

## Family *Taenariiventaceae*

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### Etymology

[Tae.na.ri.i.vi.ven.ta'ce.ae] N.L. fem. n. *Taenariivivens*, referring to the type genus *Taenariivivens*; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Taenariiventaceae*, the *Taenariivivens* family

### Nomenclatural type

Genus *Taenariivivens*

### Description

The family belongs to the order *Omnitrophales*, class *Omnitrophia*, phylum *Omnitrophota*. Where known, cells are < 0.3 µm. Genomes encode ADP/ATP translocases, very large ORFs, and are consistent with predicted respiratory pathways. Assemblies assigned to the family have been recovered from ground water, wastewater, geothermal springs, soil, and saline sediments. Where data is available, assemblies originated from samples taken at circumneutral pH and temperatures close to 10 °C. The nomenclatural type for the family is the genus *Taenariivivens*.

### Classification

*Bacteria* » *Omnitrophota* » *Omnitrophia* » *Omnitrophales* » *Taenariiventaceae*

### References

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

### Registry URL

<https://seqco.de/i:23688>

## 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)