

Resource Summary Report

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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 thiohydantoin 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).