

Resource Summary Report

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MG-RAST

RRID:SCR_004814

Type: Tool

Proper Citation

MG-RAST (RRID:SCR_004814)

Resource Information

URL: <http://metagenomics.anl.gov/>

Proper Citation: MG-RAST (RRID:SCR_004814)

Description: An automated analysis platform for metagenomes providing quantitative insights into microbial populations based on sequence data. The server primarily provides upload, quality control, automated annotation and analysis for prokaryotic metagenomic shotgun samples.

Abbreviations: MG RAST

Synonyms: The Metagenomics RAST server, Metagenomics RAST, MG-RAST - metagenomics analysis server

Resource Type: data analysis service, production service resource, service resource, analysis service resource

Defining Citation: [PMID:18803844](#)

Keywords: metagenome, base pair, sequence, phylogenetic, functional analysis, data sharing, metadata, protein, micro biome, analysis platform, bio.tools

Funding: NIAID contract HHSN272200900040C;
DOE contract DE-AC02-06CH11357

Availability: Acknowledgement requested, Public, Account required

Resource Name: MG-RAST

Resource ID: SCR_004814

Alternate IDs: OMICS_01456, biotools:mg-rast

Alternate URLs: <http://metagenomics.nmpdr.org>, <https://bio.tools/mg-rast>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260806T054406+0000

Ratings and Alerts

No rating or validation information has been found for MG-RAST.

No alerts have been found for MG-RAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1137 mentions in open access literature.

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

Przemieniecki SW, et al. (2025) The Impact of Nanoparticles and Molecular Forms of TiO₂ on the Rhizosphere of Plants in the Example of Common Wheat (*Triticum aestivum* L.)- Shifts in Microbiome Structure and Predicted Microbial Metabolic Functions. *International journal of molecular sciences*, 26(2).

Rungsihiranrut A, et al. (2025) Metagenomic analysis reveals the roles of Actinobacteria in plasticizer-contaminated landfills and aids in identifying key degraders. *Scientific reports*, 15(1), 18157.

González-Rosales C, et al. (2025) A global deep terrestrial biosphere core microbiome. *ISME communications*, 5(1), ycaf176.

Ricci F, et al. (2025) Chemosynthesis enhances net primary production and nutrient cycling in a hypersaline microbial mat. *The ISME journal*, 19(1).

Tavares TCS, et al. (2025) Characterization of antibiotic resistance genes in soils from agroecosystems of the Brazilian Amazon. *Frontiers in microbiology*, 16, 1508157.

Soffritti I, et al. (2025) Harnessing probiotics and bacteriophages to fight *Salmonella* and limit the use of antibiotics in broilers: a study in commercial conditions. *Poultry science*, 104(10), 105595.

Li AD, et al. (2025) Metatranscriptomic time series insight into antibiotic resistance genes and mobile genetic elements in wastewater systems under antibiotic selective pressure. *BMC microbiology*, 25(1), 45.

Wang J, et al. (2025) Whole-genome sequencing and metagenomics reveal diversity and prevalence of *Listeria* spp. from soil in the Nantahala National Forest. *Microbiology spectrum*, 13(1), e0171224.

Senawin S, et al. (2025) Microbiota profiles and antimicrobial resistance genes in sow fecal samples from farms with and without antibiotic use. *Animal bioscience*, 38(11), 2487.

Zhang J, et al. (2025) Administration of a Recombinant Fusion Protein of IFN- γ and CD154 Inhibited the Infection of Chicks with *Salmonella enterica*. *Veterinary sciences*, 12(2).

Grosche A, et al. (2025) The chemosynthetic biofilm microbiome of deep-sea hydrothermal vents across space and time. *Environmental microbiome*, 20(1), 88.

Lang M, et al. (2025) Benchmarking the methods for predicting base pairs in RNA-RNA interactions. *Bioinformatics (Oxford, England)*, 41(6).

Parwin N, et al. (2025) Metagenomic analysis of microbiome spatial dynamics in urban river confluence affected by city wastewater. *Genomics & informatics*, 23(1), 27.

Chan YL, et al. (2025) *Bifidobacterium lactis* ameliorates AOM/DSS-induced inflammation, dysbiosis, and colonic precancerous lesions. *Applied microbiology and biotechnology*, 109(1), 69.

Joos L, et al. (2025) Year-long, multiple-timepoint field studies show the importance of spatiotemporal dynamics and microbial functions in agricultural soil microbiomes. *mSystems*, 10(7), e0011225.

Faure G, et al. (2025) TIGR-Tas: A family of modular RNA-guided DNA-targeting systems in prokaryotes and their viruses. *Science (New York, N.Y.)*, 388(6746), eadv9789.

Samson R, et al. (2025) Deciphering the comprehensive microbiome of glacier-fed Ganges and functional aspects: implications for one health. *Microbiology spectrum*, 13(8), e0172024.

Contreras-de la Rosa PA, et al. (2025) Exploring the microbial communities in coastal cenote and their hidden biotechnological potential. *Microbial genomics*, 11(4).

Hancock TL, et al. (2025) Microcystis bloom control using hydrogen peroxide and floating sodium percarbonate algaecide Lake Guard Oxy in Florida. *Applied and environmental microbiology*, 91(12), e0195025.

Qiu D, et al. (2025) Global variation in plant-beneficial bacteria in soil under pesticide stress. *Nature communications*, 16(1), 10685.