A high-speed search engine pLink 2 with systematic evaluentification of cross-linked peptides

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Citation Report

#	Article	IF	CITATIONS
1	Discovery of Interacting Proteins of ABA Receptor PYL5 via Covalent Chemical Capture. ACS Chemical Biology, 2019, 14, 2557-2563.	3 <b>.</b> 4	3
2	Insights into the assembly and architecture of a Staufen-mediated mRNA decay (SMD)-competent mRNP. Nature Communications, 2019, 10, 5054.	12.8	27
3	An integrated workflow for crosslinking mass spectrometry. Molecular Systems Biology, 2019, 15, e8994.	7.2	120
4	Improving mass spectrometry analysis of protein structures with arginine-selective chemical cross-linkers. Nature Communications, 2019, 10, 3911.	12.8	45
5	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein–Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. Analytical Chemistry, 2020, 92, 1874-1882.	6.5	20
6	Smart Cutter: An Efficient Strategy for Increasing the Coverage of Chemical Cross-Linking Analysis. Analytical Chemistry, 2020, 92, 1097-1105.	6.5	6
7	To Cleave or Not To Cleave in XL-MS?. Journal of the American Society for Mass Spectrometry, 2020, 31, 196-206.	2.8	60
8	Structural Insights into the Roles of Metazoan-Specific Splicing Factors in the Human Step 1 Spliceosome. Molecular Cell, 2020, 80, 127-139.e6.	9.7	26
9	Vaccinia Virus Immunomodulator A46: Destructive Interactions with MAL and MyD88 Shown by Negative-Stain Electron Microscopy. Structure, 2020, 28, 1271-1287.e5.	3.3	5
10	Dimerization regulates the human APC/C-associated ubiquitin-conjugating enzyme UBE2S. Science Signaling, 2020, 13, .	3.6	12
11	Mapping the native interaction surfaces of PREP1 with PBX1 by cross-linking mass-spectrometry and mutagenesis. Scientific Reports, 2020, 10, 16809.	3.3	9
12	Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. Nature Methods, 2020, 17, 985-988.	19.0	23
13	DNA Binding Reorganizes the Intrinsically Disordered C-Terminal Region of PSC in Drosophila PRC1. Journal of Molecular Biology, 2020, 432, 4856-4871.	4.2	6
14	Structural snapshots of human pre-60S ribosomal particles before and after nuclear export. Nature Communications, 2020, 11, 3542.	12.8	44
15	Mechanism of protein-guided folding of the active site U2/U6 RNA during spliceosome activation. Science, 2020, 370, .	12.6	50
16	Integrated Structural Modeling of Full-Length LRH-1 Reveals Inter-domain Interactions Contribute to Receptor Structure and Function. Structure, 2020, 28, 830-846.e9.	3.3	22
17	Decision Tree Searching Strategy to Boost the Identification of Cross-Linked Peptides. Analytical Chemistry, 2020, 92, 13702-13710.	6.5	3
18	Structure of the human sodium leak channel NALCN in complex with FAM155A. Nature Communications, 2020, 11, 5831.	12.8	24

#	Article	IF	CITATIONS
19	Generation of Aggregates of $\hat{l}$ ±-Lactalbumin by UV-B Light Exposure. Journal of Agricultural and Food Chemistry, 2020, 68, 6701-6714.	5.2	21
20	Molecular architecture of the human 17S U2 snRNP. Nature, 2020, 583, 310-313.	27.8	63
21	Identification of Sulfenylated Cysteines in Arabidopsis thaliana Proteins Using a Disulfide-Linked Peptide Reporter. Frontiers in Plant Science, 2020, 11, 777.	3.6	31
22	Harmonizing structural mass spectrometry analyses in the mass spec studio. Journal of Proteomics, 2020, 225, 103844.	2.4	7
23	Structure of complete Pol II–DSIF–PAF–SPT6 transcription complex reveals RTF1 allosteric activation. Nature Structural and Molecular Biology, 2020, 27, 668-677.	8.2	98
24	Use of Multiple Ion Fragmentation Methods to Identify Protein Cross-Links and Facilitate Comparison of Data Interpretation Algorithms. Journal of Proteome Research, 2020, 19, 2758-2771.	3.7	3
25	Expanding the Depth and Sensitivity of Cross-Link Identification by Differential Ion Mobility Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. Analytical Chemistry, 2020, 92, 10495-10503.	6.5	32
26	Structural basis of human full-length kindlin-3 homotrimer in an auto-inhibited state. PLoS Biology, 2020, 18, e3000755.	5.6	26
27	Rett syndrome-causing mutations compromise MeCP2-mediated liquid–liquid phase separation of chromatin. Cell Research, 2020, 30, 393-407.	12.0	80
28	A synthetic peptide library for benchmarking crosslinking-mass spectrometry search engines for proteins and protein complexes. Nature Communications, 2020, 11, 742.	12.8	62
