

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, data processing software, software resource

Keywords: image processing software, diffraction image, mtz file

Resource Name: iMosflm

Resource ID: SCR_014217

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260807T042816+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 332 mentions in open access literature.

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

Engemann R, et al. (2026) In Situ Insights into Enhanced Cooperative Ligand Exchange Kinetics via Solvent-Induced Restacking in a 2D Metal-Organic Framework. *Journal of the American Chemical Society*, 148(13), 13940.

Glaser AW, et al. (2026) Phosphatase SHP2 pathogenic mutations enhance activity by altering conformational sampling. *Proceedings of the National Academy of Sciences of the United States of America*, 123(3), e2513851123.

Sato H, et al. (2026) Biochemical and structural analyses of metallo- β -lactamase VIM-28: impact of substitutions at residues 224 and 228 on substrate profile, stability, and zinc affinity. *Microbiology spectrum*, 14(3), e0278825.

Waterson AG, et al. (2026) Identification of KLHL12 Ligands Using Fragment-Based Methods. *Journal of medicinal chemistry*, 69(7), 7709.

Du W, et al. (2026) Mining of natural diversity enables efficient and expressible peptide asparaginyl ligases. *Nature communications*, 17(1).

Konstantoulea K, et al. (2026) A functional amyloid scaffold shapes insect egg coats. *bioRxiv : the preprint server for biology*.

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

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

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.

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 YF177.1 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.

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

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

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

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

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.

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