

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

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CCP4

Resource Name: PDBe - Protein Data Bank in Europe

Resource ID: SCR_004312

Alternate IDs: r3d100012791, biotools:pdbe, nlx_32372

Alternate URLs: <https://bio.tools/pdbe>, <https://doi.org/10.17616/R3J226>

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260801T190239+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Wojnowska M, et al. (2025) Structural basis for collagen recognition by the Streptococcus pyogenes M3 protein and its involvement in biofilm. eLife, 14.

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.

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

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).

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.

Perez-Illana M, et al. (2021) Cryo-EM structure of enteric adenovirus HAdV-F41 highlights structural variations among human adenoviruses. *Science advances*, 7(9).

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

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Weis F, et al. (2019) Elucidation of the viral disassembly switch of tobacco mosaic virus. *EMBO reports*, 20(11), e48451.

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.

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

Davey NE, et al. (2019) An intrinsically disordered proteins community for ELIXIR. *F1000Research*, 8.

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).

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.

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.

Qu K, et al. (2018) Structure and architecture of immature and mature murine leukemia virus capsids. *Proceedings of the National Academy of Sciences of the United States of America*, 115(50), E11751.