Resource Summary Report

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BioLiP

RRID:SCR_027685
Type: Tool

Proper Citation

BioLiP (RRID:SCR_027685)

Resource Information

URL: https://www.aideepmed.com/BioLiP/

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Description: Semi-manually curated database for biologically relevant ligand-protein binding interactions. Structure data are collected primarily from Protein Data Bank (PDB), with biological insights mined from literature and other specific databases. Database used for serving needs of ligand-protein docking, virtual ligand screening and protein function annotation.BioLiP2 offers significantly greater coverage of nucleic acid-protein interactions, and interactions involving large complexes, integrates structural alignment algorithms with structure prediction techniques, which enables composite protein structure and sequence-based searching.

Synonyms: BioLiP2

Resource Type: data or information resource, database

Defining Citation: PMID:23087378, PMID:37522378

Keywords: curated database, ligand-protein binding interactions, ligand-protein docking, virtual ligand screening, protein function annotation,

Funding: National Science Foundation ;
NIGMS GM083107;
NIGMS GM084222

Availability: Free, Freely available

Resource Name: BioLiP

Resource ID: SCR_027685

Record Creation Time: 20251120T080608+0000

Record Last Update: 20260801T191429+0000

Ratings and Alerts

No rating or validation information has been found for BioLiP.

No alerts have been found for BioLiP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 115 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Erckert K, et al. (2025) bindNode24: Competitive binding residue prediction with 60???% smaller model. Computational and structural biotechnology journal, 27, 1060.

Rodrigues CHM, et al. (2025) CSM-Potential2: A comprehensive deep learning platform for the analysis of protein interacting interfaces. Proteins, 93(1), 209.

Yang C, et al. (2025) The optimised model of predicting protein-metal ion ligand binding residues. IET systems biology, 19(1), e70001.

Kim S, et al. (2025) Deep learning molecular interaction motifs from receptor structures alone. Journal of cheminformatics, 17(1), 113.

Gao S, et al. (2025) Predicting the binding residues of four small molecule ligands by utilizing ensemble algorithms with additional correlation features. Scientific reports, 15(1), 39243.

Guan M, et al. (2025) SpatConv Enables the Accurate Prediction of Protein Binding Sites by a Pretrained Protein Language Model and an Interpretable Bio-spatial Convolution. Research (Washington, D.C.), 8, 0773.

Hu F, et al. (2025) MegSite: an accurate nucleic acid-binding residue prediction method based on multimodal protein language model. Briefings in bioinformatics, 26(5).

Wang Z, et al. (2025) ProCV: A 3D similarity grouping method for enhanced protein pocket recognition and ligand interaction analysis. iScience, 28(4), 112305.

Chenhe Z, et al. (2025) Integrating machine learning and molecular dynamics simulation to decipher the molecular network of dioxin-associated liposarcoma. Scientific reports, 15(1), 40072.

Essien C, et al. (2025) Predicting the location of coordinated metal ion-ligand binding sites using geometry-aware graph neural networks. Computational and structural biotechnology journal, 27, 137.

Aniceto N, et al. (2025) LigExtract: Large-scale Automated Identification of Ligands from Protein Structures in the Protein Data Bank. Genomics, proteomics & bioinformatics, 23(4).

Derry A, et al. (2025) Unsupervised learning reveals landscape of local structural motifs across protein classes. Bioinformatics (Oxford, England), 41(7).

Zhang J, et al. (2025) Explainable Deep Multilevel Attention Learning for Predicting Protein Carbonylation Sites. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e2500581.

Tahmid MT, et al. (2025) TransBind allows precise detection of DNA-binding proteins and residues using language models and deep learning. Communications biology, 8(1), 568.

Dai X, et al. (2025) Topological deep learning for enhancing peptide-protein complex prediction. Communications chemistry, 8(1), 347.

Gheeraert A, et al. (2025) DIONYSUS: a database of protein-carbohydrate interfaces. Nucleic acids research, 53(D1), D387.

Gamouh H, et al. (2025) Hybrid protein-ligand binding residue prediction with protein language models: does the structure matter? Bioinformatics (Oxford, England), 41(8).

Zhang Z, et al. (2025) LABind: identifying protein binding ligand-aware sites via learning interactions between ligand and protein. Nature communications, 16(1), 7712.

Yuan Q, et al. (2024) Genome-scale annotation of protein binding sites via language model and geometric deep learning. eLife, 13.

Kwiatkowski A, et al. (2024) ATP-Triggered Fe(CN)2CO Synthon Transfer from the Maturase HypCD to the Active Site of Apo-[NiFe]-Hydrogenase. Journal of the American Chemical Society, 146(45), 30976.