Phylum *Krumholzibacteriota*

Etymology
[Krum.hol.zi.bac.te.ri.o'ta] **N.L. neut. n.** *Krumholzibacterium*, a genus name ; *-ota*, ending to denote a phylum; **N.L. neut. pl. n.** *Krumholzibacteriota*, the Krumholzibacterium phylum

Nomenclatural type
Genus *Krumholzibacterium*

Description
Youssef et al. (2019): The candidatus phylum *Krumholzibacteriota* is defined by eight genomic assemblies (Zgenome0171T, Zgenome0218, Zgenome0207_2, Zgenome0274_1, UBA2172, UBA4771, UBA4783, and ex4484_7) recovered using genome-resolved metagenomics from three distinct habitats (Zodletone spring sediment, Suncor tailing pond, and Guyamas basin), as well as 16S rRNA gene sequences from uncultured representatives in a wide range of terrestrial, marine, and aquatic habitats that are predominantly anoxic or hypoxic. The genome assembly Zgenome0171T serves as the type material and is deposited in GenBank under Biosample accession number SAMN09745294 and WGS accession number QTKG00000000. Genomic analysis predicted Gram-negative cell walls, and rod-shaped cells with heterotrophic lifestyle, and the ability to degrade glucose, mannose, alanine, aspartate, glutamate, and methionine and production of acetate and formate as fermentation end products.

Classification
Bacteria » *Krumholzibacteriota*

References
Effective publication: Youssef et al., 2019 [1]

Registry URL
https://seqco.de/i:41783

References

1. Youssef et al. (2019). Candidatus Krumholzibacterium zodletonense gen. nov., sp nov, the first representative of the candidate phylum Krumholzibacteriota phyl. nov. recovered from an anoxic sulfidic spring using genome resolved metagenomics. *Systematic and Applied Microbiology*. DOI: 10.1016/j.syapm.2018.11.002