

Species *Elulimicrobium humile*^{TS}

Etymology

[hu.mi'le] L. neut. adj. *humile*, humble, low

Nomenclatural type

[NCBI Assembly: GCA_009919195.1](#)^{TS}

Description

This species displays a consistently low abundance when detected between the months of July and October, and a geographic range restricted to the tree northernmost lakes on the Chattahoochee River (USA): lakes Lanier, West Point, and Eufaula. According to the genome assembly, WB6_2A_207 is 3.79 Mbp long with 1,298 contigs (N50: 4 kbp) and 34.3% G+C content. It includes 4,108 predicted proteins as well as 90 non-coding RNA loci (87 tRNA, 1 rRNA, and 2 tmRNA). The estimated coding density is 94.1%. Based on genome annotation, this organism is predicted to have sucrose and oxidase activity and the capability of gelatin and arginine dihydrolase activity. The type material is the genome WB6_2A_207, deposited in the NCBI database with Genome Accession RGCK00000000 and BioSample SAMN10223143.

Classification

Bacteria » *Elulimicrobiota* » *Elulimicrobiia* » *Elulimicrobiales* » *Elulimicrobiaceae* » *Elulimicrobium* » *Elulimicrobium humile*^{TS}

References

Effective publication: Rodriguez-R et al., 2020 [1]

Registry URL

<https://seqco.de/i:516>

References

1. Rodriguez-R et al. (2020). Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. *Environmental Microbiology*. DOI:10.1111/1462-2920.15112