

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: analysis service resource, data analysis service, production service resource, 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: 20260912T200134+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 1165 mentions in open access literature.

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

Khurajog B, et al. (2026) Effectiveness of probiotic supplementation on growth performance, gut microbiota, and Salmonella reduction in broiler chicks challenged with Salmonella Typhimurium. Scientific reports, 16(1), 6983.

Yash , et al. (2026) Dataset on ecological health and microbial communities of coastal aquaculture ponds from surrounding region of Sundarban mangroves. Data in brief, 65, 112542.

Ismaeil M, et al. (2026) Predictive functional profiling of 16S rRNA genes amplicons reveals bioremediation and sulfur metabolism capacity in thermophilic hot spring bacteriomes. Scientific reports, 16(1).

Rout AK, et al. (2026) Metagenomic insights into microbial diversity, xenobiotic and plastic-degrading enzymes in sediments of river Yamuna at Agra. Frontiers in microbiology, 17, 1828736.

Machineski GDS, et al. (2026) Riparian Forest Restoration Drives the Recovery of Soil Chemistry, Microbial Community Structure, and Enzymatic Activity in the Itaipu Reservoir Protection Zone. Microorganisms, 14(2).

Ortigoza PYA, et al. (2026) Biogas production using the microbial community present in the soil from Deception Island, maritime Antarctica. Environmental science and pollution research international, 33(17), 8426.

Akanmu AM, et al. (2026) Dietary plant extracts reduce methane emission and modulate rumen microbial functionality in Merino lambs. Scientific reports, 16(1).

Özdemir K, et al. (2026) Characterization of a Boron-Tolerant Nocardia niigatensis Isolated from Boron-Rich Soils: Physiological, Enzymatic, and Genomic Insights. Microorganisms, 14(2).

Chung B, et al. (2026) Plant litter chemistry and associated changes in microbial decomposition under drought. *mBio*, 17(6), e0043826.

Afshar Jahanshahi D, et al. (2026) MiGPC: a comprehensive catalog of enzybiotics from environmental metagenomes. *Scientific reports*, 16(1).

Anil , et al. (2026) Microbial zonation and functional roles in the gut of white grub (*Maladera insanabilis*) larvae. *Scientific reports*, 16(1).

Enebe MC, et al. (2026) Microbial membrane transport genes in maize rhizosphere under fertilization - a preliminary study. *Scientific reports*, 16(1).

Tamang S, et al. (2026) Metagenomic analysis of bacterial diversity, antibiotic resistance, and functional profiles in the ice core samples from two glaciers of Sikkim Himalaya. *Scientific reports*, 16(1).

da Silveira Bastos IMA, et al. (2026) Worldwide diversity and ecology of mangrove fungi: a systematic review of ITS metabarcoding studies and a quantitative, integrative analysis of raw sequence data. *World journal of microbiology & biotechnology*, 42(7).

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

Yaghoubi Khanghahi M, et al. (2025) Transcriptomic, biochemical, and microbiome assessments into drought and salinity tolerance in durum wheat mediated by plant growth-promoting bacteria. *Physiology and molecular biology of plants : an international journal of functional plant biology*, 31(12), 2121.

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.

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.