Genus *Izemobacterium*

Etymology

[I.ze.mo.bac.te'ri.um] **Gr. neut. n.** *izema*, a settling down, sediment; **N.L. neut. n.** *bacterium*, rod; **N.L. neut. n.** *Izemobacterium*, a bacterium from settling or subsurface environments

Nomenclatural type

Species *Izemobacterium crustae*$^{\mathrm{Ts}}$

Description

The description of the genus is identical to that given for the type species.
The MAG encodes a nearly complete glycolytic pathway and a complete lactate fermentation pathway, while gluconeogenesis and the tricarboxylic acid cycle are absent, consistent with a fermentative lifestyle and partial oxidative metabolism typical of anaerobic or microaerophilic organisms. An F_1F_0-type ATP synthase is present, suggesting energy generation linked to proton or sodium motive force. No carbon fixation pathways were detected, supporting a heterotrophic mode of nutrition. Genes for β-glucosidase and pullulanase indicate conserved oligosaccharide degradation, and biosynthetic pathways for several amino acids (serine, threonine, glutamine, cysteine, and glycine) are present. The MAG also encodes ferrous iron uptake systems, a complete DNA degradation locus (including extracellular nucleases, ABC transporters, and salvage enzymes), and a conserved sporulation gene set (spoIIIE, spoVG, kapD, spsF), consistent with endospore formation.

Classification

Bacteria » *Bacillota* » *Bacilli* » *Izemoplasmatales* » *Izemoplasmataceae* » *Izemobacterium*

References

Effective publication: Viver, Robador, 2026 [1]

Registry URL

https://seqco.de/i:54823

References

1. Viver, Robador (2026). Genomic insights into Izemobacterium crustae gen. nov., sp. nov., reveal metabolic adaptations for persistence in the oceanic crust. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2025.126679