

# 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:** data or information resource, database, data repository, service resource, storage service resource

**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.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 39 mentions in open access literature.

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

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).

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.

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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.

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

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Shao C, et al. (2017) Multivariate Analyses of Quality Metrics for Crystal Structures in the PDB Archive. *Structure* (London, England : 1993), 25(3), 458.

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.

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

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.

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