Resource Summary Report

Generated by NIF on May 15, 2025

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

Defining Citation: PMID:25261217

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

Funding:

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: 20250514T061701+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 71 mentions in open access literature.

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

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.

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.

Tomaszewski KL, et al. (2024) Enhanced Staphylococcus aureus protection by uncoupling of the ?-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.

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.

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.

Wu CG, et al. (2023) Extended regulation interface coupled to the allosteric network and disease mutations in the PP2A-B56? 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.

Felker D, et al. (2023) Mapping interactions of calmodulin and neuronal NO synthase by crosslinking and mass spectrometry. The Journal of biological chemistry, 300(1), 105464.

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

Boegholm N, et al. (2023) The IFT81-IFT74 complex acts as an unconventional RabL2 GTPase-activating protein during intraflagellar transport. The EMBO journal, 42(18), e111807.

Koutná E, et al. (2023) Multivalency of nucleosome recognition by LEDGF. Nucleic acids research, 51(18), 10011.