Resource Summary Report

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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 application, software resource, image processing software, software toolkit, data processing software

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

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

Record Last Update: 20260819T044427+0000

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 334 mentions in open access literature.

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

Román-Trufero M, et al. (2026) A Novel Potent and Selective GCN2 Inhibitor, APL-4098, Has Antileukemic Activity through Dysregulation of Mitochondrial Function. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1846.

Charaka V, et al. (2026) HP1? recruits RING1A to ubiquitinate histone H2A for BRCA1-mediated resection of double-stand breaks. iScience, 29(2), 114582.

Cervantes Rincón T, et al. (2026) Analysis of West Nile disease convalescents identifies human monoclonal antibodies protective against West Nile and related orthoflaviviruses. Immunity, 59(7), 2015.

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. iScience, 29(7), 116513.

Besaw JE, et al. (2026) Structural characterization of the Cu(II)-NTA spin label on ?-helices by X-ray crystallography and electron paramagnetic resonance. Structure (London, England : 1993), 34(4), 645.

Esdar C, et al. (2025) M4205 (IDRX-42) Is a Highly Selective and Potent Inhibitor of Relevant Oncogenic Driver and Resistance Variants of KIT in Cancer. Molecular cancer therapeutics, 24(7), 1040.

Benjamin JS, et al. (2025) 23ME-01473, an Fc Effector-Enhanced Anti-ULBP6/2/5 Antibody, Restores NK Cell-Mediated Antitumor Immunity through NKG2D and Fc?RIIIa Activation. Cancer research communications, 5(3), 476.

Tangpeerachaikul A, et al. (2025) Zidesamtinib Selective Targeting of Diverse ROS1 Drug-Resistant Mutations. Molecular cancer therapeutics, 24(7), 1005.

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

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

Raig ND, et al. (2025) Type-II kinase inhibitors that target Parkinson's Disease-associated LRRK2. bioRxiv : the preprint server for biology.

Raig ND, et al. (2025) Type II kinase inhibitors that target Parkinson's disease-associated LRRK2. Science advances, 11(23), eadt2050.

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

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

Machner L, et al. (2025) Mechanism of SHP2 activation by bis-Tyr-phosphorylated Gab1. Structure (London, England : 1993).

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.

Pinkas DM, et al. (2024) A BTB extension and ion-binding domain contribute to the pentameric structure and TFAP2A binding of KCTD1. Structure (London, England : 1993), 32(10), 1586.

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