
Species *Blautia caccae*

Etymology

[cac'cae] **N.L. gen. n.** *caccae*, of faeces, referring to the source of isolate

Nomenclatural type

Strain: CLA SR-H028 = DSM 118556 = LMG 33609

Description

The genome size is 5.83 Mbp, G+C percentage is 46.73%, with 98.73% completeness and 0.63% contamination. The closest relative to strain CLA-SR-H028 was *Blautia hominis* (98.66%) based on 16S rRNA gene analysis. ANI comparison identified CLA-SR-H028 as a novel species within the genus *Blautia*, with all values being below the species threshold. GTDB-Tk classification as 'Blautia sp001304935' confirmed the proposition of a novel species within *Blautia*. Functional analysis showed the strain has 158 transporters, 18 secretion genes, and predicted utilization of cellobiose, sucrose, starch and production of propionate, acetate, cobalamin, and folate. In total, 353 CAZymes were identified, with 53 different glycoside hydrolase families and 15 glycoside transferase families represented. The strain CLA-SR-H028 (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Blautia* » *Blautia caccae*

References

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

Registry URL

<https://seqco.de/i:48044>

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](https://doi.org/10.1038/s41467-025-59229-9)