

## Species *Multiplicimicrobium inquinatum*<sup>Ts</sup>

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### Etymology

[in.qui.na'tum] L. neut. adj. *inquinatum*, polluted or defiled, referring to the recovery of this organism from wastewater

### Nomenclatural type

[NCBI Assembly: GCA\\_002344825.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Multiplicimicrobium*. Estimated genome size for this species is between 2 and 2.25 Mb with a %GC content of 46.35-46.78 %. Very large ORFs or partial homologs to very large ORFs, containing domains associated with cellular adhesion, an ADP/ATP translocase, and genes associated with respiratory complex I, II, IV and V are encoded by genomes of this species. The presence of cytochrome c oxidase in the genome indicates that this species is likely aerobic, and nitric oxide is predicted as an alternative terminal electron acceptor. A reversible acetyl-CoA synthetase is also encoded by genomes of this species, and may be indicative of acetate utilization, or fermentation of sugars to acetate. All genes required for the production of the Type-4a pilus are present in genomes of this species. Assemblies for this species originated from activated sludge bioreactor samples. The nomenclatural type for the species is the genome GCA\_002344825.1.

### Classification

*Bacteria* » *Omnitrophota* » *Omnitrophia* » *Omnitrophales* » *Aquinolibacteriaceae* » *Multiplicimicrobium* » *Multiplicimicrobium inquinatum*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:23679>

## 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)