Resource Summary Report

Generated by dkNET on Apr 16, 2025

BIND

RRID:SCR_003576
Type: Tool

Proper Citation

BIND (RRID:SCR_003576)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC165503/

Proper Citation: BIND (RRID:SCR_003576)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 17, 2022. Designed to capture protein function, defined at molecular level as set of other molecules with which protein interacts or reacts along with molecular outcome. Archives biomolecular interaction, complex and pathway information. A web-based system is available to query, view and submit records. BIND continues to grow with the addition of individual submissions as well as interaction data from the PDB and a number of large-scale interaction and complex mapping experiments using yeast two hybrid, mass spectrometry, genetic interactions and phage display.

Abbreviations: BIND

Synonyms: Biomolecular Interaction Network Database

Resource Type: database, data or information resource

Defining Citation: PMID:12519993

Keywords: interaction, protein, protein-protein interaction, small molecule-protein, nucleic acid-protein, small molecule, nucleic acid

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: BIND

Resource ID: SCR_003576

Alternate IDs: nlx_11393

Old URLs: http://bind.ca/

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250412T054847+0000

Ratings and Alerts

No rating or validation information has been found for BIND.

No alerts have been found for BIND.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 179 mentions in open access literature.

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

Weerasekera R, et al. (2024) Vibrio cholerae RbmB is an ?-1,4-polysaccharide lyase with biofilm-disrupting activity against Vibrio polysaccharide (VPS). PLoS pathogens, 20(12), e1012750.

de Guzman JCC, et al. (2024) Selective protease inhibitors from secondary metabolites of Philippine medicinal plants against porcine epidemic diarrhea virus: A computational veterinary drug discovery approach. Open veterinary journal, 14(9), 2192.

Hussain M, et al. (2024) Computational modeling of cyclotides as antimicrobial agents against Neisseria gonorrhoeae PorB porin protein: integration of docking, immune, and molecular dynamics simulations. Frontiers in chemistry, 12, 1493165.

Hu B, et al. (2024) Enterococcus faecalis provides protection during scavenging in carrion crow (Corvus corone). Zoological research, 45(3), 451.

Zheng J, et al. (2024) Network pharmacology, computational biology integrated surface plasmon resonance technology reveals the mechanism of ellagic acid against rotavirus. Scientific reports, 14(1), 7548.

Di Vincenzo R, et al. (2024) Oriented display of HIV-1 Env trimers by a novel coupling

strategy enhances B cell activation and phagocytosis. Frontiers in immunology, 15, 1344346.

Kumar S, et al. (2024) Isatin-tethered halogen-containing acylhydrazone derivatives as monoamine oxidase inhibitor with neuroprotective effect. Scientific reports, 14(1), 1264.

Khoramjoo M, et al. (2024) Protocol to identify biomarkers in patients with post-COVID condition using multi-omics and machine learning analysis of human plasma. STAR protocols, 5(2), 103041.

Kumar BH, et al. (2023) Identification of phytochemical as a dual inhibitor of PI3K and mTOR: a structure-based computational approach. Molecular diversity, 27(5), 2015.

Kauppila M, et al. (2023) Toward Corneal Limbus In Vitro Model: Regulation of hPSC-LSC Phenotype by Matrix Stiffness and Topography During Cell Differentiation Process. Advanced healthcare materials, 12(29), e2301396.

Mirzakhani H, et al. (2023) Integration of circulating microRNAs and transcriptome signatures identifies early-pregnancy biomarkers of preeclampsia. Clinical and translational medicine, 13(11), e1446.

Aakula A, et al. (2023) PP2A methylesterase PME-1 suppresses anoikis and is associated with therapy relapse of PTEN-deficient prostate cancers. Molecular oncology, 17(6), 1007.

Meng X, et al. (2023) The role of an amphiphilic helix and transmembrane region in the efficient acylation of the M2 protein from influenza virus. Scientific reports, 13(1), 18928.

Sahu A, et al. (2023) In-silico and in-vitro study reveals ziprasidone as a potential aromatase inhibitor against breast carcinoma. Scientific reports, 13(1), 16545.

Haqqani AS, et al. (2023) Proteome Profiling of Brain Vessels in a Mouse Model of Cerebrovascular Pathology. Biology, 12(12).

Newman CS, et al. (2022) Initiation of genomics-assisted breeding in Virginia-type peanuts through the generation of a de novo reference genome and informative markers. Frontiers in plant science, 13, 1073542.

Kondoh K, et al. (2022) Identification of Key Genes and Pathways Associated with Preeclampsia by a WGCNA and an Evolutionary Approach. Genes, 13(11).

Askarzadeh M, et al. (2022) Design, synthesis, in vitro ?-glucosidase inhibition, docking, and molecular dynamics of new phthalimide-benzenesulfonamide hybrids for targeting type 2 diabetes. Scientific reports, 12(1), 10569.

Khan S, et al. (2021) Predicting the Ultimate Axial Capacity of Uniaxially Loaded CFST Columns Using Multiphysics Artificial Intelligence. Materials (Basel, Switzerland), 15(1).

Ghafouri F, et al. (2021) Omics Multi-Layers Networks Provide Novel Mechanistic and Functional Insights Into Fat Storage and Lipid Metabolism in Poultry. Frontiers in genetics, 12, 646297.