

Resource Summary Report

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

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: 20260821T194132+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 25 mentions in open access literature.

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

Trendel J, et al. (2026) Rapid photo-crosslinking in living cells reveals protein-nucleic acid dynamics on a timescale of minutes. *Nucleic acids research*, 54(7).

Abelenda JA, et al. (2026) The chromatin reader MBD4 regulates temperature- and flowering-responsive transcription by recognizing histone arginine methylation. *Plant communications*, 7(6), 101869.

Stowell JAW, et al. (2026) Phosphorylation-dependent tuning of mRNA deadenylation rates. *Nature structural & molecular biology*, 33(1), 63.

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.