Resource Summary Report

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ICM Browser

RRID:SCR_014878
Type: Tool

Proper Citation

ICM Browser (RRID:SCR_014878)

Resource Information

URL: http://www.molsoft.com/icm_browser.html

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Description: Molecular graphics environment which provides biologists and chemists with representations of proteins, DNA, RNA, and multiple sequence alignments. Users can build, annotate, and edit interactive views and slides of molecules. Users can also superimpose protein structures, search PDB, measure distanaces and angles, and view and make high resolution images of alignments.

Synonyms: ICM-Browser

Resource Type: software resource

Keywords: drug design, molecular graphics design, protein, protein structure, multiple sequence alignments

Funding:

Availability: Free, Available for download

Resource Name: ICM Browser

Resource ID: SCR_014878

License URLs: http://www.molsoft.com/terms-of-use.html

Record Creation Time: 20220129T080322+0000

Record Last Update: 20250410T070539+0000

Ratings and Alerts

No rating or validation information has been found for ICM Browser.

No alerts have been found for ICM Browser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Namoto K, et al. (2024) NIBR-LTSi is a selective LATS kinase inhibitor activating YAP signaling and expanding tissue stem cells in vitro and in vivo. Cell stem cell, 31(4), 554.

Poleboyina SM, et al. (2023) Homology Modeling, Screening, and Identification of Potential FOXO6 Inhibitors Curtail Gastric Cancer Progression: an In Silico Drug Repurposing Approach. Applied biochemistry and biotechnology.

Overduin M, et al. (2022) Progressive membrane-binding mechanism of SARS-CoV-2 variant spike proteins. iScience, 25(8), 104722.

Singh KS, et al. (2021) IspH inhibitors kill Gram-negative bacteria and mobilize immune clearance. Nature, 589(7843), 597.

Mokaya J, et al. (2020) Hepatitis B virus resistance to tenofovir: fact or fiction? A systematic literature review and structural analysis of drug resistance mechanisms. Wellcome open research, 5, 151.

Kinyanyi D, et al. (2019) Comparative in silico study of congocidine congeners as potential inhibitors of African swine fever virus. PloS one, 14(8), e0221175.

Zou B, et al. (2018) Prediction of sensitivity to gefitinib/erlotinib for EGFR mutations in NSCLC based on structural interaction fingerprints and multilinear principal component analysis. BMC bioinformatics, 19(1), 88.

Kinyanyi D, et al. (2018) In silico structural and functional prediction of African swine fever virus protein-B263R reveals features of a TATA-binding protein. PeerJ, 6, e4396.

Zou B, et al. (2017) Deciphering mechanisms of acquired T790M mutation after EGFR inhibitors for NSCLC by computational simulations. Scientific reports, 7(1), 6595.

Naschberger A, et al. (2017) Structural Evidence for a Role of the Multi-functional Human

Glycoprotein Afamin in Wnt Transport. Structure (London, England : 1993), 25(12), 1907.

Kuzmanic A, et al. (2017) Changes in the free-energy landscape of p38? MAP kinase through its canonical activation and binding events as studied by enhanced molecular dynamics simulations. eLife, 6.

Glukhova A, et al. (2017) Structure of the Adenosine A1 Receptor Reveals the Basis for Subtype Selectivity. Cell, 168(5), 867.

Bradley AR, et al. (2017) MMTF-An efficient file format for the transmission, visualization, and analysis of macromolecular structures. PLoS computational biology, 13(6), e1005575.

Diehl WE, et al. (2016) Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. Cell, 167(4), 1088.

Hua T, et al. (2016) Crystal Structure of the Human Cannabinoid Receptor CB1. Cell, 167(3), 750.

Skowronska-Krawczyk D, et al. (2015) P16INK4a Upregulation Mediated by SIX6 Defines Retinal Ganglion Cell Pathogenesis in Glaucoma. Molecular cell, 59(6), 931.

Singh SP, et al. (2012) Prediction of the three-dimensional structure of serine/threonine protein kinase pto of Solanum lycopersicum by homology modelling. Bioinformation, 8(5), 212.