

Resource Summary Report

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SCÅTTER

RRID:SCR_017271

Type: Tool

Proper Citation

SCÅTTER (RRID:SCR_017271)

Resource Information

URL: <http://www.bioisis.net>

Proper Citation: SCÅTTER (RRID:SCR_017271)

Description: Software JAVA based application for basic analysis of Small Angle X-ray Scattering datasets.

Resource Type: service resource, data access protocol, software resource, production service resource, web service, analysis service resource

Keywords: analysis, data, dataset, small, angle, X ray, scattering, SAXS, BIOISIS

Funding: Department of Energy Office of Science Integrated Diffraction Analysis Technologies ;
National Cancer Institute Structural Cell Biology of DNA Repair Machines ;
National Institute of General Medical Sciences project MINOS

Availability: Restricted

Resource Name: SCÅTTER

Resource ID: SCR_017271

Alternate URLs: <https://bl1231.als.lbl.gov/scatter/>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260729T044432+0000

Ratings and Alerts

No rating or validation information has been found for SCÅTTER.

No alerts have been found for SCÅTTER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Olp MD, et al. (2025) Multivalent nucleosome scaffolding by bromodomain and extraterminal domain tandem bromodomains. *The Journal of biological chemistry*, 301(3), 108289.

Rambo RP, et al. (2025) Information theory optimization of signals from small-angle scattering measurements. *Biophysical journal*, 124(15), 2511.

Brosey CA, et al. (2025) NADH-bound AIF activates the mitochondrial CHCHD4/MIA40 chaperone by a substrate-mimicry mechanism. *The EMBO journal*, 44(4), 1220.

Thamkachy R, et al. (2024) Structural basis for Mis18 complex assembly and its implications for centromere maintenance. *EMBO reports*, 25(8), 3348.

Jones BE, et al. (2024) Developing an in situ LED irradiation system for small-angle X-ray scattering at B21, Diamond Light Source. *Journal of synchrotron radiation*, 31(Pt 4), 763.

Kaundal S, et al. (2024) RNA-dependent RNA polymerase of predominant human norovirus forms liquid-liquid phase condensates as viral replication factories. *Science advances*, 10(51), eadp9333.

Gurusaran M, et al. (2024) The crystal structure of SUN1-KASH6 reveals an asymmetric LINC complex architecture compatible with nuclear membrane insertion. *Communications biology*, 7(1), 138.

Bianco S, et al. (2024) Mechanical release of homogenous proteins from supramolecular gels. *Nature*, 631(8021), 544.

Murray DT, et al. (2024) Correlating Conformational Equilibria with Catalysis in the Electron Bifurcating EtfABCX of *Thermotoga maritima*. *Biochemistry*, 63(1), 128.

Vieira MFM, et al. (2024) The pathogen-encoded signalling receptor Tir exploits host-like intrinsic disorder for infection. *Communications biology*, 7(1), 179.

Brosey CA, et al. (2024) Chemical screening by time-resolved X-ray scattering to discover allosteric probes. *Nature chemical biology*, 20(9), 1199.

Dunce JM, et al. (2024) BRCA2 stabilises RAD51 and DMC1 nucleoprotein filaments through a conserved interaction mode. *Nature communications*, 15(1), 8292.

Iqbal H, et al. (2023) A solution structure analysis reveals a bent collagen triple helix in the complement activation recognition molecule mannan-binding lectin. *The Journal of*

biological chemistry, 299(2), 102799.

Macdonald R, et al. (2023) The Shr receptor from *Streptococcus pyogenes* uses a cap and release mechanism to acquire heme-iron from human hemoglobin. *Proceedings of the National Academy of Sciences of the United States of America*, 120(5), e2211939120.

Petrvalska O, et al. (2023) 14-3-3 protein inhibits CaMKK1 by blocking the kinase active site with its last two C-terminal helices. *Protein science : a publication of the Protein Society*, 32(11), e4805.

Stelfox AJ, et al. (2023) Crystal structure and solution state of the C-terminal head region of the narxovirus receptor binding protein. *mBio*, 14(5), e0139123.

Motycka B, et al. (2023) Amino Acid Residues Controlling Domain Interaction and Interdomain Electron Transfer in Cellobiose Dehydrogenase. *Chembiochem : a European journal of chemical biology*, 24(22), e202300431.

Crichton JH, et al. (2023) Structural maturation of SYCP1-mediated meiotic chromosome synapsis by SYCE3. *Nature structural & molecular biology*, 30(2), 188.

Cuesta-Hernández HN, et al. (2023) An allosteric switch between the activation loop and a c-terminal palindromic phospho-motif controls c-Src function. *Nature communications*, 14(1), 6548.

Gurusaran M, et al. (2023) Molecular insights into LINC complex architecture through the crystal structure of a luminal trimeric coiled-coil domain of SUN1. *Frontiers in cell and developmental biology*, 11, 1144277.