Resource Summary Report

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ZMM

RRID:SCR_005741
Type: Tool

Proper Citation

ZMM (RRID:SCR_005741)

Resource Information

URL: http://www.zmmsoft.com

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Description: ZMM is a molecular modeling program for theoretical studies of systems of any complexity: small molecules, peptides, proteins, nucleic acids, and ligand-receptor complexes. ZMM searches optimal structures in the space of generalized coordinates: torsion angles, bond angles, bond lengths, positions free molecules and ions, and orientation of free molecules. Any generalized coordinate may be kept fixed. Molecules and fragments that are not expected to undergo significant conformational changes may be treated as rigid bodies. Popular molecular modeling programs usually work in the space of Cartesian coordinates of atoms. During energy minimization of a big system, many Cartesian coordinates-variables move collectively. For example, rotation of a benzene ring around the C-Ph bond in the Cartesian-coordinates space involves collective motion of 33 variables. In the generalized-coordinates space, this rotation involves variation of just one torsion angle. In ZMM, any fragment of a molecular system may be treated as either rigid or flexible. The generalized-coordinates method saves large computational resources if only a small part of a system is considered flexible. Examples are ligand-protein and protein-protein interactions. The savings occur because the sampling space is reduced and because molecular interactions within rigid fragments are not computed. * ZMM runs on Windows 95, 98, 2000, XP, UNIX, and Linux * ZMM can be used via the command-line interface * ZMM can also be used at Windows via a graphical user interface

Abbreviations: ZMM

Synonyms: ZMM - Molecular Modeling Program

Resource Type: data processing software, data visualization software, software application, software resource

Keywords: molecule, molecular model, peptide, protein, nucleic acid, ligand-receptor complex, small molecule

Availability: Commercial license

Resource Name: ZMM

Resource ID: SCR_005741

Alternate IDs: nlx_149201

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260912T195630+0000

Ratings and Alerts

No rating or validation information has been found for ZMM.

No alerts have been found for ZMM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Bykhovskaia M, et al. (2021) SNARE complex alters the interactions of the Ca2+ sensor synaptotagmin 1 with lipid bilayers. Biophysical journal, 120(4), 642.

Siepi M, et al. (2020) Molecular Dissection of dH3w, A Fluorescent Peptidyl Sensor for Zinc and Mercury. Sensors (Basel, Switzerland), 20(3).

Siepi M, et al. (2019) Denatured lysozyme-coated carbon nanotubes: a versatile biohybrid material. Scientific reports, 9(1), 16643.

Nikolaev MV, et al. (2017) TRPV1 activation power can switch an action mode for its polypeptide ligands. PloS one, 12(5), e0177077.

Maleeva G, et al. (2017) Voltage-Dependent Inhibition of Glycine Receptor Channels by Niflumic Acid. Frontiers in molecular neuroscience, 10, 125.

Rossokhin AV, et al. (2014) Block of GABA(A) receptor ion channel by penicillin: electrophysiological and modeling insights toward the mechanism. Molecular and cellular neurosciences, 63, 72.

Bruhova I, et al. (2013) Energy for wild-type acetylcholine receptor channel gating from different choline derivatives. Biophysical journal, 104(3), 565.

De Rosa M, et al. (2013) Novel promising linezolid analogues: rational design, synthesis and biological evaluation. European journal of medicinal chemistry, 69, 779.

Bruhova I, et al. (2010) A homology model of the pore domain of a voltage-gated calcium channel is consistent with available SCAM data. The Journal of general physiology, 135(3), 261.

Lewis SN, et al. (2010) Virtual Screening as a Technique for PPAR Modulator Discovery. PPAR research, 2010, 861238.

Blanchet J, et al. (2007) Acidic residues on the voltage-sensor domain determine the activation of the NaChBac sodium channel. Biophysical journal, 92(10), 3513.

Tikhonov DB, et al. (2007) Sodium channels: ionic model of slow inactivation and state-dependent drug binding. Biophysical journal, 93(5), 1557.