

Register list for 38 new names from Eremiobacterota including Xenobiaceae fam. nov.

Submitted by Ferrari, Belinda

Table 1: Complete list of names proposed in the current register list.

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|-------------------------------|---|--|------------------------|---------------------|---|
| Class <i>Xenobiia</i> | [Xe.no.bi'ia] N.L. neut. n. <i>Xenobium</i> , foreign life, referencing the artificial environment from which it was recovered; <i>-ia</i> , ending to denote a class; N.L. neut. pl. n. <i>Xenobiia</i> , the <i>Xenobium</i> class | Class defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. Defined as a class-level lineage based on UBP9 in Parks et al (2017). | <i>Eremiobacterota</i> | <i>Xenobium</i> | seqco.de/i:31316 |
| Class <i>Eremiobacteria</i> | [E.re.mi.o.bac.te'ri.a] N.L. masc. n. <i>Eremiobacter</i> , a rod from a desert; <i>-ia</i> , ending to denote a class; N.L. neut. pl. n. <i>Eremiobacteria</i> , the <i>Eremiobacter</i> class | Class defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Eremiobacterota</i> | <i>Eremiobacter</i> | seqco.de/i:41723 |
| Order <i>Eremiobacterales</i> | [E.re.mi.o.bac.te.ra'les] N.L. masc. n. <i>Eremiobacter</i> , a rod from a desert; <i>-ales</i> , ending to denote an order; N.L. fem. pl. n. <i>Eremiobacterales</i> , the <i>Eremiobacter</i> order | Order defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Eremiobacteria</i> | <i>Eremiobacter</i> | seqco.de/i:41907 |
| Order <i>Xenobiales</i> | [Xe.no.bi.a'les] N.L. neut. n. <i>Xenobium</i> , foreign life, referencing the artificial environment from which it was recovered; <i>-ales</i> , ending to denote an order; N.L. fem. pl. n. <i>Xenobiales</i> , the <i>Xenobium</i> order | Order defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. Defined as an order-level lineage based on UBA4705 in Parks et al (2017). | <i>Xenobiia</i> | <i>Xenobium</i> | seqco.de/i:31315 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|------------------------------------|---|---|-------------------------|--|---|
| Family <i>Eremiobacteraceae</i> | [E.re.mi.o.bac.ter.a.ce'ae] N.L. masc. n. <i>Eremiobacter</i> , a rod from a desert; N.L. suff. <i>-aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Eremiobacteraceae</i> , the Eremiobacter family | Family defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Eremiobacterales</i> | <i>Eremiobacter</i> | seqco.de/i:41908 |
| Family <i>Xenobiaceae</i> | [Xe.no.bi.a.ce'ae] N.L. neut. n. <i>Xenobium</i> , foreign life, referencing the artificial environment from which it was recovered; <i>-aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Xenobiaceae</i> , the Xenobium family | Family defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. Defined as a family-level lineage based on UBA4705 in Parks et al (2017). | <i>Xenobiales</i> | <i>Xenobium</i> | seqco.de/i:41921 |
| Genus <i>Xenobium</i> | [Xe.no'bi.um] Gr. adj. <i>xenos</i> , strange, foreign; Gr. masc. n. <i>bios</i> , life; N.L. neut. n. <i>Xenobium</i> , foreign life, referencing the artificial environment from which it was recovered | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Xenobiaceae</i> | <i>Xenobium occultum</i> ^{Ts} | seqco.de/i:41922 |
| Genus <i>Cybelea</i> | [Cy.be'le.a] N.L. fem. n. <i>Cybelea</i> , a bacterium named after Cybele, an ancient Anatolian earth goddess, in reference to the recovery from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Cybelea septentrionalis</i> ^{Ts} | seqco.de/i:42538 |
| Genus <i>Erabacter</i> | [Era.bac'ter] Gr. fem. n. <i>era</i> , <i>-ae</i> , earth; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Erabacter</i> , earth bacterium, in reference to the recovery from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Erabacter solicola</i> ^{Ts} | seqco.de/i:43329 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|---------------------------|--|--|-------------------------|---|---|
