

Resource Summary Report

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Biological Biochemical Image Database

RRID:SCR_003474

Type: Tool

Proper Citation

Biological Biochemical Image Database (RRID:SCR_003474)

Resource Information

URL: <http://bbid.irp.nia.nih.gov/>

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Description: Database of images of putative biological pathways, macromolecular structures, gene families, and cellular relationships. It is of use to those who are working with large sets of genes or proteins using cDNA arrays, functional genomics, or proteomics. The rationale for this collection is that: # Except in a few cases, information on most biological pathways in higher eukaryotes is non-existent, incomplete, or conflicting. # Similar biological pathways differ by tissue context, developmental stages, stimulatory events, or for other complex reasons. This database allows comparisons of different variations of pathways that can be tested empirically. # The goal of this database is to use images created directly by biomedical scientists who are specialists in a particular biological system. It is specifically designed to NOT use average, idealized or redrawn pathways. It does NOT use pathways defined by computer algorithm or information search approaches. # Information on biological pathways in higher eukaryotes generally resides in the images and text of review papers. Much of this information is not easily accessible by current medical reference search engines. # All images are attributable to the original authors. All pathways or other biological systems described are graphic representations of natural systems. Each pathway is to be considered a work in progress. Each carries some degree of error or incompleteness. The end user has the ultimate responsibility to determine the scientific correctness and validity in their particular biological system. Image/pathway submissions are welcome.

Abbreviations: BBID

Synonyms: BBID-Biological Biochemical Image Database

Resource Type: data or information resource, data repository, database, image collection, image repository, service resource, storage service resource

Defining Citation: [PMID:11099263](#)

Keywords: eukaryota, gene, gene family, biochemical, biological role, cdna, cdna array, cellular relationship, genomics, macromolecule, protein, proteomics, image, pathway, structure, annotation, cell, macromolecular structure, protein, functional genomics, proteomics

Funding: NIH Blueprint for Neuroscience Research

Availability: IMAGES MAY NOT BE USED WITHOUT BOTH THE WRITTEN PERMISSION FROM THE ORIGINAL PUBLISHER AND THE BBID DATABASE ADMINISTRATOR., The community can contribute to this resource

Resource Name: Biological Biochemical Image Database

Resource ID: SCR_003474

Alternate IDs: nif-0000-00205

Alternate URLs: <http://bbid.grc.nia.nih.gov/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260829T182135+0000

Ratings and Alerts

No rating or validation information has been found for Biological Biochemical Image Database.

No alerts have been found for Biological Biochemical Image Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Banerjee A, et al. (2023) Combinatorial Effects of miRNAs in HSV-2 Infection of Macrophages: An In Silico and In Vitro Integration Approach. *Vaccines*, 11(9).

Elias MH, et al. (2022) A Systematic Review of Candidate miRNAs, Its Targeted Genes and Pathways in Chronic Myeloid Leukemia-An Integrated Bioinformatical Analysis. *Frontiers in oncology*, 12, 848199.

Notararigo S, et al. (2021) Evaluation of an O2-Substituted (1-3)-??-D-Glucan, Produced by *Pediococcus parvulus* 2.6, in ex vivo Models of Crohn's Disease. *Frontiers in microbiology*, 12, 621280.

Zhou Q, et al. (2021) Coix Seed Diet Ameliorates Immune Function Disorders in Experimental Colitis Mice. *Nutrients*, 14(1).

Darzi M, et al. (2021) Gene co-expression network analysis reveals immune cell infiltration as a favorable prognostic marker in non-uterine leiomyosarcoma. *Scientific reports*, 11(1), 2339.

Mohamad MA, et al. (2020) A Review of Candidate Genes and Pathways in Preeclampsia-An Integrated Bioinformatical Analysis. *Biology*, 9(4).

Fustaino V, et al. (2017) Characterization of epithelial-mesenchymal transition intermediate/hybrid phenotypes associated to resistance to EGFR inhibitors in non-small cell lung cancer cell lines. *Oncotarget*, 8(61), 103340.

Liu X, et al. (2016) Personalized characterization of diseases using sample-specific networks. *Nucleic acids research*, 44(22), e164.

Budak G, et al. (2015) Reconstruction of the temporal signaling network in Salmonella-infected human cells. *Frontiers in microbiology*, 6, 730.

Tan KL, et al. (2014) Transcriptional profiling of the postnatal brain of the Ts1Cje mouse model of Down syndrome. *Genomics data*, 2, 314.

Jin L, et al. (2014) Pathway-based analysis tools for complex diseases: a review. *Genomics, proteomics & bioinformatics*, 12(5), 210.