

Genus *Caldisaccharidevorator*

Etymology

[Cal.di.sac.cha.ri.de.vo.ra'tor] L. **masc. adj.** *caldus*, hot; L. **neut. n.** *saccharum*, sugar; L. **masc. n.** *devorator*, devourer; N.L. **masc. n.** *Caldisaccharidevorator*, hot sugar devourer

Nomenclatural type

Species *Caldisaccharidevorator sinensis*^{T5}

Description

Genomes belonging to the genus have been recovered from metagenomic sequence data from thermal environments from Malaysia and China. GC content range between 55-57%. ANI and AAI values among members of the genus are incongruent, although ANI values > 75% are observed among the two species in the genus. Based on available genome data, the genus likely comprise aerobic polysaccharide-degrading species, with the low-affinity terminal oxidase (CoxABC) conserved in the genus. Approximately 100 glycoside hydrolases (GHs) are encoded by genomes in the genus with > 40 GH families represented. No hydrogenases were predicted for genomes belonging to this genus.

Classification

Bacteria » *Armatimonadota* » *Fervidibacteria* » *Fervidibacterales* » *Fervidibacteraceae* » *Caldisaccharidevorator*

References

Effective publication: Nou et al., 2024 [1]

Registry URL

<https://seqco.de/i:44082>

References

1. Nou et al. (2024). Genome-guided isolation of the hyperthermophilic aerobe *Fervidibacter sacchari* reveals conserved polysaccharide metabolism in the Armatimonadota. *Nature Communications*. DOI:10.1038/s41467-024-53784-3