

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>

Proper Citation: Pathosystems Resource Integration Center (RRID:SCR_004154)

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: service resource, data analysis service, bioinformatics resource center, data or information resource, database, 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: 20260731T042701+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 [kravitz2](#) .

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.

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

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

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

Y??lmaz 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.

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.

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).

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.

L??pez 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).

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

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.

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.

Wasney M, et al. (2025) Uniform bacterial genetic diversity along the guts of mice inoculated with human stool. *bioRxiv : the preprint server for biology*.

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.

Pal A, et al. (2025) Machine learning-based approach for identification of new resistance associated mutations from whole genome sequences of *Mycobacterium tuberculosis*. *Bioinformatics advances*, 5(1), vbaf050.

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.

Zheng H, et al. (2025) Microbiological Diagnostic Performance and Clinical Effect of Metagenomic Next-Generation Sequencing for the Detection of Immunocompromised Patients With Community-Acquired Pneumonia. *Infection and drug resistance*, 18, 1223.

Poudel S, et al. (2025) Interpreting roles of mutations associated with the emergence of *S. aureus* USA300 strains using transcriptional regulatory network reconstruction. *eLife*, 12.

Gilbert NE, et al. (2025) A bloom of a single bacterium shapes the microbiome during outdoor diatom cultivation collapse. *mSystems*, 10(6), e0037525.