

Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

xiSEARCH

RRID:SCR_018395

Type: Tool

Proper Citation

xiSEARCH (RRID:SCR_018395)

Resource Information

URL: <https://www.rappsilberlab.org/software/xisearch/>

Proper Citation: xiSEARCH (RRID:SCR_018395)

Description: Software and algorithm for analyzing protein protein cross linking mass spectrometry data. Library of routines for peptide based mass spectrometry. Contains search engine for identification of crosslinked peptides.

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

Defining Citation: [PMID:26719564](#)

Keywords: Protein analysis, mass spectrometry, protein cross linking, XL-MS, cross-linking mass spectrometry, data analysis, peptide mass spectrometry, crosslinked peptide identification

Funding: Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: xiSEARCH

Resource ID: SCR_018395

Alternate URLs: <https://github.com/Rappsilber-Laboratory/xisearch>

License: Apache License 2.0

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260729T044445+0000

Ratings and Alerts

No rating or validation information has been found for xiSEARCH.

No alerts have been found for xiSEARCH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Xia Y, et al. (2025) Phosphoglycerate Kinase Can Adopt a Topologically Misfolded Form that is More Stable than its Native State. bioRxiv : the preprint server for biology.

Ciancone A, et al. (2025) Expanding the Crosslinking Mass Spectrometry Toolbox With Vinyl Sulfone Crosslinkers. Molecular & cellular proteomics : MCP, 24(12), 101315.

Gireesh A, et al. (2025) Nucleosome interaction of the CPC secures centromeric chromatin integrity and chromosome segregation fidelity. The EMBO journal, 44(22), 6556.

Wang M, et al. (2025) Molecular mechanism targeting condensin for chromosome condensation. The EMBO journal, 44(3), 705.

Horne CR, et al. (2025) Unconventional binding of calmodulin to CHK2 kinase inhibits catalytic activity. The Biochemical journal, 482(23), 1759.

Tan W, et al. (2025) MORC2 is a phosphorylation-dependent DNA compaction machine. Nature communications, 16(1), 5606.

Yu J, et al. (2025) Substrate recognition by human separase. Science advances, 11(46), eady9807.

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

Kwiatkowski A, et al. (2024) ATP-Triggered Fe(CN)₂CO Synthon Transfer from the Maturase HypCD to the Active Site of Apo-[NiFe]-Hydrogenase. Journal of the American Chemical Society, 146(45), 30976.

Stankunas E, et al. (2024) Docking a flexible basket onto the core of the nuclear pore complex. Nature cell biology, 26(9), 1504.

Fischer L, et al. (2024) Rescuing error control in crosslinking mass spectrometry. Molecular systems biology, 20(9), 1076.

Absmeier E, et al. (2023) Specific recognition and ubiquitination of translating ribosomes by mammalian CCR4-NOT. *Nature structural & molecular biology*, 30(9), 1314.

Flacht L, et al. (2023) Integrative structural analysis of the type III secretion system needle complex from *Shigella flexneri*. *Protein science : a publication of the Protein Society*, 32(4), e4595.

Tremel S, et al. (2021) Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. *Nature communications*, 12(1), 1564.

Rodriguez Carvajal A, et al. (2021) The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. *eLife*, 10.

Lenz S, et al. (2021) Reliable identification of protein-protein interactions by crosslinking mass spectrometry. *Nature communications*, 12(1), 3564.

Rose J, et al. (2021) The functionality of plant mechanoproteins (forisomes) is dependent on the dual role of conserved cysteine residues. *International journal of biological macromolecules*, 193(Pt B), 1332.

Higashi TL, et al. (2020) A Structure-Based Mechanism for DNA Entry into the Cohesin Ring. *Molecular cell*, 79(6), 917.

Alc??n P, et al. (2020) FANCD2-FANCI is a clamp stabilized on DNA by monoubiquitination of FANCD2 during DNA repair. *Nature structural & molecular biology*, 27(3), 240.

Ahel J, et al. (2020) Moyamoya disease factor RNF213 is a giant E3 ligase with a dynein-like core and a distinct ubiquitin-transfer mechanism. *eLife*, 9.