

Andrea Sinz

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

6,156
citations

76326

40
h-index

88630

70
g-index

153
all docs

153
docs citations

153
times ranked

5683
citing authors

#	ARTICLE	IF	CITATIONS
1	The megakaryocytic transcription factor ARID3A suppresses leukemia pathogenesis. <i>Blood</i> , 2022, 139, 651-665.	1.4	20
2	Cross-Linking Mass Spectrometry for Investigating Protein Conformations and Protein-Protein Interactions – A Method for All Seasons. <i>Chemical Reviews</i> , 2022, 122, 7500-7531.	47.7	101
3	Modulation of transcriptional mineralocorticoid receptor activity by casein kinase 1. <i>FASEB Journal</i> , 2022, 36, e22059.	0.5	0
4	Different Oligomeric States of the Tumor Suppressor p53 Show Identical Binding Behavior Towards the S100 β Homodimer. <i>ChemBioChem</i> , 2022, , .	2.6	2
5	IGF2BP1 is a targetable SRC/MAPK-dependent driver of invasive growth in ovarian cancer. <i>RNA Biology</i> , 2021, 18, 391-403.	3.1	21
6	Oncogenic Potential of the Dual-Function Protein MEX3A. <i>Biology</i> , 2021, 10, 415.	2.8	10
7	First 3D-Structural Data of Full-Length Guanylyl Cyclase 1 in Rod-Outer-Segment Preparations of Bovine Retina by Cross-Linking/Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2021, 433, 166947.	4.2	3
8	Probing glycation potential of dietary sugars in human blood by an integrated in vitro approach. <i>Food Chemistry</i> , 2021, 347, 128951.	8.2	3
9	An anti-HER2 nanobody binds to its antigen HER2 via two independent paratopes. <i>International Journal of Biological Macromolecules</i> , 2021, 182, 502-511.	7.5	5
10	A rapid and reliable liquid chromatography/mass spectrometry method for SARS-CoV-2 analysis from gargle solutions and saliva. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 6503-6511.	3.7	14
11	Cross-Linking/Mass Spectrometry Combined with Ion Mobility on a timsTOF Pro Instrument for Structural Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 11442-11450.	6.5	26
12	High-throughput characterization of photocrosslinker-bearing ion channel variants to map residues critical for function and pharmacology. <i>PLoS Biology</i> , 2021, 19, e3001321.	5.6	13
13	A Diazirine-Modified Membrane Lipid to Study Peptide/Lipid Interactions – Chances and Challenges. <i>Chemistry - A European Journal</i> , 2021, 27, 14586-14593.	3.3	5
14	Native mass spectrometry identifies the HybG chaperone as carrier of the Fe(CN) $_2$ CO group during maturation of <i>E. coli</i> [NiFe]-hydrogenase 2. <i>Scientific Reports</i> , 2021, 11, 24362.	3.3	7
15	Cross-linking/mass spectrometry to get a closer view on protein interaction networks. <i>Current Opinion in Biotechnology</i> , 2020, 63, 48-53.	6.6	64
16	The Isotope-Labeled, MS-Cleavable Cross-Linker Disuccinimidyl Dibutyric Urea for Improved Cross-Linking/Mass Spectrometry Studies. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 183-189.	2.8	13
17	A biuret-derived, MS-cleavable cross-linking reagent for protein structural analysis: A proof-of-principle study. <i>Journal of Mass Spectrometry</i> , 2020, 55, e4449.	1.6	1
18	Exploring GPCR-arrestin interfaces with genetically encoded crosslinkers. <i>EMBO Reports</i> , 2020, 21, e50437.	4.5	24

