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

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: 20260728T043521+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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

Conesa P, et al. (2023) Scipion3: A workflow engine for cryo-electron microscopy image processing and structural biology. Biological imaging, 3, e13.

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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.

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.

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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.

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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.

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Melero R, et al. (2020) Continuous flexibility analysis of SARS-CoV-2 spike prefusion structures. IUCrJ, 7(Pt 6), 1059.

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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.