

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 29, 2026

BioXTAS RAW

RRID:SCR_025769

Type: Tool

Proper Citation

BioXTAS RAW (RRID:SCR_025769)

Resource Information

URL: <https://bioxtas-raw.readthedocs.io/en/latest/>

Proper Citation: BioXTAS RAW (RRID:SCR_025769)

Description: Software tool as GUI based Python program for reduction and analysis of small-angle X-ray solution scattering (SAXS) data. Small-angle scattering data reduction and analysis. Available on Windows, macOS (and OS X), and Linux.

Synonyms: BioXTAS RAW 2

Resource Type: software application, software resource

Defining Citation: [PMID:29021737](#), [PMID:38322719](#)

Keywords: reduction and analysis of small-angle X-ray solution scattering data, small-angle X-ray solution scattering data,

Funding: US Department of Energy ;
NIGMS P30 GM138395

Availability: Free, Freely available,

Resource Name: BioXTAS RAW

Resource ID: SCR_025769

License: GNU GPL v3

Record Creation Time: 20240920T053257+0000

Record Last Update: 20260727T040844+0000

Ratings and Alerts

No rating or validation information has been found for BioXTAS RAW.

No alerts have been found for BioXTAS RAW.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 63 mentions in open access literature.

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

Ma E, et al. (2025) A large C-terminal Rad52 segment acts as a chaperone to Form and Stabilize Rad51 Filaments. Nature communications, 16(1), 5589.

Bandekar SJ, et al. (2025) Structural basis for regulation of CELSR1 by a compact module in its extracellular region. Nature communications, 16(1), 3972.

Wang T, et al. (2025) Nucleotide-specific RNA conformations and dynamics within ribonucleoprotein condensates. bioRxiv : the preprint server for biology.

Yun MK, et al. (2025) Isoleucine Binding and Regulation of Escherichia coli and Staphylococcus aureus Threonine Dehydratase (IlvA). Biochemistry, 64(13), 2793.

Malard F, et al. (2025) Molecular basis for the calcium-dependent activation of the ribonuclease EndoU. Nature communications, 16(1), 3110.

Ramírez-Larrota JS, et al. (2025) Biochemical and structural characterization of the human gut microbiome metallopeptidase IgAse provides insight into its unique specificity for the Fab' region of IgA1 and IgA2. PLoS pathogens, 21(7), e1013292.

Baral R, et al. (2025) A general mechanism for initiating the bacterial general stress response. eLife, 13.

Li T, et al. (2025) Crystal structure of Isthmin-1 and reassessment of its functional role in pre-adipocyte signaling. Nature communications, 16(1), 3580.

Petrova ZO, et al. (2025) The role of kinase domain dimerization in EGFR activation. Structure (London, England : 1993).

Dao TP, et al. (2024) Short disordered termini and proline-rich domain are major regulators of UBQLN1/2/4 phase separation. Biophysical journal, 123(11), 1449.

Grosjean N, et al. (2024) A hemoprotein with a zinc-mirror heme site ties heme availability to carbon metabolism in cyanobacteria. Nature communications, 15(1), 3167.

Pérez-Jover I, et al. (2024) Allosteric control of dynamin-related protein 1 through a disordered C-terminal Short Linear Motif. Nature communications, 15(1), 52.

Ostan NKH, et al. (2024) A secreted bacterial protein protects bacteria from cationic antimicrobial peptides by entrapment in phase-separated droplets. PNAS nexus, 3(4), pgae139.

Wang H, et al. (2024) Structural basis for antibody-mediated NMDA receptor clustering and endocytosis in autoimmune encephalitis. Nature structural & molecular biology, 31(12), 1987.

Koduru T, et al. (2024) A molten globule ensemble primes Arf1-GDP for the nucleotide switch. Proceedings of the National Academy of Sciences of the United States of America, 121(39), e2413100121.

Ravala SK, et al. (2024) Structural and dynamic changes in P-Rex1 upon activation by PIP3 and inhibition by IP4. eLife, 12.

Sanchez-Martinez S, et al. (2024) Labile assembly of a tardigrade protein induces biostasis. Protein science : a publication of the Protein Society, 33(4), e4941.

Priest JM, et al. (2024) Structural insights into the formation of repulsive netrin guidance complexes. Science advances, 10(7), eadj8083.

Yang CY, et al. (2024) Reverse hierarchical DED assembly in the cFLIP-procaspase-8 and cFLIP-procaspase-8-FADD complexes. Nature communications, 15(1), 8974.

Malard F, et al. (2024) Molecular Basis for the Calcium-Dependent Activation of the Ribonuclease EndoU. Research square.