

Resource Summary Report

Generated by [dkNET](#) 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 [dkNET](#) .

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).

Mueller AU, et al. (2025) Real-time capture of ??N transcription initiation intermediates reveals mechanism of ATPase-driven activation by limited unfolding. bioRxiv : the preprint server for biology.

Drobiazko A, et al. (2025) Molecular basis of foreign DNA recognition by BREX anti-phage immunity system. Nature communications, 16(1), 1825.

Schultz K, et al. (2025) Snapshots of acyl carrier protein shuttling in human fatty acid synthase. Nature, 641(8062), 520.

Carr KD, et al. (2025) Protein identification using Cryo-EM and artificial intelligence guides improved sample purification. Journal of structural biology: X, 11, 100120.

Hamm CW, et al. (2025) Inorganic polyphosphate and the stringent response coordinately control cell division and cell morphology in Escherichia coli. mBio, 16(2), e0351124.

Hu J, et al. (2025) Establishing a universal IVRP method for quadrivalent HPV vaccines to replace in vivo potency tests. NPJ vaccines, 10(1), 55.

Liu X, et al. (2025) Structure, identification and characterization of the RibD-enolase complex in *Francisella*. *bioRxiv : the preprint server for biology*.

Xiao X, et al. (2025) Cryo-EM structures define the electron bifurcating flavobicluster and ferredoxin binding site in an archaeal Nfn-Bfu transhydrogenase. *The Journal of biological chemistry*, 301(4), 108410.

Shahid T, et al. (2025) Structural dynamics of DNA unwinding by a replicative helicase. *Nature*, 641(8061), 240.

Alom MS, et al. (2025) Protein bL38 facilitates incorporation of uL6 during assembly of the 50S subunit in *Flavobacterium johnsoniae*. *Nucleic acids research*, 53(4).

Adu OF, et al. (2025) Structures and functions of the limited natural polyclonal antibody response to parvovirus infection. *Proceedings of the National Academy of Sciences of the United States of America*, 122(8), e2423460122.

Asahi K, et al. (2025) Cryo-EM structure of the bacterial intramembrane metalloprotease RseP in the substrate-bound state. *Science advances*, 11(9), eadu0925.

Wang Y, et al. (2025) Filamentation activates bacterial Avs5 antiviral protein. *Nature communications*, 16(1), 2408.