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

Defining Citation: DOI:10.1093/bib/bbp043

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

Funding: NIGMS GM077678;
NIGMS GM080746;
NIGMS GM75742

Availability: Free to the research community, Fee for commercial use

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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Borowska-Beszta M, et al. (2024) Comparative genomics, pangenomics, and phenomic studies of Pectobacterium betavasculorum 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.

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

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.

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.

Deeg CM, et al. (2020) From the Inside Out: an Epibiotic Bdellovibrio Predator with an Expanded Genomic Complement. Journal of bacteriology, 202(8).

Paley S, et al. (2019) The MultiOmics Explainer: explaining omics results in the context of a pathway/genome database. BMC bioinformatics, 20(1), 399.

Deeg CM, et al. (2019) Chromulinavorax destructans, a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum Dependentiae. PLoS pathogens, 15(5), e1007801.

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).

Sabir JS, et al. (2016) The nuclear genome of Rhazya stricta and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae. Scientific reports, 6, 33782.

Weber T, et al. (2016) The secondary metabolite bioinformatics portal: Computational tools to facilitate synthetic biology of secondary metabolite production. Synthetic and systems biotechnology, 1(2), 69.

Naithani S, et al. (2016) FragariaCyc: A Metabolic Pathway Database for Woodland Strawberry Fragaria vesca. Frontiers in plant science, 7, 242.

Guimarães 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 Methylomicrobium 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.

Demir E, et al. (2010) The BioPAX community standard for pathway data sharing. Nature biotechnology, 28(9), 935.