

Resource Summary Report

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[xia2 pipeline](#)

RRID:SCR_015746

Type: Tool

Proper Citation

xia2 pipeline (RRID:SCR_015746)

Resource Information

URL: <https://xia2.github.io/>

Proper Citation: xia2 pipeline (RRID:SCR_015746)

Description: Data processing software that performs X-ray diffraction data processing. It handles multi-pass, multi-wavelength data sets and supports remote access to synchrotron facilities.

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

Defining Citation: [PMID:23793152](#)

Keywords: xray, diffraction, data processing, synchrotron, multi-pass, multi-wavelength, bio.tools

Availability: Open Source, Available for download

Resource Name: xia2 pipeline

Resource ID: SCR_015746

Alternate IDs: biotools:xia2

Alternate URLs: <https://bio.tools/xia2>

License: BSD License

License URLs: <https://xia2.github.io/license.html>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260912T200103+0000

Ratings and Alerts

No rating or validation information has been found for xia2 pipeline.

No alerts have been found for xia2 pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Hope I, et al. (2025) Crystallographic fragment screening of CDK2-cyclin A: FragLites map sites of protein-protein interaction. 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.

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.

McGregor NGS, et al. (2022) Synthesis of broad-specificity activity-based probes for exo-? -mannosidases. Organic & biomolecular chemistry, 20(4), 877.

Kantsadi AL, et al. (2022) Structures of SAS-6 coiled coil hold implications for the polarity of the centriolar cartwheel. Structure (London, England : 1993), 30(5), 671.

Tuekprakhon A, et al. (2022) Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum. Cell, 185(14), 2422.

Zhang S, et al. (2022) Scaffolding Protein GspB/OutB Facilitates Assembly of the Dickeya dadantii Type 2 Secretion System by Anchoring the Outer Membrane Secretin Pore to the Inner Membrane and to the Peptidoglycan Cell Wall. mBio, 13(3), e0025322.

Hulce KR, et al. (2022) Inhibiting a dynamic viral protease by targeting a non-catalytic cysteine. Cell chemical biology, 29(5), 785.

Hammond CM, et al. (2021) DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. Molecular cell, 81(12), 2533.

York A, et al. (2021) Structure-based modeling and dynamics of MurM, a Streptococcus pneumoniae penicillin resistance determinant present at the cytoplasmic membrane. Structure (London, England : 1993), 29(7), 731.

Robinson RA, et al. (2021) Simultaneous binding of Guidance Cues NET1 and RGM blocks extracellular NEO1 signaling. Cell, 184(8), 2103.

Scott AJ, et al. (2021) Constructing ion channels from water-soluble α -helical barrels. *Nature chemistry*, 13(7), 643.

Dick SD, et al. (2020) Structural Basis for the Activation and Target Site Specificity of CDC7 Kinase. *Structure (London, England : 1993)*, 28(8), 954.

Harvey EP, et al. (2020) Identification of a Covalent Molecular Inhibitor of Anti-apoptotic BFL-1 by Disulfide Tethering. *Cell chemical biology*, 27(6), 647.

Dong C, et al. (2020) Structural Basis for the Binding Selectivity of Human CDY Chromodomains. *Cell chemical biology*, 27(7), 827.

Rozbesky D, et al. (2020) Drosophila OTK Is a Glycosaminoglycan-Binding Protein with High Conformational Flexibility. *Structure (London, England : 1993)*, 28(5), 507.

Butt BG, et al. (2020) Non-native fold of the putative VPS39 zinc finger domain. *Wellcome open research*, 5, 154.

Ben-Nun Y, et al. (2020) Identification of a Structural Determinant for Selective Targeting of HDMX. *Structure (London, England : 1993)*, 28(7), 847.

Yuan M, et al. (2019) Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. *Cell host & microbe*, 25(6), 873.

Landry AP, et al. (2019) A Catalytic Trisulfide in Human Sulfide Quinone Oxidoreductase Catalyzes Coenzyme A Persulfide Synthesis and Inhibits Butyrate Oxidation. *Cell chemical biology*, 26(11), 1515.