

# New species (and genus) belonging to Cloacimonadota

Submitted by Klimek, Dominika

## Genus *Digestoria*

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### Etymology

[Di.ges.to'ri.a] **L. fem. adj.** *digestoria*, promoting digestion; **N.L. fem. n.** *Digestoria*, a microbe promoting digestion, referring to its role in anaerobic digestion

### Nomenclatural type

Species *Digestoria delfosse*<sup>Ts</sup>

### Description

Bacteria associated with this genus belong to the *Cloacimonadota* phylum and have been found mainly in anaerobic digestion systems so far.

### Classification

*Incertae sedis* (Bacteria) » *Digestoria*

### References

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

### Registry URL

<https://seqco.de/i:52909>

## Species *Cloacimonas fortuita*

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### 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](#)<sup>Ts</sup>

### 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>

## Species *Digestoria delfosse*<sup>ts</sup>

### Etymology

[del.fos.se'i] **N.L. gen. n.** *delfosse*, of Delfosse, named in honor of former group leader, Dr. Philippe Delfosse

### Nomenclatural type

[NCBI Assembly: GCA\\_056337095.1](#)<sup>Ts</sup>

### Description

The genome of *Digestoria delfosse* in OTU\_1 is complete and closed, 2.3 Mbp long, with a GC content of 54.3%, and it contains two rRNA operons. The species represents a distinct lineage defined by ANI  $\geq$  95% to its known relatives. Therefore, only the novel genus and species are formally established, while all higher-level ranks remain unnamed pending further phylogenomic resolution of the phylum. *D. delfosse* encodes a complete glycolysis pathway with exception for pyruvate kinase, previously shown to be replaced by pyruvate orthophosphate dikinase in *Cloacimonadota* genomes, and the microorganism can oxidize pyruvate further to acetyl-CoA and acetate. It is capable of beta-oxidation and protein degradation (i.e., encoding multiple peptidases) with a complete metabolism of histidine to glutamate.

### Classification

*Incertae sedis* (Bacteria) » *Digestoria* » *Digestoria delfosse*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:55908>

## 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

## Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:d2lcq-ea** submitted by **Klimek, Dominika** and including 3 new names has been successfully validated.

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