# Species Allofontibacter lacus

#### Etymology

[la'cus] L. gen. n. lacus, of a lake

### Nomenclatural type

INSDC Nucleotide: RGRP00000000.1 Ts

#### Description

We propose to name PEL1, the most complete and persistent genomospecies of clade IIIb in the freshwater ecosystems sample, as *Allofontibacter lacus* sp. nov. [formerly "*Candidatus* Fonsibacter lacus"]. In addition to the previously described properties of the genus *Allonsibacter* corrig. Henson, et al (2018), the proposed species is described as follows. Small, curved rod cells of approximately  $1 \times 0.2 \, \mu m$ . Partial genome sequence WB8\_6\_001 with estimated completeness of 77.5% and contamination of 0.9% is 1.08 Mbp in size, with 1375 predicted genes, a coding density of 92.0%, and a G + C content of 35.9%. WB8\_6\_001 has an ANI of 84.9% and AAI of 87.0% with the *Allofontibacter communis* corrig. Henson et al (2018) [formerly "*Ca.* Fonsibacter ubiquis"] str. LSUCC0530T genome, the only currently described member of the *Allofontibacter* genus. The type material for this species is the genome WB8\_6\_001, identified in the freshwater lakes along the Chattahoochee River, Southeast USA. The representative genome is available in GenBank under accession number <u>SAMN102235538</u>.

#### Classification

Bacteria » Pseudomonadota » Alphaproteobacteria » Candidatus Pelagibacterales » Candidatus Pelagibacteraceae » Candidatus Allofontibacter » "Allofontibacter lacus"

#### References

Effective publication: Tsementzi et al., 2019 [1] Corrigendum: Oren, Garrity, 2021 [2] (from "Candidatus Fonsibacter lacus")

## Registry URL

https://seqco.de/i:454

## References

- Tsementzi et al. (2019). Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus "Candidatus Fonsibacter" and proposal of Ca. Fonsibacter lacus sp. nov. Systematic and Applied Microbiology. DOI:10.1016/j.syapm.2019.03.007
- 2. Oren, Garrity (2021). Candidatus List No. 2. Lists of names of prokaryotic Candidatus taxa. *International Journal of Systematic and Evolutionary Microbiology*. DOI:10.1099/ijsem.0.004671