| Genus <i>Tyrphobacter</i> | [Tyr.pho.ba'cter] Gr. n. <i>tyrpha</i> , -ae, peat; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Tyrphobacter</i> , bacterium from the peat, in reference to the recovery from peatlands | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Tyrphobacter aquilonaris</i> ^{TS} | seqco.de/i:43316 |
| Genus <i>Nyctobacter</i> | [Nyc.to.ba'cter] Gr. fem. n. <i>Nyx</i> , primordial goddess of the night in Greek mythology; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Nyctobacter</i> , referring to a bacterium capable of 'dark' carbon fixation (chemolithoautotrophy), as well as the long and dark winter of Antarctica | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Nyctobacter psychrophilus</i> ^{TS} | seqco.de/i:42523 |
| Genus <i>Velthaea</i> | [Vel.tha'ea] N.L. fem. n. <i>Velthaea</i> , bacterium named after ancient Etruscan earth god Veltha, in reference to to the recovery from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Velthaea versatilis</i> ^{TS} | seqco.de/i:43525 |
| Genus <i>Tumulicola</i> | [Tu.mu.li'co.la] L. masc. n. <i>tumulus</i> , mound, hill; L. masc. / fem. suff. <i>-cola</i> , inhabitant, dweller; N.L. fem. n. <i>Tumulicola</i> , mound-dweller, in reference to the recovery from a palsa (mound) | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Tumulicola scandinaviensis</i> ^{TS} | seqco.de/i:43732 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|------------------------------|--|--|--------------------------|---|---|
| Genus <i>Elarobacter</i> | [E.la.ro.bac'ter] Gr. fem. n. <i>Elara</i> , maiden in Greek mythology who was hidden beneath the earth, where she gave birth to Tityus; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Elarobacter</i> , in reference to a bacterium recovered from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Elarobacter winogradsky</i> ^{TS} | seqco.de/i:41726 |
| Genus <i>Mawsoniella</i> | [Maw.so'ni.el.la] N.L. fem. dim. n. <i>Mawsoniella</i> , in honor of Sir Douglas Mawson, an Australian Antarctic explorer and pioneer | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Eremiobacteraceae</i> | <i>Mawsoniella australis</i> ^{TS} | seqco.de/i:42719 |
| Genus <i>Eremiobacter</i> | [E.re.mi.o.bac'ter] Gr. fem. n. <i>eremia</i> , desert, wilderness; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Eremiobacter</i> , a rod from a desert | Type genus of Eremiobacterota. Genus defined based on phylogenomics of 38 conserved marker genes and the lack of any named close relative at the time. | <i>Eremiobacteraceae</i> | <i>Eremiobacter antarcticus</i> ^{TS} | seqco.de/i:42508 |
| Genus <i>Bruticola</i> | [Bru.ti.co'la] L. masc. n. <i>brutus</i> , of animals, beasts; L. masc. / fem. suff. <i>-cola</i> , inhabitant, dweller; N.L. fem. n. <i>Bruticola</i> , animal-dweller, in reference to the mammal (baboon) fecal microbiome | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Xenobiaceae</i> | <i>Bruticola papionis</i> ^{TS} | seqco.de/i:41962 |
| Genus <i>Meridianibacter</i> | [Me.ri.di.a.ni.bac'ter] L. masc. adj. <i>meridianus</i> , southern; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Meridianibacter</i> , southern bacterium, in reference to the recovery from Antarctic soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Meridianibacter frigidus</i> ^{TS} | seqco.de/i:43148 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|---|--|---|-------------------------|--|---|
| Genus <i>Zemelea</i> | [Ze.me.le'a] N.L. fem. n. <i>Zemelea</i> , , named for Zemele, Lithuanian earth goddess, in reference to the recovery from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Zemelea palustris</i> ^{Ts} | seqco.de/i:48243 |