29	Structure of the transcription coactivator SAGA. Nature, 2020, 577, 717-720.	27.8	112
30	Evidence of Allosteric Coupling between Substrate Binding and Adx Recognition in the Vitamin D Carbon-24 Hydroxylase CYP24A1. Biochemistry, 2020, 59, 1537-1548.	2.5	11
31	Molecular Topology of RNA Polymerase I Upstream Activation Factor. Molecular and Cellular Biology, 2020, 40, .	2.3	8
32	An experimentally generated peptide database increases the sensitivity of XL-MS with complex samples. Journal of Proteomics, 2020, 220, 103754.	2.4	5
33	Cleavable Cross-Linkers and Mass Spectrometry for the Ultimate Task of Profiling Protein–Protein Interaction Networks <i>in Vivo</i> . Journal of Proteome Research, 2021, 20, 78-93.	3.7	55
34	A composite filter for low FDR of protein-protein interactions detected by in vivo cross-linking. Journal of Proteomics, 2021, 230, 103987.	2.4	11
35	Pre-termination Transcription Complex: Structure and Function. Molecular Cell, 2021, 81, 281-292.e8.	9.7	62
36	Affinity and chemical enrichment strategies for mapping lowâ€abundance protein modifications and proteinâ€interaction networks. Journal of Separation Science, 2021, 44, 310-322.	2.5	6

#	Article	IF	CITATIONS
37	Defining the architecture of the human TIM22 complex by chemical crosslinking. FEBS Letters, 2021, 595, 157-168.	2.8	7
39	Selective crossâ€linking of coinciding protein assemblies by inâ€gel crossâ€linking mass spectrometry. EMBO Journal, 2021, 40, e106174.	7.8	32
40	Unraveling the surface glycoprotein interaction network by integrating chemical crosslinking with MS-based proteomics. Chemical Science, 2021, 12, 2146-2155.	7.4	10
41	Glycan–protein cross-linking mass spectrometry reveals sialic acid-mediated protein networks on cell surfaces. Chemical Science, 2021, 12, 8767-8777.	7.4	14
42	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. Nature Communications, 2021, 12, 502.	12.8	307
43	Identification of Native Cross-Links in <i>Bacillus subtilis</i> Proteome Research, 2021, 20, 1809-1816.	3.7	9
44	Proteomic characterization of the human lens and Cataractogenesis. Expert Review of Proteomics, 2021, 18, 119-135.	3.0	8
46	Molecular architecture of the endocytic TPLATE complex. Science Advances, 2021, 7, .	10.3	31
48	Cryo-EM structure of the yeast TREX complex and coordination with the SR-like protein Gbp2. ELife, 2021, 10, .	6.0	20
50	Automated error log resolution. , 2021, , .		1
51	Interfaces with Structure Dynamics of the Workhorses from Cells Revealed through Cross-Linking Mass Spectrometry (CLMS). Biomolecules, 2021, 11, 382.	4.0	8
52	LinX: A Software Tool for Uncommon Cross-Linking Chemistry. Journal of Proteome Research, 2021, 20, 2021-2027.	3.7	5
53	Integrative proteomics identifies thousands of distinct, multi-epitope, and high-affinity nanobodies. Cell Systems, 2021, 12, 220-234.e9.	6.2	38
54	The structure of a virus-encoded nucleosome. Nature Structural and Molecular Biology, 2021, 28, 413-417.	8.2	40
56	Structural insights into preinitiation complex assembly on core promoters. Science, 2021, 372, .	12.6	104
57	pDeepXL: MS/MS Spectrum Prediction for Cross-Linked Peptide Pairs by Deep Learning. Journal of Proteome Research, 2021, 20, 2570-2582.	3.7	4
58	MS Annika: A New Cross-Linking Search Engine. Journal of Proteome Research, 2021, 20, 2560-2569.	3.7	26
60	Structures of the human Mediator and Mediator-bound preinitiation complex. Science, 2021, 372, .	12.6	85

#	ARTICLE	IF	CITATIONS
61	Recent progress in mass spectrometry-based strategies for elucidating protein–protein interactions. Cellular and Molecular Life Sciences, 2021, 78, 5325-5339.	5.4	53
62	Repurposing of synaptonemal complex proteins for kinetochores in Kinetoplastida. Open Biology, 2021, 11, 210049.	3.6	28
63	Retention time prediction using neural networks increases identifications in crosslinking mass spectrometry. Nature Communications, 2021, 12, 3237.	12.8	22
64	Ribosome-Amplified Metabolism, RAMBO, Measured by NMR Spectroscopy. Biochemistry, 2021, 60, 1885-1895.	2.5	2
65	Chemical Synthesis of Activityâ€Based E2â€Ubiquitin Probes for the Structural Analysis of E3 Ligaseâ€Catalyzed Transthiolation. Angewandte Chemie - International Edition, 2021, 60, 17171-17177.	13.8	46
66	HSP-90/kinase complexes are stabilized by the large PPIase FKB-6. Scientific Reports, 2021, 11, 12347.	3.3	4
