

# Archaea from terrestrial arthropods

Submitted by Protasov, Evgenii

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

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Bathycorpusculaceae</i>	[Ba.thy.cor.pus.cu.la'ce.ae] N.L. neut. n. <i>Bathycorpusculum</i> , referring to the type genus <i>Bathycorpusculum</i> ; <i>-aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Bathycorpusculaceae</i> , the <i>Bathycorpusculum</i> family	The family is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Bathyarchaeales</i>	<i>Bathycorpusculum</i>	<a href="https://seqco.de/i:32518">seqco.de/i:32518</a>
Genus <i>Methanorbis</i>	[Me.than.or'bis] N.L. neut. n. <i>methanum</i> , methane; L. masc. n. <i>orbis</i> , a disk; N.L. masc. n. <i>Methanorbis</i> , a methane-producing disk	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Cells are ovoid cocci 1–3 µm. Non-motile. H <sub>2</sub> and CO <sub>2</sub> are the substrates for methanogenesis; formate can substitute H <sub>2</sub> . Acetate and formate are required for growth. The temperature range is 25–40 °C.	<i>Methanocorpusculaceae</i>	<i>Methanorbis furvi</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32539">seqco.de/i:32539</a>
Genus <i>Bathycorpusculum</i>	[Ba.thy.cor.pus'cu.lum] Gr. pref. <i>bathy-</i> , deep, especially deep sea (from the Greek <i>bathys</i> , deep); L. neut. n. <i>corpusculum</i> , a little body, a particle; N.L. neut. n. <i>Bathycorpusculum</i> , a particle from the deep sea	The genus identified by metagenomic analyses. Putative mixotrophic CO <sub>2</sub> -reducing acetogens that use H <sub>2</sub> and amino acids as electron donors.	<i>Bathycorpusculaceae</i>	<i>Bathycorpusculum acetigenes</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32517">seqco.de/i:32517</a>
Genus <i>Methanofilum</i>	[Me.tha.no.fi'lum] N.L. pref. <i>methano-</i> , pertaining to methane; L. neut. n. <i>filum</i> , a thread or string; N.L. neut. n. <i>Methanofilum</i> , a methane-producing thread.	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Methanospirillaceae</i>	<i>Methanofilum arcanum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32513">seqco.de/i:32513</a>

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Genus <i>Methanofrustulum</i>	[Me.tha.no.frus'tu.lum] N.L. pref. <i>methano-</i> , pertaining to methane; L. neut. dim. n. <i>frustum</i> , morsel, crumb (of food); N.L. neut. n. <i>Methanofrustulum</i> , a methane-producing crumb	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Methanosarcinaceae</i>	<i>Methanofrustulum fimpullorum</i> <sup>TS</sup>	<a href="https://seqco.de/i:32514">seqco.de/i:32514</a>
Genus <i>Methanarmilla</i>	[Me.than.ar.mil'la] N.L. neut. n. <i>methanum</i> , methane; L. fem. n. <i>armilla</i> , bracelet; N.L. fem. n. <i>Methanarmilla</i> , methane-producing bracelet, referring to the short chains of cells formed by the type species	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods or coccobacilli, 0.6 µm in width and 1–1.8 µm in length. Cells occur singly, in pairs or in short chains. Gram positive. Nonmotile. Require complex medium with acetate, yeast extract, trypticase, volatile fatty acids, coenzyme M. Optimum temperature is 37–40° C. Use H <sub>2</sub> + CO <sub>2</sub> or formate + CO <sub>2</sub> as substrates for methanogenesis.	<i>Methanobacteriaceae</i>	<i>Methanarmilla wolini</i> <sup>TS</sup>	<a href="https://seqco.de/i:32439">seqco.de/i:32439</a>
Genus <i>Methanobaculum</i>	[Me.tha.no.ba'cu.lum] N.L. pref. <i>methano-</i> , pertaining to methane; L. neut. n. <i>baculum</i> , small rod; N.L. neut. n. <i>Methanobaculum</i> , a small methane-producing rod.	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Straight short rods with slightly tapered ends that occur singly, in pairs, or in short chains. Non-motile. Gram-positive. Strict anaerobe. Use H <sub>2</sub> + CO <sub>2</sub> as substrates for methanogenesis, growth on formate is poor. Grow poorly on mineral medium with vitamins. Yeast extract, casamino acids, and rumen fluid strongly stimulate growth. Optimum temperature is 30–37 °C.	<i>Methanobacteriaceae</i>	<i>Methanobaculum cuticulare</i> <sup>TS</sup>	<a href="https://seqco.de/i:32445">seqco.de/i:32445</a>
