

# Atabeyarchaeia classis nov.

Submitted by Valentin-Alvarado, Luis

## Abstract

Atabeyarchaeia and Freyarchaeia represent two distinct lineages within the Asgard superphylum, expanding our understanding of archaeal diversity and metabolic capabilities. Genomic analyses reveal that Atabeyarchaeia are likely non-methanogenic acetogenic chemoheterotrophs with potential for lithoautotrophic growth using H<sub>2</sub> as an electron donor. They possess pathways for degrading amino acids and other carbon compounds, including the ability to metabolize C<sub>1</sub>, C<sub>3</sub>, and C<sub>5</sub> compounds, which is uncommon among Asgard archaea. Freyarchaeia, originally described as a separate lineage, shares some metabolic features with Atabeyarchaeia but exhibits distinct characteristics. Both groups are positioned within the Asgard clade, with phylogenetic analyses using multiple marker gene sets (including 47 archaeal clusters of orthologous genes, 15 ribosomal protein genes, and the 16S rRNA gene) consistently placing Atabeyarchaeia as a sister group to Freyarchaeia. Despite sharing only 40-45% average amino acid identity with other Asgard genomes, both lineages are classified within the Asgardarchaeota phylum, adhering to the Genome Taxonomy Database (GTDB) standards. The proposed classification establishes Atabeyarchaeum as the type genus for the family Atabeyarchaeaceae, order Atabeyarchaeales, and class Atabeyarchaeia, while maintaining Freyarchaeia as a distinct lineage within the same phylum. This research highlights the metabolic diversity within the Asgard superphylum and provides insights into the potential roles of these archaea in carbon cycling and their interactions with other microbial communities in various ecosystems.

## Class *Freyarchaeia*

### Etymology

[Fre.y.ar.chae'i.a] N.L. neut. n. *Freyarchaeum*, referring to the type genus Freyarchaeum; *-ia*, ending to denote a class; N.L. neut. pl. n. *Freyarchaeia*, the Freyarchaeum class

### Nomenclatural type

Genus *Freyarchaeum*

### Description

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.

### Classification

*Archaea* » *Asgardarchaeota* » *Freyarchaeia*

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:48235>

## Class *Atabeyarchaeia*

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**Etymology**

[A.ta.be.y.ar.chae'i.a] **N.L. neut. n.** *Atabeyarchaeum*, referring to the type genus *Atabeyarchaeum*; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Atabeyarchaeia*, the *Atabeyarchaeum* class

**Nomenclatural type**

Genus *Atabeyarchaeum*

**Description**

Based on protein content and compositional features, we infer that *Atabeyarchaeia* 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 *Freyarchaeia*. 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 *Atabeyarchaeum* as the type genus for the family *Atabeyarchaeaceae*, the order *Atabeyarchaeales*, the class *Atabeyarchaeia* with the *Asgardarchaeota* phylum.

**Classification**

*Archaea* » *Asgardarchaeota* » *Atabeyarchaeia*

**References**

Effective publication: Valentin-Alvarado et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:33330>

## Order *Freyarchaeales*

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**Etymology**

[Fre.y.ar.chae.a'les] **N.L. neut. n.** *Freyarchaeum*, referring to the type genus *Freyarchaeum*; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Freyarchaeales*, the *Freyarchaeum* order

**Nomenclatural type**

Genus *Freyarchaeum*

### Description

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.

### Classification

*Archaea* » *Asgardarchaeota* » *Freyarchaeia* » *Freyarchaeales*

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

### Registry URL

<https://seqco.de/i:48236>

## Order *Atabeyarchaeales*

### Etymology

[A.ta.be.y.ar.chae.a'les] **N.L. neut. n.** *Atabeyarchaeum*, referring to the type genus Atabeyarchaeum; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Atabeyarchaeales*, the Atabeyarchaeum order

### Nomenclatural type

Genus *Atabeyarchaeum*

### Description

Based on protein content and compositional features, we infer that Atabeyarchaeia 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 Freyarchaeia. 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 Atabeyarchaeum as the type genus for the family Atabeyarchaeaceae, the order Atabeyarchaeales, the class Atabeyarchaeia with the Asgardarchaeota phylum.

### Classification

*Archaea* » *Asgardarchaeota* » *Atabeyarchaeia* » *Atabeyarchaeales*

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

### Registry URL

<https://seqco.de/i:48234>

## Family *Freyarchaeaceae*

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### Etymology

[Fre.y.ar.chae.a'ce.ae] N.L. neut. n. *Freyarchaeum*, referring to the type genus *Freyarchaeum*; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Freyarchaeaceae*, the *Freyarchaeum* family

### Nomenclatural type

Genus *Freyarchaeum*

### Description

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.

