# **Resource Summary Report**

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# PDBj - Protein Data Bank Japan

RRID:SCR\_008912 Type: Tool

#### **Proper Citation**

PDBj - Protein Data Bank Japan (RRID:SCR\_008912)

#### **Resource Information**

URL: http://www.pdbj.org/

Proper Citation: PDBj - Protein Data Bank Japan (RRID:SCR\_008912)

**Description:** PDBj (Protein Data Bank Japan) maintains a centralized PDB archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB, the BMRB in USA and the PDBe in EU.

Abbreviations: PDBj

Synonyms: PDBj, Protein Data Bank Japan

**Resource Type:** storage service resource, data or information resource, service resource, database, data repository

**Keywords:** protein, macromolecule, structure, sequence, ligand, binding site, nmr, molecule, gold standard

**Funding:** Japan Science and Technology Agency ; NBDC - National Bioscience Database Center

**Availability:** PDB data, Text and images are free of all copyright restrictions. You can use them free of charge. When you reprint or cite them, Please also cite us as follows: Protein Data Bank Japan (PDBj) Please also see Terms of Use page.

Resource Name: PDBj - Protein Data Bank Japan

Resource ID: SCR\_008912

Alternate IDs: nlx\_151484

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250509T055913+0000

# **Ratings and Alerts**

No rating or validation information has been found for PDBj - Protein Data Bank Japan.

No alerts have been found for PDBj - Protein Data Bank Japan.

### Data and Source Information

Source: SciCrunch Registry

# **Usage and Citation Metrics**

We found 37 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Xu W, et al. (2023) Announcing the launch of Protein Data Bank China as an Associate Member of the Worldwide Protein Data Bank Partnership. Acta crystallographica. Section D, Structural biology, 79(Pt 9), 792.

Ichimaru K, et al. (2022) Cooperative regulation of PBI1 and MAPKs controls WRKY45 transcription factor in rice immunity. Nature communications, 13(1), 2397.

Westbrook JD, et al. (2022) PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. Journal of molecular biology, 434(11), 167599.

Shao C, et al. (2022) Simplified quality assessment for small-molecule ligands in the Protein Data Bank. Structure (London, England : 1993), 30(2), 252.

Behzadi P, et al. (2022) Worldwide Protein Data Bank (wwPDB): A virtual treasure for research in biotechnology. European journal of microbiology & immunology, 11(4), 77.

Kojima H, et al. (2020) Cyclization Reaction-Based Turn-on Probe for Covalent Labeling of Target Proteins. Cell chemical biology, 27(3), 334.

Hosoe Y, et al. (2019) Structural and functional properties of Grb2 SH2 dimer in CD28 binding. Biophysics and physicobiology, 16, 80.

Tsai JY, et al. (2019) Roles of the Hydrophobic Gate and Exit Channel in Vigna radiata Pyrophosphatase Ion Translocation. Journal of molecular biology, 431(8), 1619.

Martinez X, et al. (2019) Molecular Graphics: Bridging Structural Biologists and Computer Scientists. Structure (London, England : 1993), 27(11), 1617.

Korkmaz S, et al. (2018) Investigation of protein quaternary structure via stoichiometry and symmetry information. PloS one, 13(6), e0197176.

Hiroaki H, et al. (2018) Spatial Overlap of Claudin- and Phosphatidylinositol Phosphate-Binding Sites on the First PDZ Domain of Zonula Occludens 1 Studied by NMR. Molecules (Basel, Switzerland), 23(10).

Birnbaum MD, et al. (2018) A Rapid and Precise Mutation-Activated Fluorescence Reporter for Analyzing Acute Mutagenesis Frequency. Cell chemical biology, 25(8), 1038.

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Kono T, et al. (2017) A RuBisCO-mediated carbon metabolic pathway in methanogenic archaea. Nature communications, 8, 14007.

Shimada A, et al. (2017) A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. Science advances, 3(7), e1603042.

Kinjo AR, et al. (2017) Protein Data Bank Japan (PDBj): updated user interfaces, resource description framework, analysis tools for large structures. Nucleic acids research, 45(D1), D282.

Rose PW, et al. (2017) The RCSB protein data bank: integrative view of protein, gene and 3D structural information. Nucleic acids research, 45(D1), D271.

Plöchinger M, et al. (2016) Functional Update of the Auxiliary Proteins PsbW, PsbY, HCF136, PsbN, TerC and ALB3 in Maintenance and Assembly of PSII. Frontiers in plant science, 7, 423.

Sugiyama S, et al. (2016) Molecular mechanism underlying promiscuous polyamine recognition by spermidine acetyltransferase. The international journal of biochemistry & cell biology, 76, 87.

Rose PW, et al. (2015) The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. Nucleic acids research, 43(Database issue), D345.