

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

Submitted by Chuvochina, Maria

## Order *Australimonadales*

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### Etymology

[Aus.tra.li.mo.na.da'les] N.L. fem. n. *Australimonas*, type genus of the order; *-ales*, ending to denote an order; N.L. fem. pl. n. *Australimonadales*, the Australimonas order

### Nomenclatural type

Genus *Australimonas*

### Description

The description of Australimonadales is the same as that of Australimonas. The former name for this order is UBA2963.

### Classification

*Bacteria* » *Chloroflexota* » *Dehalococcoidia* » *Australimonadales*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46751>

## Order *Eutrophobiales*

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### Etymology

[Eu.tro.pho.bi.a'les] N.L. masc. n. *Eutrophobius*, type genus of the order; *-ales*, ending to denote an order; N.L. fem. pl. n. *Eutrophobiales*, the Eutrophobius order

### Nomenclatural type

Genus *Eutrophobius*

### Description

The description of Eutrophobiales is the same as that of Eutrophobius. The former name for this order is UBA4486.

### Classification

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Eutrophobiales*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46757>

## Family *Australimonadaceae*

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### Etymology

[Aus.tra.li.mo.na.da.ce'ae] N.L. fem. n. *Australimonas*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Australimonadaceae*, the Australimonas family

### Nomenclatural type

Genus *Australimonas*

**Description**

The description of Australimonadaceae is the same as for Australimonas. The former name for this family is UBA2963.

**Classification**

*Bacteria* » *Chloroflexota* » *Dehalococcoidia* » *Australimonadales* » *Australimonadaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46750>

## Family *Marisalimonadaceae*

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**Etymology**

[Ma.ri.sa.li.mo.na.da.ce'ae] N.L. fem. n. *Marisalimonas*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Marisalimonadaceae*, the *Marisalimonas* family

**Nomenclatural type**

Genus *Marisalimonas*

**Description**

The description of Marisalimonadaceae is the same as for Marisalimonas. The former name for this family is AAA536-G10.

**Classification**

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Puniceispirillales* » *Marisalimonadaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46752>

## Family *Salivitaceae*

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**Etymology**

[Sa.li.vi.ta.ce'ae] N.L. fem. n. *Salivita*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Salivitaceae*, the *Salivita* family

**Nomenclatural type**

Genus *Salivita*

**Description**

The description of Salivitaceae is the same as that of Salivita. The former name for this family is HTCC2089.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Salivitaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46755>

## Family *Eutrophomonadaceae*

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**Etymology**

[Eu.tro.pho.mo.na.da.ce'ae] N.L. fem. n. *Eutrophomonas*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Eutrophomonadaceae*, the Eutrophomonas family

**Nomenclatural type**

Genus *Eutrophomonas*

**Description**

The description of Eutrophomonadaceae is the same as that of Eutrophomonas. The former name for this family is UBA3031.

**Classification**

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophomonadaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46753>

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**Family *Eutrophobiaceae***

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**Etymology**

[Eu.tro.pho.bi.a.ce'ae] N.L. masc. n. *Eutrophobius*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Eutrophobiaceae*, the Eutrophobius family

**Nomenclatural type**

Genus *Eutrophobius*

**Description**

The description of Eutrophobiaceae is same as that of Eutrophobius. The former name for this family is UBA4486.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Eutrophobiales* » *Eutrophobiaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46756>

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**Family *Eutrophovitaceae***

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**Etymology**

[Eu.tro.pho.vi.ta.ce'ae] N.L. fem. n. *Eutrophovita*, type genus of the family; *-aceae*, ending to denote a family; N.L. fem. pl. n. *Eutrophovitaceae*, the Eutrophovita family

**Nomenclatural type**

Genus *Eutrophovita*

**Description**

The description of Eutrophovitaceae is same as that of Eutrophovita. The former name for this family is UBA3031.

**Classification**

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophovitaceae*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46754>

## Genus *Australimonas*

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### Etymology

[Aus.tra.li.mo'nas] L. adj. *australis*, southern; N.L. fem. n. *monas*, a unit; N.L. fem. n. *Australimonas*, a unit from the south, referring to Australia where the organism was found

### Nomenclatural type

Species *Australimonas brisbanensis*<sup>Ts</sup>

### Description

The description is identical to that of the type species.

### Classification

*Bacteria* » *Chloroflexota* » *Dehalococcoidia* » *Australimonadales* » *Australimonadaceae* » *Australimonas*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46730>

## Genus *Marisalimonas*

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### Etymology

[Ma.ri.sa.li.mo'nas] L. neut. n. *mare*, the sea; L. masc. n. *sal*, salt; N.L. fem. n. *monas*, a unit; N.L. fem. n. *Marisalimonas*, a microbe occurring in saline conditions in the sea

### Nomenclatural type

Species *Marisalimonas marina*<sup>Ts</sup>

### Description

The former name for this genus is AAA536-G10. The description is identical to that of the type species.

