

Resource Summary Report

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NCBI BioSystems Database

RRID:SCR_004690

Type: Tool

Proper Citation

NCBI BioSystems Database (RRID:SCR_004690)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/biosystems/>

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Description: Database that provides access to biological systems and their component genes, proteins, and small molecules, as well as literature describing those biosystems and other related data throughout Entrez. A biosystem, or biological system, is a group of molecules that interact directly or indirectly, where the grouping is relevant to the characterization of living matter. BioSystem records list and categorize components, such as the genes, proteins, and small molecules involved in a biological system. The companion FLink tool, in turn, allows you to input a list of proteins, genes, or small molecules and retrieve a ranked list of biosystems. A number of databases provide diagrams showing the components and products of biological pathways along with corresponding annotations and links to literature. This database was developed as a complementary project to (1) serve as a centralized repository of data; (2) connect the biosystem records with associated literature, molecular, and chemical data throughout the Entrez system; and (3) facilitate computation on biosystems data. The NCBI BioSystems Database currently contains records from several source databases: KEGG, BioCyc (including its Tier 1 EcoCyc and MetaCyc databases, and its Tier 2 databases), Reactome, the National Cancer Institute's Pathway Interaction Database, WikiPathways, and Gene Ontology (GO). It includes several types of records such as pathways, structural complexes, and functional sets, and is designed to accommodate other record types, such as diseases, as data become available. Through these collaborations, the BioSystems database facilitates access to, and provides the ability to compute on, a wide range of biosystems data. If you are interested in depositing data into the BioSystems database, please contact them.

Abbreviations: BioSystems

Synonyms: BioSystems Database, NCBI BioSystems

Resource Type: data analysis service, data or information resource, data repository, storage service resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:19854944](#)

Keywords: pathway, disease, gene, protein, small molecule, literature, computation, image, biomarker, drug, structural complex, functional set, biological system, molecule, gold standard, bio.tools

Funding: NIH

Resource Name: NCBI BioSystems Database

Resource ID: SCR_004690

Alternate IDs: r3d100011033, biotools:biosystems, nlx_69646

Alternate URLs: <https://bio.tools/biosystems>, <https://doi.org/10.17616/R31K80>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260801T190243+0000

Ratings and Alerts

No rating or validation information has been found for NCBI BioSystems Database.

No alerts have been found for NCBI BioSystems Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 118 mentions in open access literature.

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

Alqhtani HA, et al. (2025) Evaluation of L-carnitine's protective properties against AlCl₃-induced brain, liver, and renal toxicity in rats. PloS one, 20(1), e0317939.

Zhao W, et al. (2025) GoFCards: an integrated database and analytic platform for gain of function variants in humans. Nucleic acids research, 53(D1), D976.

Modawe GA, et al. (2025) Association of Plasma Cholesterol Profile in Sudanese Patients with Hypertension. Annals of African medicine, 24(3), 586.

Jiang SD, et al. (2024) Chromosome-level genome assembly of a stored-product psocid, Liposcelis tricolor (Psocodea: Liposcelididae). Scientific data, 11(1), 1310.

Shi H, et al. (2024) RefMetaPlant: a reference metabolome database for plants across five major phyla. *Nucleic acids research*, 52(D1), D1614.

Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. *Nucleic acids research*, 52(D1), D1478.

Fazmiya MJA, et al. (2024) Efficacy of a vaginal suppository formulation prepared with *Acacia arabica* (Lam.) Willd. gum and *Cinnamomum camphora* (L.) J. Presl. in heavy menstrual bleeding analyzed using a machine learning technique. *Frontiers in pharmacology*, 15, 1331622.

Garcia-Vi??ola V, et al. (2024) Simultaneous Analysis of Organic Acids, Glycerol and Phenolic Acids in Wines Using Gas Chromatography-Mass Spectrometry. *Foods (Basel, Switzerland)*, 13(2).

Moreno-Loshuertos R, et al. (2023) A Mutation in Mouse MT-ATP6 Gene Induces Respiration Defects and Opposed Effects on the Cell Tumorigenic Phenotype. *International journal of molecular sciences*, 24(2).

Carbonetto P, et al. (2023) Interpreting structure in sequence count data with differential expression analysis allowing for grades of membership. *bioRxiv : the preprint server for biology*.

Carbonetto P, et al. (2023) GoM DE: interpreting structure in sequence count data with differential expression analysis allowing for grades of membership. *Genome biology*, 24(1), 236.

Morales-Ferra DL, et al. (2023) Chemical Characterization, Antilipidemic Effect and Anti-Obesity Activity of *Ludwigia octovalvis* in a Murine Model of Metabolic Syndrome. *Plants (Basel, Switzerland)*, 12(13).

Sit YT, et al. (2023) Synergistic roles of DYRK1A and GATA1 in trisomy 21 megakaryopoiesis. *JCI insight*, 8(23).

Gholami M, et al. (2022) Association of miRNA targetome variants in LAMC1 and GNB3 genes with colorectal cancer and obesity. *Cancer medicine*, 11(21), 3923.

Chen H, et al. (2022) Tracing Bai-Yue Ancestry in Aboriginal Li People on Hainan Island. *Molecular biology and evolution*, 39(10).

Vinogradov AE, et al. (2022) Cellular Biogenetic Law and Its Distortion by Protein Interactions: A Possible Unified Framework for Cancer Biology and Regenerative Medicine. *International journal of molecular sciences*, 23(19).

Mishra A, et al. (2022) Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. *Brain : a journal of neurology*, 145(6), 1992.

Li X, et al. (2022) Expanding the Coverage of Metabolic Landscape in Cultivated Rice with Integrated Computational Approaches. *Genomics, proteomics & bioinformatics*, 20(4), 702.

Hasani Fard AH, et al. (2022) MiR-106b-5p Regulates the Reprogramming of Spermatogonial Stem Cells into iPSC (Induced Pluripotent Stem Cell)-Like Cells. Iranian biomedical journal, 26(4), 291.

Mota LFM, et al. (2022) Integrating genome-wide association study and pathway analysis reveals physiological aspects affecting heifer early calving defined at different ages in Nelore cattle. Genomics, 114(4), 110395.