

# Resource Summary Report

Generated by T1D on Jul 30, 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:** software application, software resource, data analysis software, data processing software

**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:** 20260729T044218+0000

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## Ratings and Alerts

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

No alerts have been found for Protein Databank Fun.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

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.