

# Fontibacterium commune gen. nov. sp. nov.

Submitted by Thrash, Cameron

## Genus *Fontibacterium*

### Etymology

[Fon.ti.bac.te'ri.um] **L. masc. n.** *fons*, a spring; **N.L. neut. n.** *bacterium*, a rod, bacterium; **N.L. neut. n.** *Fontibacterium*, a bacterium from a spring

### Nomenclatural type

Species *Fontibacterium commune*<sup>Ts</sup>

### Description

Aerobic, chemoorganoheterotrophic, and oligotrophic. Cells are small, curved rods roughly 1 × 0.1 µm. Non-motile. On the basis of phylogenomics and 16S rRNA gene phylogenetics, subclade IIIb/LD12 occurs on a separate branch within the *Pelagibacteraceae* (SAR11), sister to subclade IIIa containing strains HIMB114 and IMCC9063. Owing to the depth of branching between these clades using concatenated protein-coding genes, and the 92 and 91% 16S rRNA gene sequence identity with HIMB114 and IMCC9063, respectively, we propose LSUCC0530 and subclade IIIb/LD12 as a novel genus in the *Pelagibacteraceae*.

### Classification

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium*

### References

Effective publication: Henson et al., 2018 [1]  
*Emendavit*: Tsementzi et al., 2019 [2]

### Registry URL

<https://seqco.de/i:453>

## Species *Fontibacterium commune*<sup>Ts</sup>

### Etymology

[com.mu'ne] **L. neut. adj.** *commune*, common

### Nomenclatural type

NCBI Assembly: [GCA\\_002688585.1](https://ncbi.nlm.nih.gov/assembly/GCA_002688585.1)<sup>Ts</sup>

### Reference Strain

[Strain sc|0039474](https://ncbi.nlm.nih.gov/strain/sc/0039474): LSUCC0530

### Description

In addition to the properties given in the genus description, the species is described as follows. Growth occurs at temperatures between 23 °C and 30 °C, but not at 11 °C or below, nor at 35 °C or above. Optimal salinity is 1.45 and below, and growth occurs between 0.36 and 4.68. At optimal temperature and salinity, cells divide at an average rate of 0.52 day<sup>-1</sup>. Genome size is 1.16 Mbp, with 1271 predicted genes, and a GC content of 29.02% (calculated). LSUCC0530 had an ANI of 75.3 and 75.9% and an AAI of 58.1 and 59.7% with HIMB114 and IMCC9063, respectively. The genome is available on GenBank under accession number CP024034.

### Classification

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium commune*<sup>Ts</sup>

### References

Effective publication: Henson et al., 2018 [1]

### Registry URL

<https://seqco.de/i:457>

## References

1. Henson et al. (2018). Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. *The ISME Journal*. DOI:10.1038/s41396-018-0092-2
2. 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

## Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:eh4rag03** submitted by **Thrash, Cameron** and including 2 new names has been successfully validated.

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