

Species *Velesiimonas alkalicola*^{Ts}

Etymology

[a.l.ka.li'co.la] N.L. neut. n. *alkali*, alkaline; N.L. fem. suff. *-cola*, an inhabitant of; N.L. fem. n. *alkalicola*, inhabitant of alkaline environments

Nomenclatural type

[NCBI Assembly: GCA_013626165.1](#)^{Ts}

Description

This species is the nomenclatural type for the genus *Velesiimonas*. The predicted genome size of this species is quite small in comparison to other *Omnitrophota*, at approximately 1.3 Mb. The % GC content of the genome is 37.82 %. No parasitism- or predation-associated genes are encoded by the genome for this species, and limited genes for energy metabolism are predicted for this genome, although, like other members in the phylum, the Type-4a pilus machinery is encoded. An Rnf complex, along with a respiratory F-type ATPase (complex V) are encoded by the genome of this species. The anaerobic sample from which the genome was derived was taken from serpentinized groundwater from an alkaline spring, in the Cedars, California, USA. The nomenclatural type for the species is GCA_013626165.1.

Classification

Incertae sedis (Bacteria) » *Velesiimonadales* » *Velesiimonadaceae* » *Velesiimonas* » *Velesiimonas alkalicola*^{Ts}

References

Effective publication: Seymour et al., 2023 [1]

Registry URL

<https://seqco.de/i:23736>

References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. [DOI:10.1038/s41564-022-01319-1](https://doi.org/10.1038/s41564-022-01319-1)