

# Register list for 31 new names from Prabhu et al. 2024

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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<br><i>Australimonadales</i>   | [Aus.tra.li.mo.na.da'les]<br><b>N.L. fem. n.</b> <i>Australimonas</i> ,<br>type genus of the order; -<br><i>ales</i> , ending to denote an<br>order; <b>N.L. fem. pl. n.</b><br><i>Australimonadales</i> , the<br><i>Australimonas</i> order          | The description of Australimonadales is the same as that of<br><i>Australimonas</i> . The former name for this order is UBA2963.  | <i>Dehalococcoidia</i>     | <i>Australimonas</i> | <a href="https://seqco.de/i:46751">seqco.de/i:46751</a> |
| Order <i>Eutrophobiales</i>         | [Eu.tro.pho.bi.a'les] <b>N.L.</b><br><b>masc. n.</b> <i>Eutrophobius</i> ,<br>type genus of the order; -<br><i>ales</i> , ending to denote an<br>order; <b>N.L. fem. pl. n.</b><br><i>Eutrophobiales</i> , the<br><i>Eutrophobius</i> order           | The description of Eutrophobiales is the same as that of<br><i>Eutrophobius</i> . The former name for this order is UBA4486.      | <i>Gammaproteobacteria</i> | <i>Eutrophobius</i>  | <a href="https://seqco.de/i:46757">seqco.de/i:46757</a> |
| Family<br><i>Australimonadaceae</i> | [Aus.tra.li.mo.na.da.ce'ae]<br><b>N.L. fem. n.</b> <i>Australimonas</i> ,<br>type genus of the family; -<br><i>aceae</i> , ending to denote a<br>family; <b>N.L. fem. pl. n.</b><br><i>Australimonadaceae</i> , the<br><i>Australimonas</i> family    | The description of Australimonadaceae is the same as for<br><i>Australimonas</i> . The former name for this family is UBA2963.    | <i>Australimonadales</i>   | <i>Australimonas</i> | <a href="https://seqco.de/i:46750">seqco.de/i:46750</a> |
| Family<br><i>Marisalimonadaceae</i> | [Ma.ri.sa.li.mo.na.da.ce'ae]<br><b>N.L. fem. n.</b><br><i>Marisalimonas</i> , type genus<br>of the family; <i>-aceae</i> ,<br>ending to denote a family;<br><b>N.L. fem. pl. n.</b><br><i>Marisalimonadaceae</i> , the<br><i>Marisalimonas</i> family | The description of Marisalimonadaceae is the same as for<br><i>Marisalimonas</i> . The former name for this family is AAA536-G10. | <i>Puniceispirillales</i>  | <i>Marisalimonas</i> | <a href="https://seqco.de/i:46752">seqco.de/i:46752</a> |

| Proposed Taxon                   | Etymology  | Description  | Parent Taxon           | Type                 | Registry URL  |
|----------------------------------|--|--|------------------------|----------------------|---|
| Family <i>Salivitaceae</i>       | [Sa.li.vi.ta.ce'ae] N.L. fem. n. <i>Salivita</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Salivitaceae</i> , the <i>Salivita</i> family                         | The description of <i>Salivitaceae</i> is the same as that of <i>Salivita</i> . The former name for this family is HTCC2089.           | <i>Pseudomonadales</i> | <i>Salivita</i>      | <a href="https://seqco.de/i:46755">seqco.de/i:46755</a> |
| Family <i>Eutrophomonadaceae</i> | [Eu.tro.pho.mo.na.da.ce'ae] N.L. fem. n. <i>Eutrophomonas</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Eutrophomonadaceae</i> , the <i>Eutrophomonas</i> family | The description of <i>Eutrophomonadaceae</i> is the same as that of <i>Eutrophomonas</i> . The former name for this family is UBA3031. | <i>Burkholderiales</i> | <i>Eutrophomonas</i> | <a href="https://seqco.de/i:46753">seqco.de/i:46753</a> |
| Family <i>Eutrophobiaceae</i>    | [Eu.tro.pho.bi.a.ce'ae] N.L. masc. n. <i>Eutrophobius</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Eutrophobiaceae</i> , the <i>Eutrophobius</i> family         | The description of <i>Eutrophobiaceae</i> is same as that of <i>Eutrophobius</i> . The former name for this family is UBA4486.         | <i>Eutrophobiales</i>  | <i>Eutrophobius</i>  | <a href="https://seqco.de/i:46756">seqco.de/i:46756</a> |
| Family <i>Eutrophovitaceae</i>   | [Eu.tro.pho.vi.ta.ce'ae] N.L. fem. n. <i>Eutrophovita</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; N.L. fem. pl. n. <i>Eutrophovitaceae</i> , the <i>Eutrophovita</i> family        | The description of <i>Eutrophovitaceae</i> is same as that of <i>Eutrophovita</i> . The former name for this family is UBA3031.        | <i>Burkholderiales</i> | <i>Eutrophovita</i>  | <a href="https://seqco.de/i:46754">seqco.de/i:46754</a> |