| Genus <i>Lustribacter</i> | [Lus.tri.bac'ter] L. neut. n. <i>lustrum</i> , bog; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Lustribacter</i> , bacterium from the bog, in reference to the recovery from a bog | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Lustribacter telmatis</i> ^{Ts} | seqco.de/i:42844 |
| Genus <i>Tityobacter</i> | [Ti.ty.o.ba'cter] Gr. masc. n. <i>Tityos</i> , in Greek mythology, giant born from the earth, son of Elara; N.L. masc. n. <i>bacter</i> , a rod; N.L. masc. n. <i>Tityobacter</i> , bacterium named after Tityos (giant born from the earth), in reference to the recovery from soil | Genus defined based on 16S rRNA phylogeny and phylogenomic analysis of 15 ribosomal proteins and the GTDB. | <i>Baltobacteraceae</i> | <i>Tityobacter terrigena</i> ^{Ts} | seqco.de/i:43379 |
| Species <i>Cybelea septentrionalis</i> ^{Ts} | [sep.ten.tri.o.na'lis] L. fem. adj. <i>septentrionalis</i> , northern | Obligate heterotroph. Hydrogen oxidation using Group 1h [NiFe] hydrogenase. Organic substrates include peptides, amino acids, carboxylates, taurine, urea, sarcosine, PVA, arylsulfates, poly- and oligosaccharides, sugars, fluoroacetate. Degradation of β -glucan (GH1, GH16), cellulose/ β -glucan (GH5_40), chitin (GH18), β -D-galactoside (GH35), and xyloglucan (GH74). PHA storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Cybelea</i> | NCBI Assembly: GCA_003158175.1 ^{Ts} | seqco.de/i:43849 |
| Species <i>Tyrphobacter aquilonaris</i> ^{Ts} | [aqui.lo.na'ris] L. masc. adj. <i>aquilonaris</i> , northern, northerly | Obligate heterotroph. Organic substrates include peptides, amino acids, carboxylates, methanol, poly- and oligosaccharides, sugars. PHA storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Tyrphobacter</i> | NCBI Assembly: GCA_003133745.1 ^{Ts} | seqco.de/i:43739 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|--|---|---|------------------------|--|---|
| Species <i>Mawsoniella australis</i> ^{Ts} | [aus.tra'lis] L. fem. adj. <i>australis</i> , southern, of the south wind, in reference to the recovery from the southern continent of Antarctica | Obligate heterotroph. Hydrogen oxidation using Group 1h [NiFe] hydrogenase. Organic substrates include peptides, amino acids, carboxylates, sarcosine, oligosaccharides, sugars, catechol, 4hydroxybenzoate. PHA storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Mawsoniella</i> | NCBI Assembly: GCA_014304875.1 ^{Ts} | seqco.de/i:42720 |
| Species <i>Eremiobacter antarcticus</i> ^{Ts} | [an.tar'cti.cus] L. masc. adj. <i>antarcticus</i> , southern, pertaining to Antarctica | Heterotroph and autotroph. Hydrogenotrophic chemolithoautotrophy using Group 1h [NiFe] hydrogenase and CBB cycle; capable of using atmospheric H ₂ . Organic substrates include peptides, amino acids, carboxylates, acetate, sarcosine, formate, methanol, poly- and oligosaccharides, sugars, catechol, 4-hydroxybenzoate. Glycogen storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Eremiobacter</i> | NCBI Assembly: GCA_003244105.1 ^{Ts} | seqco.de/i:42509 |
| Species <i>Bruticola papionis</i> ^{Ts} | [pa.pi.o'nis] N.L. gen. n. <i>papionis</i> , pertaining to Papio, the primate genus that includes baboons | Obligate heterotroph. Fermentative (no respiration). Organic substrates include peptides, amino acids, citrate, starch, maltodextrin, glucose. Bidirectional Fe-only hydrogenases (for redox balance?). Glycogen storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Bruticola</i> | NCBI Assembly: GCA_002407045.1 ^{Ts} | seqco.de/i:41963 |
