Resource Summary Report

Generated by dkNET on Apr 16, 2025

PDB-Dev

RRID:SCR_016185
Type: Tool

Proper Citation

PDB-Dev (RRID:SCR_016185)

Resource Information

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

Proper Citation: PDB-Dev (RRID:SCR_016185)

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: data repository, service resource, 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: 20250416T063749+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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.

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.

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

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.

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.

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.

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.

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

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

Sali A, et al. (2021) From integrative structural biology to cell biology. The Journal of biological chemistry, 296, 100743.

Kaake RM, et al. (2021) Characterization of an A3G-VifHIV-1-CRL5-CBF? 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.