67	Reliable identification of protein-protein interactions by crosslinking mass spectrometry. Nature Communications, 2021, 12, 3564.	12.8	69
68	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. MBio, 2021, 12, e0142321.	4.1	20
69	The Odorant-Binding Proteins of the Spider Mite Tetranychus urticae. International Journal of Molecular Sciences, 2021, 22, 6828.	4.1	7
70	A new non-classical fold of varroa odorant-binding proteins reveals a wide open internal cavity. Scientific Reports, 2021, 11, 13172.	3.3	4
71	Diethynyl Phosphinates for Cysteineâ€Selective Protein Labeling and Disulfide Rebridging. Angewandte Chemie - International Edition, 2021, 60, 15359-15364.	13.8	35
72	Diethinylphosphinate für die Cysteinâ€selektive Proteinmarkierung und Disulfidâ€Verbrückung. Angewandte Chemie, 2021, 133, 15487-15492.	2.0	2
73	Chemical Synthesis of Activityâ€Based E2â€Ubiquitin Probes for the Structural Analysis of E3 Ligaseâ€Catalyzed Transthiolation. Angewandte Chemie, 2021, 133, 17308-17314.	2.0	5
74	Large-scale ratcheting in a bacterial DEAH/RHA-type RNA helicase that modulates antibiotics susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	6
75	Crossâ€linking reactions in food proteins and proteomic approaches for their detection. Mass Spectrometry Reviews, 2022, 41, 861-898.	5.4	12
76	Accurate Retention Time Prediction Based on Monolinked Peptide Information to Confidently Identify Cross-Linked Peptides. Journal of the American Society for Mass Spectrometry, 2021, 32, 2410-2416.	2.8	1
77	Towards low false discovery rate estimation for protein-protein interactions detected by chemical cross-linking. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140655.	2.3	4
78	In-Cell Labeling and Mass Spectrometry for Systems-Level Structural Biology. Chemical Reviews, 2022, 122, 7647-7689.	47.7	17

#	Article	IF	Citations
79	Allosteric transcription stimulation by RNA polymerase II super elongation complex. Molecular Cell, 2021, 81, 3386-3399.e10.	9.7	17
80	New insights into the mechanisms of age-related protein-protein crosslinking in the human lens. Experimental Eye Research, 2021, 209, 108679.	2.6	4
81	Structural insights into how Prp5 proofreads the pre-mRNA branch site. Nature, 2021, 596, 296-300.	27.8	28
82	Synthesis, LC-MS/MS analysis, and biological evaluation of two vaccine candidates against ticks based on the antigenic PO peptide from R. sanguineus linked to the p64K carrier protein from Neisseria meningitidis. Analytical and Bioanalytical Chemistry, 2021, 413, 5885-5900.	3.7	3
83	Photo-activatable Ub-PCNA probes reveal new structural features of the <i>Saccharomyces cerevisiae</i> Polî-/PCNA complex. Nucleic Acids Research, 2021, 49, 9374-9388.	14.5	5
84	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. Chemical Reviews, 2022, 122, 7386-7414.	47.7	24
85	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. Structure, 2021, 29, 1014-1028.e8.	3.3	9
86	A resource of high-quality and versatile nanobodies for drug delivery. IScience, 2021, 24, 103014.	4.1	19
87	Basic pH reversed-phase liquid chromatography (bRPLC) in combination with tip-based strong cation exchange (SCX-Tip), ReST, an efficient approach for large-scale cross-linked peptide analysis. Analytica Chimica Acta, 2021, 1179, 338838.	5.4	7
88	Mapping protein interactions in the active TOM-TIM23 supercomplex. Nature Communications, 2021, 12, 5715.	12.8	28
89	Molecular characterization of a complex of apoptosis-inducing factor $1$ with cytochrome c oxidase of the mitochondrial respiratory chain. Proceedings of the National Academy of Sciences of the United States of America, 2021, $118$ , .	7.1	20
90	A novel recognition site for polyubiquitin and ubiquitin-like signals in an unexpected region of proteasomal subunit Rpn1. Journal of Biological Chemistry, 2021, 297, 101052.	3.4	8
91	Covalently Engineered Nanobody Chimeras for Targeted Membrane Protein Degradation. Journal of the American Chemical Society, 2021, 143, 16377-16382.	13.7	99
92	Spontaneous protein–protein crosslinking at glutamine and glutamic acid residues in long-lived proteins. Biochemical Journal, 2021, 478, 327-339.	3.7	5
94	Epitope and Paratope Mapping of PD-1/Nivolumab by Mass Spectrometry-Based Hydrogen–Deuterium Exchange, Cross-linking, and Molecular Docking. Analytical Chemistry, 2020, 92, 9086-9094.	6.5	38
95	Mechanism of protein cleavage at asparagine leading to protein–protein cross-links. Biochemical Journal, 2019, 476, 3817-3834.	3.7	22
