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: 20250417T065206+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 1119 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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).

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.

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.

Brzeszcz J, et al. (2024) Bacteria degrading both n-alkanes and aromatic hydrocarbons are prevalent in soils. Environmental science and pollution research international, 31(4), 5668.

Mustafa AS, et al. (2024) Spatial Variations in the Nasal Microbiota of Staff Working in a Healthcare-Associated Research Core Facility. Medical principles and practice : international journal of the Kuwait University, Health Science Centre, 33(1), 66.

Kiran A, et al. (2024) The African Human Microbiome Portal: a public web portal of curated metagenomic metadata. Database : the journal of biological databases and curation, 2024.

Maitre A, et al. (2024) Differential interactions of Rickettsia species with tick microbiota in Rh. sanguineus and Rh. turanicus. Scientific reports, 14(1), 20674.

Indio V, et al. (2024) Shotgun metagenomic investigation of foodborne pathogens and antimicrobial resistance genes in artisanal fermented meat products from the Mediterranean area. Italian journal of food safety, 13(2), 12210.

Barno AR, et al. (2024) Snow viruses and their implications on red snow algal blooms. mSystems, 9(5), e0008324.

Fagunwa O, et al. (2024) The Human Gut and Dietary Salt: The Bacteroides/Prevotella Ratio as a Potential Marker of Sodium Intake and Beyond. Nutrients, 16(7).

Papadimitriou K, et al. (2024) Study of the Microbiome of the Cretan Sour Cream Staka Using Amplicon Sequencing and Shotgun Metagenomics and Isolation of Novel Strains with an Important Antimicrobial Potential. Foods (Basel, Switzerland), 13(7).

Lahiani M, et al. (2024) Early Developmental Exposure to Triclosan Impacts Fecal Microbial Populations, IgA and Functional Activities of the Rat Microbiome. Journal of xenobiotics, 14(1), 193.

Zhou T, et al. (2024) MAMI: a comprehensive database of mother-infant microbiome and probiotic resources. Nucleic acids research, 52(D1), D738.

Masuda Y, et al. (2024) Global soil metagenomics reveals distribution and predominance of Deltaproteobacteria in nitrogen-fixing microbiome. Microbiome, 12(1), 95.

Guo W, et al. (2024) Seasonal stability of the rumen microbiome contributes to the adaptation patterns to extreme environmental conditions in grazing yak and cattle. BMC biology, 22(1), 240.

Msango K, et al. (2024) Variation and functional profile of gut bacteria in the scarab beetle, Anomala dimidiata, under a cellulose-enriched microenvironment. Scientific reports, 14(1), 22400.

Dörr AK, et al. (2024) RiboSnake - a user-friendly, robust, reproducible, multipurpose and documentation-extensive pipeline for 16S rRNA gene microbiome analysis. GigaByte (Hong Kong, China), 2024, gigabyte132.

Power JF, et al. (2024) A genus in the bacterial phylum Aquificota appears to be endemic to Aotearoa-New Zealand. Nature communications, 15(1), 179.

Malik AA, et al. (2024) Bacterial population-level trade-offs between drought tolerance and resource acquisition traits impact decomposition. The ISME journal, 18(1).

Corrêa PS, et al. (2024) Interaction between methanotrophy and gastrointestinal nematodes infection on the rumen microbiome of lambs. FEMS microbiology ecology, 100(6).