Resource Summary Report

Generated by NIF on Apr 20, 2025

cryoSPARC

RRID:SCR_016501
Type: Tool

Proper Citation

cryoSPARC (RRID:SCR_016501)

Resource Information

URL: https://cryosparc.com/

Proper Citation: cryoSPARC (RRID:SCR_016501)

Description: Software integrated platform used for obtaining 3D structural information from single particle cryo-EM data. Enables automated, high quality and high-throughput structure discovery of proteins, viruses and molecular complexes for research and drug discovery.

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

Defining Citation: PMID:28165473

Keywords: Structura Biotechnology Inc., data, processing, analysis, image, single, particle, cryo-EM, structure, discovery, automated, protein, virus, molecular, complex

Funding:

Availability: Available free of charge for academic users with a valid institutional email address, Trail available

Resource Name: cryoSPARC

Resource ID: SCR_016501

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250420T015354+0000

Ratings and Alerts

No rating or validation information has been found for cryoSPARC.

No alerts have been found for cryoSPARC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1744 mentions in open access literature.

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

Pourmal S, et al. (2025) Autoinhibition of dimeric NINJ1 prevents plasma membrane rupture. Nature, 637(8045), 446.

van der Velden TT, et al. (2025) Menaquinone-specific turnover by Mycobacterium tuberculosis cytochrome bd is redox regulated by the Q-loop disulfide bond. The Journal of biological chemistry, 301(2), 108094.

Roberts JR, et al. (2025) Structural basis for catalysis and selectivity of phospholipid synthesis by eukaryotic choline-phosphotransferase. Nature communications, 16(1), 111.

Song Y, et al. (2025) Structural basis of human VANGL-PRICKLE interaction. Nature communications, 16(1), 132.

Mullard RM, et al. (2025) The N-terminus of the Clostridioides difficile transferase A component directs toxin activity and potency. mBio, 16(1), e0240524.

Fort J, et al. (2025) The conserved lysine residue in transmembrane helix 5 is pivotal for the cytoplasmic gating of the L-amino acid transporters. PNAS nexus, 4(1), pgae584.

Zhang J, et al. (2025) Structural basis for the interaction between the Drosophila RTK Sevenless (dROS1) and the GPCR BOSS. Nature communications, 16(1), 808.

Yang X, et al. (2025) Structural insights into human topoisomerase 3? DNA and RNA catalysis and nucleic acid gate dynamics. Nature communications, 16(1), 834.

Freitas MM, et al. (2025) The bile acid-sensitive ion channel is gated by Ca2+-dependent conformational changes in the transmembrane domain. bioRxiv : the preprint server for biology.

Huang Y, et al. (2025) A single residue switch mediates the broad neutralization of Rotaviruses. Nature communications, 16(1), 838.

Jungfer K, et al. (2025) Mechanistic determinants and dynamics of cA6 synthesis in type III

CRISPR-Cas effector complexes. Nucleic acids research, 53(2).

Shin H, et al. (2025) Structural basis of directionality control in large serine integrases. bioRxiv : the preprint server for biology.

Seddon C, et al. (2025) Cryo-EM structure and evolutionary history of the conjugation surface exclusion protein TraT. Nature communications, 16(1), 659.

Kim S, et al. (2025) Cryo-EM structures reveal the H+/citrate symport mechanism of Drosophila INDY. Life science alliance, 8(4).

Bal?kç? E, et al. (2025) Structure of the Nipah virus polymerase complex. The EMBO journal, 44(2), 563.

Wei F, et al. (2025) Drug inhibition and substrate transport mechanisms of human VMAT2. Nature communications, 16(1), 323.

Bernhard H, et al. (2025) Structural basis of Spliced Leader RNA recognition by the Trypanosoma brucei cap-binding complex. Nature communications, 16(1), 685.

Chen Z, et al. (2025) A broadly neutralizing antibody against the SARS-CoV-2 Omicron sub-variants BA.1, BA.2, BA.2.12.1, BA.4, and BA.5. Signal transduction and targeted therapy, 10(1), 14.

Wells JN, et al. (2025) Reconstitution of human DNA licensing and the structural and functional analysis of key intermediates. Nature communications, 16(1), 478.

Wang L, et al. (2025) Structural insights into the LGR4-RSPO2-ZNRF3 complexes regulating WNT/?-catenin signaling. Nature communications, 16(1), 362.