

## Identification of d -arabinan-degrading enzymes in mycobacteria

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*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection

Detailed methods are in the manuscript, however we used Chromeleon V.6.8 for all HPLC analysis.

Data analysis

Graphpad Prism v8.0.1 or v9.3.1 was used for graphing/plotting/statistical analysis. Proteomics were analysed using MaxQuant version 1.6.12.052. RNASeq was analysed by Rsubread package. IQ-TREE v.1.6.12 was used to generate maximum likelihood phylogenies using automatic model selection and ClustalOmega was used for alignments.

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The proteomics dataset was deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD039984 (<http://www.ebi.ac.uk/pride/archive/projects/PXD039984>). For RNASeq experiments raw sequencing reads were mapped to Bacteroides cellulosilyticus DSM 14838 (GCA\_000158035) downloaded from Ensembl (assembly ID ASM15803v1).

## Human research participants

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Reporting on sex and gender

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

N/A

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

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## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

No statistical method was used to pre-determine sample size. For statistical analysis at least three biological replicates were used.

Data exclusions

No data were excluded.

Replication

For all analysis at least 2 technical replicates but typically 3 were used. Replication of the data was successful and no data has been omitted.

Randomization

The experimental design does not require randomization.

Blinding

No blinding was applied due to the nature of these experiments.

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## Methods

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<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
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