

Register list for 44 new names including *Proruminomicrobium quisquiliarum* 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>Ruminimicrobiellum</i>	[Ru.mi.ni.mi.cro'bi.ell.um] L. neut. n. <i>rumen</i> , the rumen; N.L. dim. neut. n. <i>microbiellum</i> , a small microbe; N.L. neut. n. <i>Ruminimicrobiellum</i> , a small microbe that occurs in the rumen	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Ruminimicrobiellum bubulum</i> ^{Ts}	seqco.de/i:24029
Genus <i>Ruminimicrobium</i>	[Ru.mi.ni.mi.cro'bi.um] L. neut. n. <i>rumen</i> , the rumen; N.L. neut. n. <i>microbium</i> , microbe; N.L. neut. n. <i>Ruminimicrobium</i> , a microbe that occurs in the rumen	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Ruminimicrobium bovinum</i> ^{Ts}	seqco.de/i:24028
Genus <i>Proruminimicrobium</i>	[Pro.ru.mi.ni.mi.cro'bi.um] L. pref. pro , (temporally) prior, fore-; N.L. neut. n. <i>Ruminimicrobium</i> , a microbe that occurs in the rumen; N.L. neut. n. <i>Proruminimicrobium</i> , a bacterial genus ancestral to <i>Ruminimicrobium</i> .	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Proruminimicrobium quisquiliarum</i> ^{Ts}	seqco.de/i:32939

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Praeruminimicrobium</i>	[Prae.ru.mi.ni.mi.cro'bi.um] L. pref. prae- , before; N.L. neut. n. Ruminimicrobium , a microbe that occurs in the rumen; N.L. neut. n. Praeruminimicrobium , a bacterial genus ancestral to Ruminimicrobium	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Praeruminimicrobium purgament</i> ^{Ts}	seqco.de/i:32937
Genus <i>Parendomicrobium</i>	[Par.en.do.mi.cro'bi.um] L. adj. par , equal, like; N.L. neut. n. Endomicrobium , a bacterial genus; N.L. neut. n. Parendomicrobium , a bacterial genus like Endomicrobium	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Parendomicrobium reticulitermitis</i> ^{Ts}	seqco.de/i:24030
Genus <i>Ectomicrobium</i>	[Ec.to.mi.cro'bi.um] Gr. adv. ektos , outside, external; N.L. neut. n. microbium , microbe; N.L. neut. n. Ectomicrobium , a microbe that occurs on the outside (of another organism).	A bacterial genus defined by metagenome-assembled genomes. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Ectomicrobium neotermitis</i> ^{Ts}	seqco.de/i:24026
Genus <i>Endomicrobiellum</i>	[En.do.mi.cro.bi.ell'um] Gr. pref. endon , within; N.L. neut. n. microbium , microbe; L. neut. dim. n. suff. -ellum , diminutive ending; N.L. neut. dim. n. Endomicrobiellum , a small microbe that occurs within (a host cell).	A bacterial genus identified by genomic, single-cell amplified genomes and metagenome-assembled genome. All members of the genus are intracellular symbionts of termite gut flagellates. The genus is defined by phylogenomic analysis as a monophyletic group that shows a relative evolutionary divergence (RED) similar to that of the neighboring genera.	<i>Endomicrobiaceae</i>	<i>Endomicrobiellum trichonymphae</i> ^{Ts}	seqco.de/i:24027
Species <i>Endomicrobiellum africanum</i>	[a.fri.ca'num] N.L. neut. adj. africanum , of Africa, African, referring to the geographic origin of the host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.2 mol% and the estimated genome size is 1.1 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031281995.1 ^{Ts}	seqco.de/i:32922

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Endomicrobiellum cubanum</i>	[cu.ba'num] N.L. neut. adj. <i>cubanum</i> , of Cuba, Cuban, referring to the geographic origin of the host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.1 mol% and the estimated genome size is 1.4 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031269735.1 ^{Ts}	seqco.de/i:32919
Species <i>Endomicrobiellum porotermitis</i>	[po.ro.ter'mi.tis] N.L. gen. n. <i>porotermitis</i> , of Porotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 37.2 mol% and the estimated genome size is 1.1 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031289055.1 ^{Ts}	seqco.de/i:32925
Species <i>Endomicrobiellum incisitermitis</i>	[in.ci.si.ter'mi.tis] N.L. gen. n. <i>incisitermitis</i> , of Incisitermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.2 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031275795.1 ^{Ts}	seqco.de/i:32923
Species <i>Endomicrobiellum cryptotermitis</i>	[cryp.to.ter'mi.tis] N.L. gen. n. <i>cryptotermitis</i> , of Cryptotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.1 mol% and the estimated genome size is 1.2 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031257835.1 ^{Ts}	seqco.de/i:32920
Species <i>Endomicrobiellum calonymphae</i>	[ca.lo.nym'phae] N.L. gen. n. <i>calonymphae</i> , of Calonympha, referring to the host flagellate.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 32.4 mol% and the estimated genome size is 0.9 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031269945.1 ^{Ts}	seqco.de/i:32915
Species <i>Endomicrobiellum mastotermitis</i>	[mas.to.ter'mi.tis] N.L. gen. n. <i>mastotermitis</i> , of Mastotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.0 mol% and the estimated genome size is 0.9 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031272445.1 ^{Ts}	seqco.de/i:32914

