

Register list for 27 new names including *Avelusimicrobium faecis* sp. nov.

Submitted by Mies, Undine Sophie

Genus *Avelusimicrobium*

Etymology

[Av.e.lu.si.mi.cro'bi.um] **L. fem. n.** *avis*, bird; **N.L. neut. n.** *Elusimicrobium*, a bacterial genus; **N.L. neut. n.** *Avelusimicrobium*, a genus related to *Elusimicrobium* that occurs in birds

Nomenclatural type

Species *Avelusimicrobium excrementipullorum*^{TS}

Description

The genus comprises only metagenome-assembled genomes. Occur in the hindgut of birds and mammals. 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* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Avelusimicrobium*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:42385>

Genus *Proelusimicrobium*

Etymology

[Pro.e.lu.si.mi.cro'bi.um] **Gr. prep.** *pro*, before; **N.L. neut. n.** *Elusimicrobium*, a bacterial genus; **N.L. neut. n.** *Proelusimicrobium*, the ancestral *Elusimicrobium*

Nomenclatural type

Species *Proelusimicrobium excrementi*^{TS}

Description

The genus comprises only metagenome-assembled genomes. Occur in the hindgut of chicken, various ruminants, humans, pigs and baboons. 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* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Proelusimicrobium*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49126>

Species *Avelusimicrobium alvi*

Etymology

[al'vi] **L. fem. gen. n.** *alvi*, of the bowel

Nomenclatural type

[NCBI Assembly: GCA_905200775.1](#) ^{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 54% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium alvi*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49151>

Species *Avelusimicrobium aviculae*

Etymology

[a.vi'cu.lae] **L. gen. n.** *aviculae*, of a small bird, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_944324655.1](#) ^{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 48% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium aviculae*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49144>

Species *Avelusimicrobium bubulum*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_902798835.1](#) ^{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 46% and the estimated genome size is 1.4 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium bubulum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49148>

Species *Avelusimicrobium caledoniense*

Etymology

[ca.le.do.ni.en'se] **N.L. neut. adj.** *caledoniense*, of or pertaining to Scotland, where the genome was assembled.

Nomenclatural type

[NCBI Assembly: GCA_902793205.1](#) ^{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 47% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium caledoniense*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49150>

Species *Avelusimicrobium cornigerorum*

Etymology

[cor.ni.ge.ro'rum] **L. gen. pl. n.** *cornigerorum*, of horned cattle, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_002309715.1](#) ^{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 45% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium cornigerorum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49132>

Species *Avelusimicrobium excrementipullorum*^{Ts}

Etymology

[ex.cre.men.ti.pul.lo'rum] **L. neut. n.** *excrementum*, excrement; **L. masc. n.** *pullus*, a young chicken; **N.L. gen. pl. n.** *excrementipullorum*, of young chicken excrement

Nomenclatural type

[NCBI Assembly: GCA_944327025.1](#)^{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 53% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium excrementipullorum*^{Ts}

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:42386>

Species *Avelusimicrobium faecicola*

Etymology

[fae.ci'co.la] **L. fem. n.** *faex*, dregs; **L. fem. n. suff.** *-cola*, inhabitant; **N.L. fem. n.** *faecicola*, inhabitant of feces

Nomenclatural type

[NCBI Assembly: GCA_021636085.1](#)^{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 50% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium faecicola*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49146>

Species *Avelusimicrobium faecis*

Etymology

[fae'cis] **L. gen. n.** *faecis*, of faeces, referring to the isolation source.

Nomenclatural type

[NCBI Assembly: GCA_934636855.1](#) ^{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 54% and the estimated genome size is 1.4 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium faecis*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49149>

Species *Avelusimicrobium fimicola*

Etymology

[fi.mi'co.la] **L. neut. n.** *fimum*, dung, excrement; **L. fem. n. suff.** *-cola*, inhabitant; **N.L. fem. n.** *fimicola*, dung dweller, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_900541355.1](#) ^{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 47% and the estimated genome size is 1.6 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium fimicola*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49145>

Species *Avelusimicrobium gallicola*

Etymology

[gal.li'co.la] **L. masc. n.** *gallus*, rooster, chicken; **L. fem. n. suff.** *-cola*, inhabitant; **L. fem. n.** *gallicola*, inhabitant of chickens

Nomenclatural type

[NCBI Assembly: GCF_002159705.1](#) ^{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 52% and the estimated genome size is 1.6 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Avelusimicrobium* » *Avelusimicrobium gallicola*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49133>

Species *Avelusimicrobium gallinaceum*

Etymology

[gal.li.na'ce.um] **L. neut. adj.** *gallinaceum*, of or belonging to poultry, fowl, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_944324965.1](#) ^{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 49% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Avelusimicrobium* » *Avelusimicrobium gallinaceum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49134>

Species *Avelusimicrobium intestinale*

Etymology

[in.tes.ti.na'le] **N.L. neut. adj.** *intestinale*, of or belonging to the intestine, intestinal, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_902765225.1](#) ^{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 48% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium intestinale*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49135>

