

Resource Summary Report

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iMosflm

RRID:SCR_014217

Type: Tool

Proper Citation

iMosflm (RRID:SCR_014217)

Resource Information

URL: <http://www.mrc-lmb.cam.ac.uk/harry/imosflm/ver721/introduction.html>

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Description: Software which processes diffraction data/images and produces an MTZ file of reflection indices with their intensities, standard deviations, and other parameters. The MTZ file is passed onto other programs of the CCP4 program suite for further data reduction. iMosflm processes data from CCD and pixel detectors. It is available for Windows, Mac OSX and Linux platforms. Tutorials are available at the website.

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

Keywords: image processing software, diffraction image, mtz file

Resource Name: iMosflm

Resource ID: SCR_014217

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260728T043435+0000

Ratings and Alerts

No rating or validation information has been found for iMosflm .

No alerts have been found for iMosflm .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 326 mentions in open access literature.

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

Chatterjee S, et al. (2025) Ancestral Sequence Reconstruction of the Ethylene-Forming Enzyme. *Biochemistry*, 64(15), 3432.

Gieselmann L, et al. (2025) Profiling of HIV-1 elite neutralizer cohort reveals a CD4bs bnAb for HIV-1 prevention and therapy. *Nature immunology*, 26(11), 2016.

Saharan K, et al. (2025) Structure-function studies of a nucleoplasmin isoform from *Plasmodium falciparum*. *The Journal of biological chemistry*, 301(4), 108379.

Georgakopoulos ND, et al. (2025) Tetrazole-containing naphthalene bis-sulfonamide Keap1-Nrf2 interaction inhibitors with unexpected binding modes. *Redox biology*, 88, 103924.

Khandokar Y, et al. (2025) Molecular basis for presentation of N-myristoylated peptides by the chicken YF1?7.1 molecule. *The Journal of biological chemistry*, 301(7), 110253.

Pham S, et al. (2025) Conformational flexibility is a critical factor in designing broad-spectrum human norovirus protease inhibitors. *Journal of virology*, 99(2), e0175724.

Shiojima Y, et al. (2025) Crystal Structure of CcGH131B, a Protein Belonging to Glycoside Hydrolase Family 131 from the Basidiomycete *Coprinopsis cinerea*. *Journal of applied glycoscience*, 72(2), 7202104.

Shin OS, et al. (2024) Crimean-Congo hemorrhagic fever survivors elicit protective non-neutralizing antibodies that target 11 overlapping regions on glycoprotein GP38. *Cell reports*, 43(7), 114502.

Shahri MA, et al. (2024) Deciphering the structure of a multi-drug resistant *Acinetobacter baumannii* short-chain dehydrogenase reductase. *PloS one*, 19(2), e0297751.

Wachino J-i, et al. (2024) Hydroxyhexylitaconic acids as potent IMP-type metallo-?-lactamase inhibitors for controlling carbapenem resistance in Enterobacterales. *Microbiology spectrum*, 12(3), e0234423.

Pijning T, et al. (2024) Structural and time-resolved mechanistic investigations of protein hydrolysis by the acidic proline-specific endoprotease from *Aspergillus niger*. *Protein science : a publication of the Protein Society*, 33(1), e4856.

Ghafoori SM, et al. (2024) RNA Binding Properties of SOX Family Members. *Cells*, 13(14).

Fernando MC, et al. (2024) The structure of KRASG12C bound to divarasib highlights features of potent switch-II pocket engagement. *Small GTPases*, 15(1), 1.

Nguyen MC, et al. (2024) Molecular insight into interactions between the Taf14, Yng1 and Sas3 subunits of the NuA3 complex. *Nature communications*, 15(1), 5335.

May AJ, et al. (2024) Structural and antigenic characterization of novel and diverse Henipavirus glycoproteins. *bioRxiv : the preprint server for biology*.

Nguy AKL, et al. (2024) Non-Canonical Cytochrome P450 Enzymes in Nature. *bioRxiv : the preprint server for biology*.

Cross EM, et al. (2024) A functional and structural comparative analysis of large tumor antigens reveals evolution of different importin β -dependent nuclear localization signals. *Protein science : a publication of the Protein Society*, 33(2), e4876.

Edgar RCS, et al. (2024) On-target, dual aminopeptidase inhibition provides cross-species antimalarial activity. *mBio*, 15(6), e0096624.

Chen X, et al. (2024) The presence of broadly neutralizing anti-SARS-CoV-2 RBD antibodies elicited by primary series and booster dose of COVID-19 vaccine. *PLoS pathogens*, 20(6), e1012246.

Ke Z, et al. (2024) N terminus of SARS-CoV-2 nonstructural protein 3 interrupts RNA-driven phase separation of N protein by displacing RNA. *The Journal of biological chemistry*, 300(11), 107828.