Species *Izemobacterium crustae*Ts

Etymology
[crus'tae] **L. gen. n.** *crustae*, from crust, referring to the subseafloor oceanic crust from which this organism was recovered

Nomenclatural type
NCBI Assembly: GCA_052978905.1 Ts

Description
The MAG is 2.2 Mb with a GC content of 33.6%, completeness 97.78%, contamination 5.58%. Phylogenomic analysis places it within the family *Izemoplasmataceae*. The AAI value of the MAG and the close relative species *Izemoplasma acidinucleici* was 57.18%. 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. 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* » *Izemobacterium crustae*Ts

References
Effective publication: Viver, Robador, 2026 [1]

Registry URL
https://seqco.de/i:54822

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