Resource Summary Report

Generated by RRID on Apr 17, 2025

XDS Program Package

RRID:SCR_015652
Type: Tool

Proper Citation

XDS Program Package (RRID:SCR_015652)

Resource Information

URL: http://xds.mpimf-heidelberg.mpg.de/

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Description: Software for x-ray detection and processing single-crystal monochromatic diffraction data recorded by the rotation method. XDS can process data images from CCD-, imaging-plate-, multiwire-, and pixel-detectors in a variety of formats.

Abbreviations: XDS

Synonyms: XDS, XDS Package

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

Keywords: x-ray detection, monochromatic diffraction, single-crystal, image processing, multi-segment detector, nfs environment

Funding:

Availability: Free, Available for download, License required for commercial use, Runs on Linux, Runs on Mac OS

Resource Name: XDS Program Package

Resource ID: SCR_015652

Alternate URLs: https://strucbio.biologie.uni-konstanz.de/xdswiki/index.php/Xds

Record Creation Time: 20220129T080326+0000

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Ratings and Alerts

No rating or validation information has been found for XDS Program Package.

No alerts have been found for XDS Program Package.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 322 mentions in open access literature.

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

Markusson S, et al. (2025) Nanobodies against the myelin enzyme CNPase as tools for structural and functional studies. Journal of neurochemistry, 169(1), e16274.

Nakazawa Y, et al. (2025) Structure and function of a ?-1,2-galactosidase from Bacteroides xylanisolvens, an intestinal bacterium. Communications biology, 8(1), 66.

Le Bas A, et al. (2025) Structure of WzxE the lipid III flippase for Enterobacterial Common Antigen polysaccharide. Open biology, 15(1), 240310.

Yudenko A, et al. (2025) Structural basis of signaling complex inhibition by IL-6 domain-swapped dimers. Structure (London, England : 1993), 33(1), 171.

Hulin-Curtis S, et al. (2024) A targeted single mutation in influenza A virus universal epitope transforms immunogenicity and protective immunity via CD4+ T cell activation. Cell reports, 43(6), 114259.

Ray R, et al. (2024) Eliciting a single amino acid change by vaccination generates antibody protection against group 1 and group 2 influenza A viruses. Immunity, 57(5), 1141.

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. Cell, 187(6), 1440.

Chen Y, et al. (2023) Structural definition of HLA class II-presented SARS-CoV-2 epitopes reveals a mechanism to escape pre-existing CD4+ T cell immunity. Cell reports, 42(8), 112827.

Ren X, et al. (2023) Structural basis for ATG9A recruitment to the ULK1 complex in mitophagy initiation. Science advances, 9(7), eadg2997.

Thai E, et al. (2023) Molecular determinants of cross-reactivity and potency by VH3-33 antibodies against the Plasmodium falciparum circumsporozoite protein. Cell reports, 42(11), 113330.

Ray S, et al. (2023) High-resolution structures with bound Mn2+ and Cd2+ map the metal import pathway in an Nramp transporter. eLife, 12.

Healy MD, et al. (2023) Structure of the endosomal Commander complex linked to Ritscher-Schinzel syndrome. Cell, 186(10), 2219.

Motouchi S, et al. (2023) Identification of enzymatic functions of osmo-regulated periplasmic glucan biosynthesis proteins from Escherichia coli reveals a novel glycoside hydrolase family. Communications biology, 6(1), 961.

Hara M, et al. (2023) Centromere/kinetochore is assembled through CENP-C oligomerization. Molecular cell, 83(13), 2188.

Racle J, et al. (2023) Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes. Immunity, 56(6), 1359.

Hattne J, et al. (2023) Electron counting with direct electron detectors in MicroED. Structure (London, England : 1993), 31(12), 1504.

Martinez-Martin I, et al. (2023) Titin domains with reduced core hydrophobicity cause dilated cardiomyopathy. Cell reports, 42(12), 113490.

Rodarte JV, et al. (2023) Structures of drug-specific monoclonal antibodies bound to opioids and nicotine reveal a common mode of binding. Structure (London, England : 1993), 31(1), 20.

Huber EM, et al. (2022) Structural insights into cooperative DNA recognition by the CCAAT-binding complex and its bZIP transcription factor HapX. Structure (London, England : 1993), 30(7), 934.

Bolgi O, et al. (2022) Dipeptidyl peptidase 9 triggers BRCA2 degradation and promotes DNA damage repair. EMBO reports, 23(10), e54136.