

# Register list for 44 new names including *Proruminomicrobium quisquiliarum* sp. nov.

Submitted by Mies, Undine Sophie

## Genus *Ruminimicrobiellum*

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### Etymology

[Ru.mi.ni.mi.cro'bi.ell.um] L. neut. n. *rumen*, the rumen; N.L. dim. neut. n. *microbiellum*, a small microbe; N.L. neut. n. *Ruminimicrobiellum*, a small microbe that occurs in the rumen

### Nomenclatural type

Species *Ruminimicrobiellum bubulum*<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobiellum*

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:24029>

## Genus *Ruminimicrobium*

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### Etymology

[Ru.mi.ni.mi.cro'bi.um] L. neut. n. *rumen*, the rumen; N.L. neut. n. *microbium*, microbe; N.L. neut. n. *Ruminimicrobium*, a microbe that occurs in the rumen

### Nomenclatural type

Species *Ruminimicrobium bovinum*<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobium*

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:24028>

## Genus *Proruminimicrobium*

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**Etymology**

[Pro.ru.mi.ni.mi.cro'bi.um] L. **pref.** *pro*, (temporally) prior, fore-; **N.L. neut. n.** *Ruminimicrobium*, a microbe that occurs in the rumen; **N.L. neut. n.** *Proruminimicrobium*, a bacterial genus ancestral to Ruminimicrobium.

**Nomenclatural type**

Species *Proruminimicrobium quisquiliarum*<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Proruminimicrobium*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32939>

## Genus *Praeruminimicrobium*

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**Etymology**

[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

**Nomenclatural type**

Species *Praeruminimicrobium purgament*<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Praeruminimicrobium*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32937>

## Genus *Parendomicrobium*

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**Etymology**

[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

**Nomenclatural type**

Species *Parendomicrobium reticulitermitis*<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Parendomicrobium*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:24030>

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**Genus *Ectomicrobium***

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**Etymology**

[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).

**Nomenclatural type**

Species *Ectomicrobium neotermitis*<sup>T5</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ectomicrobium*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:24026>

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**Genus *Endomicrobiellum***

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**Etymology**

[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).

**Nomenclatural type**

Species *Endomicrobiellum trichonymphae*<sup>T5</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:24027>

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**Species *Endomicrobiellum africanum***

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**Etymology**

[a.fri.ca'num] N.L. neut. adj. *africanum*, of Africa, African, referring to the geographic origin of the host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031281995.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum africanum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32922>

## Species *Endomicrobiellum cubanum*

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**Etymology**

[cu.ba'num] N.L. neut. adj. *cubanum*, of Cuba, Cuban, referring to the geographic origin of the host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031269735.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum cubanum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32919>

## Species *Endomicrobiellum porotermitis*

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**Etymology**

[po.ro.ter'mi.tis] N.L. gen. n. *porotermitis*, of *Porotermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031289055.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum porotermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32925>

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**Species *Endomicrobiellum incisitermitis***

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**Etymology**

[in.ci.si.ter'mi.tis] N.L. gen. n. *incisitermitis*, of *Incisitermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031275795.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum incisitermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32923>

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**Species *Endomicrobiellum cryptotermitis***

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**Etymology**

[cryp.to.ter'mi.tis] N.L. gen. n. *cryptotermitis*, of *Cryptotermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031257835.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum cryptotermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32920>

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**Species *Endomicrobiellum calonymphae***

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**Etymology**

[ca.lo.nym'phae] N.L. gen. n. *calonymphae*, of *Calonympha*, referring to the host flagellate.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031269945.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum calonymphae*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32915>

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**Species *Endomicrobiellum mastotermis***

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**Etymology**

[mas.to.ter'mi.tis] N.L. **gen. n.** *mastotermis*, of Mastotermes, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031272445.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum mastotermis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32914>

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**Species *Endomicrobiellum neotermis***

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**Etymology**

[ne.o.ter'mi.tis] N.L. **gen. n.** *neotermis*, of Neotermes, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031282355.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum neotermis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32912>

## Species *Endomicrobiellum pyrsonymphae*

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### Etymology

[pyr.so.nym'phae] N.L. gen. n. *pyrsonymphae*, of *Pyrsonympha*, referring to the host flagellate.

