Resource Summary Report

Generated by SPARC SAWG on Jul 30, 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 application, software resource

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: 20260727T040824+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 33 mentions in open access literature.

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

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 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.

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.

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.

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.

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.

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

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.

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.

Kone?ná K, et al. (2025) Functional characterization of 16 variants found in the LDL receptor gene. Journal of lipid research, 66(9), 100873.

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.

Tang J, et al. (2025) Targeting N-Myc in neuroblastoma with selective Aurora kinase A degraders. Cell chemical biology, 32(2), 352.

Schumann J, et al. (2024) Ten-electron count rule for the binding of adsorbates on single-atom alloy catalysts. Nature chemistry, 16(5), 749.

Camargo PG, et al. (2024) Py-CoMFA, docking, and molecular dynamics simulations of Leishmania (L.) amazonensis arginase inhibitors. Scientific reports, 14(1), 11575.

Tourkova IL, et al. (2024) Chloride/proton antiporters ClC3 and ClC5 support bone formation in mice. Bone reports, 21, 101763.

Hossain A, et al. (2024) Role of cold shock proteins B and D in Aeromonas salmonicida subsp. salmonicida physiology and virulence in lumpfish (Cyclopterus lumpus). Infection and immunity, 92(8), e0001124.

Nelic D, et al. (2024) Agonist-selective activation of individual G-proteins by muscarinic receptors. Scientific reports, 14(1), 9652.

Saillant V, et al. (2024) HssS activation by membrane heme defines a paradigm for two-component system signaling in Staphylococcus aureus. mBio, 15(6), e0023024.