Resource Summary Report

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PDBe - Protein Data Bank in Europe

RRID:SCR_004312 Type: Tool

Proper Citation

PDBe - Protein Data Bank in Europe (RRID:SCR_004312)

Resource Information

URL: http://www.ebi.ac.uk/pdbe/

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Description: The European resource for the collection, organization and dissemination of data on biological macromolecular structures. In collaboration with the other worldwide Protein Data Bank (wwPDB) partners - the Research Collaboratory for Structural Bioinformatics (RCSB) and BioMagResBank (BMRB) in the USA and the Protein Data Bank of Japan (PDBj) - they work to collate, maintain and provide access to the global repository of macromolecular structure data. The main objectives of the work at PDBe are: * to provide an integrated resource of high-quality macromolecular structures and related data and make it available to the biomedical community via intuitive user interfaces. * to maintain in-house expertise in all the major structure-determination techniques (X-ray, NMR and EM) in order to stay abreast of technical and methodological developments in these fields, and to work with the community on issues of mutual interest (such as data representation, harvesting, formats and standards, or validation of structural data). * to provide high-quality deposition and annotation facilities for structural data as one of the wwPDB deposition sites. Several sophisticated tools are also available for the structural analysis of macromolecules.

Abbreviations: PDBe

Synonyms: Protein DataBank Europe, Protein DataBank in Europe, PDBe, Protein Data Bank in Europe, Protein Data Bank Europe, Macromolecular Structure Database

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

Defining Citation: PMID:21045060, PMID:21460450, PMID:19858099

Keywords: x-ray, nmr, cryo-em, hybrid method, dna, protein, rna, sugar, ligand, virus, compound, fold, enzyme, 3d spatial image, structure, macromolecule, protein-protein interaction, gold standard, bio.tools

Funding: European Molecular Biology Laboratory; Heidelberg; Germany ; Wellcome Trust ; BBSRC ; NIH ; European Union ; MRC ; CCP4

Resource Name: PDBe - Protein Data Bank in Europe

Resource ID: SCR_004312

Alternate IDs: biotools:pdbe, nlx_32372

Alternate URLs: https://bio.tools/pdbe

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250508T064859+0000

Ratings and Alerts

No rating or validation information has been found for PDBe - Protein Data Bank in Europe.

No alerts have been found for PDBe - Protein Data Bank in Europe.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

Iwamuro T, et al. (2024) Stability of N-type inactivation and the coupling between N-type and C-type inactivation in the Aplysia Kv1 channel. Pflugers Archiv : European journal of physiology, 476(10), 1493.

Thore S, et al. (2023) Molecular details of the CPSF73-CPSF100 C-terminal heterodimer and interaction with Symplekin. Open biology, 13(11), 230221.

Ling EM, et al. (2022) A comprehensive structural analysis of the ATPase domain of human DNA topoisomerase II beta bound to AMPPNP, ADP, and the bisdioxopiperazine, ICRF193. Structure (London, England : 1993), 30(8), 1129.

Marabini R, et al. (2021) Near-atomic structure of an atadenovirus reveals a conserved capsid-binding motif and intergenera variations in cementing proteins. Science advances, 7(14).

Antolin AA, et al. (2021) Evolution of kinase polypharmacology across HSP90 drug discovery. Cell chemical biology, 28(10), 1433.

Bhamidimarri SP, et al. (2021) Acquisition of ionic copper by the bacterial outer membrane protein OprC through a novel binding site. PLoS biology, 19(11), e3001446.

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Upadhyay SK, et al. (2020) Structural basis of UCUU RNA motif recognition by splicing factor RBM20. Nucleic acids research, 48(8), 4538.

Fusani L, et al. (2020) Exploring Ligand Stability in Protein Crystal Structures Using Binding Pose Metadynamics. Journal of chemical information and modeling, 60(3), 1528.

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Dodonova SO, et al. (2019) Structure of the Ty3/Gypsy retrotransposon capsid and the evolution of retroviruses. Proceedings of the National Academy of Sciences of the United States of America, 116(20), 10048.

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Cook CE, et al. (2019) The European Bioinformatics Institute in 2018: tools, infrastructure and training. Nucleic acids research, 47(D1), D15.

Hirano Y, et al. (2019) Structural basis of phosphatidylcholine recognition by the C2-domain of cytosolic phospholipase A2?. eLife, 8.

Kolesnikova O, et al. (2018) Molecular structure of promoter-bound yeast TFIID. Nature communications, 9(1), 4666.

De Robertis M, et al. (2018) In Vivo Evaluation of a New Recombinant Hyaluronidase to Improve Gene Electro-Transfer Protocols for DNA-Based Drug Delivery against Cancer. Cancers, 10(11).

Zhang Y, et al. (2018) Alternative Mode of E-Site tRNA Binding in the Presence of a Downstream mRNA Stem Loop at the Entrance Channel. Structure (London, England : 1993), 26(3), 437.

Miller OK, et al. (2018) A new structural class of bacterial thioester domains reveals a slipknot topology. Protein science : a publication of the Protein Society, 27(9), 1651.

van Haren MJ, et al. (2018) The kinetic analysis of the N-methylation of 4-phenylpyridine by nicotinamide N-methyltransferase: Evidence for a novel mechanism of substrate inhibition. The international journal of biochemistry & cell biology, 98, 127.

Urresti S, et al. (2018) Structural studies of the unusual metal-ion site of the GH124 endoglucanase from Ruminiclostridium thermocellum. Acta crystallographica. Section F, Structural biology communications, 74(Pt 8), 496.