### Nomenclatural type

[NCBI Assembly: GCA\\_020328045.1](#) <sup>Ts</sup>

### Description

The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of *Pyrsonympha vertens*. Localized in the cytoplasm of *Pyrsonympha vertens* 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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum pyrsonymphae*

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:32910>

## Species *Endomicrobiellum trichonymphae*<sup>Ts</sup>

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### Etymology

[tri.cho.nym'phae] N.L. gen. n. *trichonymphae*, of *Trichonympha*, referring to the host flagellate

### Nomenclatural type

[NCBI Assembly: GCF\\_002355835.1](#) <sup>Ts</sup>

### Description

The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of the cellulolytic protist *Trichonympha agilis* 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 *Trichonympha* 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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum trichonymphae*<sup>Ts</sup>

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:32908>

## Species *Endomicrobiellum dinenymphae*

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### Etymology

[di.ne.nym'phae] N.L. gen. n. *dinenymphae*, of *Dinenympha*, referring to the host flagellate

### Nomenclatural type

[NCBI Assembly: GCA\\_020328135.1](#) <sup>Ts</sup>

**Description**

The species comprises only single-cell amplified genomes. Colonizes the cytoplasm of *Dinenympha*. 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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum dinenymphae*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32909>

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**Species *Endomicrobium procryptotermitis***

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**Etymology**

[pro.cryp.to.ter'mi.tis] N.L. gen. n. *procryptotermitis*, of Procryptotermes, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031279415.1](#) <sup>TS</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobium* » *Endomicrobium procryptotermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32907>

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**Species *Endomicrobium macrotermitis***

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**Etymology**

[ma.cro.ter'mi.tis] N.L. gen. n. *macrotermitis*, of Macrotermes, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031271405.1](#) <sup>TS</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobium* » *Endomicrobium macrotermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32906>



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## Species *Endomicrobium neocapritermitis*

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### Etymology

[ne.o.ca.pri.ter'mi.tis] N.L. gen. n. *neocapritermitis*, of *Neocapritermes*, referring to the termite host genus.

### Nomenclatural type

[NCBI Assembly: GCA\\_009778325.1](#)<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobium* » *Endomicrobium neocapritermitis*

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:32905>

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## Species *Endomicrobium labiotermitis*

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### Etymology

[la.bi.o.ter'mi.tis] N.L. gen. n. *labiotermitis*, of *Labiotermes*, referring to the termite host genus

### Nomenclatural type

[NCBI Assembly: GCA\\_009778965.1](#)<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobium* » *Endomicrobium labiotermitis*

### References

Effective publication: Mies et al., 2024 [1]

### Registry URL

<https://seqco.de/i:32904>

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## Species *Endomicrobium embiratermitis*

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### Etymology

[em.bi.ra.ter'mi.tis] N.L. gen. n. *embiratermitis*, of *Embiratermes*, referring to the termite host genus.

### Nomenclatural type

[NCBI Assembly: GCA\\_009781315.1](#)<sup>Ts</sup>

### Description

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobium* » *Endomicrobium embiratermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32903>

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**Species *Endomicrobiellum meruensis***

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**Etymology**

[me.ru.en'sis] N.L. gen. n. *meruensis*, of *Neotermes meruensis*, referring to the host species.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031282625.1](#) <sup>TS</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum meruensis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32927>

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**Species *Endomicrobiellum siamense***

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**Etymology**

[si.a.men'se] N.L. neut. adj. *siamense*, of Siam, Thai, referring to the geographic origin of the host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031268145.1](#) <sup>TS</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum siamense*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32917>

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**Species *Praeruminimicrobium purgament<sup>1</sup>s***

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**Etymology**

[pur.ga.men'ti] L. gen. n. *purgamenti*, from waste, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_018433585.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Praeruminimicrobium* » *Praeruminimicrobium purgamenti*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32938>

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**Species *Proruminimicrobium quisquiliarum*<sup>Ts</sup>**

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**Etymology**

[quis.qui.li.a'rum] L. gen. pl. n. *quisquiliarum*, from waste, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_018433245.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Proruminimicrobium* » *Proruminimicrobium quisquiliarum*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32940>

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**Species *Endomicrobiellum devescovinae***

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**Etymology**

[de.ves.co.vi'nae] N.L. gen. n. *devescovinae*, of *Devescovina*, referring to the flagellate host

