

Resource Summary Report

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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: service resource, production 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: 20260725T190801+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 907 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Safari M, et al. (2026) Comprehensive genomic analysis of a novel *Bacillus cereus* decomposing toluene potentially applicable in bioremediation. *Microbiology spectrum*, 14(1), e0289224.

Hu Y, et al. (2026) Global epidemiological and genetic characteristics of carbapenem-resistant *Escherichia coli* carrying blaIMP. *Microbiology spectrum*, 14(1), e0324425.

Ramesh M, et al. (2025) Age-Dependent Pleomorphism in *Mycobacterium monacense* Cultures. *Microorganisms*, 13(3).

Benhadj M, et al. (2025) Genomic Insights and Antimicrobial Potential of Newly *Streptomyces cavourensis* Isolated from a Ramsar Wetland Ecosystem. *Microorganisms*, 13(3).

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

Yibar A, et al. (2025) Integrated assessment of mucilage impact on human health using the One Health approach: Prevalence and antimicrobial resistance profiles of *Escherichia coli* and *Clostridium perfringens* in the Marmara Sea, Türkiye. *Heliyon*, 11(3), e42103.

Liu Z, et al. (2025) Functional genomic analysis of *Bacillus cereus* BC4 strain for chromium remediation in contaminated soil. *Current research in microbial sciences*, 8, 100388.

Prole JR, et al. (2025) Identification of four novel *Streptomyces* isolated from machair grassland soil using a culture-based bioprospecting strategy: *Streptomyces caledonius* sp. nov., *Streptomyces machairae* sp. nov., *Streptomyces pratisoli* sp. nov. and *Streptomyces achmelvichensis* sp. nov. *International journal of systematic and evolutionary microbiology*, 75(4).

Xu D, et al. (2025) Complete genome sequence of *Mammaliicoccus lentus* (*Staphylococcus lentus*) strain B3, isolated from mouse early-life gut microbiota. *Microbiology resource announcements*, 14(6), e0021425.

Ochiai E, et al. (2025) Molecular Structure and Biosynthesis of Pyoverdines Produced by *Pseudomonas fulva*. *Microorganisms*, 13(6).

Kiga K, et al. (2025) Development of a nonreplicative phage-based DNA delivery system and its application to antimicrobial therapies. *PNAS nexus*, 4(6), pgaf176.

Recacha E, et al. (2025) Characterization of a blaKPC-3-carrying plasmid in a clinical isolate of *Klebsiella pneumoniae* belonging to the emerging successful clone ST147. *Microbiology spectrum*, 13(7), e0233824.

Li X, et al. (2025) Systematic evaluation of phenotypic variations induced by prophages in a clinical isolate of *Pseudomonas aeruginosa*. *mSystems*, 10(9), e0042825.

Liu Z, et al. (2025) C15-bacillomycin D produced by *Bacillus amyloliquefaciens* 4-9-2 suppress *Fusarium graminearum* infection and mycotoxin biosynthesis. *Frontiers in microbiology*, 16, 1599452.

Hu W, et al. (2025) Structural basis for *Salmonella* infection by two Microviridae phages. *Communications biology*, 8(1), 1166.

Zhou Y, et al. (2025) Whole genome sequencing of *Salmonella* in poultry from China reveals the presence of blaNDM-5 in different serotypes. *Poultry science*, 104(11), 105647.

Stefan M, et al. (2025) Recurrence following invasive GAS infections in adults: Triumph of virulence or failure of immunity? *Virulence*, 16(1), 2563765.

Chakraborty S, et al. (2025) Partners in root nodule symbiosis respond uniquely to heavy metal stresses in a host genotype-dependent manner. *Scientific reports*, 15(1), 33518.

Fu Z, et al. (2025) Characterization of Alginate Utilization Strategy in a Novel Marine Bacteroidetes: Insights from *Roseihalotalea indica* gen. nov. sp. nov. TK19036T. *Marine drugs*, 23(9).

Tu J, et al. (2025) Colanic acid-mediated phage resistance enhances virulence in high-risk global clone *Escherichia coli* ST410. *PLoS pathogens*, 21(12), e1013807.