### Classification

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Puniceispirillales* » *Marisalimonadaceae* » *Marisalimonas*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46734>

## Genus *Salsuginivita*

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### Etymology

[Sal.su.gi.ni.vi'ta] L. fem. n. *salsugo*, brackish water; L. fem. n. *vita*, life; N.L. fem. n. *Salsuginivita*, a bacterium found in brackish habitats

### Nomenclatural type

Species *Salsuginivita brisbanensis*<sup>Ts</sup>

### Description

The former name for this genus is CAIYFD01. The description is identical to that of the type species.

### Classification

*Bacteria* » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Opitutaceae* » *Salsuginivita*

### References

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46748>

## Genus *Salivita*

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**Etymology**

[Sa.li.vi'ta] L. **masc. n.** *sal*, salt; L. **fem. n.** *vita*, life; N.L. **fem. n.** *Salivita*, an organism associated with saltwater

**Nomenclatural type**

Species *Salivita marina*<sup>Ts</sup>

**Description**

The former name for this genus is RGAU01. The description is identical to that of the type species.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Salivitaceae* » *Salivita*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46741>

## Genus *Eutrophobius*

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**Etymology**

[Eu.tro.pho.bi'us] Gr. **adv.** *eú*, good; Gr. **adj.** *trophos*, feeder; Gr. **masc. n.** *bios*, life; N.L. **masc. n.** *Eutrophobius*, life associated with eutrophic environments

**Nomenclatural type**

Species *Eutrophobius brisbanensis*<sup>Ts</sup>

**Description**

This is a novel group of the family and order UBA4486. The description is identical to that of the type species.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Eutrophobiales* » *Eutrophobiaceae* » *Eutrophobius*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46745>

## Genus *Eutrophocola*

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**Etymology**

[Eu.tro.pho.co'la] Gr. **adv.** *eú*, good; Gr. **adj.** *trophos*, feeder; L. **masc. / fem. suff.** *cola*, inhabitant; N.L. **fem. n.** *Eutrophocola*, referring to a microbe in eutrophic aquatic environments

**Nomenclatural type**

Species *Eutrophocola salsuginis*<sup>Ts</sup>

**Description**

The former name for this genus is RFVC01. The description is identical to that of the type species.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Pseudohongiellaceae* » *Eutrophocola*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46743>

## Genus *Eutrophomonas*

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### Etymology

[Eu.tro.pho.mo'nas] Gr. adv. *eû*, good; Gr. adj. *trophos*, feeder; L. fem. n. *monas*, a unit; N.L. fem. n. *Eutrophomonas*, a unit associated with eutrophic environments

### Nomenclatural type

Species *Eutrophomonas brisbanensis*<sup>Ts</sup>

### Description

This is a novel group of the family UBA3031 within order Burkholderiales. The description is identical to that of the type species.

### Classification

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophomonadaceae* » *Eutrophomonas*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46737>

## Genus *Eutrophosalina*

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### Etymology

[Eu.tro.pho.sa.li'na] Gr. adj. *eû*, good; Gr. adj. *trophos*, feeder; N.L. fem. adj. *salina*, salty; N.L. fem. n. *Eutrophosalina*, a microbe adapted to eutrophic and saline environments

### Nomenclatural type

Species *Eutrophosalina marina*<sup>Ts</sup>

### Description

The former name for this genus is MED-G14. The description is identical to that of the type species.

### Classification

*Bacteria* » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Eutrophosalina*

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46728>

## Genus *Eutrophovita*

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### Etymology

[Eu.tro.pho.vi'ta] Gr. adv. *eû*, good; Gr. masc. / fem. adj. *trophos*, feeder; L. fem. n. *vita*, life; N.L. fem. n. *Eutrophovita*, an organism associated with eutrophic environments

### Nomenclatural type

Species *Eutrophovita brisbanensis*<sup>Ts</sup>

**Description**

This is a novel group of the family UBA3031 within order Burkholderiales. The description is identical to that of the type species.

**Classification**

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophovitaceae* » *Eutrophovita*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46739>

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**Genus *Salinivivens***

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**Etymology**

[Sa.li.ni.vi'vens] N.L. masc. adj. *salinus*, saline; L. part. adj. *vivens*, living; N.L. masc. n. *Salinivivens*, a microbial organism thriving in saline conditions

**Nomenclatural type**

Species *Salinivivens marinus*<sup>Ts</sup>

**Description**

The former name for this genus is MED-G52. The description is identical to that of the type species.

**Classification**

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Salinivivens*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:44234>

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**Species *Marisalimonas marina*<sup>Ts</sup>**

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**Etymology**

[ma.ri'na] L. fem. adj. *marina*, of the sea, marine

**Nomenclatural type**

[NCBI Assembly: GCA\\_038131365.1](https://ncbi.nlm.nih.gov/assembly/GCA_038131365.1)<sup>Ts</sup>

**Description**

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 1.9Mbp.