| Proposed Taxon             | Etymology  | Description  | Parent Taxon              | Type  | Registry URL  |
|----------------------------|--|--|---------------------------|---|---|
| Genus <i>Australimonas</i> | [Aus.tra.li.mo'nas] L. <b>adj.</b> <i>australis</i> , southern; N.L. <b>fem. n.</b> <i>monas</i> , a unit; N.L. <b>fem. n.</b> <i>Australimonas</i> , a unit from the south, referring to Australia where the organism was found               | The description is identical to that of the type species.  | <i>Australimonadaceae</i> | <i>Australimonas brisbanensis</i> <sup>TS</sup> | <a href="https://seqco.de/i:46730">seqco.de/i:46730</a> |
| Genus <i>Marisalimonas</i> | [Ma.ri.sa.li.mo'nas] L. <b>neut. n.</b> <i>mare</i> , the sea; L. <b>masc. n.</b> <i>sal</i> , salt; N.L. <b>fem. n.</b> <i>monas</i> , a unit; N.L. <b>fem. n.</b> <i>Marisalimonas</i> , a microbe occurring in saline conditions in the sea | The former name for this genus is AAA536-G10. The description is identical to that of the type species.          | <i>Marisalimonadaceae</i> | <i>Marisalimonas marina</i> <sup>TS</sup>       | <a href="https://seqco.de/i:46734">seqco.de/i:46734</a> |
| Genus <i>Salsuginivita</i> | [Sal.su.gi.ni.vi'ta] L. <b>fem. n.</b> <i>salsugo</i> , brackish water; L. <b>fem. n.</b> <i>vita</i> , life; N.L. <b>fem. n.</b> <i>Salsuginivita</i> , a bacterium found in brackish habitats  | The former name for this genus is CAIYFD01. The description is identical to that of the type species.            | <i>Opitutaceae</i>        | <i>Salsuginivita brisbanensis</i> <sup>TS</sup> | <a href="https://seqco.de/i:46748">seqco.de/i:46748</a> |
| Genus <i>Salivita</i>      | [Sa.li.vi'ta] L. <b>masc. n.</b> <i>sal</i> , salt; L. <b>fem. n.</b> <i>vita</i> , life; N.L. <b>fem. n.</b> <i>Salivita</i> , an organism associated with saltwater  | The former name for this genus is RGAU01. The description is identical to that of the type species.              | <i>Salivitaceae</i>       | <i>Salivita marina</i> <sup>TS</sup>            | <a href="https://seqco.de/i:46741">seqco.de/i:46741</a> |
| Genus <i>Eutrophobius</i>  | [Eu.tro.pho.bi'us] Gr. <b>adv.</b> <i>eû</i> , good; Gr. <b>adj.</b> <i>trophos</i> , feeder; Gr. <b>masc. n.</b> <i>bios</i> , life; N.L. <b>masc. n.</b> <i>Eutrophobius</i> , life associated with eutrophic environments                   | This is a novel group of the family and order UBA4486. The description is identical to that of the type species. | <i>Eutrophobiaceae</i>    | <i>Eutrophobius brisbanensis</i> <sup>TS</sup>  | <a href="https://seqco.de/i:46745">seqco.de/i:46745</a> |