Genus <i>Methanovirga</i>	[Me.tha.no.vir'ga] N.L. pref. <i>methano-</i> , pertaining to methane; L. fem. n. <i>virga</i> , a rod; N.L. fem. n. <i>Methanovirga</i> , a methane-producing rod	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Methanobacteriaceae</i>	<i>Methanovirga basalitermitum</i> <sup>TS</sup>	<a href="https://seqco.de/i:32454">seqco.de/i:32454</a>

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Genus <i>Methanomicula</i>	[Me.tha.no.mi'cu.la] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. fem. n.</b> <i>micula</i> , morsel, crumb (of salt); <b>N.L. fem. n.</b> <i>Methanomicula</i> , a methane-producing crumb	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Methanomethylophilaceae</i>	<i>Methanomicula labiotermitis</i> <sup>TS</sup>	<a href="https://seqco.de/i:32531">seqco.de/i:32531</a>
Genus <i>Methanoflexus</i>	[Me.tha.no.fle'xus] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. masc. n.</b> <i>flexus</i> , a bending, turning, winding; <b>N.L. masc. n.</b> <i>Methanoflexus</i> , methane-producing (organism) with a curved shape	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Curved rods that occur singly, in pairs, or in chains. Gram positive. Nonmotile. Strict anaerobe. Require yeast extract or rumen fluid for growth. Optimum temperature is 30 °C. Use H <sub>2</sub> + CO <sub>2</sub> as substrates for methanogenesis.	<i>Methanobacteriaceae</i>	<i>Methanoflexus curvatus</i> <sup>TS</sup>	<a href="https://seqco.de/i:32447">seqco.de/i:32447</a>
Genus <i>Methanorudis</i>	[Me.tha.no.ru'dis] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. fem. n.</b> <i>rudis</i> , a small stick; <b>N.L. fem. n.</b> <i>Methanorudis</i> , a small methane-producing stick	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group.	<i>Methanobacteriaceae</i>	<i>Methanorudis spinitermitis</i> <sup>TS</sup>	<a href="https://seqco.de/i:32452">seqco.de/i:32452</a>
Genus <i>Methanolapillus</i>	[Me.tha.no.la'pil.lus] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. masc. n.</b> <i>lapillus</i> , a pebble, gem, jewel; <b>N.L. masc. n.</b> <i>Methanolapillus</i> , a methane-producing jewel	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Cells are irregular cocci, 1-2 µm. Cells occur singly or sometimes in aggregates. Nonmotile. Require complex medium with yeast extract, peptone, and casamino acids. Grow between 25-42° C. H <sub>2</sub> and methanol are the substrates for methanogenesis; methylamines can substitute methanol.	<i>Methanosarcinaceae</i>	<i>Methanolapillus millepedarum</i> <sup>TS</sup>	<a href="https://seqco.de/i:32601">seqco.de/i:32601</a>

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Genus <i>Methanocatella</i>	[Me.tha.no.ca.tel'la] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. fem. dim. n.</b> <i>catella</i> , a little chain; <b>N.L. fem. dim. n.</b> <i>Methanocatella</i> , a methane-producing chain, referring to the short chains of cells characteristic of this genus	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods or coccobacilli, 0.4–1 µm in width and 0.6–1.5 µm in length. Cells occur singly, in pairs or in chains of 4–6 cells. Gram positive. Nonmotile. Require complex medium with yeast extract, trypticase, rumen fluid, or fecal extract. Optimum temperature is 35–42 °C. Use H <sub>2</sub> + CO <sub>2</sub> as substrates for methanogenesis, some species grow poorly on formate.	<i>Methanobacteriaceae</i>	<i>Methanocatella smithii</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32432">seqco.de/i:32432</a>
Genus <i>Methanacia</i>	[Me.than.a'ci.a] <b>N.L. neut. n.</b> <i>methanum</i> , methane; <b>L. fem. n.</b> <i>acia</i> , thread, yarn; <b>N.L. fem. n.</b> <i>Methanacia</i> , a methane-producing thread	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Filamentous rods with slightly tapered ends. Gram positive. Nonmotile. Strict anaerobe. Require yeast extract for growth. Optimum temperature is 30 °C. Use H <sub>2</sub> + CO <sub>2</sub> as substrates for methanogenesis.	<i>Methanobacteriaceae</i>	<i>Methanacia filiformis</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32450">seqco.de/i:32450</a>
