

Resource Summary Report

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UCSF ChimeraX

RRID:SCR_015872

Type: Tool

Proper Citation

UCSF ChimeraX (RRID:SCR_015872)

Resource Information

URL: <https://www.cgl.ucsf.edu/chimerax/>

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Description: Software for 3D/4D image reconstruction. UCSF ChimeraX is the next-generation molecular visualization program from the Resource for Biocomputing, Visualization, and Informatics (RBVI), following UCSF Chimera.

Synonyms: ChimeraX

Resource Type: data visualization software, 3d visualization software, software application, 4d visualization software, software resource, data processing software

Keywords: 3d, 4d, image reconstruction, molecular visualization, biocomputing, informatics, rbvi, ucsf, chimera

Funding: NIGMS P41 GM103311

Resource Name: UCSF ChimeraX

Resource ID: SCR_015872

License: UCSF ChimeraX Non-Commercial Software License Agreement

License URLs: <http://www.rbvi.ucsf.edu/chimerax/docs/license.html>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T042754+0000

Ratings and Alerts

No rating or validation information has been found for UCSF ChimeraX.

No alerts have been found for UCSF ChimeraX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1825 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Mulvaney T, et al. (2026) Cryo-EM Analysis in CASP16. *Proteins*, 94(1), 447.

Larsen BB, et al. (2026) Functional and antigenic constraints on the Nipah virus fusion protein. *bioRxiv : the preprint server for biology*.

Pinto CS, et al. (2026) Actin arginylation alters myosin engagement and F-actin patterning despite structural conservation. *The Journal of cell biology*, 225(1).

Lee E, et al. (2026) *Streptococcus pneumoniae* HtrA is a dynamic and monomeric virulence factor capable of forming larger oligomeric complexes. *Protein science : a publication of the Protein Society*, 35(1), e70411.

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.

Hou Z, et al. (2026) In situ chromatin dynamics and HIV-1 nuclear trafficking. *bioRxiv : the preprint server for biology*.

Medina M, et al. (2026) Surface Morphometrics reveals local membrane thickness variation in organellar subcompartments. *The Journal of cell biology*, 225(3).

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

Lovatt C, et al. (2026) Memory engram synapse 3D macromolecular architecture visualized by cryoCLEM-guided cryoET. *Structure (London, England : 1993)*, 34(1), 100.

Kalenderoglou IE, et al. (2025) Structural basis of vilazodone dual binding mode to the serotonin transporter. *Research square*.

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.

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.

Sahan AZ, et al. (2025) Lysosomal PIP3 revealed by genetically encoded lipid biosensors. *Proceedings of the National Academy of Sciences of the United States of America*, 122(13), e2426929122.

LaFlam TN, et al. (2025) Phenotypic pleiotropy of missense variants in human B cell-confinement receptor P2RY8. *bioRxiv* : the preprint server for biology.

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

Helena-Bueno K, et al. (2025) Structurally heterogeneous ribosomes cooperate in protein synthesis in bacterial cells. *Nature communications*, 16(1), 2751.

Li S, et al. (2025) The structure of basal body inner junctions from *Tetrahymena* revealed by electron cryo-tomography. *The EMBO journal*, 44(7), 1975.

Li YC, et al. (2025) Structural insights into human PNPase in health and disease. *Nucleic acids research*, 53(4).

Duran-Roma R, et al. (2025) Native Fold Delay and its implications for co-translational chaperone binding and protein aggregation. *Nature communications*, 16(1), 1673.