

Resource Summary Report

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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: data or information resource, database

Defining Citation: [PMID:14634627](#)

Keywords: 3-dimentional, 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, r3d100011104

Alternate URLs: <https://doi.org/10.17616/R3462V>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260729T044137+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 1215 mentions in open access literature.

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

Li Z, et al. (2026) Phylogenetic and functional characterization of Asgard primases. Molecular biology and evolution, 43(1).

Duan H, et al. (2025) Blocking activation of the C1r zymogen defines a novel mode of complement inhibition. The Journal of biological chemistry, 301(3), 108301.

Bittrich S, et al. (2025) Visualizing and analyzing 3D biomolecular structures using Mol* at RCSB.org: Influenza A H5N1 virus proteome case study. Protein science : a publication of the Protein Society, 34(4), e70093.

Datta SP, et al. (2025) Evolutionary duplication of the leishmanial adaptor protein ?-SNAP plays a role in its pathogenicity. The Journal of biological chemistry, 301(5), 108427.

Peddada N, et al. (2025) Structural insights into the ubiquitin-independent midnolin-proteasome pathway. *Proceedings of the National Academy of Sciences of the United States of America*, 122(19), e2505345122.

Masuyer G, et al. (2025) Botulinum neurotoxin A mutants with enhanced ganglioside binding show improved potency and altered ganglioside selectivity. *Communications chemistry*, 8(1), 171.

Parker MC, et al. (2025) A Metric for the Entropic Purpose of a System. *Entropy (Basel, Switzerland)*, 27(2).

Hladík P, et al. (2025) Phenylacetic acid metabolism in land plants: novel pathways and metabolites. *Journal of experimental botany*, 76(12), 3427.

Crava CM, et al. (2025) Alternative strategies based on transgenic *Drosophila melanogaster* for the functional characterization of insect Ionotropic Receptors. *Biological research*, 58(1), 36.

Wang H, et al. (2025) Computational loop reconstruction based design of efficient PET hydrolases. *Communications biology*, 8(1), 934.

Manna A, et al. (2025) Sample delivery methods for protein X-ray crystallography with a special focus on sample consumption. *Nature communications*, 16(1), 9856.

Karimullina E, et al. (2025) Structural architecture of TolQ-TolR inner membrane protein complex from opportunistic pathogen *Acinetobacter baumannii*. *Science advances*, 11(14), eadq9845.

Gonzalez A, et al. (2025) A repurposed AMP binding domain reveals mitochondrial protein AMPylation as a regulator of cellular metabolism. *Nature communications*, 16(1), 7863.

He M, et al. (2025) Machine learning-powered discovery of a novel berberine derivative inducing SCD-dependent ferroptosis in osteosarcoma. *Journal of translational medicine*, 23(1), 1328.

Khilji MS, et al. (2025) Structural similarities reveal an expansive conotoxin family with a two-finger toxin fold. *Protein science : a publication of the Protein Society*, 34(11), e70333.

Ciulla DA, et al. (2025) A general assay platform to study protein pharmacology using ligand-dependent structural dynamics. *Nature communications*, 16(1), 4342.

Chen Z, et al. (2025) Development of PVTX-405 as a potent and highly selective molecular glue degrader of IKZF2 for cancer immunotherapy. *Nature communications*, 16(1), 4095.

Zheng S, et al. (2025) Navigating the unstructured by evaluating alphafold's efficacy in predicting missing residues and structural disorder in proteins. *PloS one*, 20(3), e0313812.

Kopečný DJ, et al. (2025) A monomer-dimer switch modulates the activity of plant adenosine kinase. *Journal of experimental botany*, 76(12), 3457.

Masuyer G, et al. (2025) Discovery of mono-ADP ribosylating toxins with high structural homology to *Pseudomonas* exotoxin A. *Communications biology*, 8(1), 413.