Genus <i>Methanobinarius</i>	[Me.tha.no.bi.na'ri.us] <b>N.L. pref.</b> <i>methano-</i> , pertaining to methane; <b>L. masc. adj.</b> <i>binarius</i> , consisting of two things; <b>N.L. masc. n.</b> <i>Methanobinarius</i> , methane-producing (organism) consisting of two things, referring to the pairs of cells formed by the type species	The genus is defined by relative evolutionary divergence (RED) and phylogenomic analysis as a monophyletic group. Short oval rods that occur singly, in pairs or in short chains. Gram positive. Nonmotile. Use H <sub>2</sub> + CO <sub>2</sub> as substrates for methanogenesis, might also grow poorly on formate. Grow poorly on mineral medium with vitamins; yeast extract, casamino acids, and rumen fluid strongly stimulate growth. Optimum temperature is 30–37 °C.	<i>Methanobacteriaceae</i>	<i>Methanobinarius arboriphilus</i> <sup>Ts</sup>	<a href="https://seqco.de/i:32442">seqco.de/i:32442</a>

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Species <i>Methanarmilla boviskoreani</i>	[bo.vis.ko.re.a'ni] L. <b>gen. n.</b> <i>bovis</i> , cattle; <b>N.L. masc. adj.</b> <i>koreanus</i> , Korean; <b>N.L. gen. masc. / fem. n.</b> <i>boviskoreani</i> , of Korean cattle	Cells stain Gram-positive, occur singly or in pairs or chains and are rod-shaped (1.5–1.8 µm). Cells are non-motile. The optimum pH and temperature for growth are pH 6.5–7.0 and 37–40 °C. The maximum salt (NaCl) tolerance for growth is 0.5 M (as in Lee et al., 2013). The G+C content of the type genome is 28.9 mol%, and the genome size is 2.04 Mbp.	<i>Methanarmilla</i>	NCBI Assembly: GCF_000320505.1 Ts	<a href="https://seqco.de/i:32441">seqco.de/i:32441</a>
Species <i>Methanocatella thaueri</i>	[thau'er.i] <b>N.L. gen. masc. n.</b> <i>thaueri</i> , of Thauer, named in honor of Rudolf K. Thauer for his fundamental contributions to the delineation of the biochemistry of methanogenesis	Coccobacillus, with slightly tapered ends, about 0.5 µm in width and 0.6–1.2 µm in length, occurring in pairs and short chains. Some chains may have elongated cells. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 36.9 mol%, and the genome size is 2.24 Mbp.	<i>Methanocatella</i>	NCBI Assembly: GCF_003111625.1 Ts	<a href="https://seqco.de/i:32437">seqco.de/i:32437</a>
Species <i>Methanobinarius endosymbioticus</i>	[en.do.sym.bi.o'ti.cus] <b>Gr. pref.</b> <i>endo-</i> , within; <b>N.L. masc. adj.</b> <i>symbioticus</i> , living together; <b>N.L. masc. adj.</b> <i>endosymbioticus</i> , living together within (another organism)	The species identified by metagenomic analyses. The G+C content of the type genome is 25.2 mol%, and the genome size is 1.91 Mbp.	<i>Methanobinarius</i>	NCBI Assembly: GCA_003315655.1 Ts	<a href="https://seqco.de/i:32444">seqco.de/i:32444</a>
Species <i>Methanobaculum cuticulare</i> <sup>Ts</sup>	[cu.ti.cu.la're] <b>N.L. neut. adj.</b> <i>cuticulare</i> , referring to the cuticular surface of the termite hindgut epithelium, which is colonized by this organism	The species description remains the same as in Miller (2015). The G+C content of the type genome is 26.7 mol%, and the genome size is 2.60 Mbp.	<i>Methanobaculum</i>	NCBI Assembly: GCA_001639285.1 Ts	<a href="https://seqco.de/i:32446">seqco.de/i:32446</a>
Species <i>Methanimicrococcus odontotermitis</i>	[o.don.to.ter'mi.tis] <b>N.L. gen. masc. n.</b> <i>odontotermitis</i> , referring to <i>Odontotermes</i> , the host genus	The species identified by metagenomic analyses. The G+C content of the type genome is 43.8%, and the estimated genome size is 1.88 Mbp.	<i>Methanimicrococcus</i>	NCBI Assembly: GCA_031286065.1 Ts	<a href="https://seqco.de/i:32598">seqco.de/i:32598</a>

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Species <i>Methanocatella smithii</i> <sup>Ts</sup>	[smith'i.i] N.L. gen. masc. n. <i>smithii</i> , of Smith, named after P.H. Smith, who isolated the type strain	The species identified by metagenomic analyses. The G+C content of the type genome is 31.0 mol%, and the genome size is 1.85 Mbp. Cells are short oval rods or coccobacilli with tapered ends, 0.6–0.7 µm in width and ~1.0 µm in length. Cells occur most frequently in pairs or in chains of 4–6 cells. Gram positive. Nonmotile. H <sub>2</sub> and CO <sub>2</sub> are the preferred energy sources. Growth on formate is poor. Cells grow optimally at 37 to 39 °C. (as in <a href="#">Balch et al., 1979</a> ; <a href="#">Miller, 2015</a> ).	<i>Methanocatella</i>	NCBI Assembly: GCF_000016525.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32433">seqco.de/i:32433</a>
