

# Atabeyarchaeia classis nov.

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

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Class <i>Atabeyarchaeia</i>	[A.ta.be.y.ar.chae'i.a] N.L. <b>neut. n.</b> <i>Atabeyarchaeum</i> , referring to the type genus <i>Atabeyarchaeum</i> ; <i>-ia</i> , ending to denote a class; <b>N.L. neut. pl. n.</b> <i>Atabeyarchaeia</i> , the <i>Atabeyarchaeum</i> class	Based on protein content and compositional features, we infer that <i>Atabeyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H <sub>2</sub> as an electron donor. Phylogenetic analyses using several sets of marker genes placed two complete genomes in a monophyletic group within the Asgard clade as a sister group to <i>Freyarchaeia</i> . We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only 40–45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Atabeyarchaeum</i> as the type genus for the family <i>Atabeyarchaeaceae</i> , the order <i>Atabeyarchaeales</i> , the class <i>Atabeyarchaeia</i> with the <i>Asgardarchaeota</i> phylum.	<i>Asgardarchaeota</i>	<i>Atabeyarchaeum</i>	<a href="https://seqco.de/i:33330">seqco.de/i:33330</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Class <i>Freyarchaeia</i>	[Fre.y.ar.chae'i.a] <b>N.L. neut. n.</b> <i>Freyarchaeum</i> , referring to the type genus <i>Freyarchaeum</i> ; - <i>ia</i> , ending to denote a class; <b>N.L. neut. pl. n.</b> <i>Freyarchaeia</i> , the <i>Freyarchaeum</i> class	<p>The type species for this taxonomic group were initially reconstructed by manual curation of Illumina short-read assemblies and then validated using both Nanopore and PacBio long reads. Phylogenetic analyses of this fully curated genome using several sets of marker genes placed the complete genomes in a monophyletic group within the Asgard clade as a sister group to Atabeyarchaeia. We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only &lt;45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Freyarchaeum</i> as the type genus for the family <i>Freyarchaeaceae</i>, the order <i>Freyarchaeales</i>, the class <i>Freyarchaeia</i> with the <i>Asgardarchaeota</i> phylum. Based on protein content and compositional features, we infer that <i>Freyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H<sub>2</sub> as an electron donor. This lineage was originally reconstructed and named from Guaymas Basin, located in the Gulf of California, México, and from Jinze Hot Spring (Yunnan, China). Subsequently, another group used the original data to recover similar genomes and referred to them as <i>Jordarchaeia</i>. Here, we retain the original nomenclature.</p>	<i>Asgardarchaeota</i>	<i>Freyarchaeum</i>	<a href="https://seqco.de/i:48235">seqco.de/i:48235</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Freyarchaeales</i>	[Fre.y.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Freyarchaeum</i> , referring to the type genus <i>Freyarchaeum</i> ; -ales, ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Freyarchaeales</i> , the <i>Freyarchaeum</i> order	<p>The type species for this taxonomic group were initially reconstructed by manual curation of Illumina short-read assemblies and then validated using both Nanopore and PacBio long reads. Phylogenetic analyses of this fully curated genome using several sets of marker genes placed the complete genomes in a monophyletic group within the Asgard clade as a sister group to Atabeyarchaeia. We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only &lt;45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Freyarchaeum</i> as the type genus for the family <i>Freyarchaeaceae</i>, the order <i>Freyarchaeales</i>, the class <i>Freyarchaeia</i> with the <i>Asgardarchaeota</i> phylum. Based on protein content and compositional features, we infer that <i>Freyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H<sub>2</sub> as an electron donor. This lineage was originally reconstructed and named from Guaymas Basin, located in the Gulf of California, México, and from Jinze Hot Spring (Yunnan, China). Subsequently, another group used the original data to recover similar genomes and referred to them as <i>Jordarchaeia</i>. Here, we retain the original nomenclature.