

## Species *Aquincolibacterium aerophilum*<sup>Ts</sup>

### Etymology

[æ.ro'phi.lum] Gr. masc. n. *aer*, air; N.L. masc. adj. suff. *-philus*, loving; N.L. neut. adj. *aerophilum*, air-loving

### Nomenclatural type

[NCBI Assembly: GCA\\_903884815.1](#)<sup>Ts</sup>

### Description

This species is the nomenclatural type for the genus *Aquincolibacterium*. Estimated genome size of this species is 2.7 to 3 Mb. %GC content range between 52.58 to 53.08 %. Sugar and amino acid transport systems are encoded by genomes belonging to this species, and genes associated with Embden-Meyerhof glycolysis and the TCA cycle are present, although succinate dehydrogenase are absent from genomes. For respiration, a simplified system consisting of complex I, ubiquinone, and cytochrome bd ubiquinol is feasible, and would suggest a microaerophilic lifestyle. Genomes encode a cytoplasmic group A3 [FeFe] electron bifurcating hydrogenase and conductive pili, all genes analyzed for the production of a Type-4a pilus, as well as a respiratory F-type ATPase. Acetate utilization or acetogenesis may be possible as a reversible acetyl-CoA synthetase is present in this species, which, coupled with the Group A3 [FeFe] hydrogenase may produce acetate. Very large ORFs or partial homologs to very large ORFs are encoded by this species. All assemblies originated from water from the methane-rich boreal lake Lake Alinen-Mustajärvi, Finland. The nomenclatural type for the species is the genome GCA\_903884815.1.

### Classification

*Bacteria* » *Omnitrophota* » *Omnitrophia* » *Omnitrophales* » *Aquincolibacteriaceae* » *Aquincolibacterium* » *Aquincolibacterium aerophilum*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:23678>

## 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)