

Register list for 16 new names including *Fervidibacteria* classis 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
Class <i>Fervidibacteria</i>	[Fer.vi.di.bac.ter'i.a] N.L. masc. n. <i>Fervidibacter</i> , referring to the type genus <i>Fervidibacter</i> ; <i>-ia</i> , ending to denote a class; N.L. neut. pl. n. <i>Fervidibacteria</i> , the <i>Fervidibacter</i> class	The description for the class is the same as for the order <i>Fervidibacterales</i> . Phylogenomic placement of this lineage within the <i>Armatimonadota</i> and relative evolutionary divergence supports delineation of this lineage as a class within the <i>Armatimonadota</i> .	<i>Armatimonadota</i>	<i>Fervidibacter</i>	seqco.de/i:44092
Order <i>Fervidibacterales</i>	[Fer.vi.di.bac.ter.a'les] N.L. masc. n. <i>Fervidibacter</i> , referring to the type genus <i>Fervidibacter</i> ; <i>-ales</i> , ending to denote an order; N.L. fem. pl. n. <i>Fervidibacterales</i> , the <i>Fervidibacter</i> order	Members of the order are aerobic or anaerobic, with both high- and low-affinity terminal oxidases present in the aerobic <i>Fervidibacterales</i> . All members are likely polysaccharide degraders as numerous carbohydrate active enzymes are found in all members of the order. Phylogenomics and relative evolutionary divergence places this order in the class <i>Fervidibacteria</i> .	<i>Fervidibacteria</i>	<i>Fervidibacter</i>	seqco.de/i:44091
Family <i>Fervidibacteraceae</i>	[Fer.vi.di.bac.ter.a'ce.ae] N.L. masc. n. <i>Fervidibacter</i> , referring to the type genus <i>Fervidibacter</i> ; <i>-aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Fervidibacteraceae</i> , the <i>Fervidibacter</i> family	Most members of the family are aerobic, with both the high-affinity and low-affinity terminal oxidases present in the genomes. All members are likely polysaccharide-degrading with numerous carbohydrate-active enzymes encoded by genomes of the family. GC content in the family range between 49% and 59%. The oxidative pentose phosphate pathway and the tricarboxylic acid cycle are complete for the family.	<i>Fervidibacterales</i>	<i>Fervidibacter</i>	seqco.de/i:44090

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Thermosaccharophagaceae</i>	[Ther.mo.sac.cha.ro.pha.ga'ce.ae] N.L. masc. n. <i>Thermosaccharophagus</i> , type genus of the family; <i>aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Thermosaccharophagaceae</i> , the family of the genus <i>Thermosaccharophagus</i>	The description for the family is the same as for the genus <i>Thermosaccharophagus</i> . Phylogenomic placement of this lineage and relative evolutionary divergence supports delineation of this group as a family within the <i>Fervidibacterales</i> .	<i>Fervidibacterales</i>	<i>Thermosaccharophagus</i>	seqco.de/i:44089
Genus <i>Fervidibacter</i>	[Fer.vi.di.bac'ter] L. masc. adj. <i>fervidus</i> , hot, steaming; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Fervidibacter</i> , a hot rod	Genomes belonging to the genus have been recovered from metagenomic sequence data from thermal environments in Antarctica, Canada, China, Japan, and USA. GC content within the genus range between 49% to 59%. Phylogenomic congruence and relative evolutionary divergence along with ANI and AAI values support designation of this group as a genus. ANI values among species in the genus are below species delineation guidelines. Available genome data support members of the genus largely being aerobic or microaerophilic, with subunits of both the high-affinity and low-affinity terminal oxidases encoded within the genus. Numerous glycoside hydrolases are encoded by species in the genus, supporting a likely saccharolytic lifestyle for members of the genus.	<i>Fervidibacteraceae</i>	<i>Fervidibacter saccharif</i> ^s	seqco.de/i:32166

