

Resource Summary Report

Generated by T1D on Aug 1, 2026

PDB-Dev

RRID:SCR_016185

Type: Tool

Proper Citation

PDB-Dev (RRID:SCR_016185)

Resource Information

URL: <https://pdb-dev.wwpdb.org>

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Description: Data repository for integrative/hybrid structural models of macromolecules and their assemblies. This includes atomistic models as well as multi-scale models consisting of different coarse-grained representations.

Resource Type: service resource, data repository, storage service resource

Keywords: protein, prototype, deposition, integration, hybrid, model, macromolecule, assembly, crystallography, spectroscopy, microscopy,

Funding: NSF DBI-1519158

Availability: Account required, Freely available, The research community can contribute to this resource

Resource Name: PDB-Dev

Resource ID: SCR_016185

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260801T042756+0000

Ratings and Alerts

No rating or validation information has been found for PDB-Dev.

No alerts have been found for PDB-Dev.

Data and Source Information

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Kliza KW, et al. (2024) N4BP1 functions as a dimerization-dependent linear ubiquitin reader which regulates TNF signalling. *Cell death discovery*, 10(1), 183.

Liu X, et al. (2024) An integrated structural model of the DNA damage-responsive H3K4me3 binding WDR76:SPIN1 complex with the nucleosome. *Proceedings of the National Academy of Sciences of the United States of America*, 121(33), e2318601121.

Pasani S, et al. (2024) The molecular architecture of the desmosomal outer dense plaque by integrative structural modeling. *Protein science : a publication of the Protein Society*, 33(12), e5217.

Arvindekar S, et al. (2024) Optimizing representations for integrative structural modeling using Bayesian model selection. *Bioinformatics (Oxford, England)*, 40(3).

Burmeister WP, et al. (2024) Structure and flexibility of the DNA polymerase holoenzyme of vaccinia virus. *PLoS pathogens*, 20(5), e1011652.

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.

Arvindekar S, et al. (2023) Optimizing representations for integrative structural modeling using Bayesian model selection. *bioRxiv : the preprint server for biology*.

Wang Y, et al. (2023) A tau fragment links depressive-like behaviors and cognitive declines in Alzheimer's disease mouse models through attenuating mitochondrial function. *Frontiers in aging neuroscience*, 15, 1293164.

Otsuka S, et al. (2023) A quantitative map of nuclear pore assembly reveals two distinct mechanisms. *Nature*, 613(7944), 575.

Pasani S, et al. (2023) The molecular architecture of the desmosomal outer dense plaque by integrative structural modeling. *bioRxiv : the preprint server for biology*.

Kim M, et al. (2022) Two interaction surfaces between XPA and RPA organize the preincision complex in nucleotide excision repair. *Proceedings of the National Academy of Sciences of the United States of America*, 119(34), e2207408119.

Trewhella J, et al. (2022) Recent advances in small-angle scattering and its expanding impact in structural biology. *Structure (London, England : 1993)*, 30(1), 15.

Burley SK, et al. (2022) RCSB Protein Data bank: Tools for visualizing and understanding biological macromolecules in 3D. *Protein science : a publication of the Protein Society*,

31(12), e4482.

Westbrook JD, et al. (2022) PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. *Journal of molecular biology*, 434(11), 167599.

Vallat B, et al. (2021) New system for archiving integrative structures. *Acta crystallographica. Section D, Structural biology*, 77(Pt 12), 1486.

Escobar CA, et al. (2021) Structural interactions define assembly adapter function of a type II secretion system pseudopilin. *Structure (London, England : 1993)*, 29(10), 1116.

Brilot AF, et al. (2021) CM1-driven assembly and activation of yeast γ -tubulin small complex underlies microtubule nucleation. *eLife*, 10.

Kadir SR, et al. (2021) Nanoscape, a data-driven 3D real-time interactive virtual cell environment. *eLife*, 10.

Kaake RM, et al. (2021) Characterization of an A3G-VifHIV-1-CRL5-CBF γ Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host-Pathogen Complexes. *Molecular & cellular proteomics : MCP*, 20, 100132.

Topf M, et al. (2021) Editorial: Experiments and Simulations: A Pas de Deux to Unravel Biological Function. *Frontiers in molecular biosciences*, 8, 799406.