

Species *Rhodoferax mariagerensis*

Etymology

[ma.ri.a.ge.ren'sis] **N.L. masc. adj.** *mariagerensis*, of the city of Mariager where the MAG was obtained

Nomenclatural type

[NCBI Assembly: GCA_016719055.1](#) ^{Ts}

Description

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*

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Rhodoferax* » *Rhodoferax mariagerensis*

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

<https://seqco.de/i:44118>

References

1. Petersen et al. (2025). Diversity and physiology of abundant *Rhodoferax* species in global wastewater treatment systems. *Systematic and Applied Microbiology*.
[DOI:10.1016/j.syapm.2024.126574](https://doi.org/10.1016/j.syapm.2024.126574)