

# Resource Summary Report

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## [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, image analysis 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

**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:** 20260821T194051+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 2939 mentions in open access literature.

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

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

Kannan S, et al. (2026) Evolution-guided protein design of IscB for persistent epigenome editing in vivo. *Nature biotechnology*, 44(5), 759.

Brunner HL, et al. (2026) A multivalent adaptor mechanism drives the nuclear import of proteasomes. *Nature communications*, 17(1).

Itskanov S, et al. (2026) Structural characterization of the HDV virion and its ribonucleoprotein. *Proceedings of the National Academy of Sciences of the United States of America*, 123(4), e2519809123.

Santarossa CC, et al. (2026) LetA defines a structurally distinct transporter family. *Nature*, 651(8107), 1097.

Ajjugal Y, et al. (2026) Protocol to investigate human mitochondrial transcription initiation by integrating biochemical and cryo-EM approaches. *STAR protocols*, 7(1), 104347.

Sun J, et al. (2026) B cell imprinting in children impairs antibodies to the haemagglutinin stalk. *Nature*, 653(8114), 528.

Wu F, et al. (2026) Development of VP30-targeted nanoparticles using DPS4 fusion peptides for the inhibition of Ebola virus. *Journal of nanobiotechnology*, 24(1).

Zhu C, et al. (2026) Structural dynamics of the midnolin-proteasome during ubiquitin-independent substrate turnover. *Nature communications*, 17(1).

Ettema TW, et al. (2026) Shared structural mechanisms of alternating access between the secondary peptide transporter SbmA and ABC transporters. *Nature communications*, 17(1).

Omura SN, et al. (2026) Engineering a compact high-fidelity *Staphylococcus aureus* Cas9 variant with broader targeting range and mechanistic insights into its activation. *Nature communications*, 17(1).

Lim GZ, et al. (2026) Cryo-EM structure of the SRI-HtrI complex reveals the cytoplasmic coupling in an archaeal phototaxis system. *Nature communications*, 17(1).

Muralidharan A, et al. (2026) Molecular basis for anti-jumbo phage immunity by AVAST type 5. *Molecular cell*, 86(4), 740.

Ma Q, et al. (2026) Insights into the structure and modulation of human TWIK-2. *Nature communications*, 17(1).

Xiao M, et al. (2026) Structural analysis reveals that water molecules mediate self-activation of GPR99. *Communications biology*, 9(1).

Kuhn CC, et al. (2026) Direct coupling of the human nuclear exosome adaptors NEXT and PAXT with transcription termination and processing machineries. *Nucleic acids research*, 54(4).

Sun C, et al. (2026) Molecular assemblies and pharmacology of cerebellar GABAA receptors. *Proceedings of the National Academy of Sciences of the United States of America*, 123(6), e2524504123.

Habib R, et al. (2026) Env-antibody coevolution identifies B cell priming as the principal bottleneck to HIV V2 apex broadly neutralizing antibody development. *Science immunology*, 11(116), eadz3933.

Ghosh AR, et al. (2026) Rapidly acquired HIV-1 neutralization breadth in a rhesus V2 apex knockin mouse model after a single bolus immunization. *Science immunology*, 11(116), eadz5064.

Xiong C, et al. (2026) Structural basis of Retron-Eco8-mediated antiphage defense. *Nucleic acids research*, 54(4).