

Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

[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: data processing software, software application, image analysis software, 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

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: 20260806T054640+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 2480 mentions in open access literature.

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

Samani EK, et al. (2026) Structural basis of product recognition by Mycobacterium tuberculosis fatty acid synthase. Protein science : a publication of the Protein Society, 35(1), e70412.

Huang J, et al. (2026) Cryo-EM structures of antibodies elicited by germline-targeting HIV MPER epitope scaffolds. Cell reports, 45(1), 116818.

Stolz M, et al. (2026) Architectural principles of transporter-chaperone coupling within the native MHC I peptide-loading complex. Science advances, 12(1), eaea7735.

Martins MP, et al. (2026) A disulfide redox switch mechanism regulates glycoside hydrolase function. Nature communications, 17(1), 45.

Lyu Y, et al. (2026) An open axial channel of the AAA ClpXP protease enhances degradation of specific classes of protein substrates. Protein science : a publication of the Protein Society, 35(1), e70372.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. Cell.

Ali-Ahmad A, et al. (2026) Structure and dynamics of 2x(CENP-A/H4)2 octasome reveal a possible intermediate in centromeric chromatin. Life science alliance, 9(3).

Hu W, et al. (2025) Structural basis for Salmonella infection by two Microviridae phages. Communications biology, 8(1), 1166.

Casu B, et al. (2025) Function and firing of the Streptomyces coelicolor contractile injection system requires the membrane protein CisA. eLife, 14.

Gristick HB, et al. (2025) Design and characterization of HIV-1 vaccine candidates to elicit antibodies targeting multiple epitopes. The Journal of experimental medicine, 222(10).

Will N, et al. (2025) Lipid interactions and gating hysteresis suggest a physiological role for mechanosensitive channel YnaI. Nature communications, 16(1), 7472.

Joudeh L, et al. (2025) Structural mechanism of strand exchange by the RAD51 filament. eLife, 14.

Hudina E, et al. (2025) The bacterial ESCRT-III PspA rods thin lipid tubules and increase membrane curvature through helix-?? interactions. Proceedings of the National Academy of Sciences of the United States of America, 122(32), e2506286122.

Singh RR, et al. (2025) Transcription activation mechanism of a non-canonical bacterial DNA damage response pathway. Research square.

Gaines MC, et al. (2025) Unusual cell surfaces, pili, and archaella of Thermoplasmatales archaea. The ISME journal, 19(1).

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

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

Levy A, et al. (2025) CryoDRGN-AI: Neural ab initio reconstruction of challenging cryo-EM and cryo-ET datasets. bioRxiv : the preprint server for biology.

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.

Cook M, et al. (2025) Structural insights into HIV-2 CA lattice formation and FG-pocket binding revealed by single-particle cryo-EM. Cell reports, 44(2), 115245.