96	FGF23 contains two distinct high-affinity binding sites enabling bivalent interactions with $\hat{l}\pm$ -Klotho. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31800-31807.	7.1	18
97	OpenPepXL: An Open-Source Tool for Sensitive Identification of Cross-Linked Peptides in XL-MS. Molecular and Cellular Proteomics, 2020, 19, 2157-2168.	3.8	10

#	Article	IF	CITATIONS
102	Discovery of a molecular glue promoting CDK12-DDB1 interaction to trigger cyclin K degradation. ELife, 2020, $9$ , .	6.0	114
104	Identifying and characterising Thrap3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. Wellcome Open Research, 0, 6, 260.	1.8	2
105	Structural basis of soluble membrane attack complex packaging for clearance. Nature Communications, 2021, 12, 6086.	12.8	18
107	Progress in methodologies and qualityâ€control strategies in protein crossâ€linking mass spectrometry. Proteomics, 2021, 21, e2100145.	2.2	5
115	Binding of cytochrome P450 27C1, a retinoid desaturase, to its accessory protein adrenodoxin. Archives of Biochemistry and Biophysics, 2021, 714, 109076.	3.0	7
116	Nematode CDC-37 and DNJ-13 form complexes and can interact with HSP-90. Scientific Reports, 2021, 11, 21346.	3.3	1
119	Printability of Zr41.2Ti13.8Cu12.5Ni10.0Be22.5 metallic glass on steel by laser additive manufacturing: A single-track study. Surface and Coatings Technology, 2021, 428, 127882.	4.8	4
120	Carboxypeptidase Y Assisted Disulfide-Bond Identification with Linearized Database Search. Analytical Chemistry, 2021, 93, 14940-14945.	6.5	4
124	Structural basis of Integrator-mediated transcription regulation. Science, 2021, 374, 883-887.	12.6	78
126	Cross-Linking Mass Spectrometry for Investigating Protein Conformations and Protein–Protein Interactions─A Method for All Seasons. Chemical Reviews, 2022, 122, 7500-7531.	47.7	101
127	Acyl carrier protein promotes MukBEF action in Escherichia coli chromosome organization-segregation. Nature Communications, 2021, 12, 6721.	12.8	12
129	Redox-sensitive CDC-42 clustering promotes wound closure in C.Âelegans. Cell Reports, 2021, 37, 110040.	6.4	6
130	Precise, fast and comprehensive analysis of intact glycopeptides and modified glycans with pGlyco3. Nature Methods, 2021, 18, 1515-1523.	19.0	79
132	Identification of an autoinhibitory, mitophagy-inducing peptide derived from the transmembrane domain of USP30. Autophagy, 2022, 18, 2178-2197.	9.1	21
134	Structural basis for assembly of TRAPPII complex and specific activation of GTPase Ypt31/32. Science Advances, 2022, 8, eabi5603.	10.3	10
135	A Membraneâ€Permeable and Immobilized Metal Affinity Chromatography (IMAC) Enrichable Crossâ€Linking Reagent to Advance In Vivo Crossâ€Linking Mass Spectrometry. Angewandte Chemie, 0, , .	2.0	1
136	A Membraneâ€Permeable and Immobilized Metal Affinity Chromatography (IMAC) Enrichable Crossâ€Linking Reagent to Advance Inâ€Vivo Crossâ€Linking Mass Spectrometry. Angewandte Chemie - International Edition, 2022, 61, .	13.8	29
138	Leveraging crosslinking mass spectrometry in structural and cell biology. Structure, 2022, 30, 37-54.	3.3	44

#	Article	IF	CITATIONS
139	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. Cell, 2022, 185, 361-378.e25.	28.9	87
141	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. ELife, 2021, $10$ , .	6.0	36
143	Optimized TMT-Based Quantitative Cross-Linking Mass Spectrometry Strategy for Large-Scale Interactomic Studies. Analytical Chemistry, 2022, 94, 5265-5272.	6.5	10
144	Nitrogen Mustard Alkylates and Cross-Links p53 in Human Keratinocytes. Chemical Research in Toxicology, 2022, 35, 636-650.	3.3	1
145	Characterization of protein unfolding by fast cross-linking mass spectrometry using di-ortho-phthalaldehyde cross-linkers. Nature Communications, 2022, 13, 1468.	12.8	20
146	Crucial role and mechanism of transcription-coupled DNA repair in bacteria. Nature, 2022, 604, 152-159.	27.8	29
149	Activation of the essential kinase PDK1 by phosphoinositide-driven trans-autophosphorylation. Nature Communications, 2022, 13, 1874.	12.8	22
150	Architecture of the human NALCN channelosome. Cell Discovery, 2022, 8, 33.	6.7	7
151	Reverse Chemical Ecology Suggests Putative Primate Pheromones. Molecular Biology and Evolution, 2022, 39, .	8.9	4
153	Conformational rearrangements upon start codon recognition in human 48S translation initiation complex. Nucleic Acids Research, 2022, 50, 5282-5298.	14.5	15