Species *Avelusimicrobium intestinipullorum*

Etymology

[in.tes.ti.ni.pul.lo'rum] **L. neut. adj.** *intestinum*, gut; **L. masc. n.** *pullus*, a young chicken; **L. gen. pl. n.** *intestinipullorum*, from the gut of young chicken

Nomenclatural type

[NCBI Assembly: GCA_944324635.1](#) ^{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 47% and the estimated genome size is 1.8 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium intestinipullorum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49136>

Species *Avelusimicrobium luingense*

Etymology

[lu.ing.en'se] **N.L. neut. adj.** *luingense*, of or from Luing, an island in the Inner Hebrides of Scotland, referring to the origin of the type genome from Luing cattle bred on this island

Nomenclatural type

[NCBI Assembly: GCA_900315845.1](#) ^{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 44% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium luingense*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49137>

Species *Avelusimicrobium pecoris*

Etymology

[pe.co'ris] **L. gen. n.** *pecoris*, of livestock, pertaining to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_902761975.1](#) ^{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 48% and the estimated genome size is 1.3 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium pecoris*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49147>

Species *Avelusimicrobium pullicaecorum*

Etymology

[pul.li.cae.co'rum] **L. masc. n.** *pullus*, a chicken; **N.L. neut. n.** *caecum*, caecum; **N.L. gen. pl. n.** *pullicaecorum*, of the caeca of chickens, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_944322825.1](#) ^{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 52% and the estimated genome size is 1.6 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium pullicaecorum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49140>

Species *Avelusimicrobium pullorum*

Etymology

[pul.lor'um] **L. gen. pl. n.** *pullorum*, of or belonging to young chickens, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_944323745.1](#) ^{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 50% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium pullorum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49139>

Species *Avelusimicrobium ruminicola*

Etymology

[ru.mi.ni'co.la] **L. neut. n.** *rumen*, rumen; **L. fem. n. suff.** *-cola*, inhabitant; **N.L. fem. n.** *ruminicola*, inhabitant of the rumen

Nomenclatural type

[NCBI Assembly: GCA_902764935.1](#) ^{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 47% and the estimated genome size is 1.4 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium ruminicola*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49141>

Species *Avelusimicrobium stercoris*

Etymology

[ster'co.ris] **L. gen. n.** *stercoris*, of excrement, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_002432025.1](#) ^{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 49% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Avelusimicrobium » *Avelusimicrobium stercoris*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49142>

Species *Aelusimicrobium vaccinum*

Etymology

[vac.ci'num] **L. neut. adj.** *vaccinum*, of or belonging to cattle, referring to the isolation source.

Nomenclatural type

[NCBI Assembly: GCA_902794895.1](#) ^{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 43% and the estimated genome size is 1.5 Mbp

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Aelusimicrobium » *Aelusimicrobium vaccinum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49143>

Species *Elusimicrobium euhamitermitis*

Etymology

[eu.ha.mi.ter'mi.tis] **N.L. gen. n.** *euhamitermitis*, of Euhamitermes, referring to the termite host genus.

Nomenclatural type

[NCBI Assembly: GCA_031254225.1](#) ^{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 47.5% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Elusimicrobium » *Elusimicrobium euhamitermitis*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49123>

Species *Proelusimicrobium bovinum*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_902791965.1](#)^{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% and the estimated genome size is 1.6 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Proelusimicrobium* » *Proelusimicrobium bovinum*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49128>

Species *Proelusimicrobium excrementi*^{Ts}

Etymology

[ex.cre.men'ti] **L. gen. n.** *excrementi*, of bodily excrement, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_934643455.1](#)^{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 45% and the estimated genome size is 1.7 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* » *Proelusimicrobium* » *Proelusimicrobium excrementi*^{Ts}

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49127>

Species *Proelusimicrobium tauri*

Etymology

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

Nomenclatural type

[NCBI Assembly: GCA_002311025.1](#) ^{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% and the estimated genome size is 1.5 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Proelusimicrobium » *Proelusimicrobium tauri*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49129>

Species *Proelusimicrobium volucris*

Etymology

[vo.lu'cris] **L. gen. n.** *volucris*, of or belonging to a bird, referring to the isolation source

Nomenclatural type

[NCBI Assembly: GCA_944324665.1](#) ^{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 45% and the estimated genome size is 1.6 Mbp.

Classification

Bacteria » *Elusimicrobiota* » *Elusimicrobia* » *Elusimicrobiales* » *Elusimicrobiaceae* »
Proelusimicrobium » *Proelusimicrobium volucris*

References

Effective publication: Mies et al., 2025 [1]

Registry URL

<https://seqco.de/i:49131>

References

1. Mies et al. (2025). Comparative genomics of Elusimicrobiaceae (phylum Elusimicrobiota) and description of the isolates *Elusimicrobium simillimum* sp. nov., *Elusimicrobium posterum* sp. nov., and *Parelusimicrobium proximum* gen. nov. sp. nov. *Systematic and Applied Microbiology*. [DOI:10.1016/j.syapm.2025.126606](https://doi.org/10.1016/j.syapm.2025.126606)

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:fo7io6k1** submitted by **Mies, Undine Sophie** and including 27 new names has been successfully validated.

Date of Priority: 2025-06-25 11:55 UTC

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