Species <i>Methanorudis spinitermitis</i> <sup>Ts</sup>	[spi.ni.ter'mi.tis] N.L. gen. masc. n. <i>spinitermitis</i> , of Spinitermes (the host genus)	The species identified by metagenomic analyses. The G+C content of the type genome is 25.8 mol%, and the genome size is 1.96 Mbp.	<i>Methanorudis</i>	NCBI Assembly: GCA_031286225.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32453">seqco.de/i:32453</a>
Species <i>Bathycorpusculum acidaminoxidans</i>	[a.cid.am.in.ox'i.dans] N.L. neut. n. <i>acidum aminum</i> , amino acid; N.L. pres. part. <i>oxydans</i> , to oxidize; N.L. part. adj. <i>acidaminoxidans</i> , amino acid-oxidizing	The species identified by metagenomic analyses. The G+C content of the type genome is 37.9 mol%, and the estimated genome size is 1.99 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009786255.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32516">seqco.de/i:32516</a>
Species <i>Methanocatella oralis</i>	[o.ra'lis] L. fem. adj. <i>oralis</i> , pertaining to the mouth	Cells are short, oval rods with tapered ends, 0.4–0.5 µm in width and 0.7–1.2 µm in length, occurring most frequently in pairs or short chains. Cells give a Gram-positive reaction when less than 4 d old. Ultrathin sections show a tristratified cell wall that is highly invaginated. Nonmotile (as in Miller, 2015). The G+C content of the type genome is 27.7 mol%, and the genome size is 2.14 Mbp.	<i>Methanocatella</i>	NCBI Assembly: GCF_001639275.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32436">seqco.de/i:32436</a>
Species <i>Methanofrustulum fimipullorum</i> <sup>Ts</sup>	[fi.mi.pul.lo'rum] L. neut. n. <i>fimus</i> , dung, excrement; L. masc. n. <i>pullus</i> , chicken; N.L. gen. pl. masc. n. <i>fimipullorum</i> , of chicken dung; denoting the putative origin from chicken manure	The species identified by metagenomic analyses. The G+C content of the type genome is 42.9%, and the estimated genome size is 1.93 Mbp.	<i>Methanofrustulum</i>	NCBI Assembly: GCA_012518265.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32515">seqco.de/i:32515</a>

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Species <i>Methanorbis rubei</i>	[ru'be.i] L. gen. masc. n. <i>rubei</i> , of the red, referring to the color of the host.	Ovoid cocci cells 1–3 µm. Non-motile. H <sub>2</sub> and CO <sub>2</sub> are the substrates for methanogenesis; formate can substitute H <sub>2</sub> . Yeast extract stimulates growth. The optimum temperature is 33 °C. The G+C content of the type genome is 50.2 mol%, and the genome size is 1.82 Mbp.	<i>Methanorbis</i>	NCBI Assembly: GCA_032714495.1 Ts	<a href="https://seqco.de/i:32573">seqco.de/i:32573</a>
Species <i>Methanovirga aequatorialis</i>	[ae.qua.to.ri.a'lis] L. fem. adj. <i>aequatorialis</i> , equatorial, denoting the origin of the host	The species identified by metagenomic analyses. The G+C content of the type genome is 29.3 mol%, and the genome size is 2.05 Mbp.	<i>Methanovirga</i>	NCBI Assembly: GCA_031282205.1 Ts	<a href="https://seqco.de/i:32455">seqco.de/i:32455</a>
Species <i>Bathycorpusculum termitum</i>	[ter'mi.tum] N.L. gen. pl. n. <i>termitum</i> , of termites, referring to the host	The species identified by metagenomic analyses. The G+C content of the type genome is 43.8 mol%, and the estimated genome size is 2.30 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_031254875.1 Ts	<a href="https://seqco.de/i:32524">seqco.de/i:32524</a>
Species <i>Methanoplasma cognatum</i>	[cog.na'tum] L. neut. adj. <i>cognatum</i> , related by blood, sibling, referring to the <i>Methanoplasma termitum</i> as relative	The species identified by metagenomic analyses. The G+C content of the type genome is 52.2%, and the estimated genome size is 1.61 Mbp.	<i>Methanoplasma</i>	NCBI Assembly: GCA_009777615.1 Ts	<a href="https://seqco.de/i:32526">seqco.de/i:32526</a>