156	Structure of human chromatin-remodelling PBAF complex bound to a nucleosome. Nature, 2022, 605, 166-171.	27.8	42
157	Art Research Based on Machine Learning and Artificial Intelligence. Security and Communication Networks, 2022, 2022, 1-9.	1.5	1
158	In-Depth <i>In Vivo</i> Crosslinking in Minutes by a Compact, Membrane-Permeable, and Alkynyl-Enrichable Crosslinker. Analytical Chemistry, 2022, 94, 7551-7558.	6.5	21
159	Cryo-EM structure of the human CST–Polα/primase complex in a recruitment state. Nature Structural and Molecular Biology, 2022, 29, 813-819.	8.2	40
162	Improved Peptide Backbone Fragmentation Is the Primary Advantage of MS-Cleavable Crosslinkers. Analytical Chemistry, 2022, 94, 7779-7786.	6.5	15
164	Structural basis of Tom20 and Tom22 cytosolic domains as the human TOM complex receptors. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	25
165	Genome-Wide Association Mapping of Hulless Barely Phenotypes in Drought Environment. Frontiers in Plant Science, $0,13,.$	3.6	4
166	Structural basis for c-di-AMP–dependent regulation of the bacterial stringent response by receptor protein DarB. Journal of Biological Chemistry, 2022, 298, 102144.	3.4	8

#	Article	IF	CITATIONS
167	Many kinds of oxidized proteins are present more in the urine of the elderly. Clinical Proteomics, $2022, 19, .$	2.1	2
169	Hsp multichaperone complex buffers pathologically modified Tau. Nature Communications, 2022, 13, .	12.8	11
170	Mimicked synthetic ribosomal protein complex for benchmarking crosslinking mass spectrometry workflows. Nature Communications, 2022, $13$ , .	12.8	17
171	A super pan-genomic landscape of rice. Cell Research, 2022, 32, 878-896.	12.0	99
172	Structure of Arabidopsis SOQ1 lumenal region unveils C-terminal domain essential for negative regulation of photoprotective qH. Nature Plants, 2022, 8, 840-855.	9.3	5
173	High-resolution mass spectrometry unveils the molecular changes of ovalbumin induced by heating and their influence on IgE binding capacity. Food Chemistry, 2022, 395, 133624.	8.2	10
174	Shelterin is a dimeric complex with extensive structural heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2022, $119$ , .	7.1	18
175	Binding stoichiometry and structural model of the HIV-1 Rev/importin $\hat{l}^2$ complex. Life Science Alliance, 2022, 5, e202201431.	2.8	3
176	Characterization of protein complexes in extracellular vesicles by intact extracellular vesicle crosslinking mass spectrometry (iEVXL). Journal of Extracellular Vesicles, 2022, 11, .	12.2	5
177	DPY30 acts as an ASH2L-specific stabilizer to stimulate the enzyme activity of MLL family methyltransferases on different substrates. IScience, 2022, 25, 104948.	4.1	5
178	The effect of lactulose thermal degradation products on β-lactoglobulin: Linear-, loop-, and cross-link structural modifications and reduced digestibility. Food Chemistry, 2023, 403, 134333.	8.2	2
179	An approach to nearest neighbor analysis of pigment-protein complexes using chemical cross-linking in combination with mass spectrometry. Methods in Enzymology, 2023, , 139-162.	1.0	1
180	SpotLink enables sensitive and precise identification of site nonspecific cross-links at the proteome scale. Briefings in Bioinformatics, 2022, 23, .	6.5	3
181	Alkynyl-Enrichable Carboxyl-Selective Crosslinkers to Increase the Crosslinking Coverage for Deciphering Protein Structures. Analytical Chemistry, 2022, 94, 12398-12406.	6.5	3
182	Mechanistic Insights into the Functioning of a Two-Subunit GMP Synthetase, an Allosterically Regulated, Ammonia Channeling Enzyme. Biochemistry, 2022, 61, 1988-2006.	2.5	3
183	Nanobodies and chemical cross-links advance the structural and functional analysis of PI3KÎ $\pm$ . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	8
184	Divergent polo boxes in KKT2 bind KKT1 to initiate the kinetochore assembly cascade in <i>Trypanosoma brucei</i> . Molecular Biology of the Cell, 2022, 33, .	2.1	3
185	Multistate structures of the MLL1-WRAD complex bound to H2B-ubiquitinated nucleosome.  Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12

#	Article	IF	CITATIONS
187	Chemical protein synthesis elucidates key modulation mechanism of the tyrosine-O-sulfation in inducing strengthened inhibitory activity of hirudin. Chinese Chemical Letters, 2023, 34, 107806.	9.0	3
