

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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, production service resource, data analysis service, database, analysis service resource, service resource, 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: 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: 20260808T190232+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 1114 mentions in open access literature.

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

Lee K, et al. (2026) Biological and Genomic Characterization of Two Astaxanthin-Producing *Paracoccus marcusii* Isolates as a Potential Source for Food Additives. Journal of microbiology and biotechnology, 36, e2512023.

- Naranjo E, et al. (2026) A novel biostimulant obtained from red wine lees enhances tolerance to ozone-induced abiotic stress in grapevine plants. *Frontiers in plant science*, 17, 1654494.
- Vermilya C, et al. (2026) Multiple clades of regulators contribute to bacterial phosphate homeostasis and *Staphylococcus aureus* pathogenesis. *mBio*, 17(5), e0020326.
- Alhasani ES, et al. (2026) Development of New Drug Against Multidrug-Resistant *Candidozyma* (*Candida*) *auris* by Mining the Genome of Marine Bacteria *Vibrio* sp. IRMCESH58L. *Pharmaceutics*, 18(2).
- Pal DC, et al. (2026) Whole-genome sequence and functional insights into the salt-tolerant plant growth-promoting bacterium *Priestia aryabhattai* MS3. *BMC genomics*, 27(1).
- de Santana Nazaré PGB, et al. (2026) Metabolic Specialization and Synergy in Alkane Degradation By a Microbial Consortium: An Integrated Genomic and Geochemical Approach. *Current microbiology*, 83(5).
- Önen N, et al. (2026) Whole-Genome Sequencing and Comparative Genomic Analysis of *Citrobacter farmeri* and *Enterobacter cloacae* from Unhatched Green Turtle Eggs. *Veterinary sciences*, 13(5).
- Otwinowska A, et al. (2026) Capsular specificity in temperate phages of *Klebsiella pneumoniae* is driven by diverse receptor-binding enzymes. *PLoS biology*, 24(4), e3003716.
- Qin Q, et al. (2026) Performance of metagenomic next-generation sequencing for bloodstream infections in perioperative critically ill patients- a post-hoc analysis of a prospective, multi-center cohort study. *Frontiers in cellular and infection microbiology*, 16, 1814969.
- Sabry H, et al. (2026) Phage vB_AbaM_MU1 for biocontrol of carbapenem-resistant *Acinetobacter baumannii* (CRAB) isolated from wound infection. *Virology journal*, 23(1).
- Tunvongvinis T, et al. (2026) Characterization and Production of Antimicrobial Compound by *Streptomyces* Isolated From the Ant *Polyrhachis laevis*. *International journal of microbiology*, 2026, 8925797.
- Wan T, et al. (2026) Genomic inference of sites of transmission during regional spread of blaNDM *Klebsiella pneumoniae* in Michigan. *Nature communications*, 17(1).
- Ansell TB, et al. (2026) Cryogenic electron tomography by the numbers: Charting underexplored lineages in structural cell biology. *Proceedings of the National Academy of Sciences of the United States of America*, 123(8), e2518350123.
- Jasnauskaitė M, et al. (2026) Structure and mechanism of antiphage retron Eco2. *Nature structural & molecular biology*, 33(2), 330.
- Eroglu V, et al. (2026) Genomic insights into *Rhizobium anhuiense* IY2 isolated from *Trifolium caudatum* root nodules. *Functional & integrative genomics*, 26(1).

Li X, et al. (2026) Revisiting the dihaloelimination potential of *Dehalococcoides* revealed by genomic and proteomic analyses. *Applied and environmental microbiology*, 92(6), e0020926.

Rinke JL, et al. (2026) Comparative analysis of 163 ant genomes reveals recurrent horizontal gene transfer from bacteria to ants. *GigaScience*, 15.

Ayyappan MV, et al. (2026) *Vibrio rubrogenes* sp. nov., prodigiosin producing halophilic bacterium from seaweed *Sargassum wightii* of Mandapam coast, India. *Scientific reports*, 16(1).

Omar MR, et al. (2026) Chitosan-dextran sulfate nanocapsules for enhanced tigecycline efficacy against non-typhoidal *Salmonella enterica*. *Scientific reports*, 16(1), 5016.

Steffen K, et al. (2026) Combined treatment with bacteriophages and sodium hypochlorite against *E. faecalis* biofilm in an in vitro root canal model with evaluation of bacterial resistance. *Journal of oral microbiology*, 18(1), 2687225.