

## Genus *Aceula*

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### Etymology

[Ace.u'la] N.L. fem. dim. n. *Aceula*, from the name of the locality (Ace Lake).

### Nomenclatural type

Species *Aceula laticola*<sup>Ts</sup>

### Description

The description for this genus is derived from Williams et al., 2021, and supplemented with additional information. Genome predictions designate this genus as heterotrophic and capable of the fermentation of glucose to acetyl-CoA through EMP pathway. Proteases and peptidases for the degradation of proteins to amino acids are present. Additionally, simple sugar transport and glycoside hydrolases are encoded by the genome and genes required for the synthesis of trehalose and glycogen are also present (Williams et al., 2021). A V-type ATPase, respiratory F-type ATPase and Rnf complex for ATP synthesis, and a Group 3d [NiFe] hydrogenase are present (Williams et al., 2021). All genes required for the tight-adherence complex and the production of a Type-4a pilus are present. The nomenclatural type for the genus is *Aceula laticola*, (genome designated 3300035698\_1100).

### Classification

*Bacteria* » *Omnitrophota* » “Velamenicoccia” » “Zapsychrales” » “Aceulaceae” » *Aceula*

### References

Effective publication: Williams et al., 2021 [1]

### Registry URL

<https://seqco.de/i:33275>

## References

1. Williams et al. (2021). Shedding Light on Microbial “Dark Matter”: Insights Into Novel Cloacimonadota and Omnitrophota From an Antarctic Lake. *Frontiers in Microbiology*. DOI:10.3389/fmicb.2021.741077