Resource Summary Report

Generated by RRID on Aug 13, 2026

VMD

RRID:SCR_024368
Type: Tool

Proper Citation

VMD (RRID:SCR_024368)

Resource Information

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

Proper Citation: VMD (RRID:SCR_024368)

Description: Software tool as 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.

Synonyms: vmd

Resource Type: software resource, software application

Keywords: molecular visualization, displaying, animating, analyzing, large biomolecular systems, .

Availability: Free, Available for download, Freely available,

Resource Name: VMD

Resource ID: SCR_024368

Old URLs: https://sources.debian.org/src/vmd/

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260813T055313+0000

Ratings and Alerts

No rating or validation information has been found for VMD.

No alerts have been found for VMD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 68 mentions in open access literature.

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

Alvarez G, et al. (2026) Deglycosylation induces a novel distal conformation in the mannose receptor CD206. Scientific reports, 16(1), 5239.

Abdelwahid MAS, et al. (2026) Diastereomeric Branched-Ester dBET1 Analogs Exhibit Conformation-Dependent Differences in Passive Membrane Permeability. Journal of medicinal chemistry, 69(3), 2900.

Amin KS, et al. (2026) Design and implementation of Cs/GO/TiO2 nanocomposite for controlling sulfamethoxazole. Scientific reports, 16(1).

Clark JA, et al. (2026) Solvent Models and Charge Scaling: Benchmarks for Molecular Dynamics of Glycosaminoglycans. The journal of physical chemistry. B, 130(19), 5002.

Gordiychuk M, et al. (2026) Searching for sequence features that control DNA cyclizability. PNAS nexus, 5(6), pgag167.

Camargo PG, et al. (2025) In silico evaluation of N-aryl-1,10-phenanthroline-2-amines as potential inhibitors of T. cruzi GP63 zinc-metalloprotease by docking and molecular dynamics simulations. Scientific reports, 15(1), 6036.

Seifi S, et al. (2025) Motion of fullerene nanomachines on thermally activated curved gold substrates. Scientific reports, 15(1), 10892.

Akulov V, et al. (2025) Phosphorylation-Regulated Conformational Diversity and Topological Dynamics of an Intrinsically Disordered Nuclear Receptor. The journal of physical chemistry. B, 129(30), 7719.

Camargo PG, et al. (2025) In vitro assays identified thiohydantoins with anti-trypanosomatid activity and molecular modelling studies indicated possible selective CYP51 inhibition. Scientific reports, 15(1), 465.

Marin-Toledo JP, et al. (2025) Molecular prosthetics for CFTR designed for anion selectivity outperform amphotericin B in cultured cystic fibrosis airway epithelia. bioRxiv : the preprint server for biology.

Ghavi Z, et al. (2025) Molecular dynamics insights into non-covalent functionalization of boron nitride nanotubes for doxorubicin delivery. Scientific reports, 15(1), 30213.

Motuziuk O, et al. (2025) The effect of C60 fullerene on the musculus gastrocnemius contraction in chronically alcohol-exposed rats and the potential mechanism of its action. Scientific reports, 15(1), 32651.

Singh AK, et al. (2025) Conformational Landscape of the Di- and Tripeptide Permease A Transport Cycle. Journal of chemical information and modeling, 65(12), 6198.

Garcia Jimenez D, et al. (2025) Linker Methylation as a Strategy to Enhance PROTAC Oral Bioavailability: Insights from Molecular Properties and Conformational Analysis. Journal of medicinal chemistry, 68(15), 16666.

Doran MH, et al. (2025) The hypertrophic cardiomyopathy-associated A331P actin variant enhances basal contractile activity and elicits resting muscle dysfunction. iScience, 28(2), 111816.

Dalal K, et al. (2025) Interpreting regulatory mechanisms of Hippo signaling through a deep learning sequence model. Cell genomics, 5(4), 100821.

Mohebbi A, et al. (2025) A new method based on binary mixture concept for prediction of ionic liquids critical properties using molecular dynamics simulation. Scientific reports, 15(1), 7545.

Zan B, et al. (2025) The difference between MelP5 and melittin membrane poration. Scientific reports, 15(1), 7442.

Yu S, et al. (2025) c-di-GMP inhibits rRNA methylation and impairs ribosome assembly in the presence of kanamycin. EMBO reports, 26(5), 1367.

??ulea TA, et al. (2025) Differential Inhibition by Cenobamate of Canonical Human Nav1.5 Ion Channels and Several Point Mutants. International journal of molecular sciences, 26(1).