Resource Summary Report

Generated by T1D on Aug 5, 2026

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

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

Record Last Update: 20260805T044322+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 6313 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

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

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

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.

Westhof E, et al. (2026) The RNA-Puzzles Assessments of RNA-Only Targets in CASP16. Proteins, 94(1), 218.

Yuan R, et al. (2026) CASP16 Protein Monomer Structure Prediction Assessment. Proteins, 94(1), 86.

Martins MP, et al. (2026) A disulfide redox switch mechanism regulates glycoside hydrolase function. Nature communications, 17(1), 45.

Lemaire ON, et al. (2026) Carbon-monoxide-driven bioethanol production operates through a tungsten-dependent catalyst. Nature chemical biology, 22(1), 28.

Chen Y, et al. (2026) Structure insight into FtsZ function maintaining under acid stress of Streptococcus mutans. International journal of oral science, 18(1), 3.

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting Helicobacter Pylori. Cancer reports (Hoboken, N.J.), 9(1), e70441.

Lee E, et al. (2026) Streptococcus pneumoniae HtrA is a dynamic and monomeric virulence factor capable of forming larger oligomeric complexes. Protein science : a publication of the Protein Society, 35(1), e70411.

Penning S, et al. (2026) Structural and functional specialization of Bordetella pertussis DsbA for pertussis toxin folding. Protein science : a publication of the Protein Society, 35(1), e70421.

Palte RL, et al. (2026) WRN structural flexibility showcased through fragment-based lead discovery of inhibitors. Nature communications, 17(1), 79.

Hu S, et al. (2025) Structural and functional analysis of the Nipah virus polymerase complex. Cell, 188(3), 688.

Yu Z, et al. (2025) Mechanisms of HSV-1 helicase-primase inhibition and replication fork complex assembly. Cell.

Xue J, et al. (2025) Structural mechanisms of PIP2 activation and SEA0400 inhibition in human cardiac sodium-calcium exchanger NCX1. eLife, 14.

Feng Z, et al. (2025) Structural and functional insights into the evolution of SARS-CoV-2 KP.3.1.1 spike protein. Cell reports, 44(7), 115941.

Petrova ZO, et al. (2025) The role of kinase domain dimerization in EGFR activation. Structure (London, England : 1993).

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

Benjamin JS, et al. (2025) 23ME-01473, an Fc Effector-Enhanced Anti-ULBP6/2/5 Antibody, Restores NK Cell-Mediated Antitumor Immunity through NKG2D and Fc?RIIIa Activation. Cancer research communications, 5(3), 476.

França TCC, et al. (2025) SI/II Pocket of Ras: An Opportunity for a Once "Undruggable" Target. ACS omega, 10(9), 9463.