

## Species *Rhodoferax bjergmarkensis*

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### Etymology

[bjerg.mar.ken'sis] **N.L. masc. adj.** *bjergmarkensis*, of the city of Bjergmarken, from where the MAG was obtained

### Nomenclatural type

[NCBI Assembly: GCA\\_016708345.1](#) <sup>Ts</sup>

### 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*).

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

### Classification

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

### References

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

### Registry URL

<https://seqco.de/i:44117>

## 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)