

Resource Summary Report

Generated by SPARC SAWG on Aug 29, 2026

xiNET

RRID:SCR_021010

Type: Tool

Proper Citation

xiNET (RRID:SCR_021010)

Resource Information

URL: <http://crosslinkviewer.org/>

Proper Citation: xiNET (RRID:SCR_021010)

Description: Open source web based visualization tool for exploring crosslinking mass spectrometry results. Displays residue resolution positional information including linkage sites and linked peptides, all types of crosslinking reaction product, ambiguous results and additional sequence information such as domains.

Synonyms: Crosslink Network Maps With Residue Resolution

Resource Type: data access protocol, data processing software, data visualization software, software application, software resource, web service

Defining Citation: [PMID:25648531](#)

Keywords: Crosslinking mass spectrometry data visualization, linkage sites, linked peptides, crosslinking reaction product display, crosslink network maps, maps with residue resolution

Funding: Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: xiNET

Resource ID: SCR_021010

Alternate URLs: <http://github.com/colin-combe/crosslink-viewer>

License: Apache v2

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260821T194148+0000

Ratings and Alerts

No rating or validation information has been found for xiNET.

No alerts have been found for xiNET.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Dunshee EB, et al. (2026) Human pumilio proteins use fuzzy multivalent hydrophobic interactions to recruit the CCR4-NOT deadenylase complex to repress mRNAs. The Journal of biological chemistry, 302(4), 111281.

Rawlinson SM, et al. (2025) Conformational dynamics, RNA binding, and phase separation regulate the multifunctionality of rabies virus P protein. Nature communications, 16(1), 9491.

Wydorski PM, et al. (2025) DnaJB1 chaperone inhibits tau aggregation by recognizing its N-terminus. bioRxiv : the preprint server for biology.

Dunshee EB, et al. (2025) Human Pumilio proteins use fuzzy multivalent hydrophobic interactions to recruit the CCR4-NOT deadenylase complex to repress mRNAs. bioRxiv : the preprint server for biology.

Chen K, et al. (2024) Structure of the human TIP60 complex. Nature communications, 15(1), 7092.

Horn-Ghetko D, et al. (2024) Noncanonical assembly, neddylation and chimeric cullin-RING/RBR ubiquitylation by the 1.8 MDa CUL9 E3 ligase complex. Nature structural & molecular biology, 31(7), 1083.

Wasmuth EV, et al. (2022) Allosteric interactions prime androgen receptor dimerization and activation. Molecular cell, 82(11), 2021.

Sailer C, et al. (2022) A comprehensive landscape of 60S ribosome biogenesis factors. Cell reports, 38(6), 110353.

Rafiei A, et al. (2022) Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain. eLife, 11.

Jenner A, et al. (2022) DRP1 interacts directly with BAX to induce its activation and apoptosis. The EMBO journal, 41(8), e108587.

Zhong Y, et al. (2022) The role of auxiliary domains in modulating CHD4 activity suggests mechanistic commonality between enzyme families. *Nature communications*, 13(1), 7524.

Roverato ND, et al. (2021) Parkin is an E3 ligase for the ubiquitin-like modifier FAT10, which inhibits Parkin activation and mitophagy. *Cell reports*, 34(11), 108857.

Moysa A, et al. (2021) A model of full-length RAGE in complex with S100B. *Structure (London, England : 1993)*, 29(9), 989.

Boczek EE, et al. (2021) HspB8 prevents aberrant phase transitions of FUS by chaperoning its folded RNA-binding domain. *eLife*, 10.

Ludzia P, et al. (2021) Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. *Structure (London, England : 1993)*, 29(9), 1014.

Gutierrez C, et al. (2021) Enabling Photoactivated Cross-Linking Mass Spectrometric Analysis of Protein Complexes by Novel MS-Cleavable Cross-Linkers. *Molecular & cellular proteomics : MCP*, 20, 100084.

Huang B, et al. (2021) Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. *Structure (London, England : 1993)*, 29(8), 804.

Azar DF, et al. (2020) Vaccinia Virus Immunomodulator A46: Destructive Interactions with MAL and MyD88 Shown by Negative-Stain Electron Microscopy. *Structure (London, England : 1993)*, 28(12), 1271.

Offensperger F, et al. (2020) Identification of Small-Molecule Activators of the Ubiquitin Ligase E6AP/UBE3A and Angelman Syndrome-Derived E6AP/UBE3A Variants. *Cell chemical biology*, 27(12), 1510.

Gamerding M, et al. (2019) Early Scanning of Nascent Polypeptides inside the Ribosomal Tunnel by NAC. *Molecular cell*, 75(5), 996.