Register list for 17 new names including Skiveiella danica sp. 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 *Aalborgicola*	[Aal.bor.gi'co.la] **N. L. neut. n.** *Aalborg*, the city of Aalborg; **L. suff.** *-cola*, inhabitant; **N.L. masc. n.** *Aalborgicola*, an inhabitant of Aalborg	Genus of species found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Most species are predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*. All species (except Aalborgicola danicus) have the potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.	*Burkholderiaceae*	*Aalborgicola defluviihabitans*^{Ts}	seqco.de/i:44106
Genus *Aalborgiella*	[Aal.bor.gi.el'la] **N.L. fem. dim. n.** *Aalborgiella*, bacterium named after the city Aalborg where the MAG had been retrieved	Genus of rod shaped bacteria found in activated sludge. Type species is Aalborgiella aggregata. Type species(Aalborgiella aggregata) is a rod shaped bacterium (1.4± 0.3 x 0.4±0.1 µm) abundant in activated sludge globally. Based on FISH analysis it seems to grow along filaments in activated sludge. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of branched amino acids. Presence of *narGHI* genes showed potential to reduce nitrate.	*Burkholderiaceae*	*Aalborgiella aggregata*^{Ts}	seqco.de/i:44101
		A genus of rod shaped bacteria found in activated sludge. Type species is Defluviibacillus avedoerensis. The type species is a rod shaped bacteria			

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Genus *Defluviibacillus*	[De.flu.vi.i.ba.ci'llus] **L. neut. n.** *defluvium*, sewage; **L. masc. n.** *bacillus*, rod-shaped bacterium; **N.L. masc. n.** *Defluviibacillus*, indicating a rod-shaped bacterium from sewage	(2.1± 0.4 x 0.6±0.1 µm) abundant in activated sludge globally. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids and branched amino acids. Presence of *narGHI* genes showed potential to reduce nitrate along with potential for further conversion via *norB* . It also had the potential to reduce nitrite to nitric oxide via nitrite reductase, *nirS.* Defluviibacillus avedoerensis had predicted all genes of the three pathways (polyP, glycogen and PHA) associated with Pao metabolism.	*Burkholderiaceae*	*Defluviibacillus avedoerensis*^{Ts}	seqco.de/i:44099
Genus *Egaibacter*	[E.ga.i.bac'ter] **N. L. masc. n.** *Egaa*, the city Egaa where the MAG had been retrieved; **N.L. masc. n.** *bacter*, bacterium; **N.L. masc. n.** *Egaibacter*, indicating a bacterium found in Egaa	Genus of bacteria found in activated sludge. Species generally have the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. They can also utilize branched chain amino acids (livFGHKM). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*. Potential to reduce nitrate with narGHI along with the reduction of nitrate to nitric oxide with nirS.	*Burkholderiaceae*	*Egaibacter danicus*^{Ts}	seqco.de/i:44121
Genus *Skiveiella*	[Ski.ve.i.el'la] **N.L. fem. dim. n.** *Skiveiella*, named after the city Skive where the MAG had been retrieved	Genus found in actived sludge. Type species is Skiveiella danica	*Burkholderiaceae*	*Skiveiella danica*^{Ts}	seqco.de/i:44104
Species *Aalborgicola bjergmarkensis*	[bjerg.mar.ken'sis] **N.L. masc. adj.** *bjergmarkensis*, of the city of Bjergmarken, from where the MAG was obtained	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. The *gtsABC+malK* transporters of of glucose uptake was also predicted. Potential to reduce nitrate with narGHI. Lastly it also had nitrous oxide reductase, nosZ predicted.	*Aalborgicola*	NCBI Assembly: GCA_016708725.1^{Ts}	seqco.de/i:44112

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Species *Aalborgicola danicus*	[da'ni.cus] **L. masc. adj.** *danicus*, Danish	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Can utilize branched chain amino acids (*livFGHKM*). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, acs, acetate kinase, ackA, and phosphate acetyltransferase, pta. Potential to reduce nitrate with *napAB* along with the reduction of nitrate to nitric oxide with nirS. Lastly it also had nitrous oxide reductase, nosZ predicted.	*Aalborgicola*	NCBI Assembly: GCA_016703945.1 ^{Ts}	seqco.de/i:44114
Species *Aalborgicola defluviihabitans*^{Ts}	[de.flu.vii.ha'bi.tans] **L. neut. n.** *defluvium*, sewage; **L. pres. part.** *habitans*, inhabiting; **L. masc. part. adj.** *defluviihabitans*, pertaining to the habitat where the MAG was sequenced from.	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta.* Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS.* Lastly it also had nitrous oxide reductase, *nosZ* predicted.	*Aalborgicola*	NCBI Assembly: GCA_016705575.1 ^{Ts}	seqco.de/i:44105
Species *Aalborgicola lynettensis*	[ly.net.ten'sis] **N.L. masc. adj.** *lynettensis*, of the city of Lynetten, from where the MAG was obtained	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Can utilize branched chain amino acids (*livFGHKM*) Potential to reduce nitrate with *narGHI*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.	*Aalborgicola*	NCBI Assembly: GCA_016719405.1 ^{Ts}	seqco.de/i:44113
Species *Aalborgiella aggregata*^{Ts}	[ag.gre.ga'ta] **L. fem. part. adj.** *aggregata*, joined together	Rod shaped bacterium (1.4± 0.3 x 0.4±0.1 µm) abundant in activated sludge globally. Based on FISH analysis it seems to grow along filaments in activated sludge. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for	*Aalborgiella*	NCBI Assembly: GCA_016708645.1 ^{Ts}	seqco.de/i:44100

