Species *Rhodoferax randersensis*

Etymology

[ran.der.sen'sis] **N.L. masc. adj.** *randersensis*, from the city Randers where the MAG had been retrieved

Nomenclatural type

NCBI Assembly: GCA_016718155.1 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.
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* 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 randersensis*

References

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

Registry URL

https://seqco.de/i:44115

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