

Register list for 12 new names including *Fontibacterium baikalense* sp. 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>Pelagilacustribacter</i>	[Pe.la.gi.la.cus.tri.bac'ter] L. neut. n. <i>pelagus</i> , of the sea; N.L. masc. adj. <i>lacustris</i> , belonging to a lake; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Pelagilacustribacter</i> , a freshwater genus of otherwise marine Pelagibacterales	Type species is <i>Pelagilacustribacter hypolimneticus</i> TrH-25oct19-165 (GCA_965235125.1), a metagenome-assembled genome (MAG) obtained from 150m depth from Traunsee, Austria. <i>Pelagilacustribacter</i> is a genus within marine SAR11-II (<i>Pelagibacterales</i>) that is found in deep freshwater lakes.	<i>Pelagibacteraceae</i>	<i>Pelagilacustribacter hypolimneticus</i> ^{Ts}	seqco.de/i:49884
Species <i>Fontibacterium africanum</i>	[a.fri.ca'num] N.L. neut. adj. <i>africanum</i> , pertaining to the isolation source of the MAG (Lake Malawi) and a prevalence in the African Great Lakes	Type genome is <i>Fontibacterium africanum</i> N-Mw6-13nov23-081 (GCA_965235885.1), a metagenome-assembled genome (MAG) assembled from 50 m depth from Lake Malawi, Malawi (date: 2023-11-13). N-Mw6-13nov23-081 has a genome size of 1.1 Mbp with a genomic GC content of 30%, contains 1 rRNA gene (5S rRNA) and 28 tRNAs. The genome is of high quality, consisting of 7 contigs, with a completeness of 95.2%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long- and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present only in the African Great Lakes Malawi, Tanganyika, and Kivu. The closest	<i>Fontibacterium</i>	NCBI Assembly: GCA_965235885.1 ^{Ts}	seqco.de/i:49874

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		<p>cultivated relatives are <i>Fontibacterium commune</i>, syn. '<i>Candidatus</i> Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to '<i>Cā. Allofontibacter communis</i>'), with an average amino acid identity of 68.64 % and average nucleotide identity of 71.78 % and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 68.51 % and an ANI of 71.6 %.</p> <p>Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp016882225.</p>			
Species <i>Fontibacterium baikalense</i>	[ba.i.ka.len'se] N.L. neut. adj. <i>baikalense</i> , of Baikal, referring to Lake Baikal, where this organism was identified	<p>Type genome is <i>Fontibacterium baikalense</i> Baikal-deep-G36 (GCA_009693745.1), a metagenome-assembled genome (MAG) co-assembled from 1250 m and 1350 m depth from Lake Baikal, Russia (date: 2018-03-29). Baikal-deep-G36 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 2 rRNA genes and 25 tRNAs. The genome is of high quality, consisting of 66 contigs, with a completeness of 95.2%, contamination of 3.9% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with IDBA-UD assembler from short-read sequencing (Illumina HiSeq 3000/4000). The closest cultivated relatives are <i>Fontibacterium commune</i>, syn. '<i>Candidatus</i> Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to '<i>Cā. Allofontibacter communis</i>'), with an average amino acid identity of 85.75% and average nucleotide identity of 84.65% and another newly proposed species, <i>Fontibacterium</i></p>	<i>Fontibacterium</i>	NCBI Assembly: GCA_009693745.1 Ts	seqco.de/i:49754

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		<p><i>medardicus</i> ME-17, with an AAI of 88.73% and an ANI of 87.93%.</p> <p>Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp009693745.</p>			
<p>Species <i>Fontibacterium boreale</i></p>	<p>[bo.re.a'le] L. neut. adj. <i>boreale</i>, pertaining to the boreal region of the Northern hemisphere</p>	<p>Type genome is <i>Fontibacterium boreale</i> Umea-bin-09620 (GCA_903909545.1), a metagenome-assembled genome (MAG) assembled from 1-5 m depth from Lake Bjarntjärnan, Sweden (date: 2018-01-01/07). Umea-bin-09620 has a genome size of 1 Mbp with a genomic GC content of 30.2% and contains 20 tRNAs. The genome is of high quality, consisting of 243 contigs, with a completeness of 96.4%, contamination of 0.1% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with Megahit (version 1.1.13) from short-read sequencing (Illumina MiSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in boreal lakes in Europe and North America. The closest cultivated relatives are <i>Fontibacterium commune</i>, syn. '<i>Candidatus</i> Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to '<i>Ca. Allofontibacter communis</i>'), with an average amino acid identity of 82.49% and average nucleotide identity of 81.54 % and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 84.48% and an ANI of 83.54 %. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota;</p>	<i>Fontibacterium</i>	<p>NCBI Assembly: GCA_903909545.1 Ts</p>	seqco.de/i:49872