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19	Structural analysis of 70S ribosomes by cross-linking/mass spectrometry reveals conformational plasticity. <i>Scientific Reports</i> , 2020, 10, 12618.	3.3	27
20	Flexibility of intrinsically disordered degrons in AUX/IAA proteins reinforces auxin co-receptor assemblies. <i>Nature Communications</i> , 2020, 11, 2277.	12.8	38
21	Cross-linking/mass spectrometry at the crossroads. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 5981-5987.	3.7	30
22	The COVID-19 MS Coalitionâ€”accelerating diagnostics, prognostics, and treatment. <i>Lancet, The</i> , 2020, 395, 1761-1762.	13.7	51
23	Mass Spectrometric Identification of SARS-CoV-2 Proteins from Gargle Solution Samples of COVID-19 Patients. <i>Journal of Proteome Research</i> , 2020, 19, 4389-4392.	3.7	159
24	Delineating the Molecular Basis of the Calmodulinâ€”bMunc13-2 Interaction by Cross-Linking/Mass Spectrometryâ€”Evidence for a Novel CaM Binding Motif in bMunc13-2. <i>Cells</i> , 2020, 9, 136.	4.1	7
25	A Simple Cross-Linking/Mass Spectrometry Workflow for Studying System-wide Protein Interactions. <i>Analytical Chemistry</i> , 2019, 91, 10236-10244.	6.5	113
26	Oligomeric state, hydrodynamic properties and target recognition of human Calcium and Integrin Binding protein 2 (CIB2). <i>Scientific Reports</i> , 2019, 9, 15058.	3.3	7
27	Profiling of Seed Proteome in Pea (<i>Pisum sativum</i> L.) Lines Characterized with High and Low Responsivity to Combined Inoculation with Nodule Bacteria and Arbuscular Mycorrhizal Fungi. <i>Molecules</i> , 2019, 24, 1603.	3.8	30
28	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
29	The First MS-Cleavable, Photo-Thiol-Reactive Cross-Linker for Protein Structural Studies. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 139-148.	2.8	29
30	Free radicalâ€”initiated peptide sequencing (FRIPS)â€”based crossâ€”linkers for improved peptide and protein structure analysis. <i>Mass Spectrometry Reviews</i> , 2019, 38, 187-201.	5.4	13
31	Crosslinking Mass Spectrometry Goes In-Tissue. <i>Cell Systems</i> , 2018, 6, 10-12.	6.2	27
32	Carboxyl-Photo-Reactive MS-Cleavable Cross-Linkers: Unveiling a Hidden Aspect of Diazirine-Based Reagents. <i>Analytical Chemistry</i> , 2018, 90, 2805-2809.	6.5	71
33	Vernetzung/Massenspektrometrie zur Untersuchung von Proteinstrukturen und Proteinâ€”Proteinâ€”Wechselwirkungen: Wo stehen wir und welchen Weg wollen wir einschlagen?. <i>Angewandte Chemie</i> , 2018, 130, 6498-6504.	2.0	10
34	Crossâ€”Linking/Mass Spectrometry for Studying Protein Structures and Proteinâ€”Protein Interactions: Where Are We Now and Where Should We Go from Here?. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 6390-6396.	13.8	156
35	Molecular Details of Retinal Guanylyl Cyclase 1/GCAP-2 Interaction. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 330.	2.9	9
36	Structural Investigation of Proteins and Protein Complexes by Chemical Cross-Linking/Mass Spectrometry. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 101-121.	1.6	18

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37	A cross-linking/mass spectrometry workflow based on MS-cleavable cross-linkers and the MeroX software for studying protein structures and protein-protein interactions. <i>Nature Protocols</i> , 2018, 13, 2864-2889.	12.0	157
38	Reconstitution of mammalian cleavage factor II involved in 5' processing of mRNA precursors. <i>Rna</i> , 2018, 24, 1721-1737.	3.5	36
39	Structure and mechanism of the two-component α -helical pore-forming toxin YaxAB. <i>Nature Communications</i> , 2018, 9, 1806.	12.8	46
40	The effect of simulated microgravity on the <i>Brassica napus</i> seedling proteome. <i>Functional Plant Biology</i> , 2018, 45, 440.	2.1	12
41	Mining seed proteome: from protein dynamics to modification profiles. <i>Biological Communications</i> , 2018, 63, 43-58.	0.8	15
42	Presynaptic Calmodulin targets: lessons from structural proteomics. <i>Expert Review of Proteomics</i> , 2017, 14, 223-242.	3.0	15
43	Improved single-step enrichment methods of cross-linked products for protein structure analysis and protein interaction mapping. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 2393-2400.	3.7	40
44	Combining affinity enrichment, cross-linking with photo amino acids, and mass spectrometry for probing protein kinase D2 interactions. <i>Proteomics</i> , 2017, 17, e1600459.	2.2	21
45	Azide-Modified Membrane Lipids: Synthesis, Properties, and Reactivity. <i>Langmuir</i> , 2017, 33, 4960-4973.	3.5	13
46	An Integrated Mass Spectrometry Based Approach to Probe the Structure of the Full-Length Wild-Type Tetrameric p53 Tumor Suppressor. <i>Angewandte Chemie</i> , 2017, 129, 281-285.	2.0	7
47	An Integrated Mass Spectrometry Based Approach to Probe the Structure of the Full-Length Wild-Type Tetrameric p53 Tumor Suppressor. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 275-279.	13.8	31
48	The First Zero-Length Mass Spectrometry-Cleavable Cross-Linker for Protein Structure Analysis. <i>Angewandte Chemie</i> , 2017, 129, 14743-14747.	2.0	8
49	The First Zero-Length Mass Spectrometry-Cleavable Cross-Linker for Protein Structure Analysis. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14551-14555.	13.8	50
50	To Be or Not to Be? Five Guidelines to Avoid Misassignments in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 7832-7835.	6.5	60
51	A Novel MS-Cleavable Azo Cross-Linker for Peptide Structure Analysis by Free Radical Initiated Peptide Sequencing (FRIPS). <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2039-2053.	2.8	20
52	Translational repression of the <i>Drosophila nanos</i> mRNA involves the RNA helicase Belle and RNA coating by Me31B and Trailer hitch. <i>Rna</i> , 2017, 23, 1552-1568.	3.5	66
53	Novel Concepts of MS-Cleavable Cross-linkers for Improved Peptide Structure Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2022-2038.	2.8	11
54	Dissociation Behavior of a TEMPO-Active Ester Cross-Linker for Peptide Structure Analysis by Free Radical Initiated Peptide Sequencing (FRIPS) in Negative ESI-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 56-68.	2.8	13

