## **Resource Summary Report**

Generated by NIF on Apr 29, 2025

# Molecular Dynamics Workflow (BioKepler)

RRID:SCR\_014389 Type: Tool

#### **Proper Citation**

Molecular Dynamics Workflow (BioKepler) (RRID:SCR\_014389)

#### **Resource Information**

URL: https://github.com/nbcrrolls/workflows/tree/master/Production/AmberGPUMDSimulation

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**Description:** A workflow for running molecular dynamics simulations. It can be used for allatom molecular dynamic simulations, which involve five steps of minimization, one step of heating, three steps of equilibration, and one or more instances of production. The input is a set of directories that include the MD simulation input scripts, system topology and coordinate files. Output files are list of plots, simulation trajectories, intermediate files, restart files, and the like.

**Synonyms:** Molecular Dynamics Workflow, AmberGPUMDSimulation, Molecular Dynamics Workflow Software, Amber GPUMD Simulation

**Resource Type:** workflow software, data processing software, software resource, software application

Keywords: workflow, MD, molecular dynamics, simulation, software, bio.tools

Funding: NIGMS P41GM103426

Availability: Requires Linux

Resource Name: Molecular Dynamics Workflow (BioKepler)

Resource ID: SCR\_014389

Alternate IDs: biotools:ambergpumdsimulation

Alternate URLs: http://nbcr.ucsd.edu/data/downloads/workflows/,

https://bio.tools/ambergpumdsimulation

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Record Last Update: 20250429T055639+0000

#### **Ratings and Alerts**

No rating or validation information has been found for Molecular Dynamics Workflow (BioKepler) .

No alerts have been found for Molecular Dynamics Workflow (BioKepler) .

#### Data and Source Information

Source: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Purawat S, et al. (2017) A Kepler Workflow Tool for Reproducible AMBER GPU Molecular Dynamics. Biophysical journal, 112(12), 2469.