

Calditenuis ramacidaminiphagus sp. nov.

Submitted by Lai, Dengxun

Species *Calditenuis ramacidaminiphagus*

Etymology

[ra.ma.ci.da.mi.ni.pha'gus] **L. masc. n.** *ramus*, branch; **N.L. neut. n.** *acidum aminum*, amino acid; **N.L. masc. suff.** *-phagus*, eater; **N.L. masc. adj.** *ramacidaminiphagus*, a branched-chain amino acid eater

Nomenclatural type

[NCBI Assembly: GCA_050589285.1](#)^{Ts}

Description

The type strain of *Calditenuis ramacidaminiphagus* (LZ^{Ts}) was recovered from Great Boiling Spring, Gerlach, Nevada, USA. The genome is 1,506,500 bp (estimated 1,536,304 bp) with a G+C content of 62.0%. Quality assessment using CheckM indicates 98.1% completeness and 0% contamination. The organism specializes in the metabolism of branched-chain amino acids, with propionate also incorporated as a major substrate.

Classification

Incertae sedis (Archaea) » “Caldarchaeales” » *Calditenuaceae* » *Calditenuis* » *Calditenuis ramacidaminiphagus*

References

Effective publication: Lai et al., 2026 [1]

Registry URL

<https://seqco.de/i:44020>

References

1. Lai et al. (2026). Branched-chain amino acid specialization drove diversification within Calditenuaceae (Caldarchaeia) and enables their cultivation. *Nature Communications*. DOI:10.1038/s41467-026-68859-6

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:orts0bmb** submitted by **Lai, Dengxun** and including 1 new name has been successfully validated.

Date of Priority: 2026-02-13 10:22 UTC
DOI: 10.57973/seqcode.r:orts0bmb



