

# Omnitrophota phy. nov.

Submitted by Palmer, Marike

Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Phylum <i>Omnitrophota</i>	[Om.ni.tro.pho'ta] N.L. masc. n. <i>Omnitrophus</i> , referring to the type genus Omnitrophus; - <i>ota</i> , ending to denote a phylum; N.L. neut. pl. n. <i>Omnitrophota</i> , the Omnitrophus phylum	The properties of the phylum are as given by <a href="#">Rinke et al. (2013)</a> 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 <i>Omnitrophota</i> 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 <i>Omnitrophus</i> .	<i>Bacteria</i>	<i>Omnitrophus</i>	<a href="https://seqco.de/i:23664">seqco.de/i:23664</a>