

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

Submitted by Mies, Undine Sophie

Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Avelusimicrobium</i>	[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	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.	<i>Elusimicrobiaceae</i>	<i>Avelusimicrobium excrementipullorum</i> ^{Ts}	seqco.de/i:42385
Genus <i>Proelusimicrobium</i>	[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	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.	<i>Elusimicrobiaceae</i>	<i>Proelusimicrobium excrementi</i> ^{Ts}	seqco.de/i:49126
Species <i>Avelusimicrobium alvi</i>	[al'vi] L. fem. gen. n. alvi , of the bowel	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_905200775.1 ^{Ts}	seqco.de/i:49151
Species <i>Avelusimicrobium</i>	[a.vi'cu.lae] L. gen. n. aviculae , of a small bird,	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95% average nucleotide identity (ANI)	<i>Avelusimicrobium</i>	NCBI Assembly:	seqco.de/i:49144

<i>aviculae</i> Proposed Taxon	referring to the isolation source Etymology	to the type genome. The GC content of the type genome is Description	Parent Taxon	GCA_944324655.1 ^{Ts} Type	Registry URL
		48% and the estimated genome size is 1.7 Mbp.			
Species <i>Avelusimicrobium bubulum</i>	[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 46% and the estimated genome size is 1.4 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902798835.1 ^{Ts}	seqco.de/i:49148
Species <i>Avelusimicrobium caledoniense</i>	[ca.le.do.ni.en'se] N.L. neut. adj. <i>caledoniense</i> , of or pertaining to Scotland, where the genome was assembled.	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902793205.1 ^{Ts}	seqco.de/i:49150
Species <i>Avelusimicrobium cornigerorum</i>	[cor.ni.ge.ro'rum] L. gen. pl. n. <i>cornigerorum</i> , of horned 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 45% and the estimated genome size is 1.5 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_002309715.1 ^{Ts}	seqco.de/i:49132
Species <i>Avelusimicrobium excrementipullorum</i> ^{Ts}	[ex.cre.men.ti.pul.lo'rum] L. neut. n. <i>excrementum</i> , excrement; L. masc. n. <i>pullus</i> , a young chicken; N.L. gen. pl. n. <i>excrementipullorum</i> , of young chicken excrement	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_944327025.1 ^{Ts}	seqco.de/i:42386
		The species comprises only metagenome-assembled			

Proposed Taxon Species	Etymology [fae.ci'co.la] L. fem. n. <i>faex</i> , dregs; L. fem. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>faecicola</i> , inhabitant of feces	Description 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.	Parent Taxon <i>Avelusimicrobium</i>	Type NCBI Assembly: GCA_021636085.1 ^{Ts}	Registry URL seqco.de/i:49146
Species <i>Avelusimicrobium faecis</i>	[fae'cis] L. gen. n. <i>faecis</i> , of faeces, 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 54% and the estimated genome size is 1.4 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_934636855.1 ^{Ts}	seqco.de/i:49149
Species <i>Avelusimicrobium fimicola</i>	[fi.mi'co.la] L. neut. n. <i>fimum</i> , dung, excrement; L. fem. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>fimicola</i> , dung dweller, 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 47% and the estimated genome size is 1.6 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_900541355.1 ^{Ts}	seqco.de/i:49145
Species <i>Avelusimicrobium gallicola</i>	[gal.li'co.la] L. masc. n. <i>gallus</i> , rooster, chicken; L. fem. n. suff. <i>-cola</i> , inhabitant; L. fem. n. <i>gallicola</i> , inhabitant of chickens	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCF_002159705.1 ^{Ts}	seqco.de/i:49133
Species <i>Avelusimicrobium gallinaceum</i>	[gal.li.na'ce.um] L. neut. adj. <i>gallinaceum</i> , of or belonging to poultry, fowl, 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 49% and the estimated genome size is 1.7 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_944324965.1 ^{Ts}	seqco.de/i:49134

