

## Family *Aquiviventaceae*

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### Etymology

[A.qui.vi.ven.ta'ce.ae] N.L. masc. n. *Aquivivens*, referring to the type genus *Aquivivens*; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Aquiviventaceae*, family of the genus *Aquivivens*

### Nomenclatural type

Genus *Aquivivens*

### Description

This family belongs to the order *Aquiviventales*, class *Aquiviventia*, phylum *Omnitrophota*. Observed cell sizes of organisms in this family were predominantly small (0.2 µm), but some variation in cell size has been observed. Members differ in the presence of genes encoding tight-adherence complexes, ADP/ATP translocases, and very large ORFs. Most members of this family encode diverse respiratory pathways and electron transport chain components. Genomes belonging to this family originate from groundwater, wastewater, lake and river water, geothermal springs and soil. Metagenomic samples from which assemblies were recovered largely originated from microaerobic environments with circumneutral pH. The nomenclatural type for the family is the genus *Aquivivens*.

### Classification

*Bacteria* » *Omnitrophota* » *Aquiviventia* » *Aquiviventales* » *Aquiviventaceae*

### References

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

### Registry URL

<https://seqco.de/i:23668>

## 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)