Resource Summary Report

Generated by <u>dkNET</u> on May 19, 2025

Warp

RRID:SCR_018071 Type: Tool

Proper Citation

Warp (RRID:SCR_018071)

Resource Information

URL: https://github.com/cramerlab/warp

Proper Citation: Warp (RRID:SCR_018071)

Description: Software tool that automates all preprocessing steps of cryo-EM data acquisition and enables real-time evaluation. Corrects micrographs for global and local motion, estimates local defocus and monitors key parameters for each recorded micrograph or tomographic tilt series in real time. Software includes deep-learning-based models for accurate particle picking and image denoising.

Resource Type: software application, data acquisition software, data analysis software, data processing software, software resource

Defining Citation: DOI:10.1038/s41592-019-0580-y

Keywords: Automating preprocessing step, cryo EM data acquisition, micrograph correction, particle picking, image denoising, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Warp

Resource ID: SCR_018071

Alternate IDs: BioTools:Warp, biotools:Warp

Alternate URLs: https://bio.tools/Warp, https://bio.tools/Warp, https://bio.tools/Warp

License: GNU General Public License v3.0

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250517T060349+0000

Ratings and Alerts

No rating or validation information has been found for Warp.

No alerts have been found for Warp.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Chen S, et al. (2024) Cryo-electron tomography reveals the microtubule-bound form of inactive LRRK2. bioRxiv : the preprint server for biology.

Kong WW, et al. (2024) Cryo-electron tomography reveals the packaging pattern of RuBisCOs in Synechococcus ?-carboxysome. Structure (London, England : 1993), 32(8), 1110.

Tegunov D, et al. (2021) Multi-particle cryo-EM refinement with M visualizes ribosomeantibiotic complex at 3.5?Å in cells. Nature methods, 18(2), 186.

Walls AC, et al. (2020) Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. Cell, 181(2), 281.

Tegunov D, et al. (2019) Real-time cryo-electron microscopy data preprocessing with Warp. Nature methods, 16(11), 1146.