

Resource Summary Report

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

Defining Citation: [DOI:10.1038/s41592-019-0580-y](https://doi.org/10.1038/s41592-019-0580-y)

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

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

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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 7 mentions in open access literature.

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

Mohan HM, et al. (2025) Endogenous retrovirus-like proteins recruit UBQLN2 to stress granules and shape their functional biology. *Science advances*, 11(29), eadu6354.

Chen S, et al. (2025) Cryo-electron tomography reveals the microtubule-bound form of inactive LRRK2. *eLife*, 13.

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 ribosome-antibiotic 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.