| Proposed Taxon                | Etymology   | Description   | Parent Taxon               | Type  | Registry URL  |
|-------------------------------|---|---|----------------------------|---|---|
| Genus <i>Eutrophocola</i>     | [Eu.tro.pho.co'la] Gr. adv. <i>eû</i> , good; Gr. adj. <i>trophos</i> , feeder; L. masc. / fem. suff. <i>cola</i> , inhabitant; N.L. fem. n. <i>Eutrophocola</i> , referring to a microbe in eutrophic aquatic environments | The former name for this genus is RFVC01. The description is identical to that of the type species.                                 | <i>Pseudohongiellaceae</i> | <i>Eutrophocola</i><br><i>salsuginis</i> <sup>TS</sup>    | <a href="https://seqco.de/i:46743">seqco.de/i:46743</a> |
| Genus<br><i>Eutrophomonas</i> | [Eu.tro.pho.mo'nas] Gr. adv. <i>eû</i> , good; Gr. adj. <i>trophos</i> , feeder; L. fem. n. <i>monas</i> , a unit; N.L. fem. n. <i>Eutrophomonas</i> , a unit associated with eutrophic environments                        | This is a novel group of the family UBA3031 within order Burkholderiales. The description is identical to that of the type species. | <i>Eutrophomonadaceae</i>  | <i>Eutrophomonas</i><br><i>brisbanensis</i> <sup>TS</sup> | <a href="https://seqco.de/i:46737">seqco.de/i:46737</a> |
| Genus <i>Eutrophosalina</i>   | [Eu.tro.pho.sa.li'na] Gr. adj. <i>eû</i> , good; Gr. adj. <i>trophos</i> , feeder; N.L. fem. adj. <i>salina</i> , salty; N.L. fem. n. <i>Eutrophosalina</i> , a microbe adapted to eutrophic and saline environments        | The former name for this genus is MED-G14. The description is identical to that of the type species.                                | <i>Flavobacteriaceae</i>   | <i>Eutrophosalina</i><br><i>marina</i> <sup>TS</sup>      | <a href="https://seqco.de/i:46728">seqco.de/i:46728</a> |
| Genus <i>Eutrophovita</i>     | [Eu.tro.pho.vi'ta] Gr. adv. <i>eû</i> , good; Gr. masc. / fem. adj. <i>trophos</i> , feeder; L. fem. n. <i>vita</i> , life; N.L. fem. n. <i>Eutrophovita</i> , an organism associated with eutrophic environments           | This is a novel group of the family UBA3031 within order Burkholderiales. The description is identical to that of the type species. | <i>Eutrophovitaceae</i>    | <i>Eutrophovita</i><br><i>brisbanensis</i> <sup>TS</sup>  | <a href="https://seqco.de/i:46739">seqco.de/i:46739</a> |

| Proposed Taxon  | Etymology   | Description  | Parent Taxon         | Type   | Registry URL  |
|---|---|--|----------------------|--|---|
| Genus <i>Salinivivens</i>                               | [Sa.li.ni.vi'vens] N.L. <b>masc. adj.</b> <i>salinus</i> , saline; L. <b>part. adj.</b> <i>vivens</i> , living; N.L. <b>masc. n.</b> <i>Salinivivens</i> , a microbial organism thriving in saline conditions | The former name for this genus is MED-G52. The description is identical to that of the type species.   | <i>Paracoccaceae</i> | <i>Salinivivens marinus</i> <sup>Ts</sup>    | <a href="https://seqco.de/i:44234">seqco.de/i:44234</a> |
| Species <i>Marisalimonas marina</i> <sup>Ts</sup>       | [ma.ri'na] L. <b>fem. adj.</b> <i>marina</i> , of the sea, marine   | Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin and Starch) as well as fix inorganic carbon via the Calvin cycle (rbclS). Capable of nitrate (NRT2), sulphate (ssu) and phosphorus uptake (pst, pho) and regulation, as well as osmoregulate via multiple genes (trkA, nqrF, mnh, proXV). Could have possible motility using motAB and fliGMN genes. Based on the genome reporting standards for MAGs, the estimated completeness 91.69%, contamination 0.14%, and the presence of the 5S (109 bp), 16S (1,482 bp), and 23S (2,712 bp) rRNA gene and 32 tRNAs. Type genome is defined as "high-quality" draft MAG, with six contigs, genome size of 1.9Mbps. | <i>Marisalimonas</i> | NCBI Assembly: GCA_038131365.1 <sup>Ts</sup> | <a href="https://seqco.de/i:46735">seqco.de/i:46735</a> |
| Species <i>Australimonas brisbanensis</i> <sup>Ts</sup> | [bris.ban.en'sis] N.L. <b>fem. adj.</b> <i>brisbanensis</i> , of or belonging to Brisbane   | This is a novel group of the order and family UBA2963. Inferred to degrade Mucin, and carry genes for phosphate and phosphonate transporters. Can perform osmoregulation using trkA (K <sup>+</sup> transporter) and multicomponent Na <sup>+</sup> /H <sup>+</sup> transportation (mnh). Based on the genome reporting standards for MAGs, the estimated completeness was 98.68%, contamination 0%, and the presence of the 16S (1,472 bp), and 23S (2,898 bp) rRNA gene and 46 tRNAs. Type genome is defined as "high-quality" draft MAG, and a genome size of 1.9Mbps.  | <i>Australimonas</i> | NCBI Assembly: GCA_038147155.1 <sup>Ts</sup> | <a href="https://seqco.de/i:46731">seqco.de/i:46731</a> |

