Resource Summary Report

Generated by NIF on May 4, 2025

FoXS

RRID:SCR_017269
Type: Tool

Proper Citation

FoXS (RRID:SCR_017269)

Resource Information

URL: https://modbase.compbio.ucsf.edu/foxs/

Proper Citation: FoXS (RRID:SCR_017269)

Description: Web server for computing theoretical scattering profile of structure and fitting of experimental profile. Computes SAXS profile of given atomistic model and fits it to experimental profile. Used for structural modeling applications with small angle X-ray scattering data.

Synonyms: Fast X-Ray Scattering

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

Defining Citation: PMID:23972848, PMID:27151198

Keywords: computing, theoretical, scattering, profile, structure, fitting, small, angle, X ray, data

Funding: Weizmann Institute Advancing Women in Science ;
NIGMS R01 GM083960;
NCRR U54 RR022220;
NIGMS R01 GM105404;
Rinat (Pfizer) Inc. ;
Lawrence Berkeley National Lab IDAT program ;
NIGMS P41 GM109824

Availability: Free, Available for download, Freely available

Resource Name: FoXS

Resource ID: SCR_017269

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250503T060707+0000

Ratings and Alerts

No rating or validation information has been found for FoXS.

No alerts have been found for FoXS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Trewhella J, et al. (2024) Benchmarking predictive methods for small-angle X-ray scattering from atomic coordinates of proteins using maximum likelihood consensus data. IUCrJ, 11(Pt 5), 762.

Burchert JP, et al. (2023) A small-angle X-ray scattering study of red blood cells in continuous flow. Journal of synchrotron radiation, 30(Pt 3), 582.

Bermeo S, et al. (2022) De novo design of obligate ABC-type heterotrimeric proteins. Nature structural & molecular biology, 29(12), 1266.

Trewhella J, et al. (2022) A round-robin approach provides a detailed assessment of biomolecular small-angle scattering data reproducibility and yields consensus curves for benchmarking. Acta crystallographica. Section D, Structural biology, 78(Pt 11), 1315.

Xia C, et al. (2021) Molecular mechanism of interactions between ACAD9 and binding partners in mitochondrial respiratory complex I assembly. iScience, 24(10), 103153.

Garcia-Rodriguez G, et al. (2021) Alternative dimerization is required for activity and inhibition of the HEPN ribonuclease RnlA. Nucleic acids research, 49(12), 7164.

Chesterman C, et al. (2021) Co-crystallization with diabodies: A case study for the introduction of synthetic symmetry. Structure (London, England : 1993), 29(6), 598.

Alam J, et al. (2021) Expression and analysis of the SAM-dependent RNA methyltransferase Rsm22 from Saccharomyces cerevisiae. Acta crystallographica. Section D, Structural biology, 77(Pt 6), 840.

Azmi L, et al. (2020) High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. Acta crystallographica. Section F, Structural biology communications, 76(Pt 9), 414.

Wei KY, et al. (2020) Computational design of closely related proteins that adopt two well-defined but structurally divergent folds. Proceedings of the National Academy of Sciences of the United States of America, 117(13), 7208.

Niazi M, et al. (2020) Biophysical analysis of Pseudomonas-phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. Nucleic acids research, 48(20), 11721.

Bochel AJ, et al. (2020) Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7-11 Uncovers the Mannose 6-Phosphate Binding Site of Domain 9. Structure (London, England : 1993), 28(12), 1300.

Gersch M, et al. (2019) Distinct USP25 and USP28 Oligomerization States Regulate Deubiquitinating Activity. Molecular cell, 74(3), 436.

Gabrielsen M, et al. (2019) Identification and Characterization of Mutations in Ubiquitin Required for Non-covalent Dimer Formation. Structure (London, England : 1993), 27(9), 1452.

Zhou Y, et al. (2019) Flexible Tethering of ASPP Proteins Facilitates PP-1c Catalysis. Structure (London, England : 1993), 27(10), 1485.

Yamagami R, et al. (2018) Cellular conditions of weakly chelated magnesium ions strongly promote RNA stability and catalysis. Nature communications, 9(1), 2149.

Harrer N, et al. (2018) Structural Architecture of the Nucleosome Remodeler ISWI Determined from Cross-Linking, Mass Spectrometry, SAXS, and Modeling. Structure (London, England : 1993), 26(2), 282.