

Resource Summary Report

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National Resource for Automated Molecular Microscopy

RRID:SCR_001448

Type: Tool

Proper Citation

National Resource for Automated Molecular Microscopy (RRID:SCR_001448)

Resource Information

URL: <http://nramm.scripps.edu/>

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Description: Biomedical technology research center that develops, tests and applies technology aimed toward completely automating the processes involved in solving macromolecular structures using cryo-electron microscopy. The goal is to establish a resource that will serve both as a center for high-throughput molecular microscopy as well as for transferring this technique to the research community. Current Core Technology Research and Development is focused on 4 areas: improving grid substrates and specimen preparation; further automation and optimization of image acquisition; development of an integrated single particle analysis and processing pipeline; and the development of automated high throughput EM screening. NRAMM welcomes applications of both collaborative and service projects.

Abbreviations: NRAMM

Resource Type: biomedical technology research center, training resource

Keywords: macromolecular structure, cryo-electron microscopy, macromolecule, structure, microscopy, automation, high throughput, specimen handling, image acquisition, data processing, data information integration, structural biology technology center

Funding: NIGMS 9 P41 GM103310;
NCRR 2P41RR017573

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: National Resource for Automated Molecular Microscopy

Resource ID: SCR_001448

Alternate IDs: nlx_152671

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260731T042612+0000

Ratings and Alerts

No rating or validation information has been found for National Resource for Automated Molecular Microscopy.

No alerts have been found for National Resource for Automated Molecular Microscopy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Zhu Y, et al. (2017) A deep convolutional neural network approach to single-particle recognition in cryo-electron microscopy. BMC bioinformatics, 18(1), 348.

Heymann JB, et al. (2015) Validation of 3D EM Reconstructions: The Phantom in the Noise. AIMS biophysics, 2(1), 21.