

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T133401+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 [Kravitz](#) .

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.