

Acidulidesulfobacterales ord. nov. with a novel family, two novel genera, and four novel species

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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
Order <i>Acidulidesulfobacterales</i>	[A.ci.du.li.de.sul.fo.bac.te.ri.a'les] N.L. neut. n. <i>Acidulidesulfobacterium</i> , referring to the type genus <i>Acidulidesulfobacterium</i> ; -ales, ending to denote an order; N.L. fem. pl. n. <i>Acidulidesulfobacterales</i> , the <i>Acidulidesulfobacterium</i> order	Tan et al., 2019 (modified): Facultatively anaerobic autotrophs, likely use oxygen as terminal electron acceptor and thus couple Fe(II) and sulfide oxidation to aerobic respiration under aerobic conditions in AMD water and on biofilm surface, while they may perform dissimilatory sulfate reduction, Fe(III) respiration and fermentations under anaerobic conditions in the interior of biofilms and sediments.	<i>Acidulidesulfobacteriia</i>	<i>Acidulidesulfobacterium</i>	seqco.de/i:275
Family <i>Acidulidesulfobacteriaceae</i>	[A.ci.du.li.de.sul.fo.bac.te.ri.a'ce.ae] N.L. neut. n. <i>Acidulidesulfobacterium</i> , referring to the type genus <i>Acidulidesulfobacterium</i> ; -aceae, ending to denote a family; N.L. fem. pl. n. <i>Acidulidesulfobacteriaceae</i> , the <i>Acidulidesulfobacterium</i> family		<i>Acidulidesulfobacterales</i>	<i>Acidulidesulfobacterium</i>	seqco.de/i:41968
	[A.ci.di.de.sul.fo.bac'ter] N.L. masc. adj. <i>acidus</i> , acid; L. pref. <i>de-</i> , from; L. n. <i>sulfur</i> , sulfur; N.L. pref. <i>desulfo-</i> , a dissimilatory	A genus in the order Acidulidesulfobacterales , described on the basis of metagenome-assembled genomes AP1 (Acidulidesulfobacter diazotrophicus) and AP2		<i>Acidulidesulfobacter</i>	

Genus <i>Acididesulfobacter</i> Proposed Taxon	Etymology sulfate-reducing bacterium; L. masc. n. bacter , a rod; N.L. masc. n. Acididesulfobacter , a rod-shaped sulfate reducer in acidic environments	Description (<i>Acididesulfobacter guangdongensis</i>). Established on the basis of maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins.	<i>Acidulidesulfobacteriaceae</i> Parent Taxon	<i>guangdongensis</i> ^{Ts} Type	seqco.de/i:39396 Registry URL
Genus <i>Acidulidesulfobacterium</i>	[A.ci.du.li.de.sul.fo.bac.te'ri.um] L. masc. adj. acidulus , a little sour; N.L. pref. desulfo- , dissimilatory sulfate-reducing; N.L. neut. n. bacterium , rod; N.L. neut. n. Acidulidesulfobacterium , a sulfate-reducing rod in an acidic environment	A genus in the order <i>Acidulidesulfobacteriales</i> , described on the basis of metagenome-assembled genomes AP3 (<i>Acidulidesulfobacterium ferriphilum</i>) and AP4 (<i>Acidulidesulfobacterium acidiphilum</i>). Established on the basis of maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins.	<i>Acidulidesulfobacteriaceae</i>	<i>Acidulidesulfobacterium ferriphilum</i> ^{Ts}	seqco.de/i:39397
Species <i>Acididesulfobacter diazotrophicus</i>	[di.a.zo.tro'phi.cus] Gr. pref. di- , twice, doubly; N.L. neut. n. azotum , nitrogen; N.L. pref. diazo- , pertaining to dinitrogen; N.L. masc. adj. trophicus , (from Gr. masc. adj. <i>trophikos</i>) nursing, tending; N.L. masc. adj. diazotrophicus , growing on dinitrogen	Established on the basis of Average Nucleotide Identity (ANI, using OrthoANI), 16S rRNA identity, and maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins. The type genome is AP1.	<i>Acididesulfobacter</i>	NCBI Assembly: GCA_004195025.1 ^{Ts}	seqco.de/i:42351
Species <i>Acididesulfobacter guangdongensis</i> ^{Ts}	[guang.dong.en'sis] N.L. masc. adj. guangdongensis , pertaining to Guangdong, a province of southern China, where this organism was first genomically described	Established on the basis of Average Nucleotide Identity (ANI, using OrthoANI), 16S rRNA identity, and maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins. The type genome is AP2.	<i>Acididesulfobacter</i>	NCBI Assembly: GCA_004195045.1 ^{Ts}	seqco.de/i:42752
		Established on the basis of Average Nucleotide Identity (ANI, using			

Proposed Taxon	Etiology	Description	Parent Taxon	Type	Registry URL
Species <i>Acidulidesulfobacterium acidiphilum</i>	[a.ci.di.phi'lum] Gr. masc. adj. <i>acidus</i> , sour, acid; N.L. neut. adj. <i>philos</i> , loving; N.L. neut. adj. <i>acidiphilum</i> , acid-loving	Established on the basis of Average Nucleotide Identity (ANI, using OrthoANI), 16S rRNA identity, and maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins. The type genome is AP4.	<i>Acidulidesulfobacterium</i>	NCBI Assembly: GCA_008534395.1 ^{Ts}	seqco.de/i:54849
Species <i>Acidulidesulfobacterium ferriphilum</i> ^{Ts}	[fer.ri.phi'lum] L. neut. n. <i>ferrum</i> , iron; N.L. neut. adj. <i>philum</i> , loving; N.L. neut. adj. <i>ferriphilum</i> , iron-loving	Established on the basis of Average Nucleotide Identity (ANI, using OrthoANI), 16S rRNA identity, and maximum-likelihood phylogenetic reconstruction using the concatenated alignment of 16 ribosomal proteins. The type genome is AP3.	<i>Acidulidesulfobacterium</i>	NCBI Assembly: GCA_004195035.1 ^{Ts}	seqco.de/i:42041