

Species *Aquilimus communis*^{Ts}

Etymology

[com.mu'nis] **L. masc. adj.** *communis*, common

Nomenclatural type

[Genome sci|0003638](https://seqco.de/sci/0003638) ^{Ts}

Description

Etymology. The species name 'communis' refers to the fact that the specie is found in a wide range of water environments, from rivers and bays to freshwater lakes.

Brief description. The genome of *A. communis* MZLE-42 (ENA accession number GCA_965268555) had a coding density of 96.78%, and the circular, complete genome has a size of 1,377,870 bp. The species has a GC content of 44.9%, which is similar to other representatives of this order. It possesses one rRNA operon and 39 tRNA genes. It was isolated from the epilimnion (0.5 m depth) of the Žlutice Reservoir, but recruitment analysis also show that it is present in the Římov Reservoir (Czech Republic), Lake Biwa (Japan), and in Delaware River and Bay (USA). It has an average nucleotide identity between 77 – 82% with other isolates on this genus, the closest one being *A. zluticensis* MZLE-12. Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales;f__Nanopelagicaceae;g__AAA044-D11;s__.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus* » *Aquilimus communis*^{Ts}

References

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

Registry URL

<https://seqco.de/i:51025>

References

1. Chiriak 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)