

Phylum *Acidulidesulfobacteriota*

Etymology

[A.ci.du.li.de.sul.fo.bac.te.ri.o'ta] **N.L. neut. n.** *Acidulidesulfobacterium*, referring to the type genus *Acidulidesulfobacterium*; *-ota*, ending to denote a phylum; **N.L. neut. pl. n.** *Acidulidesulfobacteriota*, the *Acidulidesulfobacterium* phylum

Nomenclatural type

Genus *Acidulidesulfobacterium*

Description

Acidulidesulfobacteriota represents an ecologically significant group in sulfur-rich environments including artificial acid mine drainage and hydrothermal sulfides. Phylogenomic and 16S rRNA gene analyses indicated that this lineage represents a distinct phylum-level clade, leading us to propose the designation *Acidulidesulfobacteriota*. Notably, the concatenated DsrAB protein phylogeny and the mixed enzyme types involved in Dsr-dependent dissimilatory sulfur metabolism suggest that *Acidulidesulfobacteriota* may represent a transitional lineage in the evolutionary shift from reductive to oxidative Dsr metabolism.

Classification

Bacteria » *Acidulidesulfobacteriota*

References

Effective publication: Ren et al., 2025 [1]

Registry URL

<https://seqco.de/i:50994>

References

1. Ren et al. (2025). New insights into the evolution and metabolism of the bacterial phylum Candidatus Acidulodesulfobacteriota through metagenomics. *Environmental Microbiome*. [DOI:10.1186/s40793-025-00779-2](https://doi.org/10.1186/s40793-025-00779-2)