

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

DAMMIF

RRID:SCR_028444

Type: Tool

Proper Citation

DAMMIF (RRID:SCR_028444)

Resource Information

URL: <https://www.embl-hamburg.de/biosaxs/dammif.html>

Proper Citation: DAMMIF (RRID:SCR_028444)

Description: Software tool for rapidly determining the low-resolution three-dimensional shape of biological macromolecules in solution using Small-Angle X-ray Scattering (SAXS) data. Used for rapid ab-initio shape determination in small-angle scattering.

Synonyms: Dummy Atom Model Fast

Resource Type: software application, software resource

Defining Citation: [PMID:27630371](#)

Keywords: EMBL Hamburg BioSAXS group, determining low-resolution three-dimensional shape of biological macromolecules, macromolecules in solution, Small-Angle X-ray Scattering,

Availability: Free, Available for download

Resource Name: DAMMIF

Resource ID: SCR_028444

Record Creation Time: 20260514T062433+0000

Record Last Update: 20260905T133612+0000

Ratings and Alerts

No rating or validation information has been found for DAMMIF.

No alerts have been found for DAMMIF.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.