Resource Summary Report

Generated by NIF on Apr 22, 2025

LSQMAN

RRID:SCR_015751
Type: Tool

Proper Citation

LSQMAN (RRID:SCR_015751)

Resource Information

URL: http://xray.bmc.uu.se/usf/lsqman_man.html

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Description: Software for alignment, comparison of macromolecules, and performing least-squares superpositioning of biomacromolecules. The program offers a superset of the LSQ-functionality inside O and removes some of the limitations and irritations of the LSQ-commands.

Resource Type: software resource, data processing software, data analysis software, software application

Defining Citation: PMID:15299650

Keywords: least-square, least-squares superpositioning, biomacromolecule, alignment, comparison

Funding:

Availability: Free for academic use, Commercially available, Available for download

Resource Name: LSQMAN

Resource ID: SCR_015751

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250422T055908+0000

Ratings and Alerts

No rating or validation information has been found for LSQMAN.

No alerts have been found for LSQMAN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 106 mentions in open access literature.

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

Jaiswal R, et al. (2025) Cryo-EM structure of AAV2 Rep68 bound to integration site AAVS1: insights into the mechanism of DNA melting. Nucleic acids research, 53(3).

Jaiswal R, et al. (2024) Cryo-EM Structure of AAV2 Rep68 bound to integration site AAVS1: Insights into the mechanism of DNA melting. bioRxiv : the preprint server for biology.

Weiergräber OH, et al. (2022) Structure and Dynamics of Human Chemokine CCL16-Implications for Biological Activity. Biomolecules, 12(11).

Flecken M, et al. (2020) Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. Cell, 183(2), 457.

Bracher A, et al. (2020) Structure and conformational cycle of a bacteriophage-encoded chaperonin. PloS one, 15(4), e0230090.

Mönkemeyer L, et al. (2019) Chaperone Function of Hgh1 in the Biogenesis of Eukaryotic Elongation Factor 2. Molecular cell, 74(1), 88.

Corbett KS, et al. (2019) Design of Nanoparticulate Group 2 Influenza Virus Hemagglutinin Stem Antigens That Activate Unmutated Ancestor B Cell Receptors of Broadly Neutralizing Antibody Lineages. mBio, 10(1).

Miles TF, et al. (2018) Viral GPCR US28 can signal in response to chemokine agonists of nearly unlimited structural degeneracy. eLife, 7.

Gabrielsen M, et al. (2017) A General Strategy for Discovery of Inhibitors and Activators of RING and U-box E3 Ligases with Ubiquitin Variants. Molecular cell, 68(2), 456.

Moulinier L, et al. (2017) MiSynPat: An integrated knowledge base linking clinical, genetic, and structural data for disease-causing mutations in human mitochondrial aminoacyl-tRNA synthetases. Human mutation, 38(10), 1316.

Ou X, et al. (2017) Ion- and water-binding sites inside an occluded hourglass pore of a trimeric intracellular cation (TRIC) channel. BMC biology, 15(1), 31.

Shishovs M, et al. (2016) Structure of AP205 Coat Protein Reveals Circular Permutation in ssRNA Bacteriophages. Journal of molecular biology, 428(21), 4267.

Scharf L, et al. (2016) Structural basis for germline antibody recognition of HIV-1 immunogens. eLife, 5.

Geng Y, et al. (2016) Structural mechanism of ligand activation in human calcium-sensing receptor. eLife, 5.

Alguel Y, et al. (2016) Structure of eukaryotic purine/H(+) symporter UapA suggests a role for homodimerization in transport activity. Nature communications, 7, 11336.

Eyal Z, et al. (2016) A novel pleuromutilin antibacterial compound, its binding mode and selectivity mechanism. Scientific reports, 6, 39004.

Groothuizen FS, et al. (2015) MutS/MutL crystal structure reveals that the MutS sliding clamp loads MutL onto DNA. eLife, 4, e06744.

Arnold LH, et al. (2015) Phospho-dependent Regulation of SAMHD1 Oligomerisation Couples Catalysis and Restriction. PLoS pathogens, 11(10), e1005194.

Drögemüller J, et al. (2015) Determination of RNA polymerase binding surfaces of transcription factors by NMR spectroscopy. Scientific reports, 5, 16428.

Yang S, et al. (2015) Structural insights into the substrate specificity of two esterases from the thermophilic Rhizomucor miehei. Journal of lipid research, 56(8), 1616.