicoccaceae*

Etymology

[Ve.la.mi.ni.coc.ca'ce.ae] **N.L. masc. n.** *Velaminicoccus*, referring to the type genus *Velaminicoccus*; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Velaminicoccaceae*, the *Velaminicoccus* family

Nomenclatural type

Genus *Velaminicoccus*

Description

This family belongs to the order *Velaminicoccales*, class *Velaminicoccia*, phylum *Omnitrophota*. When known, cells are small (< 0.3 µm). Very large ORFS, or genomic scaffolds homologous to very large ORFs are found in all genomes in the family. Most genomes encode tight-adherence complexes and genes for acetogenesis through the bacterial Wood-Ljungdahl pathway. Assemblies assigned to the family have been recovered from ground- and wastewater. The nomenclatural type for the family is the genus *Velaminicoccus*.

Classification

Bacteria » *Omnitrophota* » *Velaminicoccia* » *Velaminicoccales* » *Velaminicoccaceae*

References

Effective publication: Seymour et al., 2023 [1]

Registry URL

<https://seqco.de/i:23750>

References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. [DOI:10.1038/s41564-022-01319-1](https://doi.org/10.1038/s41564-022-01319-1)