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Caldisaccharidevorator</i>	[Cal.di.sac.cha.ri.de.vo.ra'tor] L. masc. adj. <i>calidus</i> , hot; L. neut. n. <i>saccharum</i> , sugar; L. masc. n. <i>devorator</i> , devourer; N.L. masc. n. <i>Caldisaccharidevorator</i> , hot sugar devourer	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.	<i>Fervidibacteraceae</i>	<i>Caldisaccharidevorator</i> <i>sinensis</i> ^{TS}	seqco.de/i:44082

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Thermosaccharophagus</i>	[Ther.mo.sac.cha.ro.pha'gus] Gr. fem. adj. <i>therme</i> , heat; Gr. neut. n. <i>sakchar</i> , sugar; Gr. masc. adj. suff. <i>phagos</i> , eater; N.L. masc. n. <i>Thermosaccharophagus</i> , eater of sugar in high temperatures	Genomes belonging to the genus have been recovered from metagenomic sequence data from thermal environments in the USA and China. GC content range between 47% and 53%. ANI and AAI values among species are inconsistent, although all ANI values between species are below suggested species guidelines. Based on available genome data, the genus is strictly anaerobic. Between 64 and 105 glycoside hydrolases (GHs) are encoded by genomes of the genus, with > 25 GH families represented. Group 1a and 4b hydrogenases are conserved within the genus, suggesting hydrogen and formate metabolism in the genus. The core of the methyl-branch of the Wood-Ljungdahl pathway is conserved in the genus.	<i>Thermosaccharophagaceae</i>	<i>Thermosaccharophagus gerlachensis</i> ^{Ts}	seqco.de/i:44085

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Fervidibacter sacchari</i> ^{Ts}	[sac'cha.ri] N.L. gen. n. <i>sacchari</i> , of sugar	<p>Hyperthermophilic, microaerophilic, facultatively anaerobic, and grows chemoheterotrophically on monosaccharides and polysaccharides. Cells are ovoid- to rod-shaped, Gram-stain negative, and are 0.9-1.3 µm in width and 1.6-3.6 µm in length. Grows between 65 and 87.5 °C and an optimum temperature of 80 °C, and a pH range of 6.5-8.6 with an optimum pH of 7.5. Grows at an optimum O₂ concentration of 5-10%. Grows on D-arabinose, D-galactose, D-glucose, D-rhamnose, D-ribose, D-xylose, chondroitin sulfate, colloidal chitin, galactan, gellan gum, guar gum, karaya gum, locust bean gum, xanthan gum, xyloglucan, β-glucan, glycogen, starch, AFEX-pretreated corn stover, miscanthus, sugarcane bagasse, acetate and casamino acids. Grows weakly on xyloglucan under fermentation conditions. The major fatty acids (> 10%) are C16:0, C18:0 and/or cyclo-C17:0, and iso-C16:0. The major respiratory quinones (> 10%) are MK-8 and MK-9. The isolate and genomes of the species have been recovered from geothermal springs in the Great Basin, Nevada, USA. GC content of genomes range between 51-52%. Subunits for both the high-affinity and low-affinity terminal oxidases are encoded in the genomes. Genomes also encode a Group 3d [NiFe] hydrogenase, which produces hydrogen as an electron sink for NAD⁺ regeneration.</p>	<i>Fervidibacter</i>	NCBI Assembly: GCA_030520105.1 ^{Ts}	seqco.de/i:32165

