

Resource Summary Report

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BindingDB

RRID:SCR_000390

Type: Tool

Proper Citation

BindingDB (RRID:SCR_000390)

Resource Information

URL: <http://www.bindingdb.org>

Proper Citation: BindingDB (RRID:SCR_000390)

Description: Web accessible database of data extracted from scientific literature, focusing on proteins that are drug-targets or candidate drug-targets and for which structural data are present in Protein Data Bank . Website supports query types including searches by chemical structure, substructure and similarity, protein sequence, ligand and protein names, affinity ranges and molecular weight . Data sets generated by BindingDB queries can be downloaded in form of annotated SDfiles for further analysis, or used as basis for virtual screening of compound database uploaded by user. Data are linked to structural data in PDB via PDB IDs and chemical and sequence searches, and to literature in PubMed via PubMed IDs .

Synonyms: BindingDB

Resource Type: data or information resource, database

Defining Citation: [PMID:26481362](#), [PMID:17145705](#)

Keywords: drug, drug discovery, drug target, binding affinity, protein interaction, small molecule-protein interaction, interaction, protein, small molecule, FASEB list

Funding: NIGMS GM070064;
NSF 9808318;
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NIGMS R24 GM144232

Availability: Free, Freely available

Resource Name: BindingDB

Resource ID: SCR_000390

Alternate IDs: r3d100012074, nif-0000-02603

Alternate URLs: <https://doi.org/10.17616/R3ZS9T>

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260729T044000+0000

Ratings and Alerts

No rating or validation information has been found for BindingDB.

No alerts have been found for BindingDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Yang H, et al. (2018) In Silico Prediction of Chemical Toxicity for Drug Design Using Machine Learning Methods and Structural Alerts. *Frontiers in chemistry*, 6, 30.

Antolin AA, et al. (2018) Objective, Quantitative, Data-Driven Assessment of Chemical Probes. *Cell chemical biology*, 25(2), 194.

Karimzadeh M, et al. (2018) Aberration hubs in protein interaction networks highlight actionable targets in cancer. *Oncotarget*, 9(38), 25166.

Lacroix S, et al. (2018) A computationally driven analysis of the polyphenol-protein interactome. *Scientific reports*, 8(1), 2232.

Cheng F, et al. (2018) Network-based approach to prediction and population-based validation of in silico drug repurposing. *Nature communications*, 9(1), 2691.

Wang T, et al. (2018) A Computational Systems Pharmacology Approach to Investigate Molecular Mechanisms of Herbal Formula Tian-Ma-Gou-Teng-Yin for Treatment of Alzheimer's Disease. *Frontiers in pharmacology*, 9, 668.

Huo X, et al. (2018) A Component Formula of Chinese Medicine for Hypercholesterolemia Based on Virtual Screening and Biology Network. *Evidence-based complementary and alternative medicine : eCAM*, 2018, 1854972.

Song Z, et al. (2018) Systems Pharmacological Approach to Investigate the Mechanism of Acori Tatarinowii Rhizoma for Alzheimer's Disease. *Evidence-based complementary and alternative medicine : eCAM*, 2018, 5194016.

- Himmelstein DS, et al. (2017) Systematic integration of biomedical knowledge prioritizes drugs for repurposing. *eLife*, 6.
- Baptista SJ, et al. (2017) Novel PARP-1 Inhibitor Scaffolds Disclosed by a Dynamic Structure-Based Pharmacophore Approach. *PloS one*, 12(1), e0170846.
- Zheng T, et al. (2017) Designing Dietary Recommendations Using System Level Interactomics Analysis and Network-Based Inference. *Frontiers in physiology*, 8, 753.
- Fang J, et al. (2017) AlzhCPI: A knowledge base for predicting chemical-protein interactions towards Alzheimer's disease. *PloS one*, 12(5), e0178347.
- Liu J, et al. (2017) Enhance the performance of current scoring functions with the aid of 3D protein-ligand interaction fingerprints. *BMC bioinformatics*, 18(1), 343.
- Shen X, et al. (2017) Elucidation of the Anti-Inflammatory Mechanisms of Bupleuri and Scutellariae Radix Using System Pharmacological Analyses. *Mediators of inflammation*, 2017, 3709874.
- Shang J, et al. (2017) Comparative analyses of structural features and scaffold diversity for purchasable compound libraries. *Journal of cheminformatics*, 9(1), 25.
- Fang J, et al. (2017) Systems Pharmacology-Based Discovery of Natural Products for Precision Oncology Through Targeting Cancer Mutated Genes. *CPT: pharmacometrics & systems pharmacology*, 6(3), 177.
- Suh SY, et al. (2017) Systems Pharmacological Approach of Pulsatillae Radix on Treating Crohn's Disease. *Evidence-based complementary and alternative medicine : eCAM*, 2017, 4198035.
- Garattini E, et al. (2016) Lipid-sensors, enigmatic-orphan and orphan nuclear receptors as therapeutic targets in breast-cancer. *Oncotarget*, 7(27), 42661.
- Shen X, et al. (2016) Systems Pharmacology Based Study of the Molecular Mechanism of SiNiSan Formula for Application in Nervous and Mental Diseases. *Evidence-based complementary and alternative medicine : eCAM*, 2016, 9146378.
- Basse MJ, et al. (2016) 2P2ldb v2: update of a structural database dedicated to orthosteric modulation of protein-protein interactions. *Database : the journal of biological databases and curation*, 2016.