Species <i>Methanoplasma glyptotermitis</i>	[gly.pto.ter'mi.tis] N.L. gen. n. <i>glyptotermitis</i> , referring to <i>Glyptotermes</i> , the host genus	The species identified by metagenomic analyses. The G+C content of the type genome is 49.7%, and the estimated genome size is 1.84 Mbp.	<i>Methanoplasma</i>	NCBI Assembly: GCA_031267895.1 Ts	<a href="https://seqco.de/i:32527">seqco.de/i:32527</a>
Species <i>Methanimicrococcus stummii</i>	[stumm'i.i] N.L. gen. masc. n. <i>stummii</i> , of Stumm, named in honor of Claudius K. Stumm for his important contributions on the symbiosis of methanogens with anaerobic protists	Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate and Casamino acids; formate and yeast extract are stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 43.1%, and the estimated genome size is 1.78 Mbp.	<i>Methanimicrococcus</i>	NCBI Assembly: GCA_032594435.1 Ts	<a href="https://seqco.de/i:32599">seqco.de/i:32599</a>

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Species <i>Bathycorpusculum hydrogenotrophicum</i>	[hyd.ro.ge.no.tro.phi'cum] N.L. pref. <i>hydrogeno-</i> , pertaining to hydrogen; Gr. masc. adj. <i>trophikos</i> , pertaining to food; N.L. neut. adj. <i>hydrogenotrophicum</i> , feeding on hydrogen	The species identified by metagenomic analyses. The G+C content of the type genome is 43.2 mol%, and the estimated genome size is 2.24 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009783705.1 Ts	<a href="https://seqco.de/i:32521">seqco.de/i:32521</a>
Species <i>Methanovirga meridionalis</i>	[me.ri.di.o.na'lis] L. fem. adj. <i>meridionalis</i> , southern, denoting the origin of the host from the southern hemisphere (Chile).	The species identified by metagenomic analyses. The G+C content of the type genome is 23.7 mol%, and the genome size is 2.39 Mbp.	<i>Methanovirga</i>	NCBI Assembly: GCA_031289325.1 Ts	<a href="https://seqco.de/i:32458">seqco.de/i:32458</a>
Species <i>Methanovirga procula</i>	[pro.cu'la] L. fem. adj. <i>procula</i> , from far away, denoting the origin from a remote island (Réunion)	The species identified by metagenomic analyses. The G+C content of the type genome is 26.7 mol%, and the genome size is 2.38 Mbp.	<i>Methanovirga</i>	NCBI Assembly: GCA_031280375.1 Ts	<a href="https://seqco.de/i:32459">seqco.de/i:32459</a>
Species <i>Methanofilum arcanum</i> <sup>Ts</sup>	[ar.ca'num] L. neut. adj. <i>arcanum</i> , hidden mysterious	The species identified by metagenomic analyses. The G+C content of the type genome is 29.3 mol%, and the genome size is 2.05 Mbp.	<i>Methanofilum</i>	NCBI Assembly: GCA_031285085.1 Ts	<a href="https://seqco.de/i:32512">seqco.de/i:32512</a>
Species <i>Methanacia filiformis</i> <sup>Ts</sup>	[fi.li.for'mis.] L. neut. n. <i>filum</i> , a thread; L. fem. adj. suff. <i>-formis</i> , like, in the shape of; N.L. fem. adj. <i>filiformis</i> , thread-shaped	Filament-forming rods with slightly tapered ends, 0.23–0.28 µm in width by up to several hundred µm in length. Rarely occurs as single 4-µm-long cells. Nonmotile. strict anaerobe. Catalase positive. Metabolizes H <sub>2</sub> and CO <sub>2</sub> to CH <sub>4</sub> . Optimum temperature is 30 °C (range 10–33.5 °C). Optimum pH is 7.0–7.2 (range 6.0–7.5). Yeast extract (>0.01%) is required for growth (as in <a href="#">Miller, 2015</a> ). The G+C content of the type genome is 26.9 mol%, and the genome size is 2.60 Mbp.	<i>Methanacia</i>	NCBI Assembly: GCF_001639265.1 Ts	<a href="https://seqco.de/i:32451">seqco.de/i:32451</a>



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Species <i>Methanimicrococcus hacksteinii</i>	[hack.stein'i.i.] <b>N.L. gen. masc. n.</b> <i>hacksteinii</i> , of Hackstein, named in honor of Johannes H.P. Hackstein for his important contributions on the hydrogenosomes of anaerobic protists and methanogenesis in arthropod guts	Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 42.9%, and the estimated genome size is 2.04 Mbp.	<i>Methanimicrococcus</i>	NCBI Assembly: GCA_032714515.1 Ts	<a href="https://seqco.de/i:32595">seqco.de/i:32595</a>
