

# Resource Summary Report

Generated by [RRID](#) on Apr 8, 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/>

**Proper Citation:** XDS Program Package (RRID:SCR\_015652)

**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 toolkit, image processing software, data processing software, software resource

**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

**Record Last Update:** 20250407T220233+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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  $\beta$ -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 Mn<sup>2+</sup> and Cd<sup>2+</sup> 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.