

Resource Summary Report

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MolProbity

RRID:SCR_014226

Type: Tool

Proper Citation

MolProbity (RRID:SCR_014226)

Resource Information

URL: <http://molprobity.biochem.duke.edu>

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Description: A structure-validation web application which provides an expert-system consultation about the accuracy of a macromolecular structure model, diagnosing local problems and enabling their correction. MolProbity works best as an active validation tool (used as soon as a model is available and during each rebuild/refine loop) and when used for protein and RNA crystal structures, but it may also work well for DNA, ligands and NMR ensembles. It produces coordinates, graphics, and numerical evaluations that integrate with either manual or automated use in systems such as PHENIX, KiNG, or Coot.

Resource Type: web application, software resource

Defining Citation: [DOI:10.1107/S0907444909042073](https://doi.org/10.1107/S0907444909042073)

Keywords: web application, consultation, macromolecular structure, structure validation, macromolecular crystallography

Funding: Howard Hughes Medical Institute Predoctoral Fellowship ;
NIGMS GM-15000;
NIGMS GM-61302

Availability: Acknowledgement requested, Requires Java and Javascript

Resource Name: MolProbity

Resource ID: SCR_014226

Alternate URLs: <https://www.phenix->

online.org/documentation/reference/molprobitool.html

Record Creation Time: 20220129T080319+0000

Record Last Update: 20250420T014709+0000

Ratings and Alerts

No rating or validation information has been found for MolProbity.

No alerts have been found for MolProbity.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5703 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Bal?kç? E, et al. (2025) Structure of the Nipah virus polymerase complex. The EMBO journal, 44(2), 563.

Mohamed G, et al. (2025) A small antimicrobial peptide derived from a Burkholderia bacterium exhibits a broad-spectrum and high inhibiting activities against crop diseases. Plant biotechnology journal, 23(2), 430.

Berardi A, et al. (2025) The C-terminal PHDVC5HCH tandem domain of NSD2 is a combinatorial reader of unmodified H3K4 and tri-methylated H3K27 that regulates transcription of cell adhesion genes in multiple myeloma. Nucleic acids research, 53(1).

Arpin D, et al. (2025) The binding of RbgA to a critical 50S assembly intermediate facilitates YphC function in bacterial ribosomal assembly. Nucleic acids research, 53(2).

Koning HJ, et al. (2025) Structural plasticity of the coiled-coil interactions in human SFPQ. Nucleic acids research, 53(2).

Thach T, et al. (2025) Mechanistic insights into the selective targeting of P2X3 receptor by camlipixant antagonist. The Journal of biological chemistry, 301(1), 108109.

Lu X, et al. (2025) Structural insights into the activation mechanism of the human zinc-activated channel. Nature communications, 16(1), 442.

Alotaiq N, et al. (2025) Evaluation of Structure Prediction and Molecular Docking Tools for Therapeutic Peptides in Clinical Use and Trials Targeting Coronary Artery Disease.

International journal of molecular sciences, 26(2).

Vigneron SF, et al. (2025) Docking 14 million virtual isoquinuclidines against the mu and kappa opioid receptors reveals dual antagonists-inverse agonists with reduced withdrawal effects. *bioRxiv : the preprint server for biology*.

Lotz R, et al. (2025) Alternative splicing in the DBD linker region of p63 modulates binding to DNA and iASPP in vitro. *Cell death & disease*, 16(1), 4.

Gjorgjevikj D, et al. (2025) The Psu protein of phage satellite P4 inhibits transcription termination factor ? by forced hyper-oligomerization. *Nature communications*, 16(1), 550.

Robison B, et al. (2025) Engineered ipilimumab variants that bind human and mouse CTLA-4. *mAbs*, 17(1), 2451296.

Litschko C, et al. (2025) Transition transferases prime bacterial capsule polymerization. *Nature chemical biology*, 21(1), 120.

Matico R, et al. (2025) Navigating from cellular phenotypic screen to clinical candidate: selective targeting of the NLRP3 inflammasome. *EMBO molecular medicine*, 17(1), 54.

Seifert-Dávila W, et al. (2025) Structural and kinetic insights into tRNA promoter engagement by yeast general transcription factor TFIIC. *Nucleic acids research*, 53(1).

de Taeye SW, et al. (2025) Plant-produced SARS-CoV-2 antibody engineered towards enhanced potency and in vivo efficacy. *Plant biotechnology journal*, 23(1), 4.

Rahmati S, et al. (2025) Computational structure-based design of antiviral peptides as potential protein-protein interaction inhibitors of rabies virus phosphoprotein and human LC8. *Heliyon*, 11(1), e41520.

Tian Y, et al. (2025) Cross-species recognition of two porcine coronaviruses to their cellular receptor aminopeptidase N of dogs and seven other species. *PLoS pathogens*, 21(1), e1012836.

Zhang W, et al. (2025) Structural insights into the mechanism of phosphate recognition and transport by XPR1. *Nature communications*, 16(1), 18.

Yang J, et al. (2025) Nde1 Promotes Lis1 Binding to Full-Length Autoinhibited Human Dynein-1. *bioRxiv : the preprint server for biology*.