Resource Summary Report

Generated by dkNET on Apr 23, 2025

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

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

rbvi, ucsf, chimera

Funding: NIGMS P41 GM103311

Availability: Free, Available for download, Freely available

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: 20250423T060903+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 1120 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Ishida H, et al. (2025) Cryo-EM structures of the zinc transporters ZnT3 and ZnT4 provide insights into their transport mechanisms. FEBS letters, 599(1), 41.

Golan N, et al. (2025) Resilience and charge-dependent fibrillation of functional amyloid: Interactions of Pseudomonas biofilm-associated FapB and FapC amyloids. The Journal of biological chemistry, 301(2), 108096.

Eadsforth TC, et al. (2025) Pharmacological and structural understanding of the Trypanosoma cruzi proteasome provides key insights for developing site-specific inhibitors. The Journal of biological chemistry, 301(1), 108049.

Rosa D, et al. (2025) Investigation of alpha-glucosidase inhibition activity of Artabotrys sumatranus leaf extract using metabolomics, machine learning and molecular docking analysis. PloS one, 20(1), e0313592.

Kunz L, et al. (2025) Avirulence depletion assay: Combining R gene-mediated selection with bulk sequencing for rapid avirulence gene identification in wheat powdery mildew. PLoS pathogens, 21(1), e1012799.

Berksoz M, et al. (2025) Ranking Single Fluorescent Protein-Based Calcium Biosensor Performance by Molecular Dynamics Simulations. Journal of chemical information and modeling, 65(1), 338.

Vigneron SF, et al. (2025) Docking 14 million virtual isoquinuclidines against the mu and kappa opioid receptors reveals dual antagonists-inverse agonists with reduced withdrawal effects. bioRxiv: the preprint server for biology.

Graur A, et al. (2025) Using Protein Painting Mass Spectrometry to Define Ligand Receptor

Interaction Sites for Acetylcholine Binding Protein. Bio-protocol, 15(2), e5163.

Lovatt C, et al. (2025) Memory engram synapse 3D molecular architecture visualized by cryoCLEM-guided cryoET. bioRxiv: the preprint server for biology.

Nel L, et al. (2025) Structural and biochemical analysis of ligand binding in yeast Niemann-Pick type C1-related protein. Life science alliance, 8(1).

Lopez AE, et al. (2025) Legionella pneumophila IrsA, a novel, iron-regulated exoprotein that facilitates growth in low-iron conditions and modulates biofilm formation. Microbiology spectrum, 13(1), e0231324.

Ay S, et al. (2025) In vivo HIV-1 nuclear condensates safeguard against cGAS and license reverse transcription. The EMBO journal, 44(1), 166.

Guerriere TB, et al. (2025) Dehydrogenase versus oxidase function: the interplay between substrate binding and flavin microenvironment. ACS catalysis, 15(2), 1046.

Francisco S, et al. (2025) Restoring adapter protein complex 4 function with small molecules: an in silico approach to spastic paraplegia 50. Protein science: a publication of the Protein Society, 34(1), e70006.

Sanchez VA, et al. (2025) Genome evolution following an ecological shift in nectar-dwelling Acinetobacter. mSphere, 10(1), e0101024.

Zafar S, et al. (2025) Molecular dynamics simulation based prediction of T-cell epitopes for the production of effector molecules for liver cancer immunotherapy. PloS one, 20(1), e0309049.

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

Bal?kç? E, et al. (2025) Structure of the Nipah virus polymerase complex. The EMBO journal, 44(2), 563.

Draveny M, et al. (2025) Intracellular Quantification of an Antibiotic Metal Complex in Single Cells of Escherichia coli Using Cryo-X-ray Fluorescence Nanoimaging. ACS nano, 19(1), 979.

Gonda I, et al. (2025) The mycobacterial ABC transporter IrtAB employs a membrane-facing crevice for siderophore-mediated iron uptake. Nature communications, 16(1), 1133.