

Genus *Tepidihabitans*

Etymology

[Te.pi.di.ha'bi.tans] **L. masc. adj.** *tepidus*, warm; **L. pres. part.** *habitans*, inhabiting; **N.L. masc. n.** *Tepidihabitans*, inhabiting warmth

Nomenclatural type

Species *Tepidihabitans asiaticus*^{Ts}

Description

The genus *Tepidihabitans* is designated as g_JABLXZ01 in GTDB R226. In addition to *Tepidihabitans asiaticus* U4-05 (GCA_037481955.1), this genus includes several MAGs from thermophilic enrichment cultures (GCA_029907385.1; GCA_024653355.1), hot springs (GCA_023511395.1; GCA_037441285.1; GCA_937139435.1) and deep subsurface aquifers (GCA_013177935.1). A search in the GenBank database identified four nearly full length 16S rRNA gene sequences, that are part of the *Tepidihabitans* genus: KM373103 (from hypermesophilic terephthalate degrading bioreactor, Nobu et al., 2015), AY526498 (from a thermophilic anaerobic bioreactor, Roest et al., 2005), KX213957 (from a hot spring, Thiel et al., 2016) and AY297964 (from a thermophilic anaerobic bioreactor, Chen et al., 2004). Along with other genera, *Tepidihabitans* forms a separate phylogenetic cluster at the class level, which is designated as c_WOR-3 according to GTDB (Fig). This cluster is sister to "Candidatus Hydrothermia", to which the recently described pure culture sy37 (Mori et al., 2025), "Candidatus Hydrothermus pacificus" (Chuvochina et al. 2019), "Candidatus Caldipriscus" and "Candidatus Thermoproactor" (Colman et al., 2016) belong.

[Fig.pdf 46.7 KB](#)

Classification

Bacteria » "Hydrothermota" » *Tepidihabitantia* » *Tepidihabitantales* » *Tepidihabitantaceae* » *Tepidihabitans*

References

Effective publication: Slobodkina et al., 2025 [1]

Registry URL

<https://seqco.de/i:51334>

References

1. Slobodkina et al. (2025). Taxonomic and metabolic diversity of microbial communities in a thermal water stream in Uzbekistan and proposal of two new classes of uncultivated bacteria, *Desulfocorpusculia* class. nov. and *Tepidihabitantia* class. nov., named following the rules of SeqCode. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2025.126650