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		transportation of branched amino acids. Presence of *narGHI* genes showed potential to reduce nitrate.			
Species *Defluviibacillus avedoerensis*^{Ts}	[a.ve.doe.ren'sis] **N.L. masc. adj.** *avedoerensis*, of the city Avedoere from which the MAG is retrieved from	Rod shaped bacteria (2.1± 0.4 x 0.6±0.1 µm) abundant in activated sludge globally. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids and branched amino acids. Presence of *narGHI* genes showed potential to reduce nitrate along with potential for further conversion via *norB* . It also had the potential to reduce nitrite to nitric oxide via nitrite reductase, *nirS.* Defluviibacillus avedoerensis had predicted all genes of the three pathways (polyP, glycogen and PHA) associated with Pao metabolism.	*Defluviibacillus*	NCBI Assembly: GCA_016703665.1^{Ts}	seqco.de/i:44098
Species *Egaibacter danicus*^{Ts}	[da'ni.cus] **L. masc. adj.** *danicus*, Danish	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Glucose uptake of via the *gtsABC+malK* transporter was also predicted. Can utilize branched chain amino acids (*livFGHKM*). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*. Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*.	*Egaibacter*	NCBI Assembly: GCA_016707075.1^{Ts}	seqco.de/i:44120
Species *Rhodoferax bjergmarkensis*	[bjerg.mar.ken'sis] **N.L. masc. adj.** *bjergmarkensis*, of the city of Bjergmarken, from where the MAG was obtained	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Can utilize branched chain amino acids (*livFGHKM*). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, and acetate kinase, *ackA* Potential to reduce nitrate with narGHI along with the reduction of nitrate to nitric oxide	*Rhodoferax*	NCBI Assembly: GCA_016708345.1^{Ts}	seqco.de/i:44117

with *nirS*. Lastly it also had nitrous oxide reductase, nosZ predicted.

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Species *Rhodoferax mariagerensis*	[ma.ri.a.ge.ren'sis] **N.L. masc. adj.** *mariagerensis*, of the city of Mariager where the MAG was obtained	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Can utilize branched chain amino acids (*livFGHKM*) and polar amino acids (ABC.PA.A, ABC.PA.P, ABC.PA.S). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*. Potential to reduce nitrate with *narGHI*	*Rhodoferax*	NCBI Assembly: GCA_016719055.1$_{Ts}$	seqco.de/i:44118
Species *Rhodoferax odensensis*	[o.den.sen'sis] **N.L. masc. adj.** *odensensis*, pertaining to Odense, a city in Denmark where the original sample was collected	acterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Can utilize branched chain amino acids (*livFGHKM*). Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*. Potential to reduce nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.	*Rhodoferax*	NCBI Assembly: GCA_016718405.1$_{Ts}$	seqco.de/i:44116
Species *Rhodoferax randersensis*	[ran.der.sen'sis] **N.L. masc. adj.** *randersensis*, from the city Randers where the MAG had been retrieved	Bacterium found in activated sludge. Genome-wide gene annotation suggested the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*, acetate kinase, *ackA*, and phosphate acetyltransferase, *pta*. Potential to reduce nitrate with *narGHI* along with the reduction of nitrate to nitric oxide with *nirS*. Lastly it also had nitrous oxide reductase, *nosZ* predicted.	*Rhodoferax*	NCBI Assembly: GCA_016718155.1$_{Ts}$	seqco.de/i:44115
Species	[da.ni'ca] **L. fem. adj.**	Bacteria found in activated sludge. Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate		NCBI Assembly:	

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Skiveiella danica^{Ts}	*danica*, Danish	pathway. It furthermore showed potential for transportation of polar amino acids. Presence of *narGHI* genes showed potential to reduce nitrate.	*Skiveiella*	GCA_016721925.1^{Ts}	seqco.de/i:44103