

# Register list for 16 new names including *Andeanibacterium* 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
Genus <i>Andeanibacterium</i>	[An.de.a.ni.bac.te'ri.um] N.L. <b>masc. adj. andeanus</b> , pertaining to the Andes; N.L. <b>neut. n. bacterium</b> , small rod; N.L. <b>neut. n. Andeanibacterium</b> , Andean rod	A genus established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction, and phylogenomic analyses and is classified as a member of the <i>Sphingomonadaceae</i> family. Genomic metrics include ANI (79.88), AAI (61.59) and dDDH d4 (20.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 54 CAZymes, 15 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolysis were found within the MAG.	<i>Sphingomonadaceae</i>	<i>Andeanibacterium colombiense</i> <sup>TS</sup>	<a href="https://seqco.de/i:24097">seqco.de/i:24097</a>
Species <i>Cohnella colombiensis</i>	[co.lom.bi.en'sis] N.L. <b>fem. adj. colombiensis</b> , belonging to Colombia	The species is established on the basis of MiGA taxonomic novelty analysis, the taxonomic placement using maximum likelihood trees with 120 bacterial marker genes (bac120) and and the type material is the genome MAG_2441. Genomic metrics include ANI (67.06), AAI (67.21) and dDDH d4 (30.4). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 149 CAZymes, 44 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Cohnella</i>	INSDC Nucleotide: CP119317.1 <sup>TS</sup>	<a href="https://seqco.de/i:24096">seqco.de/i:24096</a>
Species <i>Brevundimonas colombiensis</i>	[co.lom.bi.en'sis] N.L. <b>fem. adj. colombiensis</b> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_833. Genomic metrics include ANI (87.3), AAI (82.62) and dDDH d4 (29.7). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 73 CAZymes, 13 of them involved in lignocellulose degradation. In addition, putative genes for protocatechuate and phtalate catabolism were found within the MAG.	<i>Brevundimonas</i>	INSDC Nucleotide: CP119326.1 <sup>TS</sup>	<a href="https://seqco.de/i:24108">seqco.de/i:24108</a>

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Species <i>Brevundimonas phytovorans</i>	[phy.to.vo'rans.] Gr. neut. n. <i>phyton</i> , plant; L. pres. part. <i>vorans</i> , devouring, destroying; N.L. fem. part. adj. <i>phytovorans</i> , plant-devouring	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1865. Genomic metrics include ANI (91.28), AAI (87.92) and dDDH d4 (40.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 39 CAZymes, 6 of them involved in lignocellulose degradation. In addition, putative genes for protocatechuate and phtalate catabolism were found within the MAG.	<i>Brevundimonas</i>	INSDC Nucleotide: CP119309.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24099">seqco.de/i:24099</a>
Species <i>Chryseobacterium colombiense</i>	[co.lom.bi.en'se.] N.L. neut. adj. <i>colombiense</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1654. Genomic metrics include ANI (88.96), AAI (95) and dDDH d4 (36.2). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 139 CAZymes, 41 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolysis were found within the MAG.	<i>Chryseobacterium</i>	INSDC Nucleotide: CP119310.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24098">seqco.de/i:24098</a>
Species <i>Pseudomonas phytovorans</i>	[phy.to.vo'rans.] Gr. neut. n. <i>phyton</i> , plant; L. pres. part. <i>vorans</i> , devouring, destroying; N.L. fem. part. adj. <i>phytovorans</i> , plant-devouring	A genus established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_876. Genomic metrics include ANI (92.18), AAI (95) and dDDH d4 (47). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 87 CAZymes, 16 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolysis were found within the MAG.	<i>Pseudomonas</i>	INSDC Nucleotide: CP119325.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24109">seqco.de/i:24109</a>
Species <i>Pseudobacter hemicellosilyticus</i>	[he.mi.cel.lu.lo.si.ly'ti.cus] N.L. neut. n. <i>hemicellulosum</i> , hemicellulose; N.L. masc. adj. <i>lyticus</i> , able to dissolve; N.L. masc. adj. <i>hemicellosilyticus</i> , hemicellulose dissolving	The species is established on the basis of MiGA taxonomic novelty analysis, the taxonomic placement using maximum likelihood trees with 120 bacterial marker genes (bac120) and the type material is the genome MAG_7. Genomic metrics include ANI (69.21), AAI (65.96) and dDDH d4 (22.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 237 CAZymes, 99 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Pseudobacter</i>	INSDC Nucleotide: CP119311.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24095">seqco.de/i:24095</a>