**Nomenclatural type**

[NCBI Assembly: GCA\\_031255495.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum devescovinae*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32926>

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**Species *Ruminimicrobiellum tauri***

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**Etymology**

[tau'ri] L. **gen. n.** *tauri*, of a steer, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_902792865.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobiellum* » *Ruminimicrobiellum tauri*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32936>

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**Species *Ruminimicrobiellum caprinum***

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**Etymology**

[ca.pri'num] L. **neut. adj.** *caprinum*, of or belonging to goats, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_017413305.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobiellum* » *Ruminimicrobiellum caprinum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32935>

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**Species *Ruminimicrobiellum bubulum*<sup>Ts</sup>**

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**Etymology**

[bu'bu.lum] L. **neut. adj.** *bubulum*, of or belonging to cattle, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_017651625.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobiellum* » *Ruminimicrobiellum bubulum*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32933>

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**Species *Parendomicrobium reticulitermitis*<sup>Ts</sup>**

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**Etymology**

[re.ti.cu.li.ter'mi.tis] N.L. gen. n. *reticulitermitis*, of *Reticulitermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031287095.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Parendomicrobium* » *Parendomicrobium reticulitermitis*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32929>

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**Species *Ectomicrobium neotermitis*<sup>Ts</sup>**

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**Etymology**

[ne.o.ter'mi.tis] N.L. gen. n. *neotermitis*, of *Neotermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031283745.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ectomicrobium* » *Ectomicrobium neotermitis*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32930>

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**Species *Ruminimicrobiellum ovillum***

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**Etymology**

[o.vil'lum] L. neut. adj. *ovillum*, of or belonging to sheep, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_002448285.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobiellum* » *Ruminimicrobiellum ovillum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32934>

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**Species *Ruminimicrobium bovinum*<sup>Ts</sup>**

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**Etymology**

[bo.vi'num] L. neut. adj. *bovinum*, of or belonging to cattle, referring to the isolation source

**Nomenclatural type**

[NCBI Assembly: GCA\\_900316875.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Ruminimicrobium* » *Ruminimicrobium bovinum*<sup>Ts</sup>

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32932>

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**Species *Endomicrobiellum guadaloupense***

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**Etymology**

[gu.a.da.lou.pen'se] N.L. neut. adj. *guadaloupense*, of Guadeloupe, referring to the geographic origin of the host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031278895.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum guadaloupense*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32924>

## Species *Endomicrobiellum basalitermitum*

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**Etymology**

[ba.sa.li.ter'mi.tum] L. adj. *basalis*, basal; L. masc. n. *termes*, a woodworm, termite; N.L. gen. masc. pl. n. *basalitermitum*, of lower (basal) termites.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031282525.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum basalitermitum*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:32913>

## Species *Endomicrobiellum agilis*

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**Etymology**

[a'gi.lis] L. gen. n. *agilis*, of *Trichonympha agilis*, referring to the host species.

**Nomenclatural type**

[NCBI Assembly: GCA\\_020328155.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* » *Endomicrobiellum agilis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32911>**Species** *Endomicrobiellum rosinitermitis***Etymology**

[roi.si.ni.ter'mi.tis] **N.L. gen. n.** *rosinitermitis*, of *Rosinitermes*, referring to the termite host genus.

**Nomenclatural type**

[NCBI Assembly: GCA\\_031287855.1](#)<sup>TS</sup>

**Description**

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.

**Classification**

*Bacteria* » *Elusimicrobiota* » *Endomicrobiia* » *Endomicrobiales* » *Endomicrobiaceae* » *Endomicrobiellum* »  
*Endomicrobiellum rosinitermitis*

**References**

Effective publication: Mies et al., 2024 [1]

**Registry URL**<https://seqco.de/i:32921>**References**

1. Mies et al. (2024). Genome reduction and horizontal gene transfer in the evolution of Endomicrobia—rise and fall of an intracellular symbiosis with termite gut flagellates. *mBio*. DOI:10.1128/mbio.00826-24

**Register List Certificate of Validation**

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List [seqco.de/r:tm1bm3q2](https://seqco.de/r:tm1bm3q2) submitted by **Mies, Undine Sophie** and including 39 new names has been successfully validated.

**Date of Priority:** 2024-05-29 02:02 UTC

DOI: 10.57973/seqcode.r:tm1bm3q2

