

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>

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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: 20260905T132748+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 1198 mentions in open access literature.

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

Xia P, et al. (2026) Genomic analysis of *Enterococcus faecium* co-carrying *optrA* and *poxTA* from a swine farm: dissemination across the human-animal-environment interface. *BMC microbiology*, 26(1), 125.

Crispim NR, et al. (2026) Heteroresistance to amikacin in *Klebsiella aerogenes* isolates from patients in an intensive care unit in Brazil. *Microbiology spectrum*, 14(4), e0283325.

Massacci FR, et al. (2026) Occurrence of oxazolidinone resistance genes in enterococci, staphylococci, and *Mammaliococcus sciuri* from swine slaughterhouse wastewater, Italy. *World journal of microbiology & biotechnology*, 42(5).

Li S, et al. (2026) Synergistic disinfection by phage PLY101 and 1,3-dibromo-5,5-dimethylhydantoin (DBDMH) against resistant *Proteus mirabilis*. *BMC microbiology*, 26(1).

Salazar-Sánchez A, et al. (2026) Construction and characterization of the first *Arcobacter butzleri* - *Escherichia coli* shuttle vector. *Archives of microbiology*, 208(6).

Miao F, et al. (2026) Antimicrobial resistance and genomic characteristics of avian *Pasteurella multocida*. *Poultry science*, 105(4), 106524.

Cardinali-Rezende J, et al. (2026) Motility and growth *Burkholderia* two-component: a new regulatory system of *Burkholderia seminalis*. *Applied microbiology and biotechnology*, 110(1).

Ren X, et al. (2026) Genomic and transcriptomic analysis reveals chitin metabolic pathways in the marine bacterium *Microbulbifer harenosus* CGMCC 1.13584T. *BMC microbiology*, 26(1).

Abebe MA, et al. (2026) In silico Design and Analysis of Engineered Proteins Containing Multi-Epitope and Immunodominant Domains Derived From *Rickettsia prowazekii* Antigens. *Bioinformatics and biology insights*, 20, 11779322261461934.

Feng Y, et al. (2026) Epidemiological and Genomic Characteristics of *bla* CTX-M and *bla* NDM-Producing *K. pneumoniae* From Dairy Cows in Henan Province, China.

Transboundary and emerging diseases, 2026, 5331014.

Syaputri Y, et al. (2026) Polyphasic Characterization of *Acetobacter indonesiensis* UNPADCC 01-5 Isolated From a Traditional Fermented Food, Oncom Merah. *Environmental microbiology reports*, 18(3), e70346.

Vazquez-Cruz C, et al. (2026) *Actinobacillus seminis* DnaK interacts with bovine transferrin, lactoferrin, and hemoglobin as a putative iron acquisition mechanism. *Folia microbiologica*, 71(2), 369.

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

Yang X, et al. (2026) Transient AdeABC-mediated eravacycline resistance in carbapenem-resistant *Acinetobacter baumannii* ST2: a mutation-independent efflux pump adaptation. *Annals of clinical microbiology and antimicrobials*, 25(1), 8.

Luo S, et al. (2026) Biological characterization of multidrug-resistant *Pseudomonas aeruginosa* phage PaeP_Ls and its efficacy in septic mice. *Microbiology spectrum*, 14(2), e0205025.

Ghevondyan D, et al. (2026) Genomic and chemical insights into a human lectin-binding extracellular polysaccharides from *Parageobacillus toebii* strain H-70. *PloS one*, 21(1), e0340423.

Liao CH, et al. (2026) Hidden burden of intestinal *Klebsiella pneumoniae* in Taiwan: insights into pathogenic potentials and genomic diversity. *Gut pathogens*, 18(1).

Mfopit YM, et al. (2026) Identification of Sialidase-Producing Bacteria in the Tsetse Gut and Characterisation of a *Paenibacillus* Sialidase: A Potential Tool for Paratransgenic Control of African Trypanosomes. *Research square*.

Liu Y, et al. (2026) Characterization and complete genomic sequence of a novel phage BUCT805 infecting *Serratia marcescens* and its anti-biofilm activities. *Microbiology spectrum*, 14(4), e0311925.

Escalante-Beltrán A, et al. (2026) Draft Genome Sequence of *Bacillus* sp. Strain 11B20, a Promising Plant-Growth Promoting Bacterium Associated with Maize (*Zea mays* L.) in the Yaqui Valley, Mexico. *Microorganisms*, 14(2).