

Genus *Aquilimus*

Etymology

[A.qui.li'mus] **L. fem. n.** *aqua*, water; **L. masc. n.** *limus*, silt or alluvies; **N.L. masc. n.** *Aquilimus*, a microbe from alluvial or pelagial zones of freshwaters

Nomenclatural type

Species *Aquilimus communis*^{Ts}

Description

The isolates have streamlined circular genomes with sizes between 1.37 and 1.44 Mb, low GC content for *Actinomycetota*, ranging from 43.3 to 45%, and high coding densities ~95.6%. All isolates encode one rRNA operon and between 37 to 42 tRNA genes. They are auxotrophic for some amino acids and vitamins. They encode for actinorhodopsins, heliorhodopsins, and the biosynthesis pathway of the retinal. Recruitment analysis of 1720 metagenomes suggests that *Aquilimus* members are not particularly abundant, although some species are distributed on different continents and seem to be constantly recovered throughout the year, at least in the case of the Řimov Reservoir (Czech Republic). The current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales;f__Nanopelagicaceae;g__AAA044-D11.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus*

References

Effective publication: Chiriac et al., 2025 [1]

Registry URL

<https://seqco.de/i:51011>

References

1. Chiriac et al. (2025). Ecological success in freshwater lakes: insights from novel cultivated lineages of the abundant Nanopelagicales order. *Microbiome*. DOI: [10.1186/s40168-025-02272-x](https://doi.org/10.1186/s40168-025-02272-x)