</p>	<i>Freyarchaeia</i>	<i>Freyarchaeum</i>	<a href="https://seqco.de/i:48236">seqco.de/i:48236</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Atabeyarchaeales</i>	[A.ta.be.y.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Atabeyarchaeum</i> , referring to the type genus <i>Atabeyarchaeum</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Atabeyarchaeales</i> , the <i>Atabeyarchaeum</i> order	<p>Based on protein content and compositional features, we infer that <i>Atabeyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H<sub>2</sub> as an electron donor. Phylogenetic analyses using several sets of marker genes placed two complete genomes in a monophyletic group within the Asgard clade as a sister group to <i>Freyarchaeia</i>. We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only 40–45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Atabeyarchaeum</i> as the type genus for the family <i>Atabeyarchaeaceae</i>, the order <i>Atabeyarchaeales</i>, the class <i>Atabeyarchaeia</i> with the <i>Asgardarchaeota</i> phylum.</p>	<i>Atabeyarchaeia</i>	<i>Atabeyarchaeum</i>	<a href="https://seqco.de/i:48234">seqco.de/i:48234</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Freyarchaeaceae</i>	[Fre.y.ar.chae.a'ce.ae] <b>N.L. neut. n.</b> <i>Freyarchaeum</i> , referring to the type genus <i>Freyarchaeum</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Freyarchaeaceae</i> , the <i>Freyarchaeum</i> family	<p>The type species for this taxonomic group were initially reconstructed by manual curation of Illumina short-read assemblies and then validated using both Nanopore and PacBio long reads. Phylogenetic analyses of this fully curated genome using several sets of marker genes placed the complete genomes in a monophyletic group within the Asgard clade as a sister group to Atabeyarchaeia. We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only &lt;45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Freyarchaeum</i> as the type genus for the family <i>Freyarchaeaceae</i>, the order <i>Freyarchaeales</i>, the class <i>Freyarchaeia</i> with the <i>Asgardarchaeota</i> phylum. Based on protein content and compositional features, we infer that <i>Freyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H<sub>2</sub> as an electron donor. This lineage was originally reconstructed and named from Guaymas Basin, located in the Gulf of California, México, and from Jinze Hot Spring (Yunnan, China). Subsequently, another group used the original data to recover similar genomes and referred to them as <i>Jordarchaeia</i>. Here, we retain the original nomenclature.</p>	<i>Freyarchaeales</i>	<i>Freyarchaeum</i>	<a href="https://seqco.de/i:48237">seqco.de/i:48237</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Atabeyarchaeaceae</i>	[A.ta.be.y.ar.chae.a'ce.ae] <b>N.L. neut. n.</b> <i>Atabeyarchaeum</i> , referring to the type genus <i>Atabeyarchaeum</i> ; -aceae, ending to denote a family; <b>N.L.</b> <b>fem. pl. n.</b> <i>Atabeyarchaeaceae</i> , the <i>Atabeyarchaeum</i> family	Based on protein content and compositional features, we infer that <i>Atabeyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H <sub>2</sub> as an electron donor. Phylogenetic analyses using several sets of marker genes placed two complete genomes in a monophyletic group within the Asgard clade as a sister group to <i>Freyarchaeia</i> . We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only 40–45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Atabeyarchaeum</i> as the type genus for the family <i>Atabeyarchaeaceae</i> , the order <i>Atabeyarchaeales</i> , the class <i>Atabeyarchaeia</i> with the <i>Asgardarchaeota</i> phylum.	<i>Atabeyarchaeales</i>	<i>Atabeyarchaeum</i>	<a href="https://seqco.de/i:48233">seqco.de/i:48233</a>
