

## Phylum *Omnitrophota*

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### Etymology

[Om.ni.tro.pho'ta] N.L. masc. n. *Omnitrophus*, referring to the type genus *Omnitrophus*; *-ota*, ending to denote a phylum; N.L. neut. pl. n. *Omnitrophota*, the *Omnitrophus* phylum

### Nomenclatural type

Genus *Omnitrophus*

### Description

The properties of the phylum are as given by [Rinke et al. \(2013\)](#) with the following modifications. Members of this phylum typically have small cells, with cells of approximately 0.2 µm identified in several classes. However, metagenomic DNA containing members of the *Omnitrophota* is also frequently recovered from larger cell fractions after serial filtration and larger cells have been observed in some members of the phylum. Members typically have reduced genomes, although complete biosynthetic pathways are typically encoded, with genomes ranging between 1 and 3 Mb. Genome data suggest syntrophic or host-independent acetogenic pathways, or alternatively, diverse respiratory pathways for their predicted energy metabolism. Parasitism- and predator-related genes are common in the phylum, including tight-adherence complexes, type 2 or 3 F-type ATPases, ADP/ATP translocases, and putative adhesive megaproteins, multiple copies of the Type 4a pilus complex is encoded by all members of the phylum. This phylum is closely related or part of the PVC superphylum, with a close evolutionary relationship to the *Ratteibacteria*. The nomenclatural type of the phylum is the genus *Omnitrophus*.

### Classification

*Bacteria* » *Omnitrophota*

### References

Effective publication: Rinke et al., 2013 [1]  
*Corrigendum*: Seymour et al., 2023 [2] (from “*Omnitrophica*”)

### Registry URL

<https://seqco.de/i:23664>

## References

1. Rinke et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*. DOI:10.1038/nature12352
2. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade *Omnitrophota*. *Nature Microbiology*. DOI:10.1038/s41564-022-01319-1