

Resource Summary Report

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Pathosystems Resource Integration Center

RRID:SCR_004154

Type: Tool

Proper Citation

Pathosystems Resource Integration Center (RRID:SCR_004154)

Resource Information

URL: <http://www.patricbrc.org/portal/portal/patric/Home>

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Description: A Bioinformatics Resource Center bacterial bioinformatics database and analysis resource that provides researchers with an online resource that stores and integrates a variety of data types (e.g. genomics, transcriptomics, protein-protein interactions (PPIs), three-dimensional protein structures and sequence typing data) and associated metadata. Datatypes are summarized for individual genomes and across taxonomic levels. All genomes, currently more than 10 000, are consistently annotated using RAST, the Rapid Annotations using Subsystems Technology. Summaries of different data types are also provided for individual genes, where comparisons of different annotations are available, and also include available transcriptomic data. PATRIC provides a variety of ways for researchers to find data of interest and a private workspace where they can store both genomic and gene associations, and their own private data. Both private and public data can be analyzed together using a suite of tools to perform comparative genomic or transcriptomic analysis. PATRIC also includes integrated information related to disease and PPIs. The PATRIC project includes three primary collaborators: the University of Chicago, the University of Manchester, and New City Media. The University of Chicago is providing genome annotations and a PATRIC end-user genome annotation service using their Rapid Annotation using Subsystem Technology (RAST) system. The National Centre for Text Mining (NaCTeM) at the University of Manchester is providing literature-based text mining capability and service. New City Media is providing assistance in website interface development. An FTP server and download tool are available.

Abbreviations: PATRIC

Synonyms: PathoSystems Resource Integration Center, PATRIC, Pathosystems Resource Integration Center

Resource Type: data analysis service, data or information resource, database, service resource, bioinformatics resource center, production service resource, analysis service resource

Defining Citation: [PMID:24225323](#), [PMID:17142235](#)

Keywords: genomics, genome, transcriptomics, protein-protein interaction, sequence typing, proteobacteria, brucella, rickettsia, coxiella, coronavirus, calicivirus, lyssavirus, virus, hepatitis a, hepatitis e, pathway, proteome, metabolic pathway, drug, vaccine, diagnostics, FASEB list

Funding: NIAID

Availability: Free, Public, Acknowledgement requested

Resource Name: Pathosystems Resource Integration Center

Resource ID: SCR_004154

Alternate IDs: r3d100010142, OMICS_01658, nlx_17476

Alternate URLs: <http://patricbrc.vbi.vt.edu/portal/portal/patric/Home>, <https://doi.org/10.17616/R3WS3X>

Old URLs: <http://patric.vbi.vt.edu/>

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260801T042544+0000

Ratings and Alerts

No rating or validation information has been found for Pathosystems Resource Integration Center.

No alerts have been found for Pathosystems Resource Integration Center.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1083 mentions in open access literature.

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

Y??Imaz S, et al. (2025) Genome mining of Bacillus thuringiensis strain SY49.1 reveals novel candidate pesticidal and bioactive compounds. Pest management science, 81(1), 298.

Sedrakyan A, et al. (2025) Molecular Epidemiology and In-Depth Characterization of *Klebsiella pneumoniae* Clinical Isolates from Armenia. *International journal of molecular sciences*, 26(2).

Sato N, et al. (2025) stana: an R package for metagenotyping analysis and interactive application based on clinical data. *NAR genomics and bioinformatics*, 7(1), lqae191.

Mahfouz AM, et al. (2025) Genetic determinants of silver nanoparticle resistance and the impact of gamma irradiation on nanoparticle stability. *BMC microbiology*, 25(1), 18.

López L, et al. (2025) A plasmid with the bla CTX-M gene enhances the fitness of *Escherichia coli* strains under laboratory conditions. *Microbiology (Reading, England)*, 171(1).

Li Z, et al. (2025) Characterization of OXA232-Producing Carbapenem-Resistant *Klebsiella pneumoniae*: Genomic Analysis and Virulence Assessment. *Polish journal of microbiology*, 74(1), 82.

Wang B, et al. (2025) *Lactobacillus rhamnosus* P118 enhances host tolerance to *Salmonella* infection by promoting microbe-derived indole metabolites. *eLife*, 13.

Xue Z, et al. (2025) *Helicobacter pylori* antimicrobial resistance and gene variants in Shandong Province. *Scientific reports*, 15(1), 34244.

Vermilya C, et al. (2025) Multiple clades of regulators contribute to bacterial phosphate homeostasis and pathogenesis. *bioRxiv : the preprint server for biology*.

Muruzabal-Galarza A, et al. (2025) Multiomic data analyses unveiled a novel phenol-soluble modulin that induces trapping of extracellular lipases at the surface of *Staphylococcus aureus* cells. *mBio*, 16(11), e0185625.

Huang X, et al. (2025) Phenotypic and genomic characterization of *Paenibacillus salivarius* sp. nov., isolated from the human oral cavity. *BMC microbiology*, 25(1), 737.

Passari AK, et al. (2025) Comparative genomics of the *Streptomyces* genus: insights into multi-stress-resistant genes for bioremediation. *World journal of microbiology & biotechnology*, 41(12), 492.

Rahmdel S, et al. (2025) Beyond commensalism: genomic insights into micrococcin P1-producing *Staphylococcus chromogenes*. *mSphere*, 10(12), e0073325.

Qu J, et al. (2025) Deep Amplicon Sequencing Reveals Culture-dependent Clonal Selection of *Mycobacterium tuberculosis* in Clinical Samples. *Genomics, proteomics & bioinformatics*, 22(6).

Khan ZA, et al. (2025) Survival mechanism of pancreatic tumor bacteria and their ability to metabolize chemotherapy drugs. *Microbiology spectrum*, 13(9), e0182025.

Alkhatib SA, et al. (2025) Revealing bioremediation potential of novel indigenous bacteria from oil-contaminated sites in the UAE: A combined bioinformatics and experimental validation. *PloS one*, 20(8), e0329515.

Schwardt NH, et al. (2025) A genome-wide screen in ex vivo gallbladders identifies *Listeria monocytogenes* factors required for virulence in vivo. *PLoS pathogens*, 21(3), e1012491.

McCaffrey KR, et al. (2025) Optimizing survey conditions for Burmese python detection and removal using community science data. *Scientific reports*, 15(1), 2421.

Chaggar HK, et al. (2025) *Salmonella enterica* serovar Braenderup shows clade-specific source associations and a high proportion of molecular epidemiological clustering. *Applied and environmental microbiology*, 91(4), e0259424.

Arslan A, et al. (2025) Genomic and Immunoinformatics Insights Into a Bovine-Derived *Brucella abortus* S19 Field Strain: Adaptations Impacting Vaccine Efficacy. *Veterinary medicine and science*, 11(6), e70593.