Species <i>Methanovirga australis</i>	[aus.tra'lis] <b>L. fem. adj.</b> <i>australis</i> , southern, denoting the origin of the host from the southern hemisphere (Australia)	The species identified by metagenomic analyses. The G+C content of the type genome is 26.8 mol%, and the genome size is 2.50 Mbp.	<i>Methanovirga</i>	NCBI Assembly: GCA_031272765.1 Ts	<a href="https://seqco.de/i:32456">seqco.de/i:32456</a>
Species <i>Methanorbis furvi</i> <sup>Ts</sup>	[fur'vi] <b>L. gen. masc. n.</b> <i>furvi</i> , of the black one, referring to the color of the host.	Ovoid cocci cells 1–3 µm. Non-motile. H <sub>2</sub> and CO <sub>2</sub> are the substrates for methanogenesis; formate can substitute H <sub>2</sub> . Acetate and formate are required for growth. The optimum temperature is 33 °C. The G+C content of the type genome is 50.1 mol%, and the genome size is 1.84 Mbp.	<i>Methanorbis</i>	NCBI Assembly: GCA_032714615.1 Ts	<a href="https://seqco.de/i:32572">seqco.de/i:32572</a>
Species <i>Methanoplasma poroterminis</i>	[po.ro.ter'mi.tis] <b>N.L. gen. n.</b> <i>poroterminis</i> , referring to Porotermes, the host genus	The species identified by metagenomic analyses. The G+C content of the type genome is 57.3%, and the estimated genome size is 1.69 Mbp.	<i>Methanoplasma</i>	NCBI Assembly: GCA_031290095.1 Ts	<a href="https://seqco.de/i:32528">seqco.de/i:32528</a>
Species <i>Bathycorpusculum terrae</i>	[ter'rae] <b>L. gen. n.</b> <i>terrae</i> , of the earth	The species identified by metagenomic analyses. The G+C content of the type genome is 38.1 mol%, and the estimated genome size is 1.27 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009784175.1 Ts	<a href="https://seqco.de/i:32523">seqco.de/i:32523</a>
Species <i>Methanomicula labioterminis</i> <sup>Ts</sup>	[la.bi.o.ter'mi.tis] <b>N.L. gen. n.</b> <i>labioterminis</i> , of or pertaining to Labiotermes, the genus name of the host	The species identified by metagenomic analyses. The G+C content of the type genome is 49.7%, and the estimated genome size is 1.44 Mbp.	<i>Methanomicula</i>	NCBI Assembly: GCA_009780575.1 Ts	<a href="https://seqco.de/i:32530">seqco.de/i:32530</a>
Species <i>Methanovirga basaliitermitum</i> <sup>Ts</sup>	[ba.sa.li.ter'mi.tum] <b>L. adj.</b> <i>basalis</i> , basal; <b>L. masc. n.</b> <i>termes</i> , a woodworm, a termite; <b>N.L. gen. pl. masc. n.</b> <i>basaliitermitum</i> , of lower (basal) termites	The species identified by metagenomic analyses. The G+C content of the type genome is 27.8 mol%, and the genome size is 2.18 Mbp.	<i>Methanovirga</i>	NCBI Assembly: GCA_031284445.1 Ts	<a href="https://seqco.de/i:32457">seqco.de/i:32457</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Methanimicrococcus hongohii</i>	[hon.goh'i.i.] N.L. gen. masc. n. <i>hongohii</i> , of Hongoh, named after Yuichi Hongoh in recognition of his important contributions to arthropod gut microbiology	Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate and Casamino acids; formate is stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 41.0%, and the genome size is 2.13 Mbp.	<i>Methanimicrococcus</i>	NCBI Assembly: GCA_032594095.1 Ts	<a href="https://seqco.de/i:32596">seqco.de/i:32596</a>
Species <i>Bathycorpusculum fermentans</i>	[fer.men'tans] L. part. adj. <i>fermentans</i> , fermenting	The species identified by metagenomic analyses. The G+C content of the type genome is 37.8 mol%, and the estimated genome size is 1.86 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009787175.1 Ts	<a href="https://seqco.de/i:32520">seqco.de/i:32520</a>
Species <i>Methanolapillus ohkumae</i>	[oh.ku'mae] N.L. gen. masc. n. <i>ohkumae</i> , of Ohkuma, named after Moriya Ohkuma in recognition of his important contributions to arthropod gut microbiology	Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, formate, and coenzyme M; yeast extract is stimulatory. The optimum temperature is 37 °C. The G+C content of the type genome is 41.0%, and the estimated genome size is 1.84 Mbp.	<i>Methanolapillus</i>	NCBI Assembly: GCA_032594355.1 Ts	<a href="https://seqco.de/i:32603">seqco.de/i:32603</a>
