Resource Summary Report

Generated by dkNET on Sep 4, 2026

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: 20260904T001136+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 127 mentions in open access literature.

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

Amorim AMB, et al. (2026) ViralBindPredict: empowering viral protein-ligand binding sites through deep learning and protein sequence-derived insights. GigaScience, 15.

Mou M, et al. (2026) Accurate Identification of Protein Binding Sites for All Drug Modalities Using ALLSites. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(10), e16530.

Porollo A, et al. (2026) SPPIDER-seq: Sequence-based partner-aware predictor of protein-protein interaction sites. bioRxiv : the preprint server for biology.

Ding K, et al. (2026) Deconvolving mutation effects on protein stability and function with disentangled protein language models. bioRxiv : the preprint server for biology.

Ashford P, et al. (2026) Gene duplication is associated with gene diversification and potential neofunctionalization in lung cancer evolution. Genome research, 36(3), 561.

Su Y, et al. (2026) Deciphering the molecular networks of 3-methylcholanthrene-induced clear cell renal cell carcinoma through multi-omics integration. Scientific reports, 16(1), 4411.

Porollo A, et al. (2026) SPPIDER-seq: sequence-based partner-aware predictor of protein-protein interaction sites. Bioinformatics (Oxford, England), 42(7).

Zheng W, et al. (2026) Deep-learning-based single-domain and multidomain protein structure prediction with D-I-TASSER. Nature biotechnology, 44(4), 641.

Chen H, et al. (2026) Automatically Defining Protein Words for Diverse Functional Predictions Based on Attention Analysis of a Protein Language Model. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(21), e21970.

Zhang W, et al. (2026) Deciphering DEL pocket patterns through contrastive learning. Nature communications, 17(1).

Carpenter KA, et al. (2026) Drug-Target Interaction Prediction with PIGLET. bioRxiv : the preprint server for biology.

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.

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.

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

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).

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.