

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/>

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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: data or information resource, database, service resource, storage service resource, 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, r3d100010910

Alternate URLs: <https://doi.org/10.17616/R3RP75>, <https://doi.org/10.17616/R3RP75>

Record Creation Time: 20220129T080250+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 46 mentions in open access literature.

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

Kagaya Y, et al. (2026) Structure Modeling Protocols for Protein Multimer and RNA in CASP16 With Enhanced MSAs, Model Ranking, and Deep Learning. *Proteins*, 94(1), 167.

Unno M, et al. (2025) Capturing a glycosylase reaction intermediate in DNA repair by freeze-trapping of a pH-responsive hOGG1 mutant. *Nucleic acids research*, 53(14).

Bekker GJ, et al. (2025) Protein Data Bank Japan: Improved tools for sequence-oriented analysis of protein structures. *Protein science : a publication of the Protein Society*, 34(3), e70052.

Xu D, et al. (2024) Effect and mechanism of curcumin on colon cancer cell senescence through early growth response 1 (EGR1). *Translational cancer research*, 13(7), 3251.

Xie Q, et al. (2023) Molecular Mechanisms of Functional Modulation of Transcriptional Coactivator PC4 via Phosphorylation on Its Intrinsically Disordered Region. *ACS omega*, 8(16), 14572.

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.

Fukunishi Y, et al. (2022) Computer simulation of molecular recognition in biomolecular system: from in silico screening to generalized ensembles. *Biophysical reviews*, 14(6), 1423.

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

Qin S, et al. (2022) mRNA-based therapeutics: powerful and versatile tools to combat diseases. *Signal transduction and targeted therapy*, 7(1), 166.

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

Kataoka K, et al. (2022) A cryptic phosphate-binding pocket on the SPFH domain of human stomatin that regulates a novel fibril-like self-assembly. *Current research in structural biology*, 4, 158.

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.

Robson B, et al. (2020) Bioinformatics studies on a function of the SARS-CoV-2 spike glycoprotein as the binding of host sialic acid glycans. *Computers in biology and medicine*, 122, 103849.

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.

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

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.

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

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