

Species *Duberdicusella sinuisediminis*^{Ts}

Etymology

[si.nu.i.se.di.mi'nis] L. masc. n. *sinus*, a bay; L. gen. n. *sediminis*, of sediment; N.L. gen. n. *sinuisediminis*, of sediment from a bay

Nomenclatural type

[NCBI Assembly: GCA_003644445.1](#)^{Ts}

Description

This species is the nomenclatural type for the genus *Duberdicusella*. Estimated genome size for this species ranges between 1.3 to 1.8 Mb. GC content for this species is 34.9-35.9 %. No large ORFs are predicted for members of this species. Genes associated mainly with an acetogenic metabolic scheme, along with an Rnf complex, and respiratory complex V (F-type ATPase) are encoded by the genomes of the species. A conductive pilin, a membrane-bound Group 4g [NiFe] and cytoplasmic Group A3 [FeFe] hydrogenases, and all components for the tight-adherence complex (Tad) and Type-4a pili are encoded by the genomes. Additionally, a "symbiotic" F-type ATPase is also encoded by the genomes. All assemblies assigned to this species originated from deep-sea hydrothermal vent sediment samples from Guaymas Basin, Gulf of California, Mexico, with some derived from samples with a reported temperature of 28 °C. The type for the species is the genome GCA_003644525.1.

Classification

Bacteria » *Omnitrophota* » "Velamenicoccia" » *Duberdicusellales* » *Duberdicusellaceae* » *Duberdicusella* » *Duberdicusella sinuisediminis*^{Ts}

References

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

Registry URL

<https://seqco.de/i:23742>

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)