GROMACS

RRID:SCR_014565
Type: Tool

Proper Citation

GROMACS (RRID:SCR_014565)

Resource Information

URL: http://www.gromacs.org

Description: A software package created to perform molecular dynamics. It is primarily designed for biochemical molecules like proteins, lipids and nucleic acids that have many complicated bonded interactions, but it can also be used for research on non-biological systems, such as polymers.

Resource Name: GROMACS

Proper Citation: GROMACS (RRID:SCR_014565)

Resource Type: Resource, software resource, software toolkit, simulation software, software application

Keywords: simulation, molecular dynamics, software package, software toolkit, biochemical, molecule, protein, lipid, nucleic acid, bond interaction

Resource ID: SCR_014565


References: DOI:10.1016/0010-4655(95)00042-E

Availability: Free, Available for download

Website Status: Last checked up
Ratings and Alerts

No rating or validation information has been found for GROMACS.

No alerts have been found for GROMACS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1949 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Pawar A, et al. (2020) Screening of natural compounds that targets glutamate racemase of Mycobacterium tuberculosis reveals the anti-tubercular potential of flavonoids. Scientific reports, 10(1), 949.

Herhaus L, et al. (2020) TBK1-mediated phosphorylation of LC3C and GABARAP-L2 controls autophagosome shedding by ATG4 protease. EMBO reports, 21(1), e48317.


Hsu CC, et al. (2020) The Order-Disorder Continuum: Linking Predictions of Protein
Structure and Disorder through Molecular Simulation. Scientific reports, 10(1), 2068.


Xu Y, et al. (2020) Molecular Simulation Elaborating the Mechanism of 1?-Hydroxy Alantolactone Inhibiting Ubiquitin-Conjugating Enzyme UbcH5s. Scientific reports, 10(1), 141.


