

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## PDB Validation Server

RRID:SCR\_018135

Type: Tool

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### Proper Citation

PDB Validation Server (RRID:SCR\_018135)

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### 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 application, service resource, software resource, standalone software

**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:** 20260728T043541+0000

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### Ratings and Alerts

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

No alerts have been found for PDB Validation Server.

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### 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 [nidm-terms](#) .

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  $\beta$ -1,2-glucan-associated glycoside hydrolase family 1  $\beta$ -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).

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).

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*.

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.