

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: service resource, software application, 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: 20260905T133054+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 57 mentions in open access literature.

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

Melicher F, et al. (2026) Structural and functional characterization of the newly identified Photorhabdus laumondii tumor necrosis factor-like lectin. The FEBS journal, 293(4), 1168.

Rajeshwari R, et al. (2026) Potent and selective indole-based inhibitors targeting disease-transmitting mosquitoes. RSC medicinal chemistry, 17(2), 1166.

Lepesheva GI, et al. (2026) Cryo-EM reveals an ensemble of cytochrome P450 reductase conformations in solution. Protein science : a publication of the Protein Society, 35(2), e70448.

Troisi R, et al. (2026) The Binding of 3-O-Methylfluorescein Phosphate to the Catalytic Domain of the Human CDC25B Phosphatase: A Structural Investigation. Chembiochem : a European journal of chemical biology, 27(7), e202600010.

Leiva Martel HN, et al. (2026) Roles of acidic residues in SpeG acetyltransferases-insights into importance for kinetic activity and polyamine binding in allosteric and acceptor sites. The Biochemical journal, 483(6), 1075.

Idikuda V, et al. (2026) Lipid bilayers determine allostery but not intrinsic affinity of cAMP to pacemaker channels. Nature communications, 17(1).

Rawal Y, et al. (2026) Structural insight into how RAD51 paralog exchange regulates RAD51 filament formation. Nature structural & molecular biology, 33(5), 768.

Mieher JL, et al. (2026) The structure of Streptococcus gordonii surface protein SspB in complex with TEV peptide provides clues to oral streptococcal adherence to salivary agglutinin. Infection and immunity, 94(3), e0046725.

Hu H, et al. (2026) Cryo-electron microscopy structure of the budding yeast telomerase holoenzyme. Science (New York, N.Y.), 391(6792), eadz5344.

Gardner CL, et al. (2026) Demonstration of in vivo efficacy, cryo-EM-epitope identification, and breadth of two anti-alphavirus bispecific single domain antibodies. Journal of virology, 100(1), e0187525.

Zafar H, et al. (2026) Breaking barriers: transitioning from X-ray crystallography to cryo-EM for structural studies. Acta crystallographica. Section D, Structural biology, 82(Pt 3), 253.

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.

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

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.

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.

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.

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.

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