Species *Cloacimonas fortuita*

Etymology
[for.tu.i'ta] **L. fem. adj.** *fortuita*, accidental, fortuitous, by chance; referring to the accidental isolation of the strain

Nomenclatural type
NCBI Assembly: GCA_056337045.1 [Ts]

Description
Cloacimonas fortuita was co-isolated from an enrichment culture of a methanogenic reactor containing anaerobic wastewater sludge, alongside its archaeal syntrophic partner *Methanothrix* and other minor bacterial species. The genome of this species is 1.98 Mb in length, with a GC content of 36.6%, and encodes 1591 genes, including 1529 protein-coding genes. Based on the functional annotation, it is presumed to perform syntrophic propionate oxidation via an alternative pathway. Genome of this species and its relative *C. acidaminovorans* have an Average Nucleotide Identity of 78.3%, which is below the species-level cut-off (95%) but above the genus-level threshold (>70%). Therefore, we would like to claim a new species within the known *Cloacimonas* genus.

Classification
Bacteria » *Cloacimonadota* » *Cloacimonadia* » *Cloacimonadales* » *Cloacimonadaceae* » *Cloacimonas* » *Cloacimonas fortuita*

References
Effective publication: Calusinska et al., 2026 [1]

Registry URL
https://seqco.de/i:52907

References

1. Calusinska et al. (2026). Phylum-wide propionate degradation and its potential connection to poly-gamma-glutamate biosynthesis in *Candidatus* Cloacimonadota phylum. *The ISME Journal*. DOI:10.1093/ismejo/wrag055