| Species <i>Zemelea palustris</i> ^{Ts} | [pa.lus'tris] L. fem. adj. <i>palustris</i> , marshy, swampy | Obligate heterotroph. Anaerobic respiration: nitrate. Organic substrates include peptides, amino acids, carboxylates, sarcosine, formate, poly- and oligosaccharides, sugars. PHA storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Zemelea</i> | NCBI Assembly: GCA_003134695.1 ^{Ts} | seqco.de/i:41948 |
| Species <i>Meridianibacter frigidus</i> ^{Ts} | [fri'gi.dus] L. masc. adj. <i>frigidus</i> , cold | Obligate heterotroph. Organic substrates include peptides, amino acids, carboxylates, poly- and oligosaccharides, sugars. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Meridianibacter</i> | NCBI Assembly: GCA_003243975.1 ^{Ts} | seqco.de/i:43149 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|--|---|--|---------------------|---|---|
| Species <i>Lustribacter telmatis</i> ^{Ts} | [tel'ma.tis] Gr. n. <i>telma</i> , swamp; N.L. gen. n. <i>telmatis</i> , of the bog | Obligate heterotroph. Hydrogen oxidation using Group 1h [NiFe] hydrogenase. Anaerobic respiration: urocanate. Organic substrates include peptides, amino acids, carboxylates, taurine, urea, cyanate, acetate, formate, alcohols (including methanol, ethanol), arylsulfates, alkanesulfonates, oligosaccharides, sugars, fluoroacetate, halobenzoate, phenoxypropionate, ethylbenzene, 4-hydroxybenzoate, 4-sulfocatechol. PHA storage; glycogen storage. Motile by flagella. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Lustribacter</i> | NCBI Assembly: GCA_003164045.1 ^{Ts} | seqco.de/i:42845 |
| Species <i>Cybelea palsarum</i> | [pal.sa'rum] N.L. fem. n. <i>palsa</i> , peat mound (from Finnish <i>palsa</i>); N.L. gen. pl. n. <i>palsarum</i> , from <i>palsa</i> wetlands | Obligate heterotroph. Organic substrates include peptides, amino acids, carboxylates, taurine, urea, sarcosine, PVA, arylsulfates, poly- and oligosaccharides, sugars, fluoroacetate. Degradation of β -glucan (GH1, GH16), cellulose/ β -glucan (GH5_40), chitin (GH18), β -D-galactoside (GH35), and xyloglucan (GH74). PHA storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Cybelea</i> | NCBI Assembly: GCA_003166915.1 ^{Ts} | seqco.de/i:43705 |
| Species <i>Xenobium occultum</i> ^{Ts} | [oc.cul'tum] L. neut. adj. <i>occultum</i> , hidden | Obligate heterotroph. Microaerobic; anaerobic respiration by DNRA. Fermentative. Organic substrates include peptides, amino acids, carboxylates, glycerol, poly- and oligosaccharides, sugars, 4-hydroxybenzoate. Degradation of β -glucosides (GH3), cellulose (endoglucanase GH5_5), starch (cyclomaltodextrinase GH13, and GH13_2; 4- α -glucanotransferase GH77), maltodextrin (GH13_21), α -glucans (GH31), trehalose (GH37), and xyloglucan (GH74). PHA storage; glycogen storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Xenobium</i> | NCBI Assembly: GCA_002423485.1 ^{Ts} | seqco.de/i:43215 |
| Species <i>Erabacter solicola</i> ^{Ts} | [so.li.co'la] L. neut. n. <i>solum</i> , soil; L. masc. / fem. suff. <i>-cola</i> , inhabitant, dweller; N.L. masc. n. <i>solicola</i> , inhabitant of the soil | Obligate heterotroph. Organic substrates include peptides, amino acids, carboxylates, sarcosine, poly- and oligosaccharides, sugars. PHA storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Erabacter</i> | NCBI Assembly: GCA_003136895.1 ^{Ts} | seqco.de/i:43330 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|---|--|---|--------------------|--|---|
| Species <i>Nyctobacter psychrophilus</i> ^{Ts} | [psy.chro'phi.lus] Gr. adj. <i>psychros</i> , cold; Gr. adj. <i>philos</i> , loving; N.L. masc. adj. <i>psychrophilus</i> , cold-loving | Heterotroph and autotroph. Hydrogenotrophic chemolithoautotrophy using Group 1h [NiFe] hydrogenase and CBB cycle; capable of using atmospheric H ₂ . Organic substrates include peptides, amino acids, carboxylates, poly- and oligosaccharides, sugars. PHA storage; glycogen storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Nyctobacter</i> | NCBI Assembly: GCA_014305025.1 ^{Ts} | seqco.de/i:42524 |
