Species *Aalborgicola defluviihabitans*^{Ts}

Etymology

[de.flu.vii.ha'bi.tans] **L. neut. n.** *defluvium*, sewage; **L. pres. part.** *habitans*, inhabiting; **L. masc. part. adj.** *defluviihabitans*, pertaining to the habitat where the MAG was sequenced from.

Nomenclatural type

NCBI Assembly: GCA_016705575.1 ^{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* » *Burkholderiaceae* » *Aalborgicola* » *Aalborgicola defluviihabitans*^{Ts}

References

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

Registry URL

https://seqco.de/i:44105

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