

Register list for 5 new names including *Chordibacter* gen. nov.

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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
Family <i>Seribacteraceae</i>	[Se.ri.bac.te.ra'ce.ae] N.L. masc. n. <i>Seribacter</i> , referring to the type genus <i>Seribacter</i> ; <i>-aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Seribacteraceae</i> , the <i>Seribacter</i> family	Members of the family <i>Seribacteraceae</i> are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 71 MAGs belonging to this family were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgoland spring blooms which fell into 6 clusters. <i>Seribacteraceae</i> belongs to the order <i>Opitutaes</i> , class <i>Verrucomicrobiae</i> , and phylum <i>Verrucomicrobiota</i> (based on GTDB taxonomy). Formerly identified as family MB11C04. Two FISH probes for members of this family have been developed (probe c17-1166 and c21-472 from Orellana et al., 2022) and previously used to describe that members of this genus are short rods (Orellana et al., 2022). The type genus is <i>Seribacter</i> and the corresponding type material is the metagenome-assembled genome r4, which shows 99.5% ANI to a previously described representative of the MB11C04 family (MB5 from Orellana et al., 2022).	<i>Opitutaes</i>	<i>Seribacter</i>	seqco.de/i:44057
Genus <i>Chordibacter</i>	[Chor.di.bac'ter] L. masc. adj. <i>chordus</i> , late-born; N.L. masc. n. <i>bacter</i> , rod; N.L. masc. n. <i>Chordibacter</i> , late blooming rod-shaped bacteria	Members of the <i>Chordibacter</i> genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 17 MAGs belonging to this genus were recovered in the 2011, 2012, 2016, and 2018 Helgoland spring blooms. <i>Chordibacter</i> belongs to the family <i>Seribacteraceae</i> , formerly known as MB11C04, order <i>Opitutaes</i> , class <i>Verrucomicrobiae</i> , and phylum <i>Verrucomicrobiota</i> . Formerly identified as genus MB11C04. A FISH probe for this family has been developed (probe c17-1166 from Orellana et al., 2022) and previously used to describe that members of this genus are short rods of length and width 0.9 and 0.8 µm respectively (Orellana et al., 2022).	<i>Seribacteraceae</i>	<i>Chordibacter forsetii</i> ^{TS}	seqco.de/i:44038
		Members of the <i>Seribacter</i> genus are predicted to be			

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Genus <i>Seribacter</i>	[Se.ri.bac'ter] L. masc. adj. serus , late; N.L. masc. n. bacter , rod; N.L. masc. n. Seribacter , late blooming rod-shaped bacteria	aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 11 MAGs belonging to this genus were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgoland spring blooms. <i>Seribacter</i> belongs to the family <i>Seribacteraceae</i> fam. nov., order <i>Opitutales</i> , class <i>Verrucomicrobiae</i> , and phylum <i>Verrucomicrobiota</i> . Formerly identified as genus MB11C04 in family MB11C04. A FISH probe for this family has been developed (probe c21-472 from Orellana <i>et al.</i> 2022) and previously used to describe that members of the this genus are short rods of length and width 1.2 and 1.0 µm respectively (Orellana <i>et al.</i> 2022). Orellana, L.H., Francis, T.B., Ferraro, M., Hehemann, J.-H., Fuchs, B.M., Amann, R.I. (2022) <i>Verrucomicrobiota</i> are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME J, 630–41, Doi: 10.1038/s41396-021-01105-7.	<i>Seribacteraceae</i>	<i>Seribacter sulfatis</i> ^{Ts}	seqco.de/i:44039
Species <i>Chordibacter forsetii</i> ^{Ts}	[for.se.ti'i] N.L. gen. masc. n. forsetii , of Forseti, the Scandinavian god of justice and reconciliation resident on Helgoland	Members of the <i>Chordibacter</i> genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 17 MAGs belonging to this genus were recovered in the 2011, 2012, 2016, and 2018 Helgoland spring blooms. This genome is estimated to be 92.7% complete with 2.2% redundancy. It has a GC content of 44.3% and a genome size of 2.12 Mbp. The 5S, 16S, and 23S rRNA genes were identified in the genome. <i>Chordibacter forsetii</i> belongs to the family MB11C04, order <i>Opitutales</i> , class <i>Verrucomicrobiae</i> , and phylum <i>Verrucomicrobiota</i> . Formerly identified as genus MB11C04 and species MB11C04. A FISH probe for this family has been developed (probe c17-1166 from Orellana <i>et al.</i> , 2022) and previously used to describe that members of this genus are short rods of length and width 0.9 and 0.8 µm respectively (Orellana <i>et al.</i> , 2022). The type species is <i>Chordibacter forsetii</i> and the corresponding type material is the metagenome-assembled genome ERZ814923, which shows 99.3% ANI to a previously described representative of the MB11C04 family (MB1 from Orellana <i>et al.</i> , 2022).	<i>Chordibacter</i>	NCBI Assembly: GCA_964187505.1 ^{Ts}	seqco.de/i:44036
		Members of the <i>Seribacter</i> genus are predicted to be aerobic and heterotrophic marine bacteria dwelling in surface waters. A total of 45 MAGs belonging to this			

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Species <i>Seribacter sulfatis</i> ^{Ts}	[sul.fa'tis] N.L. gen. n. <i>sulfatis</i> , of sulfate, referring to the Marine Verrucomicrobiota encoding many sulfatases	genus were recovered in the 2010, 2011, 2012, 2016, 2018 and 2020 Helgolander blooms. This genome is estimated to be 94.2% complete with 0% redundancy. It has a GC content of 42.6% and a genome size of 2.53 Mbp. The 5S, 16S, and 23S rRNA genes were identified in the genome (Table S8). <i>Seribacter sulfatis</i> belongs to the family <i>Seribacteraceae</i> fam. nov., order <i>Opitutales</i> , class <i>Verrucomicrobiae</i> , and phylum <i>Verrucomicrobiota</i> . Formerly identified as genus MB11C04 and species MB11C04, in the family MB11C04. A FISH probe for this family has been developed (probe c21-472 from Orellana et al., 2022) and previously used to describe that members of this genus are short rods of length and width 1.2 and 1.0 µm respectively (Orellana et al., 2022). The type species is <i>Seribacter sulfatis</i> and the corresponding type material is the metagenome-assembled genome ERZ816379, which shows 99.5% ANI to a previously described representative of the MB11C04 family (MB5 from Orellana et al., 2022).	<i>Seribacter</i>	NCBI Assembly: GCA_964187635.1 ^{Ts}	seqco.de/i:44037