

Register list for 7 new names including *Tiamatella incendiivivens* sp. nov. gen. nov.

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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
Genus <i>Calypsonella</i>	[Ca.lyp.so.nel'la] N.L. dim. fem. n. <i>Calypsonella</i> , little Calypso, referring to a Nereid water spirit in Greek mythology	Members of this taxon were identified at Mariner on the Valu Fa Ridge in the Lau Basin and Lucky Strike, Mid-Atlantic Ridge. A phylogenomic reconstruction using 53 archaeal marker genes places MAGs of this genus in a well-supported monophyletic clade. Using AAI, MAGs are approximately 56% similar to <i>Aeropyrum pernix</i> , and they could not be related to any previously described genus using GTDB-Tk taxonomic analysis. The 16S rRNA gene recovered from the type genome is approximately 96 to 97% similar to the 16S rRNA genes of <i>Aeropyrum pernix</i> , <i>Aeropyrum camini</i> , <i>Thermoplasma maritimum</i> and <i>Stetteria hydrogenophila</i> , consistent with the level of 16S rRNA gene sequence divergence seen between the genera <i>Aeropyrum</i> , <i>Stetteria</i> and <i>Thermoplasma</i> (~96–97%). Based on ANI analysis, each of the three MAGs in this genus represents a distinct species (~73–75% similarity). Functional gene analysis suggests that members of this genus are likely non-motile anaerobes, and they may utilize protein-rich carbon sources and at least one member may reduce sulfur, thiosulfate, polysulfides or selenite.	<i>Acidilobaceae</i>	<i>Calypsonella navitae</i> ^{ts}	seqco.de/i:33278

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Tiamatella</i>	[Ti.a.ma.tel'la] N.L. dim. fem. n. <i>Tiamatella</i> , little Tiamat, referring to an ancient Mesopotamian primordial sea goddess	Delineation of this genus is supported by AAI, phylogenomic analysis, 16S rRNA gene comparison and taxonomic assignment in GTDB. MAGs assigned to this genus have been identified at two hydrothermal vent fields along the Eastern Lau Spreading Center (ABE and Tui Malila), Mariner vent field on the Valu Fa Ridge, Lau Basin, the Lower Cone of the deep-sea Brothers volcano along the Kermadec arc and Lucky Strike vent field along the Mid-Atlantic Ridge. Members of this taxon are approximately 51–54% similar to <i>Aeropyrum pernix</i> and 50–52% similar to <i>Caldisphaera lagunensis</i> by AAI. They form a well-supported monophyletic clade in a concatenated phylogenomic tree constructed using 53 archaeal genes. A 16S rRNA gene recovered from the type genome shows ~89 to 91% similarity to <i>Aeropyrum pernix</i> , <i>Aeropyrum camini</i> , <i>Thermoplasma maritimum</i> and <i>Stetteria hydrogenophila</i> . Based on functional genomic analysis, members of this genus are likely anaerobic and may utilize proteins or amino acids as carbon sources. They are auxotrophic for purines and pyrimidines. Several members of this genus also encode DMSO reductase family genes from the <i>psrA/phsA/sreA/srrA</i> clade and may utilize polysulfides, thiosulfate, sulfur, and/or selenite as energy sources. ANI analysis suggests this genus includes at least five distinct species, and motility is likely variable between species. The name proposed here is derived from a primordial Mesopotamian sea goddess depicted as both a chaotic and creative force, and it references the turbulent but biologically rich environments in which these <i>Archaea</i> inhabit.	<i>Acidilobaceae</i>	<i>Tiamatella incendiivivens</i> ^{TS}	seqco.de/i:32112

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Hestiella</i>	[he.sti.el'la] N.L. dim. fem. n. <i>Hestiella</i> , little Hestia, named for the Greek goddess of the hearth and home	Identification of this genus is supported by phylogenomic analysis, 16S rRNA comparison, AAI, environmental distribution and functional genomic differences. MAGs belonging to this genus were identified from multiple samples, over several years, from the Mariner deep-sea vent field on the Valu Fa Ridge in the Lau Basin, and from Upper and Lower Cone at the deep-sea Brothers volcano along the Kermadec arc. Based on ANI analysis, the genus includes two distinct species (92% ANI between spp.). In a concatenated gene tree using 53 archaeal marker genes, this genus forms a highly supported monophyletic clade most closely related to terrestrial <i>Caldisphaera</i> . AAI between members of this genus and <i>Caldisphaera lagunensis</i> is approximately 64.05 to 64.29%, and a full-length 16S rRNA gene recovered from the type species is 94.07% similar to <i>C. lagunensis</i> . Functional genomic analysis suggests this genus are motile anaerobic heterotrophs that degrade protein-rich carbon sources and potentially starch and/or glycogen. It may be distinguished from <i>Caldisphaera</i> by coding potential for a perchlorate/nitrate reductase gene likely used in anaerobic respiration, NAD(P)+ and pyridoxal 5- phosphate biosynthesis and, in some cases, inosine monophosphate biosynthesis. The apparent absence of superoxide dismutase genes also suggests members of this genus may be strictly anaerobic unlike their mildly aero-tolerant relative <i>C. lagunensis</i> . The name proposed for this genus references the lifestyle of these <i>Archaea</i> which thrive in the 'home-like' oasis of warmth and nourishment provided by deep-sea vents.	<i>Acidilobaceae</i>	<i>Hestiella acidicharens</i> ^{Ts}	seqco.de/i:32607
Species <i>Calypsonella navitae</i> ^{Ts}	[na'vi.tae] L. gen. n. <i>navitae</i> , of a mariner, sailor; referring both to the marine habitat and to the Mariner deep sea vent along the Eastern Lau Spreading Center	The MAG belonging to this species was assembled and binned from a hydrothermal metagenome from the 'Toilet Bowl' at Mariner deep sea vent field along the Valu Fa Ridge in the Lau Basin. The genome consists of 65 contigs totaling 1,604,348 bp in length, with a GC content of 62.4%. It encodes a near-complete 16S rRNA gene (1403 bp), a partial 23S rRNA gene, and tRNA genes for all 20 standard amino acids. Analysis with CheckM2 suggests this MAG is 98.84% complete with 0.61% contamination. Phylogenomic reconstruction places this species within <i>Calypsonella</i> . Based on functional gene analysis, this lineage is likely a non-motile anaerobe that degrades protein-rich carbon sources, and it likely grows best at ~91°C.	<i>Calypsonella</i>	NCBI Assembly: GCA_035175045.1 ^{Ts}	seqco.de/i:32612

