

## Species *Ruthenibacterium intestinale*

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### Etymology

[in.tes.ti.na'le] **N.L. neut. adj.** *intestinale*, pertaining to the intestine, from where the type strain was isolated

### Nomenclatural type

Strain: CLA-JM-H11 = DSM 114604 = LMG 33032

### Description

The genome size is 3.1 Mbp, G+C percentage is 54.69%, with 98.3% completeness and 0.0% contamination. It contains a plasmid (5,063 bp). The closest relative to strain CLA-JM-H11 is *Ruthenibacterium lactatiformans* (94.93%), the type species of this genus, based on 16S rRNA gene analysis. Placement of the isolate within the genus *Ruthenibacterium* was confirmed based on POCP comparison, with a value of 56.41% to the type species. Strain CLA-JM-H11 was confirmed to be distinct to *R. lactatiformans* based on ANI comparison (79.28%). GTDB-Tk classification confirmed this assignment as an unknown species within *Ruthenibacterium*. Functional analysis showed the strain has 143 transporters, 16 secretion genes, and predicted utilization of starch, and production of acetate, propionate, folate, and cobalamin. In total, 155 CAZymes were identified, with 27 different glycoside hydrolase families and 13 glycoside transferase families represented. The strain CLA-JM-H11 (phylum *Bacillota*, family *Oscillospiraceae*) was isolated from human faeces.

### Classification

*Bacteria* » *Bacillota* » *Clostridia* » *Eubacteriales* » *Oscillospiraceae* » *Ruthenibacterium* » *Ruthenibacterium intestinale*

### References

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

### Registry URL

<https://seqco.de/i:48068>

## 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