

Resource Summary Report

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

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;

the Biotechnology and Biological Sciences Research Council BBM0117551;

the European Commission within the Research Infrastructures programme of Horizon 2020 676559

Availability: Free, Freely available, Training online available

Resource Name: MGnify

Resource ID: SCR_016429

Alternate IDs: r3d100011192, biotools:MGnify

Alternate URLs: <https://bio.tools/MGnify>, <https://doi.org/10.17616/R34W68>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260821T194054+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 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#).

Maisto L, et al. (2026) Multifaceted human gut microbiome data associated with health and nutrition. *Frontiers in microbiology*, 17, 1722500.

Venetsianou NK, et al. (2026) LLM-Assessed Relatedness of Microbiome Study Descriptions Aligns more Strongly with Functional than with Taxonomic Profile Similarity. *Microbial ecology*, 89(1).

Vidal E, et al. (2026) ABaCo: addressing heterogeneity challenges in metagenomic data integration with adversarial generative models. *Nucleic acids research*, 54(5).

Shrestha B, et al. (2026) Global metagenomics reveals plastid diversity and unexplored algal lineages. *Nature communications*, 17(1).

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

Meaden S, et al. (2025) Phage defence-system abundances vary across environments and increase with viral density. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1934), 20240069.

Hourigan D, et al. (2025) Nisin-like biosynthetic gene clusters are widely distributed across microbiomes. *mBio*, 16(10), e0154525.

Hu G, et al. (2025) Chemical modulation of gut bacterial metabolism induces colanic acid and extends the lifespan of nematode and mammalian hosts. *PLoS biology*, 23(11),

e3002749.

Safarchi A, et al. (2025) Understanding dysbiosis and resilience in the human gut microbiome: biomarkers, interventions, and challenges. *Frontiers in microbiology*, 16, 1559521.

Woh PY, et al. (2025) Reevaluation of the gastrointestinal methanogenic archaeome in multiple sclerosis and its association with treatment. *Microbiology spectrum*, 13(4), e0218324.

Mezhibovsky E, et al. (2025) Grape polyphenols reduce fasting glucose and increase hyocholic acid in healthy humans: a meta-omics study. *NPJ science of food*, 9(1), 87.

Manske F, et al. (2025) Development of a new data management system for the study of the gut microbiome of children who are small for their gestational age. *Computational and structural biotechnology journal*, 27, 221.

Li P, et al. (2025) Best practices for developing microbiome-based disease diagnostic classifiers through machine learning. *Gut microbes*, 17(1), 2489074.

Li X, et al. (2025) Association study between intestinal microbiota dysbiosis in inflammatory bowel disease and the global disease burden growth trend. *Frontiers in medicine*, 12, 1635242.

Paul JK, et al. (2025) Exploration of Human Skin Phageome to Reveal Endolysins and Novel Antimicrobial Peptides for Therapeutic Applications. *MicrobiologyOpen*, 14(6), e70115.

Wang S, et al. (2025) An Approach to Integrate Metagenomics, Metatranscriptomics and Metaproteomics Data in Public Data Resources. *Proteomics*, 25(17-18), 33.

Kagaya Y, et al. (2025) NuFold: end-to-end approach for RNA tertiary structure prediction with flexible nucleobase center representation. *Nature communications*, 16(1), 881.

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in *Dictyostelium*. *Molecular biology of the cell*, 36(8), ar98.

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.