Resource Summary Report

Generated by dkNET on Apr 27, 2025

TomoMiner

RRID:SCR_015045

Type: Tool

Proper Citation

TomoMiner (RRID:SCR_015045)

Resource Information

URL: http://web.cmb.usc.edu/people/alber/Software/tomominer/

Proper Citation: TomoMiner (RRID:SCR_015045)

Description: Software platform for large-scale cryo electron subtomogram classification,

alignment, and averaging.

Resource Type: software resource, source code

Keywords: analysis platform, cryo electron subtomogram, subtomogram classification, subtomogram alignment, subtomogram averaging, subtomogram analysis, bio.tools

Funding:

Availability: Available for download

Resource Name: TomoMiner

Resource ID: SCR_015045

Alternate IDs: biotools:tomominer

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

Record Creation Time: 20220129T080323+0000

Record Last Update: 20250425T060041+0000

Ratings and Alerts

No rating or validation information has been found for TomoMiner.

No alerts have been found for TomoMiner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Zhao Y, et al. (2018) An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification. Bioinformatics (Oxford, England), 34(13), i227.

Frazier Z, et al. (2017) TomoMiner and TomoMinerCloud: A Software Platform for Large-Scale Subtomogram Structural Analysis. Structure (London, England: 1993), 25(6), 951.

Xu M, et al. (2017) Deep learning-based subdivision approach for large scale macromolecules structure recovery from electron cryo tomograms. Bioinformatics (Oxford, England), 33(14), i13.