

Species *Magnetomonas plexicatena*^{Ts}

Etymology

[ple.xi.ca.te'na] **L. masc. adj.** *plexus*, interwoven; **L. fem. n.** *catena*, chain; **N.L. fem. n.** *plexicatena*, an interwoven chain

Nomenclatural type

[NCBI Assembly: GCA_004376055.2](#)^{Ts}

Description

Vibrioid-shaped, cell size $2.0 \pm 0.4 \mu\text{m}$ long and $0.5 \pm 0.1 \mu\text{m}$ wide, form magnetite magnetosomes organized in chains along the long axis of the bacterial cell body. Magnetosomes present a mean length of $108 \pm 21.1 \text{ nm}$ and a mean width of $45 \pm 8.1 \text{ nm}$. Potentially capable of chemolithoautotrophy with the oxidation of sulfur compounds and carbon assimilation by Wood-Ljungdahl pathway. Potentially capable of heterotrophy by glycolysis. Not capable of nitrogen fixation. The reference strain is LBB01. The genome reference sequence of LBB01 is CP049016. G + C content 42.0%.

Classification

Bacteria » *Nitrospirota* » *Thermodesulfovibrionia* » *Thermodesulfovibrionales* » *Magnetobacteriaceae* » *Magnetomonas* » *Magnetomonas plexicatena*^{Ts}

References

Effective publication: Uzun et al., 2022 [1]
Assigned taxonomically: Uzun et al., 2022 [1]

Registry URL

<https://seqco.de/i:51019>

References

1. Uzun et al. (2022). Detection of interphylum transfers of the magnetosome gene cluster in magnetotactic bacteria. *Frontiers in Microbiology*. [DOI:10.3389/fmicb.2022.945734](https://doi.org/10.3389/fmicb.2022.945734)