

# Resource Summary Report

Generated by [dkNET](#) on Aug 11, 2026

## TomoMiner

RRID:SCR\_015045

Type: Tool

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### Proper Citation

TomoMiner (RRID:SCR\_015045)

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### 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:** source code, software resource

**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:** 20260810T040631+0000

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### Ratings and Alerts

No rating or validation information has been found for TomoMiner.

No alerts have been found for TomoMiner.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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.