

# Resource Summary Report

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## Visual Molecular Dynamics

RRID:SCR\_001820

Type: Tool

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### Proper Citation

Visual Molecular Dynamics (RRID:SCR\_001820)

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### 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:** 20260729T044016+0000

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### Ratings and Alerts

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

No alerts have been found for Visual Molecular Dynamics.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 378 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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- $\kappa$ 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 Mn<sup>2+</sup> and Cd<sup>2+</sup> map the metal import pathway in an Nramp transporter. *eLife*, 12.

Neamtu A, et al. (2023) Molecular dynamics simulations reveal the hidden EF-hand of EF-SAM as a possible key thermal sensor for STIM1 activation by temperature. *The Journal of biological chemistry*, 299(8), 104970.