Resource Summary Report

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SCIPION

RRID:SCR_016738
Type: Tool

Proper Citation

SCIPION (RRID:SCR_016738)

Resource Information

URL: http://scipion.i2pc.es/

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Description: Software framework for image processing to obtain 3D models of macromolecular complexes using Electron Microscopy. Open-source project for integration, reproducibility and validation in 3D electron microscopy. It integrates several software packages to execute workflows combining different software tools, while taking care of formats and conversions. Electron Microscopy (3DEM). waiting for pdf from Joe

Resource Type: data processing software, image processing software, software toolkit, software resource, software application

Defining Citation: PMID:27108186

Keywords: image, processing, data, 3DEM, macromolecular, complex, electron, microscopy, format, conversion, bio.tools

Funding: Spanish Ministry of Economy and Competitiveness ;
Comunidad the Madrid ;
European Union ;
Instruct

Availability: Free, Available for download, Registration required

Resource Name: SCIPION

Resource ID: SCR_016738

Alternate IDs: biotools:monores

Alternate URLs: https://github.com/I2PC/scipion, https://bio.tools/monores

License: GNU General Public License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250426T060606+0000

Ratings and Alerts

No rating or validation information has been found for SCIPION.

No alerts have been found for SCIPION.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Iudin A, et al. (2023) EMPIAR: the Electron Microscopy Public Image Archive. Nucleic acids research, 51(D1), D1503.

Kantsadi AL, et al. (2022) Structures of SAS-6 coiled coil hold implications for the polarity of the centriolar cartwheel. Structure (London, England : 1993), 30(5), 671.

Adolph MB, et al. (2021) RADX controls RAD51 filament dynamics to regulate replication fork stability. Molecular cell, 81(5), 1074.

Lee K, et al. (2021) The structure of an Hsp90-immunophilin complex reveals cochaperone recognition of the client maturation state. Molecular cell, 81(17), 3496.

Martinez SE, et al. (2021) Assembly and Cryo-EM structure determination of yeast mitochondrial RNA polymerase initiation complex intermediates. STAR protocols, 2(2), 100431.

De Wijngaert B, et al. (2021) Cryo-EM Structures Reveal Transcription Initiation Steps by Yeast Mitochondrial RNA Polymerase. Molecular cell, 81(2), 268.

Rong Y, et al. (2021) TMEM120A contains a specific coenzyme A-binding site and might not

mediate poking- or stretch-induced channel activities in cells. eLife, 10.

Adams SE, et al. (2021) A two-site flexible clamp mechanism for RET-GDNF-GFR?1 assembly reveals both conformational adaptation and strict geometric spacing. Structure (London, England : 1993), 29(7), 694.

Khan AK, et al. (2021) Cryo-EM structure of an open conformation of a gap junction hemichannel in lipid bilayer nanodiscs. Structure (London, England : 1993), 29(9), 1040.

Harastani M, et al. (2021) HEMNMA-3D: Cryo Electron Tomography Method Based on Normal Mode Analysis to Study Continuous Conformational Variability of Macromolecular Complexes. Frontiers in molecular biosciences, 8, 663121.

Zehr EA, et al. (2020) Katanin Grips the ?-Tubulin Tail through an Electropositive Double Spiral to Sever Microtubules. Developmental cell, 52(1), 118.

Sofos N, et al. (2020) Structures of the Cmr-? Complex Reveal the Regulation of the Immunity Mechanism of Type III-B CRISPR-Cas. Molecular cell, 79(5), 741.

Melero R, et al. (2020) Continuous flexibility analysis of SARS-CoV-2 Spike prefusion structures. bioRxiv : the preprint server for biology.

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Simonetti A, et al. (2020) Structural Insights into the Mammalian Late-Stage Initiation Complexes. Cell reports, 31(1), 107497.

Alsahafi N, et al. (2019) An Asymmetric Opening of HIV-1 Envelope Mediates Antibody-Dependent Cellular Cytotoxicity. Cell host & microbe, 25(4), 578.

Lee H, et al. (2019) The Cas4-Cas1-Cas2 complex mediates precise prespacer processing during CRISPR adaptation. eLife, 8.

Maluenda D, et al. (2019) Flexible workflows for on-the-fly electron-microscopy single-particle image processing using Scipion. Acta crystallographica. Section D, Structural biology, 75(Pt 10), 882.

Brown A, et al. (2018) Structures of translationally inactive mammalian ribosomes. eLife, 7.