Species *Ventrimonas faecis*ᵀ

Etymology
[fae'cis] **L. gen. n.** *faecis*, of dregs, pertaining to faeces, from where the type strain was isolated

Nomenclatural type
Strain: CLA AP-H27 = DSM 118072 = GCA_040096075 = GCA_040096075.1 = LMG 33600

Description
The genome size is 3.41 Mbp, G+C percentage is 49.27%, with 98.73% completeness and 0.63% contamination. Functional analysis showed the strain has 156 transporters, 21 secretion genes, and predicted utilization of starch, and production of acetate, propionate, L-glutamate, cobalamin, and folate. In total, 139 CAZymes were identified, with 21 different glycoside hydrolase families and 12 glycoside transferase families represented. The strain CLA-AP-H27 (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Ventrimonas* » *Ventrimonas faecis*ᵀ

References
Effective publication: Hitch et al., 2025 [1]

Registry URL
https://seqco.de/i:48228

References

1. Hitch et al. (2025). HiBC: a publicly available collection of bacterial strains isolated from the human gut. *Nature Communications*. DOI:10.1038/s41467-025-59229-9