

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

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Genus *Ruminimicrobiellum*

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*^{Ts}

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*

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*^{Ts}

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*

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*^{Ts}

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*

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*^{Ts}

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*

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*^{Ts}

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>

Genus *Ectomicrobium*

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*^{T5}

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>

Genus *Endomicrobiellum*

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*^{T5}

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>

Species *Endomicrobiellum africanum*

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](#)^{Ts}

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*

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](#)^{Ts}

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 poroitermitis*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_031289055.1](#)^{Ts}

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 poroitermitis*

References

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

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

Species *Endomicrobiellum incisitermitis*

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](#) ^{Ts}

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>

Species *Endomicrobiellum cryptotermitis*

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](#) ^{Ts}

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>

Species *Endomicrobiellum calonymphae*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_031269945.1](#) ^{Ts}

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>

Species *Endomicrobiellum mastotermis*

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](#)^{TS}

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>

Species *Endomicrobiellum neotermis*

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](#)^{TS}

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*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_020328045.1](#)^{Ts}

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*^{Ts}

Etymology

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

Nomenclatural type

[NCBI Assembly: GCF_002355835.1](#)^{Ts}

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*^{Ts}

References

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

Registry URL

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

Species *Endomicrobiellum dinenymphae*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_020328135.1](#)^{Ts}

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>

Species *Endomicrobium procryptotermitis*

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](#)^{TS}

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>

Species *Endomicrobium macrotermitis*

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](#)^{TS}

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>

Species *Endomicrobium neocapritermitis*

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](#)^{Ts}

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>

Species *Endomicrobium labiotermitis*

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](#)^{Ts}

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>

Species *Endomicrobium embiratermitis*

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](#)^{Ts}

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>

Species *Endomicrobiellum meruensis*

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](#) ^{TS}

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>

Species *Endomicrobiellum siamense*

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](#) ^{TS}

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>

Species *Praeruminimicrobium purgament*^{TS}

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_018433585.1](#)^{Ts}

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*^{Ts}

References

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

Registry URL

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

Species *Proruminimicrobium quisquiliarum*^{Ts}

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](#)^{Ts}

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*^{Ts}

References

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

Registry URL

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

Species *Endomicrobiellum devescovinae*

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](#)^{Ts}

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>

Species *Ruminimicrobiellum tauri*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_902792865.1](#)^{Ts}

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>

Species *Ruminimicrobiellum caprinum*

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](#)^{Ts}

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>

Species *Ruminimicrobiellum bubulum*^{Ts}

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](#)^{Ts}

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*^{Ts}

References

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

Registry URL

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

Species *Parendomicrobium reticulitermitis*^{Ts}

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](#)^{Ts}

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*^{Ts}

References

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

Registry URL

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

Species *Ectomicrobium neotermitis*^{Ts}

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](#)^{Ts}

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*^{Ts}

References

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

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

Species *Ruminimicrobiellum ovillum*

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](#)^{Ts}**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>

Species *Ruminimicrobium bovinum*^{Ts}

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](#)^{Ts}**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*^{Ts}

References

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

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

Species *Endomicrobiellum guadaloupense*

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](#)^{Ts}

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*

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](#)^{Ts}

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*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_020328155.1](#)^{Ts}

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](#)^{TS}

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 submitted by **Mies, Undine Sophie** and including 39 new names has been successfully validated.

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