

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: software resource, web application

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/molprobity_tool.html

Record Creation Time: 20220129T080319+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 6711 mentions in open access literature.

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

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. *iScience*, 29(7), 116513.

Pinto CS, et al. (2026) Actin arginylation alters myosin engagement and F-actin patterning despite structural conservation. *The Journal of cell biology*, 225(1).

Soma T, et al. (2026) Structure and engineering of the large serine recombinase Bxb1 for gene integration. *Molecular cell*, 86(12), 2247.

Kurihara N, et al. (2026) Molecular mechanism of MDA5 nucleation and filament formation by LGP2. *Molecular cell*, 86(4), 707.

Wang J, et al. (2026) A noncanonical transcriptional regulation in natural product biosynthesis. *Nucleic acids research*, 54(2).

Venturi M, et al. (2026) Atkinsonella hypoxylon virus capsid structure highlights the diversity of capsid proteins among the Partitiviridae. *The Journal of general virology*, 107(1).

Velázquez C, et al. (2026) Structural insights into the antibacterial function of the *Pseudomonas putida* effector Tke5. *The EMBO journal*, 45(4), 1229.

Lin LL, et al. (2026) Structural basis and pathological implications of the dimeric OS9-SEL1L-HRD1 ERAD Core Complex. *Nature communications*, 17(1).

Schütt I, et al. (2026) Inhibitors of GapN-dependent NADPH supply as potential lead compounds for novel therapeutics against *Streptococcus pyogenes*. *Virulence*, 17(1), 2609393.

Haas CM, et al. (2026) De novo design of protein nanoparticles with integrated functional motifs. *bioRxiv : the preprint server for biology*.

Gibbs E, et al. (2026) Structure and function of the RNA polymerase complex of Borna disease virus, a nuclear-replicating non-segmented negative-strand RNA virus. *Nucleic acids research*, 54(1).

Todorovi? N, et al. (2026) Major Cat Allergen Fel d 4: Structure and Identification of a Cross-Reactive IgE-Epitope-Containing Area. *Allergy*, 81(4), 1075.

Bermudes-Contreras JD, et al. (2026) Molecular dynamics simulation of thermal activation of human TRPV1. *Molecular biology research communications*, 15(1), 39.

Chung I, et al. (2026) Post-catalysis structures of mitochondrial complex I with ubiquinol-10 bound in the active site. *Nature communications*, 17(1).

Rambo BVC, et al. (2026) Capsaicin suppresses LPS-induced inflammatory responses via NLRP3/CASP-1/IL-1? axis and purinergic pathways in BV-2 microglial cells. *Purinergic signalling*, 22(1), 3.

Cao H, et al. (2026) Inhibiting Mrt4-rRNA interaction with fumaramidmycin-based derivatives as an antifungal strategy. *Nature communications*, 17(1).

He Y, et al. (2026) Site-specific ribozyme-mediated alkylation of DNA substrates. *Nucleic acids research*, 54(6).

de Sousa GF, et al. (2026) Comparative Analysis of Banana Lectins rBanLec-Like and H84T-BanLec: An In Silico and In Vitro Approach. *The protein journal*, 45(2), 318.

Osmanovi? A, et al. (2026) Virtual screening of marine coumarins and xanthenes identifies novel acid-suppressive leads targeting histamine H? receptor and gastric proton pump. *Biomolecules & biomedicine*, 26(8), 1384.

Paesen GC, et al. (2026) Structural basis for recognition of Rift Valley fever virus Gn protein by a human neutralizing monoclonal antibody with a kappa light chain. *PLoS pathogens*, 22(2), e1013926.