

Resource Summary Report

Generated by [kravitz2](#) on Aug 8, 2026

GROMACS topology editors

RRID:SCR_025013

Type: Tool

Proper Citation

GROMACS topology editors (RRID:SCR_025013)

Resource Information

URL: <https://github.com/BlankenbergLab/gmxtras/tree/main>

Proper Citation: GROMACS topology editors (RRID:SCR_025013)

Description: Software tool as set of Python scripts to modify GROMACS topology files, by adding content from different topology files and other GROMACS input files. Useful, particularly when system components are assembled outside of GROMACS, or in different steps within GROMACS. This helps prevent users from having to copy and paste significantly large blocks of text within topology files.

Abbreviations: gmxtras

Resource Type: software resource, software application

Keywords: GROMACS, topology files, force fields, modify GROMACS topology files,

Availability: Free, Available for download, Freely available

Resource Name: GROMACS topology editors

Resource ID: SCR_025013

License: MIT license

Record Creation Time: 20240221T003954+0000

Record Last Update: 20260808T043021+0000

Ratings and Alerts

No rating or validation information has been found for GROMACS topology editors.

No alerts have been found for GROMACS topology editors.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Raubenolt B, et al. (2024) Generalized open-source workflows for atomistic molecular dynamics simulations of viral helicases. GigaScience, 13.

V'kovski P, et al. (2021) Coronavirus biology and replication: implications for SARS-CoV-2. Nature reviews. Microbiology, 19(3), 155.