Resource Summary Report

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Resource for Biocomputing Visualization and Informatics

RRID:SCR_001374
Type: Tool

Proper Citation

Resource for Biocomputing Visualization and Informatics (RRID:SCR_001374)

Resource Information

URL: http://www.cgl.ucsf.edu/

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Description: Biomedical technology resource center that develops software and web-based resources for the visualization and analysis of molecular structure, and related data, at scales ranging from the atomic to the supramolecular. They create tools for handling and integrating diverse types of biomolecular data, including atomic-resolution coordinates, density maps, sequences, annotations, and networks. Their primary efforts are in the visualization and analysis of structures of molecules and molecular assemblies, enzyme sequence-structure-function relationships, and network representations of protein similarity, binding interactions, and biological pathways. They provide technologies to enable identifying the molecular bases of disease and phenotypic variation, annotating proteins of unknown function, identifying targets for drug development, designing drugs, and engineering proteins with new functions. RBVI distributes software tools, including the popular UCSF Chimera visualization and analysis package, develops and hosts the Structure-Function Linkage Database, and provides access to state-of-the-art computational resources in support of research projects in these areas.

Abbreviations: RBVI

Resource Type: training resource, biomedical technology resource center

Keywords: training resource, molecular modeling, software, molecular graphics, visualization, modeling, molecular structure, analysis, computation, computing and informatics technology center, FASEB list

Funding: NIGMS

Resource Name: Resource for Biocomputing Visualization and Informatics

Resource ID: SCR_001374

Alternate IDs: nlx_152531

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260810T040309+0000

Ratings and Alerts

No rating or validation information has been found for Resource for Biocomputing Visualization and Informatics.

No alerts have been found for Resource for Biocomputing Visualization and Informatics.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 158 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Zheng W, et al. (2025) Molecular insights and rational engineering of a compact CRISPR-Cas effector Cas12h1 with a broad-spectrum PAM. Signal transduction and targeted therapy, 10(1), 66.

Ahmadian N, et al. (2025) Molecular dynamics study of host-guest interactions between anticancer drugs and Cucurbit[8]uril nanocontainer. Scientific reports, 15(1), 43669.

Boonkua S, et al. (2025) Replacing protruding domains of MrNV virus-like particles with sialic acid binding domains enhances binding to SARS-CoV-2 susceptible cells and reduces pseudovirus infection. Scientific reports, 15(1), 25200.

Bezerra AS, et al. (2025) Synthetic Aminochalcone Prevents Hyperglycemia-Induced Anxiety and Delays Pentylenetetrazole-Induced Epileptic Crisis in Adult Zebrafish. ACS omega, 10(28), 30313.

Kaewjiw N, et al. (2025) Domperidone inhibits dengue virus infection by targeting the viral envelope protein and nonstructural protein 1. Scientific reports, 15(1), 3817.

Jaranathummakul S, et al. (2025) Multivalent display of VP28 on chimeric virus-like particles enhances binding to shrimp target tissues: A novel antiviral strategy against white spot syndrome virus. Veterinary world, 18(8), 2194.

Hu Z, et al. (2024) Emodin alleviates cholestatic liver injury by modulating Sirt1/Fxr signaling pathways. Scientific reports, 14(1), 16756.

Yu Y, et al. (2024) Nuclear pore protein POM121 regulates subcellular localization and transcriptional activity of PPAR?. Cell death & disease, 15(1), 7.

Boonkua S, et al. (2024) Development of chimeric MrNV virus-like particles capable of binding to SARS-CoV-2-susceptible cells and reducing infection by pseudovirus variants. Scientific reports, 14(1), 31431.

Simbulan AM, et al. (2024) Immunoinformatics-guided approach for designing a pan-proteome multi-epitope subunit vaccine against African swine fever virus. Scientific reports, 14(1), 1354.

Mise K, et al. (2024) NDUFS4 regulates cristae remodeling in diabetic kidney disease. Nature communications, 15(1), 1965.

Manu P, et al. (2024) Computational Mutagenesis and Inhibition of Staphylococcus aureus AgrA LytTR Domain Using Phenazine Scaffolds: Insight From a Biophysical Study. BioMed research international, 2024, 8843954.

Lu H, et al. (2023) Emodin prevents renal ischemia-reperfusion injury via suppression of p53-mediated cell apoptosis based on network pharmacology. Heliyon, 9(5), e15682.

Munguía-Robledo S, et al. (2023) Lysine Methyltransferase EhPKMT2 Is Involved in the In Vitro Virulence of Entamoeba histolytica. Pathogens (Basel, Switzerland), 12(3).

Mohammadi S, et al. (2022) Expression, characterization, and activity optimization of a novel cellulase from the thermophilic bacteria Cohnella sp. A01. Scientific reports, 12(1), 10301.

Wang Y, et al. (2022) Cryo-EM analysis of Ebola virus nucleocapsid-like assembly. STAR protocols, 3(1), 101030.

Sadeghi M, et al. (2022) Inhibitory effect of flavonoid glycosides on digestive enzymes: In silico, in vitro, and in vivo studies. International journal of biological macromolecules, 217, 714.

Dechkla M, et al. (2022) Cry4Aa and Cry4Ba Mosquito-Active Toxins Utilize Different Domains in Binding to a Particular Culex ALP Isoform: A Functional Toxin Receptor Implicating Differential Actions on Target Larvae. Toxins, 14(10).

Nguyen T, et al. (2021) Direct IgG epitope mapping on bacterial AB toxins by cryo-EM. STAR protocols, 2(4), 100852.

Pickford P, et al. (2021) Partial agonism improves the anti-hyperglycaemic efficacy of an oxyntomodulin-derived GLP-1R/GCGR co-agonist. Molecular metabolism, 51, 101242.