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Endomicrobiellum neotermitis</i>	[ne.o.ter'mi.tis] N.L. gen. n. <i>neotermitis</i> , of <i>Neotermes</i> , referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 29.0 mol% and the estimated genome size is 0.6 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031282355.1 ^{Ts}	seqco.de/i:32912
Species <i>Endomicrobiellum pyrsonymphae</i>	[pyr.so.nym'phae] N.L. gen. n. <i>pyrsonymphae</i> , of <i>Pyrsonympha</i> , referring to the host flagellate.	The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of <i>Pyrsonympha vertens</i> . Localized in the cytoplasm of <i>Pyrsonympha vertens</i> using FISH with a specific oligonucleotide probe. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type strain is 35.3 mol% and the estimated genome size is 1.3Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_020328045.1 ^{Ts}	seqco.de/i:32910
Species <i>Endomicrobiellum trichonymphae</i> ^{Ts}	[tri.cho.nym'phae] N.L. gen. n. <i>trichonymphae</i> , of <i>Trichonympha</i> , referring to the host flagellate	The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of the cellulolytic protist <i>Trichonympha agilis</i> in the termite gut. Spindle-shaped cells (0.6 µm in length and 0.3 µm in diameter). The outer membrane forms tubular extensions into the cytoplasm of the host. Localized in the cytoplasm of flagellates of the genus <i>Trichonympha</i> using FISH with a specific oligonucleotide probe. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type strain is 35.2 mol% and the estimated genome size is 1.1Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCF_002355835.1 ^{Ts}	seqco.de/i:32908
Species <i>Endomicrobiellum dinenymphae</i>	[di.ne.nym'phae] N.L. gen. n. <i>dinenymphae</i> , of <i>Dinenympha</i> , referring to the host flagellate	The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of <i>Dinenympha</i> . The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type strain is 36.0 mol% and the estimated genome size is 1.1Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_020328135.1 ^{Ts}	seqco.de/i:32909

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Endomicrobium procryptotermitis</i>	[pro.cryp.to.ter'mi.tis] N.L. gen. n. <i>procryptotermitis</i> , of Procryptotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 36.3 mol% and the estimated genome size is 2.1 Mbp.	<i>Endomicrobium</i>	NCBI Assembly: GCA_031279415.1 ^{Ts}	seqco.de/i:32907
Species <i>Endomicrobium macrotermitis</i>	[ma.cro.ter'mi.tis] N.L. gen. n. <i>macrotermitis</i> , of Macrotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 42.7 mol% and the estimated genome size is 2.0 Mbp.	<i>Endomicrobium</i>	NCBI Assembly: GCA_031271405.1 ^{Ts}	seqco.de/i:32906
Species <i>Endomicrobium neocapritermitis</i>	[ne.o.ca.pri.ter'mi.tis] N.L. gen. n. <i>neocapritermitis</i> , of Neocapritermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 39.7 mol% and the estimated genome size is 2.4 Mbp.	<i>Endomicrobium</i>	NCBI Assembly: GCA_009778325.1 ^{Ts}	seqco.de/i:32905
Species <i>Endomicrobium labiotermitis</i>	[la.bi.o.ter'mi.tis] N.L. gen. n. <i>labiotermitis</i> , of Labiotermes, referring to the termite host genus	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 38.0 mol% and the estimated genome size is 2.0 Mbp.	<i>Endomicrobium</i>	NCBI Assembly: GCA_009778965.1 ^{Ts}	seqco.de/i:32904
Species <i>Endomicrobium embiratermitis</i>	[em.bi.ra.ter'mi.tis] N.L. gen. n. <i>embiratermitis</i> , of Embiratermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 39.6 mol% and the estimated genome size is 2.0 Mbp.	<i>Endomicrobium</i>	NCBI Assembly: GCA_009781315.1 ^{Ts}	seqco.de/i:32903
Species <i>Endomicrobiellum meruensis</i>	[me.ru.en'sis] N.L. gen. n. <i>meruensis</i> , of Neotermes meruensis, referring to the host species.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 33.8 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031282625.1 ^{Ts}	seqco.de/i:32927

