

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

MeroX

RRID:SCR_014956

Type: Tool

Proper Citation

MeroX (RRID:SCR_014956)

Resource Information

URL: <http://www.stavroX.com>

Proper Citation: MeroX (RRID:SCR_014956)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on June 29,2023. Software tool for the analysis of cross-linking/mass spectrometry datasets using MS-cleavable cross-linkers. MeroX is specialized for MS/MS-cleavable cross linking reagents and identifies the specific fragmentation products of the cleavable cross links.

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

Defining Citation: [PMID:25261217](#)

Keywords: sequence analysis software, cross linking, mass spectrometry, MS cleavage, fragmentation, cleavable cross link, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MeroX

Resource ID: SCR_014956

Alternate IDs: BioTools:MeroX, biotools:MeroX

Alternate URLs: <https://bio.tools/MeroX>, <https://bio.tools/MeroX>, <https://bio.tools/MeroX>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260905T132752+0000

Ratings and Alerts

No rating or validation information has been found for MeroX.

No alerts have been found for MeroX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 74 mentions in open access literature.

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

Chen S, et al. (2025) Quantitative Glycan-Protein Cross-Linking Mass Spectrometry Using Enrichable Linkers Reveals Extensive Glycan-Mediated Protein Interaction Networks. *Analytical chemistry*, 97(3), 1584.

Dolles S, et al. (2025) Versatile Features of an Antibody Mimetic Peptide and Its Variants. *Journal of peptide science : an official publication of the European Peptide Society*, 31(3), e70005.

Planelles-Herrero VJ, et al. (2025) Elongator is a microtubule polymerase selective for polyglutamylated tubulin. *The EMBO journal*, 44(5), 1322.

McMillan SN, et al. (2025) Mavacamten inhibits myosin activity by stabilising the myosin interacting-heads motif and stalling motor force generation. *bioRxiv : the preprint server for biology*.

Hassan AH, et al. (2025) Novel archaeal ribosome dimerization factor facilitating unique 30S-30S dimerization. *Nucleic acids research*, 53(2).

Carrington G, et al. (2024) A multiscale approach reveals the molecular architecture of the autoinhibited kinesin KIF5A. *The Journal of biological chemistry*, 300(3), 105713.

Koszela J, et al. (2024) A substrate-interacting region of Parkin directs ubiquitination of the mitochondrial GTPase Miro1. *bioRxiv : the preprint server for biology*.

Hu H, et al. (2024) Spatiotemporal and direct capturing global substrates of lysine-modifying enzymes in living cells. *Nature communications*, 15(1), 1465.

Clasen MA, et al. (2024) Proteome-scale recombinant standards and a robust high-speed search engine to advance cross-linking MS-based interactomics. *Nature methods*, 21(12), 2327.

Dhillon A, et al. (2024) Structural insights into the interaction between adenovirus C5 hexon and human lactoferrin. *Journal of virology*, 98(3), e0157623.

Birklbauer MJ, et al. (2024) Proteome-wide non-cleavable crosslink identification with MS Annika 3.0 reveals the structure of the *C. elegans* Box C/D complex. *Communications*

chemistry, 7(1), 300.

Rojas Echeverri JC, et al. (2024) A Workflow for Improved Analysis of Cross-Linking Mass Spectrometry Data Integrating Parallel Accumulation-Serial Fragmentation with MeroX and Skyline. *Analytical chemistry*, 96(19), 7373.

Tomaszewski KL, et al. (2024) Enhanced Staphylococcus aureus protection by uncoupling of the α -toxin-ADAM10 interaction during murine neonatal vaccination. *Nature communications*, 15(1), 8702.

Vermeire PJ, et al. (2023) Molecular structure of soluble vimentin tetramers. *Scientific reports*, 13(1), 8841.

Huang P, et al. (2023) The intracellular helical bundle of human glucose transporter GLUT4 is important for complex formation with ASPL. *FEBS open bio*, 13(11), 2094.

Di Ianni A, et al. (2023) Structural assessment of the full-length wild-type tumor suppressor protein p53 by mass spectrometry-guided computational modeling. *Scientific reports*, 13(1), 8497.

Meng Y, et al. (2023) Phosphorylation-dependent pseudokinase domain dimerization drives full-length MLKL oligomerization. *Nature communications*, 14(1), 6804.

Franco-Echevarría E, et al. (2023) Distinct accessory roles of Arabidopsis VEL proteins in Polycomb silencing. *Genes & development*, 37(17-18), 801.

Wu CG, et al. (2023) Extended regulation interface coupled to the allosteric network and disease mutations in the PP2A-B56 γ holoenzyme. *bioRxiv : the preprint server for biology*.

Hassan AH, et al. (2023) The structural principles underlying molybdenum insertase complex assembly. *Protein science : a publication of the Protein Society*, 32(9), e4753.