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, service resource, data repository, database, 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

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250412T055326+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 dkNET.

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.

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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.

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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.

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

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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.

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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.