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Endomicrobiellum</i> <i>siamense</i>	[si.a.men'se] N.L. neut. adj. <i>siamense</i> , of Siam, Thai, referring to the geographic origin of the host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 30.8 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031268145.1 ^{Ts}	seqco.de/i:32917
Species <i>Praeruminimicrobium</i> <i>purgamenti</i> ^{Ts}	[pur.ga.men'ti] L. gen. n. <i>purgamenti</i> , from waste, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 34.6 mol% and the estimated genome size is 1.9 Mbp.	<i>Praeruminimicrobium</i>	NCBI Assembly: GCA_018433585.1 ^{Ts}	seqco.de/i:32938
Species <i>Proruminimicrobium</i> <i>quisquiliarum</i> ^{Ts}	[quis.qui.li.a'rum] L. gen. pl. n. <i>quisquiliarum</i> , from waste, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 35.1 mol% and the estimated genome size is 2.0 Mbp.	<i>Proruminimicrobium</i>	NCBI Assembly: GCA_018433245.1 ^{Ts}	seqco.de/i:32940
Species <i>Endomicrobiellum</i> <i>devescovinae</i>	[de.ves.co.vi'nae] N.L. gen. n. <i>devescovinae</i> , of Devescovina, referring to the flagellate host	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 34.1 mol% and the estimated genome size is 1.2 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031255495.1 ^{Ts}	seqco.de/i:32926
Species <i>Ruminimicrobiellum</i> <i>tauri</i>	[tau'ri] L. gen. n. <i>tauri</i> , of a steer, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 29.3 mol% and the estimated genome size is 1.5 Mbp.	<i>Ruminimicrobiellum</i>	NCBI Assembly: GCA_902792865.1 ^{Ts}	seqco.de/i:32936
Species <i>Ruminimicrobiellum</i> <i>caprinum</i>	[ca.pri'num] L. neut. adj. <i>caprinum</i> , of or belonging to goats, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 33.0 mol% and the estimated genome size is 1.7 Mbp.	<i>Ruminimicrobiellum</i>	NCBI Assembly: GCA_017413305.1 ^{Ts}	seqco.de/i:32935

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Species <i>Ruminimicrobiellum bubulum</i> ^{Ts}	[bu'bu.lum] L. neut. adj. <i>bubulum</i> , of or belonging to cattle, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.8 mol% and the estimated genome size is 1.9 Mbp.	<i>Ruminimicrobiellum</i>	NCBI Assembly: GCA_017651625.1 ^{Ts}	seqco.de/i:32933
Species <i>Parendomicrobium reticulitermitis</i> ^{Ts}	[re.ti.cu.li.ter'mi.tis] N.L. gen. n. <i>reticulitermitis</i> , of Reticulitermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 37.7 mol% and the estimated genome size is 2.3 Mbp.	<i>Parendomicrobium</i>	NCBI Assembly: GCA_031287095.1 ^{Ts}	seqco.de/i:32929
Species <i>Ectomicrobium neotermitis</i> ^{Ts}	[ne.o.ter'mi.tis] N.L. gen. n. <i>neotermitis</i> , of Neotermes, referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 41.2 mol% and the estimated genome size is 1.4 Mbp.	<i>Ectomicrobium</i>	NCBI Assembly: GCA_031283745.1 ^{Ts}	seqco.de/i:32930
Species <i>Ruminimicrobiellum ovillum</i>	[o.vil'lum] L. neut. adj. <i>ovillum</i> , of or belonging to sheep, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 32.3 mol% and the estimated genome size is 1.8 Mbp.	<i>Ruminimicrobiellum</i>	NCBI Assembly: GCA_002448285.1 ^{Ts}	seqco.de/i:32934
Species <i>Ruminimicrobium bovinum</i> ^{Ts}	[bo.vi'num] L. neut. adj. <i>bovinum</i> , of or belonging to cattle, referring to the isolation source	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.0 mol% and the estimated genome size is 1.9 Mbp.	<i>Ruminimicrobium</i>	NCBI Assembly: GCA_900316875.1 ^{Ts}	seqco.de/i:32932
Species <i>Endomicrobiellum guadaloupense</i>	[gu.a.da.lou.pen'se] N.L. neut. adj. <i>guadaloupense</i> , of Guadeloupe, referring to the geographic origin of the host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 32.5 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031278895.1 ^{Ts}	seqco.de/i:32924

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Endomicrobiellum</i> <i>basalitermitum</i>	[ba.sa.li.ter'mi.tum] L. adj. <i>basalis</i> , basal; L. masc. n. <i>termes</i> , a woodworm, termite; N.L. gen. masc. pl. n. <i>basalitermitum</i> , of lower (basal) termites.	A bacterial species identified by metagenome-assembled genomes. The species includes all bacteria with genomes that show an average nucleotide identity (ANI) of $\geq 95\%$ to the type genome. The GC content of the type genome is 30.8 mol% and the estimated genome size is 0.8 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031282525.1 ^{TS}	seqco.de/i:32913
Species <i>Endomicrobiellum</i> <i>agilis</i>	[a'gi.lis] L. gen. n. <i>agilis</i> , of <i>Trichonympha agilis</i> , referring to the host species.	The species comprises only metagenome-assembled genomes and single-cell amplified genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 36.0 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_020328155.1 ^{TS}	seqco.de/i:32911
Species <i>Endomicrobiellum</i> <i>roisinitermitis</i>	[roi.si.ni.ter'mi.tis] N.L. gen. n. <i>roisinitermitis</i> , of <i>Roisinitermes</i> , referring to the termite host genus.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI) to the type genome. The GC content of the type genome is 31.3 mol% and the estimated genome size is 1.3 Mbp.	<i>Endomicrobiellum</i>	NCBI Assembly: GCA_031287855.1 ^{TS}	seqco.de/i:32921