| Proposed Taxon  | Etymology  | Description  | Parent Taxon          | Type   | Registry URL  |
|---|--|--|-----------------------|--|---|
| Species<br><i>Eutrophosalina marina</i> <sup>Ts</sup> | [ma.ri'na] L. fem. adj. <i>marina</i> , of the sea, marine | Inferred to be marine ecotype, and can break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin, Cellulose, Sulfated polysaccharides and Starch). Also carries a polyphosphate kinase gene for polyphosphate accumulation, likely fuelling cytochrome c oxidase (coxABCD). Can perform osmoregulation using trk1 (K <sup>+</sup> transporter) and nqrF (Na <sup>+</sup> transporter). Based on the genome reporting standards for MAGs, the estimated completeness was 96.32%, contamination 0%, and the presence of the 16S (1,522 bp), and 23S (2,775 bp) rRNA gene and 34 tRNAs. Type genome is defined as "high-quality" draft MAG, having two contigs and a genome size of 1.5Mbps.  | <i>Eutrophosalina</i> | NCBI Assembly:<br>GCA_038147175.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46729">seqco.de/i:46729</a> |
| Species <i>Salivita marina</i> <sup>Ts</sup>          | [ma.ri'na] L. fem. adj. <i>marina</i> , of the sea, marine | Inferred to break down a wide range of organic carbon substrates (Chitin, Mucin, Xylan, Cellulose and Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Encodes genes for nitrate uptake (NRT2), thiosulfate oxidation (soxABCDXYZ), sulphate assimilation (cys), phosphorus uptake and regulation (pho, pst), polyphosphate kinase and phosphatase (ppa). Can perform osmoregulation (trkA, nqrF, nhaC) and is possibly motile (fliGMN, motAB). Based on the genome reporting standards for MAGs , the estimated completeness was 91.02%, contamination 1.36%, and the presence of the 5S (110bp), 16S (1,532 bp), and 23S (2,880 bp) rRNA gene and 42 tRNAs. Type genome is defined as "high-quality" draft MAG, with genome size of 3.3Mbps. | <i>Salivita</i>       | NCBI Assembly:<br>GCA_038144425.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46742">seqco.de/i:46742</a> |

| Proposed Taxon  | Etymology  | Description  | Parent Taxon         | Type   | Registry URL  |
|---|--|--|----------------------|--|---|
| Species <i>Eutrophovita brisbanensis</i> <sup>Ts</sup>  | [bris.ba.nen'sis] N.L. fem. adj. <i>brisbanensis</i> , of or belonging to Brisbane | Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Cellulose and Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Encodes genes for urea uptake and degradation (ureABC, urtABCDE), phosphorus uptake and regulation (pho, pst), polyphosphate kinase (ppk1), pyrroquinoline quinone (pqqC), thiosulfate oxidation (sox) and sulphate assimilation (cys). Based on the genome reporting standards for MAGs , the estimated completeness 92.77%, contamination 0.61%, and the presence of the 16S (1,532 bp), and 23S (2,933 bp) rRNA gene and 37 tRNAs. Type genome is defined as “high-quality” draft MAG,with genome size of 2.1 Mbps.  | <i>Eutrophovita</i>  | NCBI Assembly:<br>GCA_038147395.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46740">seqco.de/i:46740</a> |
| Species <i>Eutrophocola salsuginis</i> <sup>Ts</sup>    | [sa.lu'gi.nis] L. gen. n. <i>salsuginis</i> , of the brackish water                | Inferred to break down a Chitin and Pectin, as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Carries genes for nitrate uptake (NRT2) and anaerobic dissimilatory nitrate reduction (nirBD). Capable of sulfate assimilation (cys), phosphorus uptake and regulation (pho, pst) and polyphosphate accumulation (ppk1). Likely performing osmoregulation using trk1 (K+ transporter) and proXV (Glycine betaine) and inferred to be motile (fliGMN, motAB gene). Based on the genome reporting standards for MAGs , the estimated completeness was 93.58%, contamination 1.79%, and the presence of the 5S (106bp), 16S (1,551 bp), and 23S (2,877 bp) rRNA gene and 42 tRNAs. Type genome is defined as “high-quality” draft MAG,with genome size of 3Mbps. | <i>Eutrophocola</i>  | NCBI Assembly:<br>GCA_038147195.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46744">seqco.de/i:46744</a> |
| Species <i>Salsuginivita brisbanensis</i> <sup>Ts</sup> | [bris.ban.en'sis] N.L. fem. adj. <i>brisbanensis</i> , of or belonging to Brisbane | Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Mucin, Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Capable of nitrate uptake (NRT2), phosphorus uptake and regulation (pho, pst), polyphosphate accumulation (ppk1) and noted absence of osmoregulation genes. Based on the genome reporting standards for MAGs , the estimated completeness was 98.63%, contamination 0%, and the presence of the 16S (1,555 bp), and 23S (2, 882bp) rRNA gene and 46 tRNAs. Type genome is defined as “high-quality” draft MAG,with genome size of 2.5Mbps.   | <i>Salsuginivita</i> | NCBI Assembly:<br>GCA_038144975.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46749">seqco.de/i:46749</a> |