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55	Divide and conquer: cleavable cross-linkers to study protein conformation and protein-protein interactions. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 33-44.	3.7	100
56	Monitoring Solution Structures of Peroxisome Proliferator-Activated Receptor β upon Ligand Binding. <i>PLoS ONE</i> , 2016, 11, e0151412.	2.5	13
57	Identification of low abundance cyclophilins in human plasma. <i>Proteomics</i> , 2016, 16, 2815-2826.	2.2	8
58	Mass spectrometry-based secretome analysis of non-small cell lung cancer cell lines. <i>Proteomics</i> , 2016, 16, 2801-2814.	2.2	14
59	Protein Interaction Network of Human Protein Kinase D2 Revealed by Chemical Cross-Linking/Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 3686-3699.	3.7	14
60	Osmotic stress is accompanied by protein glycation in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 6283-6295.	4.8	47
61	Conformational Shift of a Hairpin Peptide upon Complex Formation with an Oligo-proline Peptide Studied by Mass Spectrometry. <i>ChemistrySelect</i> , 2016, 1, 3651-3656.	1.5	3
62	Integrated Workflow for Structural Proteomics Studies Based on Cross-Linking/Mass Spectrometry with an MS/MS Cleavable Cross-Linker. <i>Analytical Chemistry</i> , 2016, 88, 7930-7937.	6.5	58
63	Combining Amine-Reactive Cross-Linkers and Photo-Reactive Amino Acids for 3D-Structure Analysis of Proteins and Protein Complexes. <i>Methods in Molecular Biology</i> , 2016, 1394, 109-127.	0.9	20
64	Dissociation behavior of a bifunctional tempo-active ester reagent for peptide structure analysis by free radical initiated peptide sequencing (FRIPS) mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2015, 50, 396-406.	1.6	15
65	Structure of full-length p53 tumor suppressor probed by chemical cross-linking and mass spectrometry. <i>Proteomics</i> , 2015, 15, 2746-2755.	2.2	45
66	Chemical cross-linking and native mass spectrometry: A fruitful combination for structural biology. <i>Protein Science</i> , 2015, 24, 1193-1209.	7.6	112
67	Extending the cross-linking/mass spectrometry strategy: Facile incorporation of photo-activatable amino acids into the model protein calmodulin in <i>Escherichia coli</i> cells. <i>Methods</i> , 2015, 89, 121-127.	3.8	23
68	The Y3 ^{**} ncRNA promotes the 3' end processing of histone mRNAs. <i>Genes and Development</i> , 2015, 29, 1998-2003.	5.9	30
69	Automated Assignment of MS/MS Cleavable Cross-Links in Protein 3D-Structure Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 83-97.	2.8	197
70	The advancement of chemical cross-linking and mass spectrometry for structural proteomics: from single proteins to protein interaction networks. <i>Expert Review of Proteomics</i> , 2014, 11, 733-743.	3.0	116
71	Mapping Cell Envelope and Periplasm Protein Interactions of <i>Escherichia coli</i> Respiratory Formate Dehydrogenases by Chemical Cross-Linking and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2014, 13, 5524-5535.	3.7	9
72	Preparation of Monolithic Affinity Media for Nano-Liquid Chromatography Applications. <i>Methods in Molecular Biology</i> , 2014, 1129, 351-364.	0.9	0

