

## Species *Egaibacter danicus*<sup>Ts</sup>

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### Etymology

[da'ni.cus] **L. masc. adj.** *danicus*, Danish

### Nomenclatural type

[NCBI Assembly: GCA\\_016707075.1](#)<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.

Glucose uptake of via the *gtsABC+malK* transporter was also predicted.

Can 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* » *Egaibacter danicus*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:44120>

## 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)