Register list for Ryujinia shimokita gen. nov. sp. nov. and their lineage

Submitted by Rinke, Chris

Phylum *Ryujiniota*

Etymology
[Ry.u.ji.ni.o'ta] **N.L. fem. n.** *Ryujinia*, referring to the type genus Ryujinia; *-ota*, ending to denote a phylum; **N.L. neut. pl. n.** *Ryujiniota*, the Ryujinia phylum

Nomenclatural type
Genus *Ryujinia*

Description
Ryujiniota phyl. nov. has a global distribution and was mainly present in public shotgun metagenome datasets labelled as marine sediment metagenome, peat metagenome, sediment metagenome, soil metagenome and groundwater metagenome. The highest relative abundances of Ryujiniota were found in Costa Rica margin subsurface and east pacific subsurface metagenomes with 15.75% and 15.33%, respectively.

Classification
Bacteria » *Ryujiniota*

References
Effective publication: Sun et al., 2025 [1]
Assigned taxonomically: Sun et al., 2025 [1]

Registry URL
https://seqco.de/i:49691

Class *Ryujiniia*

Etymology
[Ry.u.ji.ni'i.a] **N.L. fem. n.** *Ryujinia*, referring to the type genus Ryujinia; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Ryujiniia*, the Ryujinia class

Nomenclatural type
Genus *Ryujinia*

Description
The description is the same as for the type genus Ryujinia

Classification
Bacteria » *Ryujiniota* » *Ryujiniia*

References
Effective publication: Sun et al., 2025 [1]

Registry URL
https://seqco.de/i:49693

Order *Ryujiniales*

Etymology
[Ry.u.ji.ni.a'les] **N.L. fem. n.** *Ryujinia*, referring to the type genus Ryujinia; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Ryujiniales*, the Ryujinia order

Nomenclatural type
Genus *Ryujinia*

Description
The description is the same as for the type genus Ryujinia

Classification
Bacteria » *Ryujiniota* » *Ryujiniia* » *Ryujiniales*

References
Effective publication: Sun et al., 2025 [1]

Registry URL
https://seqco.de/i:49694

Family *Ryujiniaceae*

Etymology
[Ry.u.ji.ni.a'ce.ae] **N.L. fem. n.** *Ryujinia*, referring to the type genus Ryujinia; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Ryujiniaceae*, the Ryujinia family

Nomenclatural type
Genus *Ryujinia*

Description
The description is the same as for the type species is Ryujinia shimokita sp. nov

Classification
Bacteria » *Ryujiniota* » *Ryujiniia* » *Ryujiniales* » *Ryujiniaceae*

References
Effective publication: Sun et al., 2025 [1]

Registry URL
https://seqco.de/i:49695

Genus *Ryujinia*

Etymology
[Ry.u.ji'ni.a] **N.L. fem. n.** *Ry.u.ji'ni.a*, named after Ryūjin (□□, lit. ‘Dragon God’) the protector deity of the sea in Japanese mythology; **N.L. fem. n.** *Ryujinia*, named after Ryūjin (□□, lit. ‘Dragon God’) the protector deity of the sea in Japanese mythology

Nomenclatural type
Species *Ryujinia shimokita*[Ts]

Description
The description is the same as for the type species is *Ryujinia shimokita* sp. nov

Classification
Bacteria » *Ryujiniota* » *Ryujiniia* » *Ryujiniales* » *Ryujiniaceae* » *Ryujinia*

References
Effective publication: Sun et al., 2025 [1]

Registry URL
https://seqco.de/i:49696

Species *Ryujinia shimokita*[Ts]

Etymology

[shi.mo.ki'ta] **N.L. fem. n.** *shimokita*, named after the sampling site, the international waters off the Shimokita Peninsula in Japan

Nomenclatural type

INSDC Nucleotide: BAAGKY000000000.1 [Ts]

Description

This uncultured species is represented by the genome 'SP_28H5_5', whose genome size is 2.0 MB, with the presence of 23S, 16S and 5S rRNA genes. *R. shimokita* is inferred to have a chemolithotrophic lifestyle, since this species encodes a nearly complete Wood–Ljungdahl (WL) pathway. It also has the potential for a heterotrophic lifestyle with substrate-level phosphorylation through glycolysis, while it lacks most genes for the citrate cycle and beta-oxidation. The type genome does not encode the ability for the oxidoreduction of nitrogen or sulphur compounds.

Classification

Bacteria » *Ryujiniota* » *Ryujiniia* » *Ryujiniales* » *Ryujiniaceae* » *Ryujinia* » *Ryujinia shimokita*[Ts]

References

Effective publication: Sun et al., 2025 [1]
Assigned taxonomically: Sun et al., 2025 [1]

Registry URL

https://seqco.de/i:49692

References

1. Sun et al. (2025). Metagenomic insights into taxonomic and functional patterns in shallow coastal and deep subseafloor sediments in the Western Pacific. *Microbial Genomics*. DOI:10.1099/mgen.0.001351

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:zf1yjhk0** submitted by **Rinke, Chris** and including 6 new names has been successfully validated.

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