Resource Summary Report

Generated by dkNET on Apr 25, 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, software resource, data processing software, software application

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: 20250425T060149+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 dkNET.

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).

Tian Y, et al. (2025) Molecular and structural basis of a subfamily of PrfH rescuing both the damaged and intact ribosomes stalled in translation. bioRxiv: the preprint server for biology.

Zou MJ, et al. (2025) Probing the Dual Role of Ca2+ in the Allochromatium tepidum LH1-RC Complex by Constructing and Analyzing Ca2+-Bound and Ca2+-Free LH1 Complexes. Biomolecules, 15(1).

Fung HYJ, et al. (2025) Nap1 and Kap114 co-chaperone H2A-H2B and facilitate targeted histone release in the nucleus. The Journal of cell biology, 224(1).

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

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

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