| Proposed Taxon  | Etymology  | Description  | Parent Taxon          | Type   | Registry URL  |
|---|--|--|-----------------------|--|---|
| Species <i>Salinivivens marinus</i> <sup>Ts</sup>       | [ma.ri'nus] L. <b>masc. adj.</b> <i>marinus</i> , of the sea                               | Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Cellulose and Starch). Capable of performing aerobic anoxygenic photosynthesis (pufLM), and thiosulfate oxidation (soxABCDXYZ), likely performing osmoregulation using trk1 (K <sup>+</sup> transporter) and proXV (Glycine betaine) and inferred to be motile (fliGMN, motAB gene). Also carries genes for phosphorus uptake and regulation (pho, pst). Based on the genome reporting standards for MAGs, the estimated completeness 94.41%, contamination 0.3%, and the presence of the 5S (108 bp), 16S (1,457 bp), and 23S (2, 718bp) rRNA gene and 32 tRNAs. Type genome is defined as "high-quality" draft MAG, with genome size of 2.6 Mbps                             | <i>Salinivivens</i>   | NCBI Assembly:<br>GCA_038142605.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46736">seqco.de/i:46736</a> |
| Species <i>Eutrophomonas brisbanensis</i> <sup>Ts</sup> | [bris.ban.en'sis] N.L. <b>fem. adj.</b> <i>brisbanensis</i> , of or belonging to Brisbane  | Inferred to break down a wide range of organic carbon substrates (Chitin, Pectin, Cellulose and Starch) as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Encodes genes for urea uptake and degradation (ureABC, urtABCDE), phosphorus uptake and regulation (pho, pst), pyrroquinoline quinone (pqqC), nitrate uptake (NRT2), thiosulfate oxidation (sox) and sulphate assimilation (cys). There is noted absence of osmoregulation genes. Based on the genome reporting standards for MAGs, the estimated completeness 98.78%, contamination 0%, and the presence of the 16S (1,532 bp), and 23S (2, 933 bp) rRNA gene and 40 tRNAs. Type genome is defined as "high-quality" draft MAG, with one contig and genome size of 2.1 Mbps. | <i>Eutrophomonas</i>  | NCBI Assembly:<br>GCA_038141705.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46738">seqco.de/i:46738</a> |
| Species <i>Nitrosopumilus brisbanensis</i>              | [bris.ban.en'sis] N.L. <b>masc. adj.</b> <i>brisbanensis</i> , of or belonging to Brisbane | Based on the genome reporting standards for MAGs, the estimated completeness was 98.63%, contamination 0%, and the presence of the 5S (111 bp), 16S (1,464 bp), and 23S (3,117 bp) rRNA gene and 43 tRNAs. Type genome is defined as "high-quality" draft MAG, with genome size of 1.3Mbps   | <i>Nitrosopumilus</i> | NCBI Assembly:<br>GCA_038152885.1<br><sup>Ts</sup> | <a href="https://seqco.de/i:46747">seqco.de/i:46747</a> |



| Proposed Taxon   | Etymology  | Description   | Parent Taxon               | Type  | Registry URL   |
|--|--|---|----------------------------|---|--|
| <p><i>Species Eutrophobius brisbanensis</i><sup>Ts</sup></p> | <p>[bris.ban.en'sis] N.L. <b>masc. adj.</b> <i>brisbanensis</i>, of or belonging to Brisbane</p> | <p>Inferred to break down a Chitin and Cellulose as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Likely performing sulfate assimilation (cys), polyphosphate accumulation (ppk1) and osmoregulation (trkA, nqrF, mnh). Based on the genome reporting standards for MAGs , the estimated completeness was 98.24%, contamination 0.88%, and the presence of the 5S (110bp), 16S (1.540 bp), and 23S (2,877 bp) rRNA gene and 46 tRNAs. Type genome is defined as “high-quality” draft MAG,with genome size of 2.7Mbps.</p> | <p><i>Eutrophobius</i></p> | <p>NCBI Assembly:<br/>GCA_038131795.1<br/><sup>Ts</sup></p> | <p><a href="https://seqco.de/i:46746">seqco.de/i:46746</a></p> |