

# Resource Summary Report

Generated by T1D on Jul 31, 2026

## LSQMAN

RRID:SCR\_015751

Type: Tool

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### Proper Citation

LSQMAN (RRID:SCR\_015751)

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### Resource Information

**URL:** [http://xray.bmc.uu.se/usf/lsqman\\_man.html](http://xray.bmc.uu.se/usf/lsqman_man.html)

**Proper Citation:** LSQMAN (RRID:SCR\_015751)

**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:** data processing software, data analysis software, software application, software resource

**Defining Citation:** [PMID:15299650](#)

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

**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:** 20260801T042753+0000

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### Ratings and Alerts

No rating or validation information has been found for LSQMAN.

No alerts have been found for LSQMAN.

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### Data and Source Information

## Usage and Citation Metrics

We found 107 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Yuste-Checa P, et al. (2025) Structural analyses define the molecular basis of clusterin chaperone function. *Nature structural & molecular biology*.

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.

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.

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.

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.

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

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

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

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.

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.