188	Genetically encoded chemical crosslinking of carbohydrate. Nature Chemistry, 2023, 15, 33-42.	13.6	17
190	Subcellular Interactomes Revealed by Merging APEX with Cross-Linking Mass Spectrometry. Analytical Chemistry, 2022, 94, 14878-14888.	6.5	5
191	A universal database reduction method based on the sequence tag strategy to facilitate large-scale database search in proteomics. International Journal of Mass Spectrometry, 2023, 483, 116966.	1.5	1
193	A toxin-deformation dependent inhibition mechanism in the T7SS toxin-antitoxin system of Gram-positive bacteria. Nature Communications, 2022, 13, .	12.8	4
195	Somatic mutation detection: a critical evaluation through simulations and reanalyses in oaks. , 0, 2, .		5
197	Mapping of the plant SnRK1 kinase signalling network reveals a key regulatory role for the class II T6P synthase-like proteins. Nature Plants, 2022, 8, 1245-1261.	9.3	41
199	Disulfide bond and crosslinking analyses reveal inter-domain interactions that contribute to the rigidity of placental malaria VAR2CSA structure and formation of CSA binding channel. International Journal of Biological Macromolecules, 2023, 226, 143-158.	7.5	2
200	Structures of transcription preinitiation complex engaged with the $\pm 1$ nucleosome. Nature Structural and Molecular Biology, 2023, 30, 226-232.	8.2	19
201	Integrative analysis reveals structural basis for transcription activation of Nurr1 and Nurr1-RXRα heterodimer. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	1
202	Structural basis of SNAPc-dependent snRNA transcription initiation by RNA polymerase II. Nature Structural and Molecular Biology, 2022, 29, 1159-1169.	8.2	5
203	Enhanced protein–protein interaction network construction promoted by in vivo cross-linking with acid-cleavable click-chemistry enrichment. Frontiers in Chemistry, 0, 10, .	3.6	6
205	Structure of nucleosome-bound human PBAF complex. Nature Communications, 2022, 13, .	12.8	11
206	Structure of a TOC-TIC supercomplex spanning two chloroplast envelope membranes. Cell, 2022, 185, 4788-4800.e13.	28.9	23
207	Exhaustive Cross-Linking Search with Protein Feedback. Journal of Proteome Research, 0, , .	3.7	4
208	The role of auxiliary domains in modulating CHD4 activity suggests mechanistic commonality between enzyme families. Nature Communications, $2022,13,.$	12.8	4
209	Mono- and Intralink Filter (Mi-Filter) To Reduce False Identifications in Cross-Linking Mass Spectrometry Data. Analytical Chemistry, 2022, 94, 17751-17756.	6.5	2
210	A quantitative interpretation of oxidative protein folding activity in Escherichia coli. Microbial Cell Factories, 2022, 21, .	4.0	0

#	Article	IF	CITATIONS
211	Identifying and characterising Thrap3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. Wellcome Open Research, 0, 6, 260.	1.8	0
212	The Crux Toolkit for Analysis of Bottom-Up Tandem Mass Spectrometry Proteomics Data. Journal of Proteome Research, 2023, 22, 561-569.	3.7	4
213	Structural basis of bacterial effector protein azurin targeting tumor suppressor p53 and inhibiting its ubiquitination. Communications Biology, 2023, 6, .	4.4	3
214	Improved Analysis of Cross-Linking Mass Spectrometry Data with Kojak 2.0, Advanced by Integration into the Trans-Proteomic Pipeline. Journal of Proteome Research, 0, , .	3.7	O
221	Transportin 1 is a major nuclear import receptor of the nitric oxide synthase interacting protein. Journal of Biological Chemistry, 2023, , $102932$ .	3.4	0
222	Cross-linking mass spectrometry for mapping protein complex topologies <i>in situ</i> i>. Essays in Biochemistry, 2023, 67, 215-228.	4.7	10
223	Mapping protein direct interactome of oxidoreductases with small molecular chemical cross-linkers in live cells. Redox Biology, 2023, 61, 102642.	9.0	1
224	A tyrosine, histidine-selective bifunctional cross-linker for protein structure analysis. Talanta, 2023, 258, 124421.	<b>5.</b> 5	3
225	Integrated mass spectrometry strategy for functional protein complex discovery and structural characterization. Current Opinion in Chemical Biology, 2023, 74, 102305.	6.1	3
226	Structural insights into DNA N6-adenine methylation by the MTA1 complex. Cell Discovery, 2023, 9, .	6.7	1
227	Linking chromatin acylation mark-defined proteome and genome in living cells. Cell, 2023, 186, 1066-1085.e36.	28.9	9
228	Regulation of 3′ splice site selection after step 1 of splicing by spliceosomal C* proteins. Science Advances, 2023, 9, .	10.3	5
