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 or information resource, analysis service resource, service resource, database, production service resource, data analysis service, bioinformatics resource center

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: OMICS_01658, nlx_17476

Alternate URLs: http://patricbrc.vbi.vt.edu/portal/portal/patric/Home

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

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250509T055640+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 999 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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).

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

Owaid HA, et al. (2025) Molecular characterization and genome sequencing of selected highly resistant clinical isolates of Pseudomonas aeruginosa and its association with the clustered regularly interspaced palindromic repeat/Cas system. Heliyon, 11(1), e41670.

Al Sium SM, et al. (2025) An insight into the genome-wide analysis of bacterial defense mechanisms in a uropathogenic Morganella morganii isolate from Bangladesh. PloS one, 20(1), e0313141.

Sivarajan V, et al. (2025) Prevalence and genomic insights of carbapenem resistant and ESBL producing Multidrug resistant Escherichia coli in urinary tract infections. Scientific reports, 15(1), 2541.

Lam HYP, et al. (2025) A Novel Bacteriophage with the Potential to Inhibit Fusobacterium nucleatum-Induced Proliferation of Colorectal Cancer Cells. Antibiotics (Basel, Switzerland), 14(1).

Yang Y, et al. (2025) High level non-carbapenemase carbapenem resistance by overlaying mutations of mexR, oprD, and ftsI in Pseudomonas aeruginosa. Microbiology spectrum, 13(1), e0139824.

Tamang P, et al. (2024) Mining Biosynthetic Gene Clusters of Pseudomonas vancouverensis Utilizing Whole Genome Sequencing. Microorganisms, 12(3).

Sid Ahmed MA, et al. (2024) Phenotypic and Genotypic Characterization of Pan-Drug-Resistant Klebsiella pneumoniae Isolated in Qatar. Antibiotics (Basel, Switzerland), 13(3).

Jastrz?b R, et al. (2024) The strain-dependent cytostatic activity of Lactococcus lactis on CRC cell lines is mediated through the release of arginine deiminase. Microbial cell factories, 23(1), 82.

Orts A, et al. (2024) A new biostimulant derived from soybean by-products enhances plant tolerance to abiotic stress triggered by ozone. BMC plant biology, 24(1), 580.

Ryu B, et al. (2024) Integrating genomic and molecular data to predict antimicrobial minimum inhibitory concentration in Klebsiella pneumoniae. Scientific reports, 14(1), 25951.

Wang X, et al. (2024) Whole genome CRISPRi screening identifies druggable vulnerabilities in an isoniazid resistant strain of Mycobacterium tuberculosis. Nature communications, 15(1), 9791.

Liu H, et al. (2024) Prevalence of ST1049-KL5 carbapenem-resistant Klebsiella pneumoniae with a blaKPC-2 and blaNDM-1 co-carrying hypertransmissible IncM1 plasmid. Communications biology, 7(1), 695.

Isaac SL, et al. (2024) Genome mining of Lactiplantibacillus plantarum PA21: insights into its antimicrobial potential. BMC genomics, 25(1), 571.

Chin HS, et al. (2024) Isolation, molecular identification, and genomic analysis of Mangrovibacter phragmitis strain ASIOC01 from activated sludge harboring the bioremediation prowess of glycerol and organic pollutants in high-salinity. Frontiers in microbiology, 15, 1415723.