

## Class *Velaminicoccia*

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### Etymology

[Ve.la.mi.ni.coc'ci.a] **N.L. masc. n.** *Velaminicoccus*, referring to the type genus *Velaminicoccus*; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Velaminicoccia*, the *Velaminicoccus* class

### Nomenclatural type

Genus *Velaminicoccus*

### Description

This class belongs to the phylum *Omnitrophota*. All previously visualized cells belonging to this class were small, and of approximately 0.2 µm. In serial-filtration experiments, most organisms were retained by filters with pore sizes at or below 0.2 µm. Genes encoding the tight-adherence complex were largely conserved, and most taxa have predicted capacity for acetogenesis through the bacterial Wood-Ljungdahl pathway. Additionally, group 4g hydrogenases were primarily observed in this class. Very large ORFs are pervasive throughout this class. Genome assemblies belonging to this class originate from lake or river water, groundwater, geothermal springs, wastewater, saline and freshwater sediment, bulk soil, and other engineered environments. The nomenclatural type for the class is the genus *Velaminicoccus* Kizina et al. 2022.

### Classification

*Bacteria* » *Omnitrophota* » *Velaminicoccia*

### References

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

### Registry URL

<https://seqco.de/i:23749>

## 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)