### Classification

*Archaea* » *Asgardarchaeota* » *Freyarchaeia* » *Freyarchaeales* » *Freyarchaeaceae*

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

### Registry URL

<https://seqco.de/i:48237>

## Family *Atabeyarchaeaceae*

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### Etymology

[A.ta.be.y.ar.chae.a'ce.ae] N.L. neut. n. *Atabeyarchaeum*, referring to the type genus *Atabeyarchaeum*; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Atabeyarchaeaceae*, the *Atabeyarchaeum* family

### Nomenclatural type

Genus *Atabeyarchaeum*

### Description

Based on protein content and compositional features, we infer that *Atabeyarchaeia* 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 *Freyarchaeia*. 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 *Atabeyarchaeum* as the type genus for the family *Atabeyarchaeaceae*, the order *Atabeyarchaeales*, the class *Atabeyarchaeia* with the *Asgardarchaeota* phylum.

**Classification**

*Archaea* » *Asgardarchaeota* » *Atabeyarchaeia* » *Atabeyarchaeales* » *Atabeyarchaeaceae*

**References**

Effective publication: Valentin-Alvarado et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:48233>

## Genus *Freyarchaeum*

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**Etymology**

[Fre.y.ar.chae'um] **N.L. fem. n.** *Freya*, the Norse Goddess most commonly associated with love and fertility; **N.L. neut. n.** *archaeum*, ancient, archaeon; **N.L. neut. n.** *Freyarchaeum*, an archaeal genus named for Freya, the Norse Goddess most commonly associated with love and fertility

**Nomenclatural type**

Species *Freyarchaeum deiterra*<sup>TS</sup>

**Description**

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.

**Classification**

*Archaea* » *Asgardarchaeota* » *Freyarchaeia* » *Freyarchaeales* » *Freyarchaeaceae* » *Freyarchaeum*

**References**

Effective publication: Valentin-Alvarado et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:48239>

## Genus *Atabeyarchaeum*

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**Etymology**

[A.ta.be.y.ar.chae'um] **N.L. fem. n.** *Atabey*, the Mother Goddess in Taíno mythology; **N.L. neut. n.** *archaeum*, ancient, an archaeon from Gr. adj. *archaios*; **N.L. neut. n.** *Atabeyarchaeum*, named for Atabey, the Mother Goddess in Taíno Puerto Rican mythology

**Nomenclatural type**

Species *Atabeyarchaeum deiterra*<sup>TS</sup>

### Description

ased on protein content and compositional features, we infer that Atabeyarchaeia 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 Freyarchaeia. 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 Atabeyarchaeum as the type genus for the family Atabeyarchaeaceae, the order Atabeyarchaeales, the class Atabeyarchaeia with the Asgardarchaeota phylum.

### Classification

*Archaea* » *Asgardarchaeota* » *Atabeyarchaeia* » *Atabeyarchaeales* » *Atabeyarchaeaceae* » *Atabeyarchaeum*

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

### Registry URL

<https://seqco.de/i:48232>

## Species *Atabeyarchaeum deiterra*<sup>Ts</sup>

### Etymology

[de.i.ter'rae] L. fem. n. *dea*, deity; L. fem. n. *terra*, of the earth; N.L. gen. n. *deiterra*, of an Earth diety

### Nomenclatural type

[NCBI Assembly: GCA\\_037310415.1](#)<sup>Ts</sup>

### Description

*Atabeyarchaeum deiterra* 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. *A. deiterra* 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.

### Classification

*Archaea* » *Asgardarchaeota* » *Atabeyarchaeia* » *Atabeyarchaeales* » *Atabeyarchaeaceae* » *Atabeyarchaeum* » *Atabeyarchaeum deiterra*<sup>Ts</sup>

### References

Effective publication: Valentin-Alvarado et al., 2024 [1]

### Registry URL

<https://seqco.de/i:48231>

## Species *Freyarchaeum deiterra*<sup>Ts</sup>

### Etymology

[de.i.ter'rae] L. fem. n. *dea*, deity; L. fem. n. *terra*, of the earth; N.L. gen. n. *deiterra*, of an Earth diety

### Nomenclatural type

[NCBI Assembly: GCA\\_037305845.1](#)<sup>Ts</sup>

**Description**

*Freyarchaeum deiteterre* has a genome size of about 3.58 Mbp with an average GC% of 40.7%, recovered from California soil. *Freyarchaeum* 16S shares less than 45% similarity with previously described Asgardarchaeota classes. *F. deiteterre* 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.

**Classification**

Archaea » Asgardarchaeota » Freyarchaeia » Freyarchaeales » Freyarchaeaceae » Freyarchaeum » Freyarchaeum deiterra<sup>ts</sup>

**References**

Effective publication: Valentin-Alvarado et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:48238>

**References**

1. Valentin-Alvarado et al. (2024). Asgard archaea modulate potential methanogenesis substrates in wetland soil. *Nature Communications*. DOI:10.1038/s41467-024-49872-z

**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:igzul8qd](https://seqco.de/r:igzul8qd) submitted by **Valentin-Alvarado, Luis** and including 10 new names has been successfully validated.

Date of Priority: 2024-08-08 08:13 UTC  
DOI: 10.57973/seqcode.r:igzul8qd