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__.			
Species <i>Fontibacterium meridianamericanum</i>	[me.ri.di.an.a.me.ri.ca'num] L. masc. adj. <i>meridianus</i> , Southerly, to the south; N.L. neut. adj. <i>americanum</i> , American; L. neut. adj. <i>meridianamericanum</i> , South American, referring to continent from the MAG was isolated	Type genome is <i>Fontibacterium meridianamericanum</i> N-IMU-22jan24-050 (GCA_965235635.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from Represa de India Muerta, a freshwater reservoir in Uruguay (date: 2024-01-22). N-IMU-22jan24-050 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 30 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 95.8%, contamination of 1.2% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in subtropical and tropical lakes in South America. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus Fonsibacter ubiquis</i> ' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Ca. Allofontibacter communis</i> '), with an average amino acid identity of 86.94% and average nucleotide identity of 84.39% and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 90.5% and an ANI of 88.11%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter;	<i>Fontibacterium</i>	NCBI Assembly: GCA_965235635.1 Ts	seqco.de/i:49882

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Fontibacterium oligotrophicum</i>	[o.li.go.tro'phi.cum] Gr. masc. adj. oligo , little; Gr. masc. adj. trophikos , nursing, tending; N.L. neut. adj. oligotrophicum , oligotrophic, referring to the low nutrient content of the isolation sites and the high abundance in oligotrophic lakes.	Type genome is <i>Fontibacterium oligotrophicum</i> N-Balt2-05jul22-047 (GCA_965235975.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from the slightly brackish part of Vistula Lagoon, Poland (date: 2022-07-05). N-Balt2-05jul22-047 has a genome size of 0.92 Mbp with a genomic GC content of 29.4% and contains 30 tRNAs. The genome is of high quality, consisting of 3 contigs, with a completeness of 96.4%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long- and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is highly abundant in oligotrophic lakes in temperate and subtropical regions. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus Fonsibacter ubiquis</i> ' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Cā. Allofontibacter communis</i> '), with an average amino acid identity of 92.57% and average nucleotide identity of 90.07% and another newly proposed species, <i>Fontibacterium medardicus</i> ME-17 (GCA_965235075.1), with an AAI of 85.45% and an ANI of 88.16%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp947497305.	<i>Fontibacterium</i>	NCBI Assembly: GCA_965235975.1 Ts	seqco.de/i:49876
		Type genome is <i>Fontibacterium scandinaviense</i> AM1_bin-0028			

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Species <i>Fontibacterium scandinaviense</i>	[scan.di.na.vi.en'se] N.L. neut. adj. <i>scandinaviense</i> , pertaining to the Scandinavian region, the isolation source of the MAG and a main occurrence in Scandinavian lakes	(GCA_903869725.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from Lake Alinen Mustajärvi, Finland (date: 2015-08-8). AM1_bin-0028 has a genome size of 1.1 Mbp with a genomic GC content of 28.9%, contains 3 rRNA genes and 31 tRNAs. The genome is of high quality, consisting of 55 contigs, with a completeness of 100%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with Megahit (version 1.1.13) from short-read sequencing (Illumina MiSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is mainly present in boreal lakes in Scandinavia. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus</i> Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Ca.</i> Allofontibacter communis'), with an average amino acid identity of 72.71 % and average nucleotide identity of 75.18 % and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 73.3 % and an ANI of 75.56 %. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp903869725.	<i>Fontibacterium</i>	NCBI Assembly: GCA_903869725.1 Ts	seqco.de/i:49875
		Type genome is <i>Fontibacterium subtropicum</i> N-SamH-20apr23-026 (GCA_965235415.1), a metagenome-assembled genome (MAG) assembled from 15 m depth from Lake Samsonvale, Australia (date: 2023-04-20). N-SamH-20apr23-026 has a genome size of 1.15 Mbp with a			

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Species <i>Fontibacterium subtropicum</i>	[sub.tro'pi.cum] N.L. neut. adj. subtropicum , pertaining to subtropical zone, the isolation source of the MAG.	genomic GC content of 29.3%, contains 3 rRNA genes and 34 tRNAs. The genome is of high quality, consisting of 100 contigs, with a completeness of 100%, contamination of 1.2% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in subtropical lakes. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus Fonsibacter ubiquis</i> ' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Ca. Allofontibacter communis</i> '), with an average amino acid identity of 88.13% and average nucleotide identity of 85.63% and another newly proposed species, <i>Fontibacterium medardicus</i> ME-17 (GCA_965235075.1), with an AAI of 90.92% and an ANI of 88.79%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp023257975.	<i>Fontibacterium</i>	NCBI Assembly: GCA_965235415.1 Ts	seqco.de/i:49877
		Type genome is <i>Fontibacterium temperatum</i> ZE-03apr19-LR-3 (GCA_964203055.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03). ZE-03apr19-LR-3 has a genome size of 0.9 Mbp with a genomic GC content of 29.4% and contains 28 tRNAs. The genome is of high quality, consisting of 3 contigs, with a completeness of 94%, contamination of 0% and strain			