229	Real-Time Library Search Increases Cross-Link Identification Depth across All Levels of Sample Complexity. Analytical Chemistry, 2023, 95, 5248-5255.	6.5	3
230	Spt6 directly interacts with Cdc73 and is required for Paf1 complex occupancy at active genes in <i>Saccharomyces cerevisiae</i> Nucleic Acids Research, 2023, 51, 4814-4830.	14.5	5
232	Cyanobacterial Phycobilisome Allostery as Revealed by Quantitative Mass Spectrometry. Biochemistry, 2023, 62, 1307-1320.	2.5	2
234	High-Sensitivity Proteome-Scale Searches for Crosslinked Peptides Using CRIMP 2.0. Analytical Chemistry, 2023, 95, 6425-6432.	6.5	4
235	Autoinhibited kinesin-1 adopts a hierarchical folding pattern. ELife, 0, 12, .	6.0	5
236	Near-atomic architecture of Singapore grouper iridovirus and implications for giant virus assembly. Nature Communications, 2023, $14$ , .	12.8	8

#	ARTICLE	IF	CITATIONS
237	Cross-linking mass spectrometry discovers, evaluates, and corroborates structures and protein–protein interactions in the human cell. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	9
238	RNA polymerase drives ribonucleotide excision DNA repair in E.Âcoli. Cell, 2023, 186, 2425-2437.e21.	28.9	6
239	In vivo cross-linking-based affinity purification and mass spectrometry for targeting intracellular protein-protein interactions. Analytica Chimica Acta, 2023, 1265, 341273.	5.4	1
240	Heterologous Expression of Plantaricin 423 and Mundticin ST4SA in Saccharomyces cerevisiae. Probiotics and Antimicrobial Proteins, 0, , .	3.9	2
241	IgE Recognition and Structural Analysis of Disulfide Bond Rearrangement and Chemical Modifications in Allergen Aggregations in Roasted Peanuts. Journal of Agricultural and Food Chemistry, 2023, 71, 9110-9119.	5.2	2
242	Affinity-Purification Combined with Crosslinking Mass Spectrometry for Identification and Structural Modeling of Host–Pathogen Protein–Protein Complexes. Methods in Molecular Biology, 2023, , 181-200.	0.9	0
244	Improved Cross-Linking Coverage for Protein Complexes Containing Low Levels of Lysine by Using an Enrichable Photo-Cross-Linker. Analytical Chemistry, 2023, 95, 9445-9452.	6.5	0
245	Crosslinker Nanocarriers Delivery to Chloroplasts for <i>In Vivo</i> Mapping of Photosynthetic Membrane Protein Complexes in Living <i>Chlamydomonas reinhardtii</i> Cells. Analytical Chemistry, 2023, 95, 9555-9563.	6.5	0
247	Cross-Linking Mass Spectrometry Uncovers Interactions Between High-Density Lipoproteins and the SARS-CoV-2 Spike Glycoprotein. Molecular and Cellular Proteomics, 2023, 22, 100600.	3.8	2
248	Proteomic Characterization of Native and Rearranged Disulfide Bonds in Proteins from Thermally Treated and Commercial Milk Samples. Journal of Agricultural and Food Chemistry, 0, , .	5.2	0
250	SeqWiz: a modularized toolkit for next-generation protein sequence database management and analysis. BMC Bioinformatics, 2023, 24, .	2.6	0
251	Structural basis of amine odorant perception by a mammal olfactory receptor. Nature, 2023, 618, 193-200.	27.8	12
252	Total Chemical Synthesis of Glycosylated TREM2 Ectodomain. ACS Chemical Neuroscience, 2023, 14, 2243-2251.	3.5	0
253	Structural insights into human co-transcriptional capping. Molecular Cell, 2023, 83, 2464-2477.e5.	9.7	8
254	Association mapping in multiple yam species (Dioscorea spp.) of quantitative trait loci for yield-related traits. BMC Plant Biology, 2023, 23, .	3.6	2
255	Evaluation of European-based polygenic risk score for breast cancer in Ashkenazi Jewish women in Israel. Journal of Medical Genetics, 2023, 60, 1186-1197.	3.2	1
256	Comparative Analysis of Chemical Cross-Linking Mass Spectrometry Data Indicates That Protein STY Residues Rarely React with $\langle i \rangle N \langle  i \rangle$ -Hydroxysuccinimide Ester Cross-Linkers. Journal of Proteome Research, $0, , .$	3.7	0
257	α-Helix-Mediated Protein Adhesion. Journal of the American Chemical Society, 2023, 145, 17125-17135.	13.7	6

#	Article	IF	CITATIONS
258	Innovation in Cross-Linking Mass Spectrometry Workflows: Toward a Comprehensive, Flexible, and Customizable Data Analysis Platform. Journal of the American Society for Mass Spectrometry, 0, , .	2.8	0
260	CaMKII autophosphorylation can occur between holoenzymes without subunit exchange. ELife, 0, 12, .	6.0	5
261	Development of Lysine Crotonylâ€Mimic Probe to Covalently Identify H3K27Cr Interacting Proteins. Chemistry - A European Journal, 2023, 29, .	3.3	0