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Fervidibacter japonicus</i>	[ja.po.ni'cus] N.L. masc. adj. <i>japonicus</i> , of Japan, the country where this organism is from	The sole genome representative of this species was recovered from a metagenome from Hishikari Mine, Japan. The GC content is 59%. The genome encodes both the high- and low-affinity terminal oxidases.	<i>Fervidibacter</i>	NCBI Assembly: GCA_002898575.1 ^{Ts}	seqco.de/i:44080
Species <i>Fervidibacter sinensis</i>	[si.nen'sis] N.L. masc. adj. <i>sinensis</i> , of China, the country where this organism is from	Genomes of this species were recovered from metagenomes from geothermal springs in Tengchong, China. GC content range between 50% and 52%. The a subunit of the high-affinity cytochrome bd ubiquinol oxidase (CydA) are encoded by the genomes of the species, but no low-affinity terminal oxidases are encoded.	<i>Fervidibacter</i>	INSDC Nucleotide: JAVHTH000000000 ^{Ts}	seqco.de/i:44079
Species <i>Thermosaccharophagus gerlachensis</i> ^{Ts}	[ger.lach.en'sis] N.L. masc. adj. <i>gerlachensis</i> , of Gerlach, the region where Great Boiling Spring is located in Nevada, where this organism is from	The sole genome representative for the species was recovered from a metagenome from Great Boiling Spring, Gerlach, Nevada, USA. GC content is 47%. No terminal oxidases are encoded by this genome, and the presence of the Wood-Ljungdahl pathway likely indicates this species is a strict anaerobe. Genes encoding a group 4d hydrogenase is present in multiple copies.	<i>Thermosaccharophagus</i>	NCBI Assembly: GCA_041538025.1 ^{Ts}	seqco.de/i:44087
Species <i>Caldisaccharidevorator sinensis</i> ^{Ts}	[si.nen'sis] N.L. masc. adj. <i>sinensis</i> , of China, the country where this organism is from	Genomes of this species were recovered from metagenomes from the geothermal spring Qiao Quan, in Tengchong, China. The GC content is approximately 56%. The low-affinity terminal oxidase CoxABC is encoded by genomes of the species.	<i>Caldisaccharidevorator</i>	INSDC Nucleotide: JAVKTG000000000 ^{Ts}	seqco.de/i:44083

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Caldisaccharidevorator malaysiensis</i>	[ma.lay.si.en'sis] N.L. masc. adj. <i>malaysiensis</i> , of Malaysia, the country where this organism is from	The sole genome representative of this species was recovered from metagenomes of microbial mats in SKY hot spring, Malaysia. The GC content is 55%. Subunits of both the high- and low-affinity terminal oxidase are encoded by the genome.	<i>Caldisaccharidevorator</i>	NCBI Assembly: GCA_025057575.1 ^{Ts}	seqco.de/i:44084
Species <i>Fervidibacter canadensis</i>	[ca.na.den'sis] N.L. masc. adj. <i>canadensis</i> , of Canada, the country where this organism is from	Genomes of this species were recovered from metagenomes from the geothermal Dewar Creek, British Columbia, Canada. GC content of genomes were approximately 57%. Subunits for both the high-affinity and low-affinity terminal oxidases are encoded in the genomes. The high-affinity respiratory H ₂ -uptake [NiFe] group 1h hydrogenases are encoded by genomes of the species, likely fueling respiration during carbon starvation.	<i>Fervidibacter</i>	NCBI Assembly: GCA_041446545.1 ^{Ts}	seqco.de/i:44081
Species <i>Thermosaccharophagus yellowstonensis</i>	[yel.low.ston.en'sis] N.L. masc. adj. <i>yellowstonensis</i> , of Yellowstone, USA, where this organism is from	The sole genome representative of the species was recovered from a metagenomes from Washburn Spring, Yellowstone National Park, Wyoming, USA. GC content is 51%. No terminal oxidases and the presence of the Wood-Ljungdahl pathway indicate that this species is likely a strict anaerobe.	<i>Thermosaccharophagus</i>	NCBI Assembly: GCA_041537945.1 ^{Ts}	seqco.de/i:44088
Species <i>Thermosaccharophagus tengchongensis</i>	[teng.chong.en'sis] N.L. masc. adj. <i>tengchongensis</i> , of Tengchong, Yunnan province, south-west China, where this organism is from	Genomes of this species were recovered from metagenomes from geothermal springs in Tengchong, China. GC content is approximately 52%. No terminal oxidases and the presence of the Wood-Ljungdahl pathway indicate that this species is likely a strict anaerobe.	<i>Thermosaccharophagus</i>	INSDC Nucleotide: JAVHTD000000000 ^{Ts}	seqco.de/i:44086