Register list for Tepidihabitans asiaticus gen. nov. sp. nov. and their lineage

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Class *Tepidihabitantia*	[Te.pi.di.ha.bi.tan'ti.a] **N.L. masc. n.** *Tepidihabitans*, the type genus of the class; **L. neut. pl. suff.** *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Tepidihabitantia*, the Tepidihabitans class	The class Tepidihabitantia is designated as c__WOR-3 in GTDB R226. In addition to Tepidihabitantales (o__UBA2258) order it includes o__B3-TA06, o__SM23-42 and other in accordance with the GTDB R226 designations. Fig.pdf 46.7 KB	*Hydrothermota*	*Tepidihabitans*	seqco.de/i:51337
Order *Tepidihabitantales*	[Te.pi.di.ha.bi.tan.ta'les] **N.L. masc. n.** *Tepidihabitans*, the type genus of the order; **L. fem. pl. suff.** *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Tepidihabitantales*, the Tepidihabitans order	The order Tepidihabitantales is designated as o_UBA2258 in GTDB R226. In addition to Tepidihabitantaceae (f_UBA2258) family it includes f__CAIPLT01, f__DTDR01, f__JBDRVQ01 and other in accordance with the GTDB R226 designations. Fig.pdf 46.7 KB	*Tepidihabitantia*	*Tepidihabitans*	seqco.de/i:51336
Family *Tepidihabitantaceae*	[Te.pi.di.ha.bi.tan.ta'ce.ae] **N.L. masc. n.** *Tepidihabitans*, the type genus of the family; **L. fem. pl. suff.** *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Tepidihabitantaceae*, the Tepidihabitans family	The family Tepidihabitantaceae is designated as f_UBA2258 in GTDB R226. In addition to Tepidihabitans genus it includes g__JAOABP01, g__UBA2258, g__UBA3079 and other in accordance with the GTDB R226 designations. Fig.pdf 46.7 KB	*Tepidihabitantales*	*Tepidihabitans*	seqco.de/i:51335

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus *Tepidihabitans*	[Te.pi.di.ha'bi.tans] **L. masc. adj.** *tepidus*, warm; **L. pres. part.** *habitans*, inhabiting; **N.L. masc. n.** *Tepidihabitans*, inhabiting warmth	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 Thermoproauctor" (Colman et al., 2016) belong. Fig.pdf 46.7 KB	*Tepidihabitantaceae*	*Tepidihabitans asiaticus*^{Ts}	seqco.de/i:51334
		Tepidihabitans asiaticus U4-05 is presented by high-quality draft metagenome-assembled genome (MAG) of a member of the *Hydrothermota* (p__WOR-3) phylum,			

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Species *Tepidihabitans asiaticus*^{Ts}	[a.si.a'ti.cus] **N.L. masc. adj.** *asiaticus*, pertaining to Asia	that was assembled from thermophilic microbial community from a hot stream formed by discharge of thermal artesian groundwater in Navoiy region (Republic of Uzbekistan). This microorganism represents 5% of the microbial community developing in the sediments under the ginger mat at a temperature of 54°C. The results of the bac120-based phylogenomic analysis confirmed that the U4-05 is a part of candidate division WOR-3 ("Candidatus Hydrothermota" according to LPSN) and, along with many MAGs, 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 Thermoproauctor" (Colman et al., 2016) belong. Analysis of the distribution of U4-05-related phylotypes shows that they are found in hot springs and thermophilic bioreactors, can occupy a significant part of the community (6-8%) and prefer moderately thermophilic conditions, neutral pH and abundance of complex organic matter. The MAG has genes for the complete Embden-Meyerhof-Parnas pathway, non-oxidative branch of the pentose-phosphate pathway and the fatty acids β-oxidation. Has only scant genes related to motility. Genes encoding most components of the tricarboxylic acid cycle are absent. Has no genes for CO2 fixation. Genes encoding components of the aerobic respiratory chain, and the F_0F_1-type H^+-transporting ATP synthase are	*Tepidihabitans*	INSDC Nucleotide: JBBFKS000000000.1^{Ts}	seqco.de/i:51333

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		absent. The genome encodes the Rnf electron-transporting complex and subunits of a V-type ATP synthase. On the basis of genome analysis, U4-05 is predicted to be an anaerobic heterotrophic bacterium with fermentative metabolism. The presence of the Rnf electron-transporting complex and subunits of a V-type ATP synthase may support ion gradient generation and ATP synthesis in the absence of a conventional electron transport chain. Fig.pdf 46.7 KB			