# Resource Summary Report

Generated by RRID on Apr 28, 2025

## RAST Server

RRID:SCR_014606
Type: Tool

## Proper Citation

RAST Server (RRID:SCR_014606)

## Resource Information

**URL:** http://rast.nmpdr.org

**Proper Citation:** RAST Server (RRID:SCR_014606)

**Description:** A SEED-quality automated service that annotates complete or nearly complete bacterial and archaeal genomes across the entire phylogenetic tree. RAST can also be used to analyze draft genomes.

**Abbreviations:** RAST

**Synonyms:** Rapid Annotation using Subsystem Technology, Rapid Annotation using Subsystem Technology Server

**Resource Type:** production service resource, service resource

**Defining Citation:** PMID:18261238

**Keywords:** microbiome, seed, annotate, genome, bacteria, archaea, service, bio.tools

**Funding:** National Science Foundation 0850546;
NIAID contract HHSN272200900040C

**Availability:** Free for the scientific community, Login required

**Resource Name:** RAST Server

**Resource ID:** SCR_014606

**Alternate IDs:** biotools:theseed

**Alternate URLs:** https://bio.tools/theseed

**Record Creation Time:** 20220129T080321+0000

**Record Last Update:** 20250426T060413+0000

## Ratings and Alerts

No rating or validation information has been found for RAST Server.

No alerts have been found for RAST Server.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 823 mentions in open access literature.

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

Mitchell DD, et al. (2025) Draft genome dataset of Streptomyces griseoincarnatus strain R-35 isolated from tidal pool sediments. Data in brief, 58, 111235.

Yakubovskij VI, et al. (2025) Phage vB_KlebPS_265 Active Against Resistant/MDR and Hypermucoid K2 Strains of Klebsiella pneumoniae. Viruses, 17(1).

Wang H, et al. (2025) In Silico Exploration of Staphylococcal Cassette Chromosome mec (SCCmec) Evolution Based on Phylogenetic Relationship of ccrAB/C. Microorganisms, 13(1).

Zhang Z, et al. (2025) Clonal Spread and Genetic Mechanisms Underpinning Ciprofloxacin Resistance in Salmonella enteritidis. Foods (Basel, Switzerland), 14(2).

Wang M, et al. (2025) Antimicrobial Resistance Genes in Clinical Escherichia coli Strains from Livestock and Poultry in Shandong Province, China During 2015-2020. Antibiotics (Basel, Switzerland), 14(1).

Almirón C, et al. (2025) Functional and genomic analyses of plant growth promoting traits in Priestia aryabhattai and Paenibacillus sp. isolates from tomato rhizosphere. Scientific reports, 15(1), 3498.

Yibar A, et al. (2025) Genomic Insight into Vibrio Isolates from Fresh Raw Mussels and Ready-to-Eat Stuffed Mussels. Pathogens (Basel, Switzerland), 14(1).

Ofosu Appiah F, et al. (2025) Emergence of Carbapenem-Resistant blaPOM-1 Harboring Pseudomonas otitidis Isolated from River Water in Ghana. Antibiotics (Basel, Switzerland), 14(1).

Park EJ, et al. (2025) Characterization of Broad Spectrum Bacteriophage vB ESM-pEJ01 and Its Antimicrobial Efficacy Against Shiga Toxin-Producing Escherichia coli in Green Juice. Microorganisms, 13(1).

Arce-Aceves MF, et al. (2025) Fitness costs of Mycobacterium tuberculosis resistant to rifampicin is compensated by rapid Th2 polarization mediated by early and high IL-4 production during mice infection. Scientific reports, 15(1), 2811.

Xie Y, et al. (2025) The prevalence of optrA-carrying Enterococci in the vaginal micro-ecology of pregnant women in late pregnancy. Microbiology spectrum, 13(1), e0213524.

Zhao J, et al. (2024) PhageGE: an interactive web platform for exploratory analysis and visualization of bacteriophage genomes. GigaScience, 13.

Yoo S, et al. (2024) Designing phage cocktails to combat the emergence of bacteriophage-resistant mutants in multidrug-resistant Klebsiella pneumoniae. Microbiology spectrum, 12(1), e0125823.

Mahadi WSW, et al. (2024) Complete genome sequence data of an Antarctic bacterium Arthrobacter sp. EM1 from the freshwater lake of the King George Island. Data in brief, 52, 109841.

Schmidt AK, et al. (2024) Targeted deletion of Pf prophages from diverse Pseudomonas aeruginosa isolates has differential impacts on quorum sensing and virulence traits. Journal of bacteriology, 206(5), e0040223.

Ofosu-Appiah F, et al. (2024) Klebsiella pneumoniae ST147 harboring blaNDM-1, multidrug resistance and hypervirulence plasmids. Microbiology spectrum, 12(3), e0301723.

Wang X, et al. (2024) Genome sequence of Shiga toxin-producing Escherichia coli jumbo bacteriophage vB_EcoM_JNE01. Microbiology resource announcements, 13(2), e0114523.

Vitt AR, et al. (2024) Diverse bacteriophages for biocontrol of ESBL- and AmpC-?-lactamase-producing E. coli. iScience, 27(2), 108826.

Du X, et al. (2024) Proximity-based defensive mutualism between Streptomyces and Mesorhizobium by sharing and sequestering iron. The ISME journal, 18(1).

Hu M, et al. (2024) Antimicrobial susceptibility and genetic characteristics of multi-drug resistant Acinetobacter baumannii isolates in Northwest China. Frontiers in microbiology, 15, 1293725.