**Classification**

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Puniceispirillales* » *Marisalimonadaceae* » *Marisalimonas* » *Marisalimonas marina*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46735>

## Species *Australimonas brisbanensis*<sup>Ts</sup>

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### Etymology

[bris.ban.en'sis] N.L. fem. adj. *brisbanensis*, of or belonging to Brisbane

### Nomenclatural type

[NCBI Assembly: GCA\\_038147155.1](#)<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Chloroflexota* » *Dehalococcoidia* » *Australimonadales* » *Australimonadaceae* » *Australimonas* » *Australimonas brisbanensis*<sup>Ts</sup>

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46731>

## Species *Eutrophosalina marina*<sup>Ts</sup>

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### Etymology

[ma.ri'na] L. fem. adj. *marina*, of the sea, marine

### Nomenclatural type

[NCBI Assembly: GCA\\_038147175.1](#)<sup>Ts</sup>

### Description

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.

### Classification

*Bacteria* » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Eutrophosalina* » *Eutrophosalina marina*<sup>Ts</sup>

### References

Effective publication: Prabhu et al., 2024 [1]

### Registry URL

<https://seqco.de/i:46729>

## Species *Salivita marina*<sup>Ts</sup>

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### Etymology

[ma.ri'na] L. fem. adj. *marina*, of the sea, marine

### Nomenclatural type

[NCBI Assembly: GCA\\_038144425.1](#)<sup>Ts</sup>



**Description**

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.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Salivitateae* » *Salivita* » *Salivita marina*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46742>

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**Species *Eutrophovita brisbanensis*<sup>Ts</sup>**

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**Etymology**

[bris.ba.nen'sis] N.L. fem. adj. *brisbanensis*, of or belonging to Brisbane

**Nomenclatural type**

[NCBI Assembly: GCA\\_038147395.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophovitateae* » *Eutrophovita* » *Eutrophovita brisbanensis*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46740>

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**Species *Eutrophocola salsuginis*<sup>Ts</sup>**

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**Etymology**

[sal.su'gi.nis] L. gen. n. *salsuginis*, of the brackish water

**Nomenclatural type**

[NCBI Assembly: GCA\\_038147195.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Pseudohongiellaceae* » *Eutrophocola* » *Eutrophocola salsuginis*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46744>

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**Species *Salsuginivita brisbanensis*<sup>Ts</sup>**

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**Etymology**

[bris.ban.en'sis] N.L. fem. adj. *brisbanensis*, of or belonging to Brisbane

**Nomenclatural type**

[NCBI Assembly: GCA\\_038144975.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Verrucomicrobiota* » *Opitutia* » *Opitutales* » *Opitutaceae* » *Salsuginivita* » *Salsuginivita brisbanensis*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46749>

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**Species *Salinivivens marinus*<sup>Ts</sup>**

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**Etymology**

[ma.ri'nus] L. masc. adj. *marinus*, of the sea

**Nomenclatural type**

[NCBI Assembly: GCA\\_038142605.1](#)<sup>Ts</sup>

**Description**

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

**Classification**

*Bacteria* » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Salinivivens* » *Salinivivens marinus*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46736>

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**Species *Eutrophomonas brisbanensis*<sup>Ts</sup>**

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**Etymology**

[bris.ban.en'sis] N.L. fem. adj. *brisbanensis*, of or belonging to Brisbane

**Nomenclatural type**

[NCBI Assembly: GCA\\_038141705.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Eutrophomonadaceae* » *Eutrophomonas* » *Eutrophomonas brisbanensis*<sup>Ts</sup>

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46738>

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**Species *Nitrosopumilus brisbanensis***

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**Etymology**

[bris.ban.en'sis] N.L. masc. adj. *brisbanensis*, of or belonging to Brisbane

**Nomenclatural type**

[NCBI Assembly: GCA\\_038152885.1](#)<sup>Ts</sup>

**Description**

Based on the genome reporting standards for MAGs, the estimated completeness was 98.63%, contamination 0%, and the presence of the %S (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

**Classification**

*Archaea* » *Thermoproteota* » *Nitrososphaeria* » *Nitrosopumilales* » *Nitrosopumilaceae* » *Nitrosopumilus* » *Nitrosopumilus brisbanensis*

**References**

Effective publication: Prabhu et al., 2024 [1]

**Registry URL**

<https://seqco.de/i:46747>

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**Species *Eutrophobius brisbanensis*<sup>Ts</sup>**

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**Etymology**

[bris.ban.en'sis] N.L. masc. adj. *brisbanensis*, of or belonging to Brisbane

**Nomenclatural type**

[NCBI Assembly: GCA\\_038131795.1](#)<sup>Ts</sup>

**Description**

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.

**Classification**

*Bacteria* » *Pseudomonadota* » *Gammaproteobacteria* » *Eutrophobiales* » *Eutrophobiaceae* » *Eutrophobius* » *Eutrophobius brisbanensis*<sup>Ts</sup>

**References**

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**References**

1. Prabhu et al. (2024). Machine learning and metagenomics identifies uncharacterized taxa inferred to drive biogeochemical cycles in a subtropical hypereutrophic estuary. *ISME Communications*.  
[DOI:10.1093/ismeco/ycae067](https://doi.org/10.1093/ismeco/ycae067)

## Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List [seqco.de/r:sfdglxu8](https://seqco.de/r:sfdglxu8) submitted by **Chuvochina, Maria** and including 29 new names has been successfully validated.

**Date of Priority:** 2024-08-12 01:22 UTC

**DOI:** 10.57973/seqcode.r:sfdglxu8