Species <i>Methanocatella millerae</i>	[mil'ler.ae] N.L. gen. fem. n. <i>millerae</i> , of Miller, named after Terry L. Miller for her contributions to the taxonomy of methanogens, in particular the genus <i>Methanobrevibacter</i>	Cells occur singly or in pairs or chains and are coccobacilli (0.5–1.2 µm) with rounded ends. Cells stain Gram-positive, are non-motile and are resistant to lysis by 10% SDS. Grows and produces methane from H <sub>2</sub> /CO <sub>2</sub> and from formate plus CO <sub>2</sub> . The optimum temperature range for growth is 36–42 °C. pH range for growth is 5.5–10.0; optimum pH is 7.0–8.0. The maximum salt tolerance for growth is 2.6 % (as in <a href="#">Rea et al., 2007</a> ). The G+C content of the type genome is 36.5 mol%, and the genome size is 2.72 Mbp.	<i>Methanocatella</i>	NCBI Assembly: GCF_900103415.1 Ts	<a href="https://seqco.de/i:32435">seqco.de/i:32435</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Methanocatella</i> <i>woesei</i>	[woe'se.i] N.L. gen. masc. n. <i>woesei</i> , of Woese, named in honor of Carl R. Woese for his pioneering contributions to the understanding of the phylogeny of methanogens and other microorganisms	Coccobacillus with slightly tapered or rounded ends, about 0.6 µm in width and 1.0 µm in length, occurring in pairs or short chains. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in <a href="#">Miller, Lin, 2002</a> ). The G+C content of the type genome is 29.9 mol%, and the genome size is 1.54 Mbp.	<i>Methanocatella</i>	NCBI Assembly: GCF_003111605.1 Ts	<a href="https://seqco.de/i:32438">seqco.de/i:32438</a>
Species <i>Methanobinarius</i> <i>arboriphilus</i> <sup>Ts</sup>	[ar.bo.ri'phi.lus] L. fem. n. <i>arboris</i> , tree; N.L. masc. adj. <i>philus</i> , friend, loving; N.L. masc. adj. <i>arboriphilus</i> , tree-loving	Cells are short rods with rounded ends, 0.5 µm in width and 1.2–1.4 µm in length. Some cells may have a slightly truncated end. They occur singly or in pairs. Growth is stimulated by trypticase peptones, yeast extract, and rumen fluid. H <sub>2</sub> and CO <sub>2</sub> may be the sole or preferred energy sources. The optimal temperature for growth was 30 to 37 °C. (as in Zeikus and Henning, 1975; Miller, 2015). The G+C content of the type genome is 25.4 mol%, and the genome size is 2.44 Mbp.	<i>Methanobinarius</i>	NCBI Assembly: GCF_002072215.1 Ts	<a href="https://seqco.de/i:32443">seqco.de/i:32443</a>
Species <i>Methanoflexus</i> <i>mossambicus</i>	[mos.sam.bi'cus] N.L. masc. adj. <i>mossambicus</i> , of Mozambique	The species identified by metagenomic analyses. The G+C content of the type genome is 24.0 mol%, and the genome size is 3.25 Mbp.	<i>Methanoflexus</i>	NCBI Assembly: GCA_031261915.1 Ts	<a href="https://seqco.de/i:32449">seqco.de/i:32449</a>
Species <i>Methanarmilla</i> <i>wolinii</i> <sup>Ts</sup>	[wo.lin'i.i.] N.L. gen. masc. n. <i>wolinii</i> , of Wolin, named in honor of Meyer J. Wolin for his singular contributions to the physiological understanding of the role of methanogens and interspecies hydrogen transfer in anaerobic habitats	Coccobacillus with slightly tapered or rounded ends, about 0.6 µm in width and 1.0–1.4 µm in length, occurring in pairs or short chains. Gram-positive. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in <a href="#">Miller, Lin, 2002</a> ). The G+C content of the type genome is 24.2 mol%, and the genome size is 2.04 Mbp.	<i>Methanarmilla</i>	NCBI Assembly: GCF_000621965.1 Ts	<a href="https://seqco.de/i:32440">seqco.de/i:32440</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Methanolapillus millepedarum</i> <sup>Ts</sup>	[mil.le.pe.da'rum] L. gen. pl. n. <i>millepedarum</i> , of millipedes	Irregular cocci cells 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. ). Requires acetate, yeast extract, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 42.9%, and the estimated genome size is 1.93 Mbp.	<i>Methanolapillus</i>	NCBI Assembly: GCA_032594115.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32600">seqco.de/i:32600</a>
Species <i>Methanolapillus africanus</i>	[a.fri.ca'nus] L. masc. adj. <i>africanus</i> , pertaining to Africa	Irregular cocci cells, 1–2 µm in diameter, non-motile. Use methanol and methylamines as methanogenesis substrates together with hydrogen. Requires acetate, yeast extract, Casamino acids, and coenzyme M. The optimum temperature is 37 °C. The G+C content of the type genome is 44.4%, and the estimated genome size is 2.10 Mbp.	<i>Methanolapillus</i>	NCBI Assembly: GCA_032714475.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32602">seqco.de/i:32602</a>
