GROMACS
RRID:SCR_014565
Type: Tool

Proper Citation
GROMACS (RRID:SCR_014565)

Resource Information
URL: http://www.gromacs.org
Proper Citation: GROMACS (RRID:SCR_014565)
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 Type: Resource, software resource, software toolkit, simulation software, software application
References: DOI:10.1016/0010-4655(95)00042-E
Keywords: simulation, molecular dynamics, software package, software toolkit, biochemical, molecule, protein, lipid, nucleic acid, bond interaction
Availability: Free, Available for download
Website Status: Last checked up
Resource Name: GROMACS
Resource ID: SCR_014565
Alternate IDs: biotools:gromacs

Alternate URLs: https://bio.tools/gromacs

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 2682 mentions in open access literature.

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


Kiriakidi S, et al. (2021) Interplay of cholesterol, membrane bilayers and the AT1R: A cholesterol consensus motif on AT1R is revealed. Computational and structural biotechnology journal, 19, 110-120.