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Species <i>Sphingomonas phytovorans</i>	[phy.to.vo'rans.] Gr. <b>neut. n.</b> <i>phyton</i> , plant; L. <b>pres. part.</b> <i>vorans</i> , devouring, destroying; N.L. <b>fem. part.</b> <b>adj.</b> <i>phytovorans</i> , plant-devouring	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_3606. Genomic metrics include ANI (80.99), AAI (80.97) and dDDH d4 (22.2). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 95 CAZymes, 29 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Sphingomonas</i>	INSDC Nucleotide: CP119314.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24103">seqco.de/i:24103</a>
Species <i>Microbacterium phytovorans</i>	[phy.to.vo'rans.] Gr. <b>neut. n.</b> <i>phyton</i> , plant; L. <b>pres. part.</b> <i>vorans</i> , devouring, destroying; N.L. <b>neut. part.</b> <b>adj.</b> <i>phytovorans</i> , plant-devouring	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_4610. Genomic metrics include ANI (82.28), AAI (73.07) and dDDH d4 (21.5). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 74 CAZymes, 31 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Microbacterium</i>	INSDC Nucleotide: CP119321.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24107">seqco.de/i:24107</a>
Species <i>Devosia phytovorans</i>	[phy.to.vo'rans.] Gr. <b>neut. n.</b> <i>phyton</i> , plant; L. <b>pres. part.</b> <i>vorans</i> , devouring, destroying; N.L. <b>fem. part.</b> <b>adj.</b> <i>phytovorans</i> , plant-devouring	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_4196. Genomic metrics include ANI (84.84), AAI (74.37) and dDDH d4 (23.5). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 90 CAZymes, 17 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Devosia</i>	INSDC Nucleotide: CP119312.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24105">seqco.de/i:24105</a>
Species <i>Microbacterium colombiense</i>	[co.lom.bi.en'se.] N.L. <b>neut.</b> <b>adj.</b> <i>colombiense</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_1911. Genomic metrics include ANI (85.9), AAI (81.1) and dDDH d4 (28.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 82 CAZymes, 30 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolysis were found within the MAG.	<i>Microbacterium</i>	INSDC Nucleotide: CP119308.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24100">seqco.de/i:24100</a>

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Species <i>Kaistia colombiensis</i>	[co.lom.bi.en'sis] N.L. fem. adj. <i>colombiensis</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_2176. Genomic metrics include ANI (86.41), AAI (77.29) and dDDH d4 (28.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 95 CAZymes, 18 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.	<i>Kaistia</i>	INSDC Nucleotide: CP119318.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24101">seqco.de/i:24101</a>
Species <i>Sphingomonas colombiensis</i>	[co.lom.bi.en'sis] N.L. fem. adj. <i>colombiensis</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_27. Genomic metrics include ANI (85.46), AAI (66.97) and dDDH d4 (20.8). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 59 CAZymes, 10 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolisis were found within the MAG.	<i>Sphingomonas</i>	INSDC Nucleotide: CP119315.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24102">seqco.de/i:24102</a>
Species <i>Pseudomonas colombiensis</i>	[co.lom.bi.en'sis] N.L. fem. adj. <i>colombiensis</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_425. Genomic metrics include ANI (86.68), AAI (86.03) and dDDH d4 (29.3). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 103 CAZymes, 19 of them involved in lignocellulose degradation. In addition, putative genes for PUR hydrolisis were found within the MAG.	<i>Pseudomonas</i>	INSDC Nucleotide: CP119322.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24106">seqco.de/i:24106</a>
Species <i>Pedobacter colombiensis</i>	[co.lom.bi.en'sis] N.L. masc. adj. <i>colombiensis</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_3858. Genomic metrics include ANI (81.7), AAI (81.02) and dDDH d4 (29.6). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 254 CAZymes, 63 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.	<i>Pedobacter</i>	INSDC Nucleotide: CP119313.1 <sup>Ts</sup>	<a href="https://seqco.de/i:24104">seqco.de/i:24104</a>

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Species <i>Andeanibacterium colombiense</i> <sup>Ts</sup>	[co.lom.bi.en'se.] N.L. neut. adj. <i>colombiense</i> , belonging to Colombia	A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction, and phylogenomic analyses and is classified as a member of the <i>Sphingomonadaceae</i> family. The type species of the genus is <i>Andeanibacterium colombiense</i> . Genomic metrics include ANI (79.88), AAI (61.59) and dDDH d4 (20.1). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 54 CAZymes, 15 of them involved in lignocellulose degradation. In addition, putative genes for PET hydrolysis were found within the MAG.	<i>Andeanibacterium</i>	INSDC Nucleotide: CP119316.1 <sup>Ts</sup>	<a href="https://seqco.de/i:31306">seqco.de/i:31306</a>