

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

PDB Validation Server

RRID:SCR_018135

Type: Tool

Proper Citation

PDB Validation Server (RRID:SCR_018135)

Resource Information

URL: <https://validate-rcsb-1.wwpdb.org/>

Proper Citation: PDB Validation Server (RRID:SCR_018135)

Description: Software tool for checking data before submitting to wwPDB. Stand alone validation server. Service designed to help to check model and experimental files prior starting data deposition.

Resource Type: software resource, software application, standalone software, service resource

Keywords: Data validation, wwPDB data submission, data deposition

Availability: Restricted

Resource Name: PDB Validation Server

Resource ID: SCR_018135

Alternate URLs: <https://validate-rcsb-2.wwpdb.org/>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260731T043019+0000

Ratings and Alerts

No rating or validation information has been found for PDB Validation Server.

No alerts have been found for PDB Validation Server.

Data and Source Information

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Montecinos F, et al. (2025) Structure of blood cell-specific tubulin and demonstration of dimer spacing compaction in a single protofilament. *The Journal of biological chemistry*, 301(2), 108132.

Zou JL, et al. (2025) Complete biosynthetic pathway of furochromones in *Saposhnikovia divaricata* and its evolutionary mechanism in Apiaceae plants. *Nature communications*, 16(1), 3109.

Rettie SA, et al. (2025) Accurate de novo design of high-affinity protein-binding macrocycles using deep learning. *Nature chemical biology*, 21(12), 1948.

Zafar H, et al. (2025) Breaking Barriers: Transitioning from X-ray Crystallography to Cryo-EM for Structural Studies of ATAD2B. *bioRxiv : the preprint server for biology*.

Haase M, et al. (2025) Re-engineering a transferase scaffold for indole C3 methylation in diketopiperazines. *Protein science : a publication of the Protein Society*, 34(9), e70254.

Henriques WS, et al. (2025) Structures reveal how the Cas1-2/3 integrase captures, delivers, and integrates foreign DNA into CRISPR loci. *Structure (London, England : 1993)*, 33(12), 2058.

Nayak AR, et al. (2025) Maackia amurensis seed lectin structure and sequence comparison with other M. amurensis lectins. *The Journal of biological chemistry*, 301(5), 108466.

Polonio P, et al. (2025) Structural basis for amyloid fibril assembly by the master cell-signaling regulator receptor-interacting protein kinase 1. *Nature communications*, 16(1), 9607.

Kumakura H, et al. (2025) A β -1,2-glucan-associated glycoside hydrolase family 1 β -glucosidase from *Streptomyces griseus*. *Protein science : a publication of the Protein Society*, 34(9), e70255.

Gutfreund C, et al. (2025) Structural insights into a DNA polymerase reading the xeno nucleic acid HNA. *Nucleic acids research*, 53(1).

Henriques WS, et al. (2025) Structures reveal how the Cas1-2/3 integrase captures, delivers, and integrates foreign DNA into CRISPR loci. *bioRxiv : the preprint server for biology*.

Coquille S, et al. (2025) Allostery and Evolution: A Molecular Journey Through the Structural and Dynamical Landscape of an Enzyme Super Family. *Molecular biology and evolution*, 42(1).

Nayak AR, et al. (2025) Structural basis for intrinsic strand displacement activity of mitochondrial DNA polymerase. *Nature communications*, 16(1), 2417.

Yasuda D, et al. (2025) Development of Keap1-Nrf2 Protein-Protein Interaction Inhibitor Activating Intracellular Nrf2 Based on the Naphthalene-2-acetamide Scaffold, and its Anti-Inflammatory Effects. *ChemMedChem*, 20(21), e202500474.

Dötsch L, et al. (2024) Discovery of the sEH Inhibitor Epoxykynin as a Potent Kynurenine Pathway Modulator. *Journal of medicinal chemistry*, 67(6), 4691.

Herbine K, et al. (2024) Structural basis for substrate binding and selection by human mitochondrial RNA polymerase. *Nature communications*, 15(1), 7134.

Lundstrøm J, et al. (2024) Elucidating the glycan-binding specificity and structure of Cucumis melo agglutinin, a new R-type lectin. *Beilstein journal of organic chemistry*, 20, 306.

Gully BS, et al. (2024) Structure of a fully assembled ?? T cell antigen receptor. *Nature*, 634(8034), 729.

Liu J, et al. (2024) The structure of mouse RIPK1 RHIM-containing domain as a homo-amyloid and in RIPK1/RIPK3 complex. *Nature communications*, 15(1), 6975.

de la Gándara Á, et al. (2024) Molecular basis for transposase activation by a dedicated AAA+ ATPase. *Nature*, 630(8018), 1003.