

# Omnitrophus fodinae sp. nov. and Omnitrophus gen. nov.

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

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Omnitrophus</i>	[Om.ni.tro'phus] L. masc. adj. <i>omnis</i> , all; Gr. n. <i>trophos</i> , feeder; N.L. masc. n. <i>Omnitrophus</i> , eating all	This monotypic genus belongs to the family <i>Omnitrophaceae</i> , order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , in the phylum <i>Omnitrophota</i> . Although only a single medium-quality genome is available for this genus currently, the historical name for the lineage represented by this phylum is based on the name of this genus. The description for this genus is the same as for the species <i>Omnitrophus fodinae</i> , the type species of the genus.	<i>Omnitrophaceae</i>	<i>Omnitrophus fodinae</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23568">seqco.de/i:23568</a>
Species <i>Omnitrophus fodinae</i> <sup>Ts</sup>	[fo.di'nae] L. gen. n. <i>fodinae</i> , of a mine, coal mine	This species is the type of the genus <i>Omnitrophus</i> . No data on cell size in the species is available. This species is represented by only one medium-quality genome, however, for historical significance, this genome serves as the nomenclatural type for the species. The %GC content of the genome is 49.56%. The estimated genome size is 2.9 Mb, with the available genome estimated to be 65 % complete. The genome available for this species encodes 2 very large ORFs with domains typically implicated in eukaryotic cell adhesion. This organism originated from groundwater sampled at Homestake Mine (Sanford Lab Homestake), South Dakota. The nomenclatural type for the species is the genome GCA_000405945.1.	<i>Omnitrophus</i>	NCBI Assembly: GCA_000405945.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23567">seqco.de/i:23567</a>