| Species <i>Velthaea versatilis</i> ^{Ts} | [ver.sa'ti.lis] L. fem. adj. <i>versatilis</i> , versatile, in reference to metabolic versatility | Heterotroph and autotroph. Hydrogenotrophic chemolithoautotrophy using Group 1h [NiFe] hydrogenase and CBB cycle; capable of using atmospheric H ₂ . Photoautotrophy; carboxysomes; photoreceptors. CO oxidation. Anaerobic respiration: sulfoxides. Assimilatory nitrate reduction. Organic substrates include peptides, amino acids, carboxylates, glycerol, taurine, urea, cyanate, sarcosine, alcohols (including methanol, ethanol), poly- and oligosaccharides, sugars, catechol, propane. PHA storage; glycogen storage. Motile by flagella (including phototaxis). Polyphosphate storage. Bidirectional [NiFe] hydrogenase (Group 3b). Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Velthaea</i> | NCBI Assembly: GCA_003134035.1 ^{Ts} | seqco.de/i:43526 |
| Species <i>Tumulicola scandinavensis</i> ^{Ts} | [scan.di.na.vi.en'sis] L. fem. n. <i>Scandinavia</i> , region in northern Europe; <i>-ensis</i> , of or from (a place); N.L. fem. adj. <i>scandinavensis</i> , from Scandinavia (Sweden) | Obligate heterotroph. CO oxidation. Organic substrates include peptides, amino acids, carboxylates, taurine, acetate, sarcosine, arylsulfates, poly- and oligosaccharides, sugars. PHA storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Tumulicola</i> | NCBI Assembly: GCA_003140835.1 ^{Ts} | seqco.de/i:43733 |
| Species <i>Cybelea tumulisoli</i> | [tu.mu.li.so'li] L. masc. n. <i>tumulus</i> , mound, hill; L. neut. n. <i>solum</i> , soil; N.L. gen. n. <i>tumulisoli</i> , from the mound soil, in reference to palsa | Obligate heterotroph. Organic substrates include peptides, amino acids, carboxylates, taurine, urea, sarcosine, PVA, arylsulfates, poly- and oligosaccharides, sugars, fluoroacetate. Degradation of β -glucan (GH1), xylan (GH10), chitin (GH18), and xyloglucan (GH74). PHA storage. Polyphosphate storage. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Cybelea</i> | NCBI Assembly: GCA_003167155.1 ^{Ts} | seqco.de/i:43786 |

| Proposed Taxon | Etymology | Description | Parent Taxon | Type | Registry URL |
|--|--|---|--------------------|--|---|
| Species <i>Elarobacter winogradskyi</i> ^{Ts} | [wi.no.grad'skiy] N.L. gen. n. <i>winogradskyi</i> , in honor of Sergei Winogradsky, Russian microbiologist and ecologist | Obligate heterotroph. CO oxidation. Organic substrates include peptides, amino acids, carboxylates, glycerol, urea, acetate, sarcosine, formate, ethanol, oligosaccharides, sugars, fluoroacetate. Degradation of trehalose (GH15), α-mannoside (GH38), and xyloglucan (GH74). PHA storage; glycogen storage. Polyphosphate storage. Motile by flagella. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Elarobacter</i> | NCBI Assembly: GCA_003134965.1 ^{Ts} | seqco.de/i:41727 |
| Species <i>Tityobacter terrigena</i> ^{Ts} | [ter.ri.ge'na] L. masc. adj. <i>terrigena</i> , born of or from the earth; L. masc. adj. <i>terrigena</i> , earth-born; in reference to the recovery from soil | Heterotroph and autotroph. CO oxidation. Hydrogenotrophic chemolithoautotrophy using Group 1h [NiFe] hydrogenase and CBB cycle; capable of using atmospheric H ₂ . Organic substrates include peptides, amino acids, carboxylates, glycerol, taurine, acetate, alcohols (including methanol, ethanol, polyvinyl alcohol), aldehydes, poly- and oligosaccharides, sugars, fluoroacetate, catechol. Glycogen storage. Polyphosphate storage. BMC for sequestering toxic metabolites. Also defined based on ANI, and phylogenies of 16S rRNA gene, 15 ribosomal proteins, and the GTDB. | <i>Tityobacter</i> | NCBI Assembly: GCA_003156715.1 ^{Ts} | seqco.de/i:43380 |