

Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 2026

Protein Databank Fun

RRID:SCR_008226

Type: Tool

Proper Citation

Protein Databank Fun (RRID:SCR_008226)

Resource Information

URL: <http://pdbfun.uniroma2.it/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 23, 2016. PDBfun is a web server for structural and functional analysis of proteins at the residue level. pdbFun gives fast access to the whole Protein Data Bank (PDB) organized as a database of annotated residues. The available data (features) range from solvent exposure to ligand binding ability, location in a protein cavity, secondary structure, residue type, sequence functional pattern, protein domain and catalytic activity. PDBfun is an integrated web tool for querying the PDB at the residue level and for local structural comparison. It integrates knowledge on single residues in protein structures coming from other databases or calculated with available or in-house developed instruments for structural analysis. Each set of different annotations represents a feature. Features are listed in PDBfun main page in orange. Features can be used for building residues selections.

Synonyms: PDBfun

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: functional, 2d, ability, activity, analysis, binding, catalytic, cavity, chain, cleft, domain, ligand, location, motif, protein, protein structure databases, residue, secondary, sequence, size, solvent, structural, structure, surface

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Protein Databank Fun

Resource ID: SCR_008226

Alternate IDs: nif-0000-21315

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260912T195701+0000

Ratings and Alerts

No rating or validation information has been found for Protein Databank Fun.

No alerts have been found for Protein Databank Fun.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Ausiello G, et al. (2005) Query3d: a new method for high-throughput analysis of functional residues in protein structures. BMC bioinformatics, 6 Suppl 4(Suppl 4), S5.

Fox JA, et al. (2005) The Bioinformatics Links Directory: a compilation of molecular biology web servers. Nucleic acids research, 33(Web Server issue), W3.