

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 [RRID](#) .

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).

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

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

Gibbs E, et al. (2026) Structural basis for domain coupling in heteromeric glycine receptors revealed by an atypical allosteric agonist. *Science advances*, 12(7), eaeb2036.

Chen LY, et al. (2026) Mesostructured Water Enhances Stability of ProteinMPNN-Designed Ubiquitin-Fold Proteins. *Journal of the American Chemical Society*, 148(7), 7363.

Liao G, et al. (2026) Evolutionary repurposing of a metabolic thiolase complex enables antibiotic biosynthesis. *Nature communications*, 17(1).

Taveira IC, et al. (2026) Docking-guided and phosphomimetic rational engineering of glucose-insensitive xylose transporters from *Trichoderma reesei*. *Microbial cell factories*, 25(1).

Fernandez-Perez J, et al. (2026) Development of an inhibitory monoclonal nanobody targeting *Streptococcus pyogenes* siderophore binding protein FtsB. *The Journal of biological chemistry*, 302(3), 111224.

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

Osmanović A, et al. (2026) Virtual screening of marine coumarins and xanthenes identifies novel acid-suppressive leads targeting histamine H₂ receptor and gastric proton pump. *Biomolecules & biomedicine*, 26(8), 1384.

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).

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

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

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

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

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

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

Todorović 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.