

Resource Summary Report

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Pathway Tools

RRID:SCR_013786

Type: Tool

Proper Citation

Pathway Tools (RRID:SCR_013786)

Resource Information

URL: <http://bioinformatics.ai.sri.com/ptools/>

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Description: A software application which supplies software tools to develop and maintain pathway/genome databases (PGDBs). These include the development of organism-specific databases, metabolic reconstruction and metabolic-flux modeling, scientific visualization and web publishing of organism-specific databases, analysis of gene-expression and metabolomics datasets, comparative genome and pathway analyses, and analysis of biological networks.

Synonyms: Pathway Tools Bioinformatics Software, Pathway Tools Software

Resource Type: software toolkit, software application, software resource, data management software

Defining Citation: [DOI:10.1093/bib/bbp043](https://doi.org/10.1093/bib/bbp043)

Keywords: software application, bioinformatics, software, software system, pathway genome database, PGDB, bio.tools

Funding: NIGMS GM077678;
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Resource Name: Pathway Tools

Resource ID: SCR_013786

Alternate IDs: biotools:pathway_tools

Alternate URLs: <http://bioinformatics.ai.sri.com/ptools/ptools-overview.html>,
https://bio.tools/pathway_tools

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Ratings and Alerts

No rating or validation information has been found for Pathway Tools.

No alerts have been found for Pathway Tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Jung S, et al. (2025) Building resource-efficient community databases using open-source software. Database : the journal of biological databases and curation, 2025.

Borowska-Beszta M, et al. (2024) Comparative genomics, pangenomics, and phenomic studies of *Pectobacterium betavascularum* strains isolated from sugar beet, potato, sunflower, and artichoke: insights into pathogenicity, virulence determinants, and adaptation to the host plant. Frontiers in plant science, 15, 1352318.

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, *Pectobacterium cacticida* and proposal for reclassification as *Alcorniella cacticida* comb. nov. Frontiers in plant science, 15, 1323790.

Smoktunowicz M, et al. (2024) Untargeted metabolomics coupled with genomics in the study of sucrose and xylose metabolism in *Pectobacterium betavascularum*. Frontiers in microbiology, 15, 1323765.

Alvarez F, et al. (2022) Genome mining of *Burkholderia ambifaria* strain T16, a rhizobacterium able to produce antimicrobial compounds and degrade the mycotoxin fusaric acid. World journal of microbiology & biotechnology, 38(7), 114.

George EE, et al. (2020) Highly Reduced Genomes of Protist Endosymbionts Show Evolutionary Convergence. Current biology : CB, 30(5), 925.

- Cannell N, et al. (2020) Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. *Current biology : CB*, 30(10), 1783.
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- Elmassry MM, et al. (2019) *Pseudomonas aeruginosa* Alters Its Transcriptome Related to Carbon Metabolism and Virulence as a Possible Survival Strategy in Blood from Trauma Patients. *mSystems*, 4(4).
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- Naithani S, et al. (2016) *FragariaCyc*: A Metabolic Pathway Database for Woodland Strawberry *Fragaria vesca*. *Frontiers in plant science*, 7, 242.
- Guimar??es L, et al. (2015) Genome informatics and vaccine targets in *Corynebacterium urealyticum* using two whole genomes, comparative genomics, and reverse vaccinology. *BMC genomics*, 16 Suppl 5(Suppl 5), S7.
- de la Torre A, et al. (2015) Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in *Methylobacterium buryatense* strain 5G(B1). *Microbial cell factories*, 14, 188.
- Orro A, et al. (2015) Genome and Phenotype Microarray Analyses of *Rhodococcus* sp. BCP1 and *Rhodococcus opacus* R7: Genetic Determinants and Metabolic Abilities with Environmental Relevance. *PloS one*, 10(10), e0139467.
- Chen JW, et al. (2012) Phenotypic and transcriptomic response of auxotrophic *Mycobacterium avium* subsp. *paratuberculosis* *leuD* mutant under environmental stress. *PloS one*, 7(6), e37884.
- Scaria J, et al. (2010) Analysis of ultra low genome conservation in *Clostridium difficile*. *PloS one*, 5(12), e15147.
- Caspi R, et al. (2010) The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. *Nucleic acids research*, 38(Database issue), D473.