

Resource Summary Report

Generated by [NIF](#) on Apr 9, 2025

Worldwide Protein Data Bank (wwPDB)

RRID:SCR_006555

Type: Tool

Proper Citation

Worldwide Protein Data Bank (wwPDB) (RRID:SCR_006555)

Resource Information

URL: <http://www.wwpdb.org/>

Proper Citation: Worldwide Protein Data Bank (wwPDB) (RRID:SCR_006555)

Description: Public global Protein Data Bank archive of macromolecular structural data overseen by organizations that act as deposition, data processing and distribution centers for PDB data. Members are: RCSB PDB (USA), PDBe (Europe) and PDBj (Japan), and BMRB (USA). This site provides information about services provided by individual member organizations and about projects undertaken by wwPDB. Data available via websites of its member organizations.

Abbreviations: wwPDB

Synonyms: World Wide Protein DataBank, wwPDB, Worldwide Protein Data Bank (wwPDB), World Wide Protein Data Bank, Worldwide Protein DataBank

Resource Type: database, data or information resource

Defining Citation: [PMID:14634627](#)

Keywords: 3-dimensional, bioinformatics, protein, research, structure, macromolecule, structural data, 3d spatial image, gold standard

Funding: NSF ;
NIGMS ;
DOE ;
NLM ;
NCI ;
NINDS ;
NIDDK ;

European Molecular Biology Laboratory ;
Heidelberg; Germany ;
Wellcome Trust ;
BBSRC ;
NIH ;
European Union ;
NBDC - National Bioscience Database Center ;
Japan Science and Technology Agency

Availability: Free, Freely available

Resource Name: Worldwide Protein Data Bank (wwPDB)

Resource ID: SCR_006555

Alternate IDs: nif-0000-23903

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250409T060534+0000

Ratings and Alerts

No rating or validation information has been found for Worldwide Protein Data Bank (wwPDB).

No alerts have been found for Worldwide Protein Data Bank (wwPDB).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1160 mentions in open access literature.

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

Li H, et al. (2025) Enhanced sampling of protein conformational changes via true reaction coordinates from energy relaxation. Nature communications, 16(1), 786.

Liu M, et al. (2025) Mechanistic insights into pachymic acid's action on triple-negative breast Cancer through TOP2A targeting. Scientific reports, 15(1), 2856.

Lopez ME, et al. (2025) Intracerebroventricular administration of a modified hexosaminidase ameliorates late-stage neurodegeneration in a GM2 mouse model. *PLoS one*, 20(1), e0315005.

, et al. (2024) EMDB-the Electron Microscopy Data Bank. *Nucleic acids research*, 52(D1), D456.

Chen X, et al. (2024) Preclinical evaluation of the SARS-CoV-2 Mpro inhibitor RAY1216 shows improved pharmacokinetics compared with nirmatrelvir. *Nature microbiology*, 9(4), 1075.

Singla A, et al. (2024) Structural basis for Retriever-SNX17 assembly and endosomal sorting. *bioRxiv : the preprint server for biology*.

Ding Y, et al. (2024) Transcriptome analysis reveals the clinical significance of CXCL13 in Pan-Gyn tumors. *Journal of cancer research and clinical oncology*, 150(3), 116.

Javornik U, et al. (2024) Unveiling the solution structure of a DNA duplex with continuous silver-modified Watson-Crick base pairs. *Nature communications*, 15(1), 7763.

Takekawa N, et al. (2024) Structural analysis of S-ring composed of FliFG fusion proteins in marine *Vibrio* polar flagellar motor. *mBio*, 15(10), e0126124.

Yang JC, et al. (2024) Loss of SELENOW aggravates muscle loss with regulation of protein synthesis and the ubiquitin-proteasome system. *Science advances*, 10(38), eadj4122.

Guo SC, et al. (2024) Dynamics of activation in the voltage-sensing domain of *Ciona* intestinalis phosphatase Ci-VSP. *Nature communications*, 15(1), 1408.

Ju X, et al. (2024) Exploring the Therapeutic Mechanism of Pingxin Dingzhi Decoction Through Network Pharmacology and Molecular Docking. *Alpha psychiatry*, 25(5), 584.

Song H, et al. (2024) Novel exosomal circEGFR facilitates triple negative breast cancer autophagy via promoting TFEB nuclear trafficking and modulating miR-224-5p/ATG13/ULK1 feedback loop. *Oncogene*, 43(11), 821.

Yue N, et al. (2024) Zn²⁺-dependent association of cysteine-rich protein with virion orchestrates morphogenesis of rod-shaped viruses. *PLoS pathogens*, 20(6), e1012311.

Kelley EH, et al. (2024) N⁶-acetyl-L-ornithine deacetylase from *Escherichia coli* and a ninhydrin-based assay to enable inhibitor identification. *Frontiers in chemistry*, 12, 1415644.

Mishra N, et al. (2024) *S. aureus* Eap is a polyvalent inhibitor of neutrophil serine proteases. *The Journal of biological chemistry*, 300(9), 107627.

Diaz N, et al. (2024) Discovery of potent small-molecule inhibitors of lipoprotein(a) formation. *Nature*, 629(8013), 945.

Burley SK, et al. (2024) RCSB Protein Data Bank: supporting research and education worldwide through explorations of experimentally determined and computationally predicted atomic level 3D biostructures. *IUCrJ*, 11(Pt 3), 279.

Wang Y, et al. (2024) A KDPG sensor RccR governs *Pseudomonas aeruginosa* carbon metabolism and aminoglycoside antibiotic tolerance. *Nucleic acids research*, 52(2), 967.

Kamuyu G, et al. (2024) Global evaluation of lineage-specific human papillomavirus capsid antigenicity using antibodies elicited by natural infection. *Nature communications*, 15(1), 1608.