Genus <i>Atabeyarchaeum</i>	[A.ta.be.y.ar.chae'um] <b>N.L. fem. n.</b> <i>Atabey</i> , the Mother Goddess in Taíno mythology; <b>N.L.</b> <b>neut. n.</b> <i>archaeum</i> , ancient, an archaeon from Gr. adj. <i>archaios</i> ; <b>N.L. neut. n.</b> <i>Atabeyarchaeum</i> , named for <i>Atabey</i> , the Mother Goddess in Taíno Puerto Rican mythology	ased on protein content and compositional features, we infer that <i>Atabeyarchaeia</i> is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H <sub>2</sub> as an electron donor. Phylogenetic analyses using several sets of marker genes placed two complete genomes in a monophyletic group within the Asgard clade as a sister group to <i>Freyarchaeia</i> . We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only 40–45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose <i>Atabeyarchaeum</i> as the type genus for the family <i>Atabeyarchaeaceae</i> , the order <i>Atabeyarchaeales</i> , the class <i>Atabeyarchaeia</i> with the <i>Asgardarchaeota</i> phylum.	<i>Atabeyarchaeaceae</i>	<i>Atabeyarchaeum</i> <i>deiterra</i> <sup>T5</sup>	<a href="https://seqco.de/i:48232">seqco.de/i:48232</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Freyarchaeum</i>	[Fre.y.ar.chae'um] <b>N.L. fem. n.</b> <i>Freya</i> , the Norse Goddess most commonly associated with love and fertility; <b>N.L. neut. n.</b> <i>archaeum</i> , ancient, archaeon; <b>N.L. neut. n.</b> <i>Freyarchaeum</i> , an archaeal genus named for Freya, the Norse Goddess most commonly associated with love and fertility	The type species for this taxonomic group were initially reconstructed by manual curation of Illumina short-read assemblies and then validated using both Nanopore and PacBio long reads. Phylogenetic analyses of this fully curated genome using several sets of marker genes placed the complete genomes in a monophyletic group within the Asgard clade as a sister group to Atabeyarchaeia. We performed phylogenetic analyses using concatenated marker sets of 47 archaeal clusters of orthologous genes (arCOGs) and 15 ribosomal protein (RP15) gene cluster, as well as the 16S rRNA gene. The new genomes share only <45% AAI when compared to other Asgard genomes, consistent with their assignment to a new phylum. Although our analyses provide evidence for distinction at the phylum level, we chose to adhere to the Genome Taxonomy Database (GTDB) for standardized microbial genome nomenclature. We establish a robust classification and propose Freyarchaeum as the type genus for the family Freyarchaeaceae, the order Freyarchaeales, the class Freyarchaeia with the Asgardarchaeota phylum. Based on protein content and compositional features, we infer that Freyarchaeia is a non-methanogenic acetogenic chemoheterotroph, with potential to grow lithoautotrophically by using H <sub>2</sub> as an electron donor. This lineage was originally reconstructed and named from Guaymas Basin, located in the Gulf of California, México, and from Jinze Hot Spring (Yunnan, China). Subsequently, another group used the original data to recover similar genomes and referred to them as Jordarchaeia. Here, we retain the original nomenclature.	<i>Freyarchaeaceae</i>	<i>Freyarchaeum deiterra</i> <sup>Ts</sup>	<a href="https://seqco.de/i:48239">seqco.de/i:48239</a>
Species <i>Atabeyarchaeum deiterra</i> <sup>Ts</sup>	[de.i.ter'rae] <b>L. fem. n.</b> <i>dea</i> , deity; <b>L. fem. n.</b> <i>terra</i> , of the earth; <b>N.L. gen. n.</b> <i>deiterra</i> , of an Earth diety	<i>Atabeyarchaeum deiterra</i> has a genome size of about 2.81 Mbp with an average GC% of 49.6%, recovered from California soil. Atabeyarchaeum 16S shares less than 75% similarity with previously described Asgardarchaeota classes. <i>A. deiterra</i> is an acetogenic chemoheterotroph like other Asgardarchaeota, including Freyarchaeia. Estimated completeness at 97.2%, contamination at 1.87%, and the presence of 16 S rRNA genes (1529 bp) and 40 tRNAs.	<i>Atabeyarchaeum</i>	NCBI Assembly: GCA_037310415.1 <sup>Ts</sup>	<a href="https://seqco.de/i:48231">seqco.de/i:48231</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Freyarchaeum</i> <i>deiterra</i> <sup>Ts</sup>	[de.i.ter'rae] L. fem. n. <i>dea</i> , deity; L. fem. n. <i>terra</i> , of the earth; N.L. <b>gen. n.</b> <i>deiterra</i> , of an Earth diety	<i>Freyarchaeum deiterra</i> has a genome size of about 3.58 Mbp with an average GC% of 40.7%, recovered from California soil. <i>Freyarchaeum</i> 16S shares less than 45% similarity with previously described Asgardarchaeota classes. <i>F. deiterra</i> is an acetogenic chemoheterotroph like other Asgardarchaeota, including other soil-associated Atabayarchaeia. Estimated completeness at 98.13%, contamination at 4.21%, and the presence of 16 S rRNA genes (1264 bp) and 38 tRNAs.	<i>Freyarchaeum</i>	NCBI Assembly: GCA_037305845.1 <sup>Ts</sup>	<a href="https://seqco.de/i:48238">seqco.de/i:48238</a>