# Species *Nanopelagicus limnae*

**Etymology**

[lim'nae] **Gr. fem. n.** *limnê*, lake; **N.L. gen. fem. n.** *limnae*, of a lake, referring to the habitat

**Nomenclatural type**

NCBI Assembly: GCF_002287885.2 $^{Ts}$

**Reference Strain**

Strain sc|0038985: MMS-21-122

**Description**

Type genome is *Nanopelagicus limnes* MMS-21-122 (GCF_002287885.2), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of 0.45±0.09 µm and diameters of 0.25±0.03 µm. The initial pure culture was lost after a few propagations to fresh medium; no growing culture is available. The initial culture grew well in sterile lake water amended with minimal carbon medium, vitamins and amino acids. *Nanopelagicus limnes* MMS-21-122 has a genome size of 1.24 Mbp and a genomic GC content of 41.5%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 38 tRNAs. It is auxotrophic for reduced sulfur sources, several amino acids (proline, ornithine, histidine, betaine) and several vitamins (B1, B2, B5, B7, B12) and possesses rhodopsins. Members of the genus *Nanopelagicus* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-ACAAGAGGTTCGTCCGTCC-3' in the 23S rRNA gene (positions 2669-2688, *E. coli* numbering). Basis for the assignment is a phylogenomic tree of 476 concatenated protein sequences, phylogenetic analysis of 16S rRNA, 23S rRNA, and rhodopsin genes, as well as average nucleotide and amino acid identities presented in Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). The closest cultivate relatives are *Nanopelagicus hibericus* MMS-21-160 (GCF_002288005.1) and *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1) with average amino acid identities of 84.5 and 81%, respectively, and average nucleotide identities of 78.6 and 77.1%, respectively.

**Classification**

*Bacteria* » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Nanopelagicus* » *Nanopelagicus limnae*

**References**

Effective publication: Neuenschwander et al., 2018 [1]
*Corrigendum*: Oren et al., 2020 [2] (from “Nanopelagicus limnes”)

**Registry URL**

https://seqco.de/i:23844

# References

1. Neuenschwander et al. (2018). Microdiversification in genome-streamlined ubiquitous freshwater Actinobacteria. *The ISME Journal*. DOI:10.1038/ismej.2017.156
2. Oren et al. (2020). Lists of names of prokaryotic Candidatus taxa. *International Journal of Systematic and Evolutionary Microbiology*. DOI:10.1099/ijsem.0.003789