

Resource Summary Report

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Protein Data Bank Site

RRID:SCR_008227

Type: Tool

Proper Citation

Protein Data Bank Site (RRID:SCR_008227)

Resource Information

URL: <http://wwwmgs.bionet.nsc.ru/mgs/gnw/pdbsite/>

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Description: Protein Data Bank (PDB) contains data on the spatial protein structures and their biologically active sites (i.e., ligand binding regions, enzyme catalytic centers, regions subjected to biochemical modifications, etc.). However, neither of the well known systems searching PDB does not provide the user with possibility to make the queries related with the active sites. A database PDBSITE storing the data on biologically active sites contained in the PDB database has been developed. PDBSITE accumulates amino acid content, structure features calculated by spatial protein structures, and physicochemical properties of sites and their spatial surroundings.

Abbreviations: PDBSITE

Resource Type: data or information resource, database

Defining Citation: [PMID:15608173](#)

Keywords: enzyme, functional, active, activity, amino acid, binding, biochemical, biological, biologically, biology, biotechnology, catalytic, dna, heterocomplex, inorganic, interaction, ligand, medicine, modification, molecular, organic, pattern, physiochemical, post-translational, primary, protein, protein sequence motifs and active sites databases, residue, rna, site, spatial, specificity, structural, structure, tertiary

Resource Name: Protein Data Bank Site

Resource ID: SCR_008227

Alternate IDs: nif-0000-21317

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260905T133151+0000

Ratings and Alerts

No rating or validation information has been found for Protein Data Bank Site.

No alerts have been found for Protein Data Bank Site.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Wang Y, et al. (2025) Homeodomain protein PRRX1 anchors the Ku heterodimers at DNA double-strand breaks to promote nonhomologous end-joining. Nucleic acids research, 53(6).