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Species <i>Fontibacterium temperatum</i>	[tem.pe.ra'tum] L. neut. adj. <i>temperatum</i> , referring to temperate climate, the species mainly occurs in lakes of the temperate region of the Northern Hemisphere	heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is highly abundant in temperate lakes of the Northern Hemisphere. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus Fonsibacter ubiquis</i> ' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Ca. Allofontibacter communis</i> '), with an average amino acid identity of 87.44% and average nucleotide identity of 85.23% and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 93.82% and an ANI of 92.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp000510845.	<i>Fontibacterium</i>	NCBI Assembly: GCA_964203055.1 Ts	seqco.de/i:49881
		Type genome is <i>Fontibacterium universale</i> N-InaE-25sep22-010 (GCA_965236175.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Inawashiro, Japan (date: 2022-09-25). N-InaE-25sep22-010 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 29 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 98.8%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing			

Proposed Taxon Species	Etymology [u.ni.ver.sa.le] adj. universale , universal, pertaining to the widespread distribution of the species	Description (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present in many lakes around the world. The closest cultivated relatives are <i>Fontibacterium commune</i> , syn. ' <i>Candidatus Fonsibacter ubiquis</i> ' LSUCC0530 (GCF_002688585.1; later reclassified to ' <i>Cā. Allofontibacter communis</i> '), with an average amino acid identity of 87.08% and average nucleotide identity of 85.18% and another newly proposed species, <i>Fontibacterium abundans</i> MiE-29 (GCA_965235095.1), with an AAI of 92.44% and an ANI of 90.87%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp000371845.	Parent Taxon	Type NCBI Assembly: GCA_965236175.1 Ts	Registry URL seqco.de/i:49878
Species <i>Pelagibacter malawiensis</i>	[ma.la.wi.en'sis] N.L. masc. adj. malawiensis , pertaining to Lake Malawi, the origin of the metagenome-assembled genome	Type genome is <i>Pelagibacter malawiensis</i> N-Mw13-23nov23-053 (GCA_965235955.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Malawi, Malawi (date: 2023-11-23). N-Mw13-23nov23-053 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 3 rRNA genes and 28 tRNAs. The genome is of high quality, consisting of 7 contigs, with a completeness of 99.5%, contamination of 0.5% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). The closest cultivated relatives are ' <i>Candidatus Pelagibacter ubique</i> SAR11 HTCC9022 (GCF_000472565.1), with an average	<i>Pelagibacter</i>	NCBI Assembly: GCA_965235955.1 Ts	seqco.de/i:49883

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		amino acid identity of 75% and average nucleotide identity of 76.4% and ' <i>Candidatus</i> Pelagibacter ubique SAR11 HTCC7211 (GCF_000155895.1), with an AAI of 74.2% and an ANI of 76.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter; s__Pelagibacter sp016870175.			
Species <i>Pelagilacustribacter hypolimneticus</i> ^{Ts}	[hy.po.lim.ne'ti.cus] G. <i>hypo</i> , below, under; N.L. neut. adj. <i>limneticus</i> , of a lake; N.L. masc. adj. <i>hypolimneticus</i> , referring to the deep zone of lakes, the hypolimnion	Type genome is <i>Pelagilacustribacter hypolimneticus</i> TrH-25oct19-165 (GCA_965235125.1), a metagenome-assembled genome (MAG) assembled from 150 m depth from Traunsee, Austria (date: 2019-10-25). TrH-25oct19-165 has a genome size of 1 Mbp with a genomic GC content of 29.2% and contains 19 tRNAs. The genome is of high quality, consisting of 87 contigs, with a completeness of 93.4%, contamination of 4.8% and strain heterogeneity of 20% as assessed with checkM. The metagenome was assembled with megahit from short-read sequencing (Illumina NovaSeq). The closest cultivated relative is <i>Cosmipelagibacter malulaniensis</i> HIMB058 (GCA_000419545.1), with an average amino acid identity of 58.8% and average nucleotide identity of 68.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__SYDM01; s__SYDM01 sp005801485.	<i>Pelagilacustribacter</i>	NCBI Assembly: GCA_965235125.1 ^{Ts}	seqco.de/i:49885