Resource Summary Report

Generated by NIF on Apr 9, 2025

FireDB

RRID:SCR_007655
Type: Tool

Proper Citation

FireDB (RRID:SCR_007655)

Resource Information

URL: http://firedb.bioinfo.cnio.es/

Proper Citation: FireDB (RRID:SCR_007655)

Description: A database of Protein Data Bank structures, ligands and annotated functional site residues. The database can be accessed by PDB codes or UniProt accession numbers as well as keywords. FireDB contains information on every chemical compound in the PDB, including their descriptions, the PDB structures in which the compounds are found and the amino acids that are in contact with the ligand.

Abbreviations: FireDB

Resource Type: database, data or information resource

Keywords: protein, protein structure, pdb, bio.tools

Funding:

Resource Name: FireDB

Resource ID: SCR_007655

Alternate IDs: nif-0000-02839, biotools:firedb

Alternate URLs: https://bio.tools/firedb

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250409T060701+0000

Ratings and Alerts

No rating or validation information has been found for FireDB.

No alerts have been found for FireDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Parker MI, et al. (2022) Delineating the RAS Conformational Landscape. Cancer research, 82(13), 2485.

Livesey BJ, et al. (2022) The properties of human disease mutations at protein interfaces. PLoS computational biology, 18(2), e1009858.

McGreig JE, et al. (2022) 3DLigandSite: structure-based prediction of protein-ligand binding sites. Nucleic acids research, 50(W1), W13.

Kihn KC, et al. (2021) Modeling the native ensemble of PhuS using enhanced sampling MD and HDX-ensemble reweighting. Biophysical journal, 120(23), 5141.

Garrido-Martín D, et al. (2018) Effect of the sequence data deluge on the performance of methods for detecting protein functional residues. BMC bioinformatics, 19(1), 67.

Pons T, et al. (2016) KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. BMC genomics, 17 Suppl 2(Suppl 2), 396.

Hu X, et al. (2016) Protein ligand-specific binding residue predictions by an ensemble classifier. BMC bioinformatics, 17(1), 470.