

Genus *Egaibacter*

Etymology

[E.ga.i.bac'ter] **N. L. masc. n.** *Egaa*, the city Egaa where the MAG had been retrieved; **N.L. masc. n.** *bacter*, bacterium; **N.L. masc. n.** *Egaibacter*, indicating a bacterium found in Egaa

Nomenclatural type

Species *Egaibacter danicus*^{Ts}

Description

Genus of bacteria found in activated sludge.

Species generally have the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway.

They can also utilize branched chain amino acids (livFGHKM).

Predicted to convert acetate to acetyl-CoA via acetyl-CoA synthetase, *acs*.

Potential to reduce nitrate with narGHI along with the reduction of nitrate to nitric oxide with nirS.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Egaibacter*

References

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

Registry URL

<https://seqco.de/i:44121>

References

1. Petersen et al. (2025). Diversity and physiology of abundant Rhodoferrax 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)