Resource Summary Report

Generated by NIF on May 16, 2025

MGnify

RRID:SCR_016429
Type: Tool

Proper Citation

MGnify (RRID:SCR_016429)

Resource Information

URL: https://www.ebi.ac.uk/metagenomics/

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Description: Portal for the analysis and exploration of metagenomic, metatranscriptomic, amplicon and assembly data. Provides functional and taxonomic analyses of user-submitted sequences, as well as analysis of publicly available metagenomic datasets held within the European Nucleotide Archive (ENA).Microbiome analysis resource in 2020.

Synonyms: , MGnify, EBI Metagenomics

Resource Type: portal, service resource, data or information resource, storage service resource, data repository

Defining Citation: PMID:31696235

Keywords: analysis, exploration, metagenomic, metatranscriptomic, amplicon, assembly, data, sequence, ENA, microbial, population, environment, bio.tools

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the Biotechnology and Biological Sciences Research Council BBI02612X1;
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Availability: Free, Freely available, Training online available

Resource Name: MGnify

Resource ID: SCR_016429

Alternate IDs: biotools:MGnify

Alternate URLs: https://bio.tools/MGnify

Record Creation Time: 20220129T080330+0000

Record Last Update: 20250516T054126+0000

Ratings and Alerts

No rating or validation information has been found for MGnify.

No alerts have been found for MGnify.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Burrows PB, et al. (2025) Decoding the chicken gastrointestinal microbiome. BMC microbiology, 25(1), 35.

Tassoulas LJ, et al. (2024) Insights into the action of the pharmaceutical metformin: Targeted inhibition of the gut microbial enzyme agmatinase. iScience, 27(2), 108900.

Rosonovski S, et al. (2024) Europe PMC in 2023. Nucleic acids research, 52(D1), D1668.

Durrant MG, et al. (2024) Bridge RNAs direct programmable recombination of target and donor DNA. Nature, 630(8018), 984.

Mora-Salguero D, et al. (2024) Long-term effects of combining anaerobic digestate with other organic waste products on soil microbial communities. Frontiers in microbiology, 15, 1490034.

Yurekten O, et al. (2024) MetaboLights: open data repository for metabolomics. Nucleic acids research, 52(D1), D640.

Birklbauer MJ, et al. (2024) Proteome-wide non-cleavable crosslink identification with MS Annika 3.0 reveals the structure of the C. elegans Box C/D complex. Communications chemistry, 7(1), 300.

Shantaram D, et al. (2024) Obesity-associated microbiomes instigate visceral adipose tissue inflammation by recruitment of distinct neutrophils. Nature communications, 15(1), 5434.

Dewar AE, et al. (2024) Bacterial lifestyle shapes pangenomes. Proceedings of the National Academy of Sciences of the United States of America, 121(21), e2320170121.

Duller S, et al. (2024) Targeted isolation of Methanobrevibacter strains from fecal samples expands the cultivated human archaeome. Nature communications, 15(1), 7593.

Zheng W, et al. (2024) Improving deep learning protein monomer and complex structure prediction using DeepMSA2 with huge metagenomics data. Nature methods, 21(2), 279.

Fernández-Calvet A, et al. (2024) Gut microbiota produces biofilm-associated amyloids with potential for neurodegeneration. Nature communications, 15(1), 4150.

Moeller AH, et al. (2024) Removal of sequencing adapter contamination improves microbial genome databases. BMC genomics, 25(1), 1033.

Molina-Sánchez MD, et al. (2024) Adaptive immunity of type VI CRISPR-Cas systems associated with reverse transcriptase-Cas1 fusion proteins. Nucleic acids research, 52(22), 14229.

Zampirolo G, et al. (2024) Tracing early pastoralism in Central Europe using sedimentary ancient DNA. Current biology : CB, 34(20), 4650.

von Meijenfeldt FAB, et al. (2023) A social niche breadth score reveals niche range strategies of generalists and specialists. Nature ecology & evolution, 7(5), 768.

Jin X, et al. (2023) Culturing of a complex gut microbial community in mucin-hydrogel carriers reveals strain- and gene-associated spatial organization. Nature communications, 14(1), 3510.

Li M, et al. (2023) Performance of Gut Microbiome as an Independent Diagnostic Tool for 20 Diseases: Cross-Cohort Validation of Machine-Learning Classifiers. Gut microbes, 15(1), 2205386.

Zimmerman S, et al. (2023) Quantifying Shared and Unique Gene Content across 17 Microbial Ecosystems. mSystems, 8(2), e0011823.

Yang P, et al. (2023) Microbiome-based enrichment pattern mining has enabled a deeper understanding of the biome-species-function relationship. Communications biology, 6(1), 391.