Species <i>Methanoflexus curvatus</i> <sup>Ts</sup>	[cur.va'tus] L. masc. adj. <i>curvatus</i> , bent, curved; referring to the shape of the cell	Curved rods with slightly tapered ends, 0.34 by 1.6 µm in size, occurring singly or in pairs. Nonmotile. Metabolizes H <sub>2</sub> and CO <sub>2</sub> , yielding CH <sub>4</sub> as the sole product. Optimum temperature is 30 °C (range 10–30 °C). Optimum pH is 7.1–7.2 (range 6.5–8.5). Complex nutritional supplements, e.g., 40% (v/v) clarified rumen fluid and nutrient broth (Difco) are required for growth ( as in Miller, 2015). The G+C content of the type genome is 25.7 mol%, and the genome size is 2.41 Mbp.	<i>Methanoflexus</i>	NCBI Assembly: GCF_001639295.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32448">seqco.de/i:32448</a>
Species <i>Methanocatella gottschalkii</i>	[gott.schalk'i.i] N.L. gen. masc. n. <i>gottschalkii</i> , of Gottschalk, named in honor of Gerhard Gottschalk for his notable contributions to the understanding of the biochemistry of methanogenesis	Coccobacillus with rounded ends, about 0.7 µm in width and 0.9 µm in length, occurring in pairs or short chains. Gram-positive reaction. Cell walls are composed of pseudomurein. Cells are resistant to lysis by SDS. Optimum temperature 37 °C. Optimum pH 7 (as in Miller, Lin, 2002). The G+C content of the type genome is 30.0 mol%, and the genome size is 1.87 Mbp.	<i>Methanocatella</i>	NCBI Assembly: GCF_003814835.1 <sup>Ts</sup>	<a href="https://seqco.de/i:32434">seqco.de/i:32434</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Methanimicrococcus labiotermitis</i>	[la.bi.o.ter'mi.tis] N.L. gen. n. <i>labiotermitis</i> , referring to Labiotermes, the host genus	The species identified by metagenomic analyses. The G+C content of the type genome is 45.5%, and the estimated genome size is 1.83 Mbp.	<i>Methanimicrococcus</i>	NCBI Assembly: GCA_009784005.1 Ts	<a href="https://seqco.de/i:32597">seqco.de/i:32597</a>
Species <i>Bathycorpusculum acetigenes</i> <sup>Ts</sup>	[a.ce.ti'ge.nes] L. neut. n. <i>acetum</i> , vinegar; Gr. suff. <i>-genes</i> , to produce; N.L. part. adj. <i>acetigenes</i> , vinegar- or acetic acid producing	The species identified by metagenomic analyses. The G+C content of the type genome is 43.4mol%, and the estimated genome size is 2.15Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009781675.1 Ts	<a href="https://seqco.de/i:32519">seqco.de/i:32519</a>
Species <i>Bathycorpusculum grumuli</i>	[gru'mu.li] L. gen. n. <i>grumuli</i> , of a little hill	The species identified by metagenomic analyses. The G+C content of the type genome is 35.5 mol%, and the estimated genome size is 2.30 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_009776805.1 Ts	<a href="https://seqco.de/i:32525">seqco.de/i:32525</a>
Species <i>Methanoplasma reticulitermitis</i>	[re.ti.cu.li.ter'mi.tis] N.L. gen. n. <i>reticulitermitis</i> , referring to Reticulitermes, the host genus	The species identified by metagenomic analyses. The G+C content of the type genome is 53.4%, and the estimated genome size is 1.34 Mbp.	<i>Methanoplasma</i>	NCBI Assembly: GCA_031287135.1 Ts	<a href="https://seqco.de/i:32529">seqco.de/i:32529</a>
Species <i>Methanorbis basalitermitum</i>	[ba.sa.li.ter'mi.tum] L. adj. <i>basalis</i> , basal; L. masc. n. <i>termes</i> , a woodworm, a termite; N.L. gen. pl. masc. n. <i>basalitermitum</i> , of lower (basal) termites	The species identified by metagenomic analyses. The G+C content of the type genome is 50.9 mol%, and the genome size is 1.27 Mbp.	<i>Methanorbis</i>	NCBI Assembly: GCA_031287415.1 Ts	<a href="https://seqco.de/i:32538">seqco.de/i:32538</a>
Species <i>Bathycorpusculum soli</i>	[so'li] L. gen. n. <i>soli</i> , of soil	The species identified by metagenomic analyses. The G+C content of the type genome is 37.5 mol%, and the estimated genome size is 1.88 Mbp.	<i>Bathycorpusculum</i>	NCBI Assembly: GCA_031277345.1 Ts	<a href="https://seqco.de/i:32522">seqco.de/i:32522</a>