262	Peroxiredoxin-1 is an H2O2 safe-guard antioxidant and signalling enzyme in M1 macrophages. Advances in Redox Research, 2023, 9, 100083.	2.1	0
263	Structure and activation of the RING E3 ubiquitin ligase TRIM72 on the membrane. Nature Structural and Molecular Biology, 2023, 30, 1695-1706.	8.2	4
264	4D-diaXLMS: Proteome-wide Four-Dimensional Data-Independent Acquisition Workflow for Cross-Linking Mass Spectrometry. Analytical Chemistry, 2023, 95, 14077-14085.	6.5	1
265	MS Annika 2.0 Identifies Cross-Linked Peptides in MS2–MS3-Based Workflows at High Sensitivity and Specificity. Journal of Proteome Research, 2023, 22, 3009-3021.	3.7	0
266	ECL 3.0: a sensitive peptide identification tool for cross-linking mass spectrometry data analysis. BMC Bioinformatics, 2023, 24, .	2.6	0
267	Higher-Order Structural Organization of the Mitochondrial Proteome Charted by In Situ Cross-Linking Mass Spectrometry. Molecular and Cellular Proteomics, 2023, 22, 100657.	3.8	2
268	The intracellular helical bundle of human glucose transporter <scp>GLUT4</scp> is important for complex formation with <scp>ASPL</scp> . FEBS Open Bio, 2023, 13, 2094-2107.	2.3	0
269	The LSF1–MDH complex functions as a scaffold to recruit β-amylase to promote starch degradation. Plant Cell, 0, , .	6.6	1
270	The Intrinsically Disordered N Terminus in Atg12 from Yeast Is Necessary for the Functional Structure of the Protein. International Journal of Molecular Sciences, 2023, 24, 15036.	4.1	0
272	A noncanonical function of SKP1 regulates the switch between autophagy and unconventional secretion. Science Advances, 2023, 9, .	10.3	2
275	DIAPH1-MFN2 interaction regulates mitochondria-SR/ER contact and modulates ischemic/hypoxic stress. Nature Communications, 2023, 14, .	12.8	3
276	Structure of the transcribing RNA polymerase II–Elongin complex. Nature Structural and Molecular Biology, 2023, 30, 1925-1935.	8.2	4
278	Autoinhibited kinesin-1 adopts a hierarchical folding pattern. ELife, 0, 12, .	6.0	1
281	Modulating Liquid–Liquid Phase Separation of Nck Adaptor Protein against Enteropathogenic <i>Escherichia coli</i> Infection. ACS Central Science, 0, , .	11.3	0
282	Chromosome-level genome assembly of hadal snailfish reveals mechanisms of deep-sea adaptation in vertebrates. ELife, $0,12,.$	6.0	1

#	Article	IF	CITATIONS
283	A mitophagy sensor PPTC7 controls BNIP3 and NIX degradation to regulate mitochondrial mass. Molecular Cell, 2024, 84, 327-344.e9.	9.7	3
284	Hypothetical chloroplast reading frame 51 encodes a photosystem I assembly factor in cyanobacteria. Plant Cell, 0, , .	6.6	0
285	PepPre: Promote Peptide Identification Using Accurate and Comprehensive Precursors. Journal of Proteome Research, 0, , .	3.7	0
286	Multi-scale structures of the mammalian radial spoke and divergence of axonemal complexes in ependymal cilia. Nature Communications, 2024, 15, .	12.8	0
287	An extensive disulfide bond network prevents tail contraction in Agrobacterium tumefaciensÂphage Milano. Nature Communications, 2024, 15, .	12.8	0
288	Structural basis for RNA polymerase II ubiquitylation and inactivation in transcription-coupled repair. Nature Structural and Molecular Biology, 2024, 31, 536-547.	8.2	0
289	Progress, Challenges and Opportunities of NMR and XL-MS for Cellular Structural Biology. Jacs Au, 2024, 4, 369-383.	7.9	0
290	Structural mechanisms of autoinhibition and substrate recognition by the ubiquitin ligase HACE1. Nature Structural and Molecular Biology, 2024, 31, 364-377.	8.2	0
291	Structural insights into histone exchange by human SRCAP complex. Cell Discovery, 2024, 10, .	6.7	0
292	RNA helicase IGHMBP2 regulates THO complex to ensure cellular mRNA homeostasis. Cell Reports, 2024, 43, 113802.	6.4	0
293	Cryo-EM analyses of dimerized spliceosomes provide new insights into the functions of B complex proteins. EMBO Journal, 2024, 43, 1065-1088.	7.8	0
294	TopBP1 utilises a bipartite GINS binding mode to support genome replication. Nature Communications, 2024, 15, .	12.8	0
297	Cryo-EM structures of the plant plastid-encoded RNA polymerase. Cell, 2024, 187, 1127-1144.e21.	28.9	0
298	Characterization of $\hat{l}^2$ -Barrel Outer Membrane Proteins and Their Interactions with Chaperones by Chemical-Crosslinking Mass Spectrometry. Methods in Molecular Biology, 2024, , 259-272.	0.9	0