Register list for Krumholzibacterium zodletonense gen. nov. sp. nov. and their lineage

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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
Phylum *Krumholzibacteriota*	[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	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,	*Bacteria*	*Krumholzibacterium*	seqco.de/i:41783

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		and methionine and production of acetate and formate as fermentation end products.			
Class *Krumholzibacteriia*	[Krum.hol.zi.bac.te.ri'i.a] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-ia*, ending to denote a class; **N.L. neut. pl. n.** *Krumholzibacteriia*, the *Krumholzibacterium* class	Youssef et al. (2019): The description is the same as for the genus *Krumholzibacterium*. Contains the order *Krumholzibacteriales*. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.	*Krumholzibacteriota*	*Krumholzibacterium*	seqco.de/i:50461
Order *Krumholzibacteriales*	[Krum.hol.zi.bac.te.ri.a'les] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-ales*, ending to denote an order; **N.L. fem. pl. n.** *Krumholzibacteriales*, the *Krumholzibacterium* order	Youssef et al. (2019): The description is the same as for the genus Krumholzibacterium. Contains the family Krumholzibacteriaceae. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine,	*Krumholzibacteriia*	*Krumholzibacterium*	seqco.de/i:42781

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.			
Family *Krumholzibacteriaceae*	[Krum.hol.zi.bac.te.ri.a'ce.ae] **N.L. neut. n.** *Krumholzibacterium*, referring to the type genus *Krumholzibacterium*; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Krumholzibacteriaceae*, the *Krumholzibacterium* family	Youssef et al. (2019): The description is the same as for the genus *Krumholzibacterium*. Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol.	*Krumholzibacteriales*	*Krumholzibacterium*	seqco.de/i:42782
Genus *Krumholzibacterium*	[Krum.hol.zi.bac.te'ri.um] **N.L. neut. n.** *bacterium*, a bacterium; **N.L. neut. n.** *Krumholzibacterium*, A bacterium named after Professor Lee Krumholz for his contributions to the fields of diversity, genetics, and physiology of micro-organisms in anaerobic habitats	Youssef et al. (2019): Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and	*Krumholzibacteriaceae*	*Krumholzibacterium zodletonense*^{Ts}	seqco.de/i:23550

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		oligpopeptides. Fermentation end products include acetate, formate, and ethanol.			
Species *Krumholzibacterium zodletonense*[Ts]	[zo.dle.to.nen'se] **N.L. neut. adj.** *zodletonense*, referring to Zodletone Spring, Oklahoma	Youssef et al. (2019): Genomic analysis predicts an anaerobic, Gram-negative, motile (flagellated) chemoorganoheterotrophic rod. Genomic analysis identified auxotrophies for proline, vitamin B6, lipoic acid, biotin, and vitamin B12. Substrates supporting growth based on genomic analysis include glucose, mannose, aspartate, alanine, asparagine, glutamate, glutamine, cysteine, serine, threonine, glycine, methionine, histidine, dipeptides, tripeptides, and oligpopeptides. Fermentation end products include acetate, formate, and ethanol. Appears to be a slow-growing member of the rare biosphere. Possesses catalase and peroxidase-encoding genes. Lacks CRISPR-Cas system. The genome assembly Zgenome0171T serves as the type material and is deposited in GenBank under Biosample accession number SAMN09745294 and WGS accession number QTKG00000000.	*Krumholzibacterium*	NCBI Assembly: GCA_003369455.1 [Ts]	seqco.de/i:307