

Resource Summary Report

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Visual Molecular Dynamics

RRID:SCR_001820

Type: Tool

Proper Citation

Visual Molecular Dynamics (RRID:SCR_001820)

Resource Information

URL: <http://www.ks.uiuc.edu/Research/vmd/>

Proper Citation: Visual Molecular Dynamics (RRID:SCR_001820)

Description: A molecular visualization program for displaying, animating, and analyzing large biomolecular systems using 3-D graphics and built-in scripting. VMD supports computers running MacOS X, Unix, or Windows, is distributed free of charge, and includes source code.

Abbreviations: VMD

Resource Type: source code, software resource

Defining Citation: [PMID:8744570](#)

Keywords: standalone software, mac os x, unix, virtual machine, windows, c++

Funding: NIGMS

Availability: Free, Freely available

Resource Name: Visual Molecular Dynamics

Resource ID: SCR_001820

Alternate IDs: OMICS_03804

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260801T191134+0000

Ratings and Alerts

No rating or validation information has been found for Visual Molecular Dynamics.

No alerts have been found for Visual Molecular Dynamics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 378 mentions in open access literature.

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

Nitsch S, et al. (2026) H4K16 acylations destabilize chromatin architecture and facilitate transcriptional response during metabolic perturbations. *Molecular cell*, 86(1), 24.

Richard AC, et al. (2025) Using Short Molecular Dynamics Simulations to Determine the Important Features of Interactions in Antibody-Protein Complexes. *Proteins*, 93(4), 812.

Fernández-Yagüe MA, et al. (2025) Mechanochemical waves in focal adhesions during cell migration. *Science advances*, 11(40), eadw6425.

Hope I, et al. (2025) Crystallographic fragment screening of CDK2-cyclin A: FragLites map sites of protein-protein interaction. *Structure (London, England : 1993)*.

Huang L, et al. (2025) Coupling of diffusion-dissolution-deformation on the nature of sorption hysteresis in nanoporous shale kerogen. *iScience*, 28(12), 113882.

Santos D, et al. (2025) The molecular mechanisms of visual chromophore release from cellular retinaldehyde-binding protein. *Structure (London, England : 1993)*, 33(8), 1436.

Kreysing JP, et al. (2025) Passage of the HIV capsid cracks the nuclear pore. *Cell*, 188(4), 930.

Tao E, et al. (2025) Drugs exhibit diverse binding modes and access routes in the Nav1.5 cardiac sodium channel pore. *The Journal of general physiology*, 157(2).

Sol Ruiz M, et al. (2025) Genetic characterization of pediatric B-cell acute lymphoblastic leukemia in Argentina uncovers molecular heterogeneity and novel variants. *Frontiers in pharmacology*, 16, 1701680.

Salvador-Garcia D, et al. (2024) A force-sensitive mutation reveals a non-canonical role for dynein in anaphase progression. *The Journal of cell biology*, 223(10).

Frank HM, et al. (2024) Structural basis of ligand specificity and channel activation in an insect gustatory receptor. *Cell reports*, 43(4), 114035.

Maksymenko K, et al. (2023) The design of functional proteins using tensorized energy calculations. *Cell reports methods*, 3(8), 100560.

Luo S, et al. (2023) Examining asymmetric pairwise pre-reaction and transition states in enzymatic catalysis by molecular dynamics simulation and quantum mechanics/molecular mechanics calculation. *STAR protocols*, 4(2), 102263.

Kührová P, et al. (2023) Sensitivity of the RNA Structure to Ion Conditions as Probed by Molecular Dynamics Simulations of Common Canonical RNA Duplexes. *Journal of chemical information and modeling*, 63(7), 2133.

Pan W, et al. (2023) Structures of NF- κ B p52 homodimer-DNA complexes rationalize binding mechanisms and transcription activation. *eLife*, 12.

Deng Q, et al. (2023) Characterization of Two Novel Rumen-Derived Exo-Polygalacturonases: Catalysis and Molecular Simulations. *Microorganisms*, 11(3).

Muscat S, et al. (2023) In silico investigation of cytochrome bc1 molecular inhibition mechanism against *Trypanosoma cruzi*. *PLoS neglected tropical diseases*, 17(1), e0010545.

Wallace M, et al. (2023) The lamin A/C Ig-fold undergoes cell density-dependent changes that alter epitope binding. *Nucleus (Austin, Tex.)*, 14(1), 2180206.

Ray S, et al. (2023) High-resolution structures with bound Mn²⁺ and Cd²⁺ map the metal import pathway in an Nramp transporter. *eLife*, 12.

Liu X, et al. (2023) Bionics design of affinity peptide inhibitors for SARS-CoV-2 RBD to block SARS-CoV-2 RBD-ACE2 interactions. *Heliyon*, 9(1), e12890.