

# Cloacimonas acidaminivorans sp. nov. and Cloacimonas gen. nov.

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## Genus *Cloacimonas*

### Etymology

[Clo.a.ci.mo'nas] L. fem. n. *cloaca*, sewer; N.L. fem. n. *monas*, monad; N.L. fem. n. *Cloacimonas*, a monad from a sewer

### Nomenclatural type

Species *Cloacimonas acidaminivorans*<sup>Ts</sup>

### Description

The description is the same as that for *Cloacimonas acidaminivorans*.

### Classification

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

### References

Effective publication: Pelletier et al., 2008 [1]  
*Corrigendum*: Oren et al., 2020 [2] (from "Cloacamonas")

### Registry URL

<https://seqco.de/i:220>

## Species *Cloacimonas acidaminivorans*<sup>Ts</sup>

### Etymology

[a.ci.da.mi.ni.vo'rans] N.L. neut. n. *acidum aminum*, amino acid; L. pres. part. *vorans*, devouring; N.L. fem. part. adj. *acidaminivorans*, amino acid-devouring

### Nomenclatural type

[NCBI Assembly: GCA\\_000146065.1](#)<sup>Ts</sup>

### Description

The complete genome of this species has been reconstructed following the metagenomic sequencing of the sludge sample obtained from the anaerobic mesophilic digester (7,000 m<sup>3</sup>) at the Evry wastewater treatment plant (250,000 population equivalents), located about 35 km south of Paris, France (48°37' 33.65"N, 2°27'53.34"E). The genome of this species is represented by a single circular chromosome consisting of 2,246,820 nucleotides with a GC content of 37.9%. The presence of the enzymes involved in the biosynthesis of lipopolysaccharides indicates that is a gram-negative bacterium, which is supported by the detection of the typical signature of gram-negative bacteria found in the *dnaK* gene. The in silico proteome analysis suggests that this species could grow on a medium that includes glucose, alanine, asparagine, aspartate, glutamate, histidine, lysine, proline, serine, and certain aliphatic carboxylic acids (succinate, lactate, and acetate). The species is inferred to be adapted to an anaerobic lifestyle and also may enable to survive under minimal oxygen concentrations. In silico proteome analysis indicated that this species might derive most of its carbon and energy from the fermentation of amino acids and it is probably a syntrophic bacterium.

### Classification

*Bacteria* » *Cloacimonadota* » *Cloacimonadia* » *Cloacimonadales* » *Cloacimonadaceae* » *Cloacimonas* » *Cloacimonas acidaminivorans*<sup>Ts</sup>

## References

Effective publication: Pelletier et al., 2008 [1]

*Corrigendum*: Oren et al., 2020 [2] (from “*Cloacamonas acidaminovorans*”)

## Registry URL

<https://seqco.de/i:173>

## References

1. Pelletier et al. (2008). “*Candidatus Cloacamonas Acidaminovorans*”: Genome Sequence Reconstruction Provides a First Glimpse of a New Bacterial Division. *Journal of Bacteriology*. [DOI:10.1128/jb.01248-07](https://doi.org/10.1128/jb.01248-07)
2. Oren et al. (2020). Lists of names of prokaryotic *Candidatus* taxa. *International Journal of Systematic and Evolutionary Microbiology*. [DOI:10.1099/ijsem.0.003789](https://doi.org/10.1099/ijsem.0.003789)

## 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:tz5nceub](https://seqco.de/r:tz5nceub) submitted by **Chuvochina, Maria** and including 2 new names has been successfully validated.

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