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Thermophilus eudorianus</i>	[eu.dor.i.a'nus] N.L. masc. adj. <i>eudorianus</i> , pertaining to Eudora, referencing to the Nereid water spirit in Greek mythology	The MAG representing this species was obtained from the Northwest Caldera Wall at the deep-sea Brothers volcano along the Kermadec arc. The MAG is composed of 10 contigs, totaling 1,522,352 bp in length, with a GC content of 54.2%. Based on CheckM2 analysis, the genome is about 95.13% complete and 0.11% contaminated, and it includes a complete 16S rRNA gene, a partial 23S rRNA gene and tRNA genes for all 20 standard amino acids. Inclusion of this MAG in <i>Thermophilus</i> is supported by 16S rRNA gene sequence identity, and its distinction as a unique species is based on geographical location at a deep-sea volcano, and ANI-based divergence between <i>Thermophilus</i> MAGs. Based on functional genomic analysis, this species is likely a non-motile, piliated anaerobic heterotroph that degrades protein-rich carbon sources and may reduce sulfur, thiosulfate, polysulfides or selenite. It is predicted to grow best at approximately 90°C. The name proposed for this species refers to an ocean-associated Nereid spirit who is the sister of Calypso, referencing the phylogenetic relationship between the <i>Calypsonella</i> and <i>Thermophilus</i> .	<i>Thermophilus</i>	NCBI Assembly: GCA_015521085.1 Ts	seqco.de/i:33329
Species <i>Tiamatella incendiivivens</i> ^{Ts}	[in.cen.di.i.vi'vens] L. neut. n. <i>incendium</i> , fire; L. pres. part. <i>vivens</i> , living; N.L. fem. adj. <i>incendiivivens</i> , living in or near the fire, referring to the active volcanic environment of Lower Cone, Brothers volcano	The MAG representing this species was obtained from a sample from the Lower Cone of the deep-sea Brothers volcano along the Kermadec arc. The genome consists of 27 contigs, totaling 1,454,292 bp in length, and has a GC content of 41.6%. Based on CheckM2, the MAG is approximately 95.79% complete with 1.74% contamination. It encodes a complete 16S rRNA gene and tRNA genes for 19 standard amino acids. Phylogenomic analysis places this genome within <i>Tiamatella</i> . Based on functional genomic analysis, this organism is likely a non-motile anaerobe that utilizes protein-rich carbon sources and may derive energy from reduction of sulfur, polysulfides, thiosulfate or selenite. It is predicted to be a hyperthermophile, growing best at approximately 80°C.	<i>Tiamatella</i>	NCBI Assembly: GCA_015522635.1 Ts	seqco.de/i:32611

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Hestiella acidicharens</i> ^{Ts}	[a.ci.di.char'ens] L. neut. adj. <i>acidum</i> , acid; N.L. part. adj. <i>charens</i> , delighting in, from Gr. v. <i>chairō</i> to rejoice or delight in; N.L. part. adj. <i>acidicharens</i> , delighting in acid	Genomes of members of this species were recovered from an acidic hydrothermal vent at Mariner on the Valu Fa Ridge in the Lau Basin and the Upper Cone of the deep-sea Brothers volcano along the Kermadec arc. MAGs range in size from approximately 1.06 to 1.48 Mbp and are in 77 to 157 contigs, with a G + C content of 39.9 to 40.2%. Based on CheckM2 estimates, MAG completeness ranges from 76.15 to 96.42%, while contamination is 0.03 to 0.39%. ANI between members of this species is >97%, and phylogenomic analysis with 53 archaeal marker genes places this species in <i>Hestiella</i> . Based on functional gene analysis, members of this species are likely motile anaerobic nitrate and/or perchlorate reducers that degrade protein-rich carbon sources, starch and/or glycogen, growing best at approximately 82 to 83°C.	<i>Hestiella</i>	NCBI Assembly: GCA_035161305.1 ^{Ts}	seqco.de/i:32609