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Avelusimicrobium intestinale</i>	[in.tes.ti.na'le] N.L. neut. adj. intestinale , of or belonging to the intestine, intestinal, 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 48% and the estimated genome size is 1.5 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902765225.1 ^{Ts}	seqco.de/i:49135
Species <i>Avelusimicrobium intestinipullorum</i>	[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	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_944324635.1 ^{Ts}	seqco.de/i:49136
Species <i>Avelusimicrobium luingense</i>	[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	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_900315845.1 ^{Ts}	seqco.de/i:49137
Species <i>Avelusimicrobium pecoris</i>	[pe.co'ris] L. gen. n. pecoris , of livestock, pertaining 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 48% and the estimated genome size is 1.3 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902761975.1 ^{Ts}	seqco.de/i:49147
Species <i>Avelusimicrobium pullicaecorum</i>	[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,	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	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_944322825.1 ^{Ts}	seqco.de/i:49140

Proposed Taxon	referring to the isolation source Etymology	content of the type genome is 52% and the estimated genome size is 1.6 Mbp. Description	Parent Taxon	Type	Registry URL
Species <i>Avelusimicrobium pullorum</i>	[pul.lor'um] L. gen. pl. n. <i>pullorum</i> , of or belonging to young chickens, 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 50% and the estimated genome size is 1.7 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_944323745.1 ^{Ts}	seqco.de/i:49139
Species <i>Avelusimicrobium ruminicola</i>	[ru.mi.ni'co.la] L. neut. n. <i>rumen</i> , rumen; L. fem. n. suff. <i>-cola</i> , inhabitant; N.L. fem. n. <i>ruminicola</i> , inhabitant of the rumen	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.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902764935.1 ^{Ts}	seqco.de/i:49141
Species <i>Avelusimicrobium stercoris</i>	[ster'co.ris] L. gen. n. <i>stercoris</i> , of excrement, 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 49% and the estimated genome size is 1.7 Mbp.	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_002432025.1 ^{Ts}	seqco.de/i:49142
Species <i>Avelusimicrobium vaccinum</i>	[vac.ci'num] L. neut. adj. <i>vaccinum</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 43% and the estimated genome size is 1.5 Mbp	<i>Avelusimicrobium</i>	NCBI Assembly: GCA_902794895.1 ^{Ts}	seqco.de/i:49143
Species	[eu.ha.mi.ter'mi.tis] N.L. gen.	The species comprises only metagenome-assembled genomes. The species includes all bacteria with more than 95%			

<i>Elusimicrobium euhamitermitis</i> Proposed Taxon	n. euhamitermitis , of Euhamitermes, referring to the termite host genus. Etymology	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. Description	<i>Elusimicrobium</i> Parent Taxon	NCBI Assembly: GCA_031254225.1 ^{Ts} Type	seqco.de/i:49123 Registry URL
Species <i>Proelusimicrobium bovinum</i>	[bo.vi'num] L. neut. adj. <i>bovinum</i> , of or belonging to or pertaining 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 38% and the estimated genome size is 1.6 Mbp.	<i>Proelusimicrobium</i>	NCBI Assembly: GCA_902791965.1 ^{Ts}	seqco.de/i:49128
Species <i>Proelusimicrobium excrementi</i> ^{Ts}	[ex.cre.men'ti] L. gen. n. <i>excrementi</i> , of bodily excrement, 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 45% and the estimated genome size is 1.7 Mbp.	<i>Proelusimicrobium</i>	NCBI Assembly: GCA_934643455.1 ^{Ts}	seqco.de/i:49127
Species <i>Proelusimicrobium tauri</i>	[tau'ri] L. gen. n. <i>tauri</i> , of a bull, 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 36% and the estimated genome size is 1.5 Mbp.	<i>Proelusimicrobium</i>	NCBI Assembly: GCA_002311025.1 ^{Ts}	seqco.de/i:49129
Species <i>Proelusimicrobium volucris</i>	[vo.lu'cris] L. gen. n. <i>volucris</i> , of or belonging to a bird, 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 45% and the estimated genome size is 1.6 Mbp.	<i>Proelusimicrobium</i>	NCBI Assembly: GCA_944324665.1 ^{Ts}	seqco.de/i:49131