

Resource Summary Report

Generated by [T1D](#) on Aug 2, 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, software application, software resource, sequence analysis software, data processing software

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: 20260801T190511+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 [T1D](#).

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.

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.

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.

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.

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

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.

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.

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

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