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: software resource, source code

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: 20260731T042617+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 kravitz2 .

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-?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.

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.