

Resource Summary Report

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UCSF Chimera

RRID:SCR_004097

Type: Tool

Proper Citation

UCSF Chimera (RRID:SCR_004097)

Resource Information

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

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Description: Software tool for interactive visualization and analysis of molecular structures and related data, including density maps, supramolecular assemblies, sequence alignments, docking results, trajectories, and conformational ensembles. High-quality images and animations can be generated. Chimera includes complete documentation and several tutorials.

Abbreviations: Chimera

Synonyms: Chimera - an Extensible Molecular Modeling System, UCSF Chimera - an Extensible Molecular Modeling System

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

Defining Citation: [PMID:15264254](#)

Keywords: molecular modeling, electron microscopy, interactive visualization and analysis, molecular structures

Funding: NCRR P41 RR001081;
NIGMS P41 GM103311

Availability: Restricted

Resource Name: UCSF Chimera

Resource ID: SCR_004097

Alternate IDs: nlx_143560

Old URLs: <http://plato.cgl.ucsf.edu/chimera/>

Record Creation Time: 20220129T080222+0000

Record Last Update: 20260903T234654+0000

Ratings and Alerts

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

No alerts have been found for UCSF Chimera.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2257 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Fatima S, et al. (2026) A novel protein truncating mutation of TTC8 causes Bardet-Biedl Syndrome (BBS) in a Pakistani family. *Genetics and molecular biology*, 49(1), e20250020.

?miga M, et al. (2026) *Porphyromonas gingivalis* produces a functional HemH ferroxidase important for its survival in a heme-limited environment. *Scientific reports*, 16(1).

Siriphanitchakorn T, et al. (2026) Reduced dengue virus pre-membrane protein-HMGB1 interaction activates host cell transcription to attenuate infection. *NPJ vaccines*, 11(1).

Chatelain FC, et al. (2026) SPARC: a structural pathogenicity algorithm for risk classification of hERG variants. *Europace : European pacing, arrhythmias, and cardiac electrophysiology : journal of the working groups on cardiac pacing, arrhythmias, and cardiac cellular electrophysiology of the European Society of Cardiology*, 28(2).

Boren C, et al. (2026) In Silico Design and Characterization of a Rationally Engineered Cas12j2 Gene Editing System for the Treatment of HPV-Associated Cancers. *International journal of molecular sciences*, 27(2).

Besli N, et al. (2026) Carvacrol Selectively Induces Mitochondria-Related Apoptotic Signaling in Primary Breast Cancer-Associated Fibroblasts. *Pharmaceuticals (Basel, Switzerland)*, 19(1).

Nellaepalli S, et al. (2026) Assembly of two functionally-distinct protein import complexes in the outer membrane of plant chloroplasts. *Nature communications*, 17(1).

Guimarães LO, et al. (2026) *Wyeomyia confusa* Lispivirus (WcLispV-SP): a novel neotropical mosquito virus in the Lispiviridae family. *Archives of virology*, 171(6).

- Koparir A, et al. (2026) Clinical and genetic heterogeneity of syndromic hearing loss and its non-syndromic hearing loss mimics. *Molecular medicine (Cambridge, Mass.)*, 32(1).
- Duan Y, et al. (2026) Asperosaponin VI Ameliorates Spontaneous Abortion by Inhibiting Trophoblast Ferroptosis via the KEAP1/NRF2/GPX4 Axis. *Antioxidants (Basel, Switzerland)*, 15(6).
- Santos-Enriquez AK, et al. (2026) Network pharmacology refined with non-ubiquity and decoy-controlled molecular docking reveals insights into *Moringa oleifera* phytochemicals targeting insulin resistance. *Frontiers in bioinformatics*, 6, 1756081.
- Kousar S, et al. (2026) Immunoinformatic-based design of a multi-epitope subunit vaccine against *Ruminococcus torques* using subtractive proteomics and molecular dynamics simulations. *Scientific reports*, 16(1).
- Chen L, et al. (2026) A conserved mycobacterial nucleomodulin hijacks the host COMPASS complex to reprogram pro-inflammatory transcription and promote intracellular survival. *eLife*, 14.
- Bravo-Villagra KM, et al. (2026) In Silico Functional and Structural Analysis of STAT4 Variants of Uncertain Significance. *Genes*, 17(1).
- Dinata R, et al. (2026) Honey Bee AMPs as a Novel Carrier Protein for the Development of a Subunit Vaccine: An Immunoinformatic Approach. *Current issues in molecular biology*, 48(1).
- Montaño GH, et al. (2026) In Silico Comparative Analysis of the Plant Growth Regulators Forchlorfenuron (CPPU) and Strigol (STG) Interacting with the Gibberellin Biosynthetic Enzyme GA3Ox2 and the Auxin Signaling Protein Receptor IAA7. *International journal of molecular sciences*, 27(7).
- Hernandez-Munguia AM, et al. (2026) Binding Affinity and Interaction Profiles of Erinacines and Erinacerins with iNOS and NF- κ B Revealed by Molecular Dynamics Simulations. *International journal of molecular sciences*, 27(7).
- Yi D, et al. (2026) Computational analysis and expression profiling of the Sulfate Transporter gene family in tomato under selenium and abiotic stress treatment. *BMC plant biology*, 26(1).
- Li BJ, et al. (2026) A Whole-Cell Catalytic System for Equol Production Based on Daidzein Reductase Engineering. *Molecules (Basel, Switzerland)*, 31(4).
- Shi R, et al. (2026) Mechanistic basis for selective Csm6-2 activation by cyclic penta-adenylate in a type III CRISPR-Cas system. *The EMBO journal*, 45(10), 3416.