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73	Structural insights into calmodulin/Munc13 interaction. <i>Biological Chemistry</i> , 2014, 395, 763-768.	2.5	4
74	Accessibilities of N-terminal myristoyl chain and cysteines in guanylyl cyclase-activating protein-2 (GCAP-2) studied by covalent labeling and mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 835-838.	1.5	1
75	Reliable Identification of Cross-Linked Products in Protein Interaction Studies by ¹³ C-Labeled p-Benzoylphenylalanine. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1628-1641.	2.8	11
76	Disulfide Linkage and Structure of Highly Stable Yeast-derived Virus-like Particles of Murine Polyomavirus. <i>Journal of Biological Chemistry</i> , 2014, 289, 10411-10418.	3.4	16
77	Pyruvate Formate-Lyase Interacts Directly with the Formate Channel FocA to Regulate Formate Translocation. <i>Journal of Molecular Biology</i> , 2014, 426, 2827-2839.	4.2	45
78	Analysis of Nidogen-1/Laminin β 1 Interaction by Cross-Linking, Mass Spectrometry, and Computational Modeling Reveals Multiple Binding Modes. <i>PLoS ONE</i> , 2014, 9, e112886.	2.5	44
79	The correlation of genome size and DNA methylation rate in metazoans. <i>Theory in Biosciences</i> , 2013, 132, 47-60.	1.4	43
80	Structural Analysis of Guanylyl Cyclase-Activating Protein-2 (GCAP-2) Homodimer by Stable Isotope-Labeling, Chemical Cross-Linking, and Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1969-1979.	2.8	32
81	Multidimensional nano-HPLC coupled with tandem mass spectrometry for analyzing biotinylated proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 2163-2173.	3.7	15
82	Monitoring Conformational Changes in Peroxisome Proliferator-Activated Receptor β by a Genetically Encoded Photoamino Acid, Cross-Linking, and Mass Spectrometry. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 4252-4263.	6.4	19
83	Structural insights into calmodulin/adenylyl cyclase 8 interaction. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 9333-9342.	3.7	14
84	Munc13-Like skMLCK Variants Cannot Mimic the Unique Calmodulin Binding Mode of Munc13 as Evidenced by Chemical Cross-Linking and Mass Spectrometry. <i>PLoS ONE</i> , 2013, 8, e75119.	2.5	4
85	Analyzing PPAR β /Ligand Interactions by Chemical Cross-Linking and High-Resolution Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 952, 287-299.	0.9	1
86	Selective selC-Independent Selenocysteine Incorporation into Formate Dehydrogenases. <i>PLoS ONE</i> , 2013, 8, e61913.	2.5	14
87	Nonconserved Ca ²⁺ /Calmodulin Binding Sites in Munc13s Differentially Control Synaptic Short-Term Plasticity. <i>Molecular and Cellular Biology</i> , 2012, 32, 4628-4641.	2.3	53
88	Analyse von Sekundärstrukturen in Peptiden mithilfe photoaktivierbarer Aminosäureanaloga. <i>Angewandte Chemie</i> , 2012, 124, 12770-12774.	2.0	3
89	Analysis of Peptide Secondary Structures by Photoactivatable Amino Acid Analogues. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 12602-12605.	13.8	33
90	Distinct Mechanisms of Calmodulin Binding and Regulation of Adenylyl Cyclases 1 and 8. <i>Biochemistry</i> , 2012, 51, 7917-7929.	2.5	28

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91	Peptide Backbone Conformation Affects the Substrate Preference of Protein Arginine Methyltransferase I. <i>Biochemistry</i> , 2012, 51, 5463-5475.	2.5	12
92	Structural Insights into Retinal Guanylylcyclase-GCAP-2 Interaction Determined by Cross-Linking and Mass Spectrometry. <i>Biochemistry</i> , 2012, 51, 4932-4949.	2.5	21
93	Phospholipases A1 from <i>Armillaria ostoyae</i> Provide Insight into the Substrate Recognition of β -Hydrolase Fold Enzymes. <i>JAOCs</i> , Journal of the American Oil Chemists' Society, 2012, 89, 1435.	1.9	1
94	Chemical Cross-Linking and High-Resolution Mass Spectrometry to Study Protein-Drug Interactions. <i>Methods in Molecular Biology</i> , 2012, 803, 205-218.	0.9	11
95	Optimizing the enrichment of cross-linked products for mass spectrometric protein analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 653-658.	1.5	86
96	StavroX-A Software for Analyzing Crosslinked Products in Protein Interaction Studies. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 76-87.	2.8	300
97	Monolithic columns with immobilized monomeric avidin: preparation and application for affinity chromatography. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 2395-2405.	3.7	17
98	A universal matrix-assisted laser desorption/ionization cleavable cross-linker for protein structure analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 155-161.	1.5	24
99	Monolithic media for applications in affinity chromatography. <i>Journal of Separation Science</i> , 2011, 34, 1958-1973.	2.5	51
100	Investigation of protein-protein interactions in living cells by chemical crosslinking and mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 3433-3440.	3.7	97
101	Forty-third annual meeting of the German Society for Mass Spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2777-2778.	3.7	0
102	Collision-induced dissociative chemical cross-linking reagent for protein structure characterization: applied Edman chemistry in the gas phase. <i>Journal of Mass Spectrometry</i> , 2010, 45, 178-189.	1.6	38
103	Fragmentation behavior of a thiourea-based reagent for protein structure analysis by collision-induced dissociative chemical cross-linking. <i>Journal of Mass Spectrometry</i> , 2010, 45, 880-891.	1.6	25
104	Computational modeling of laminin N-terminal domains using sparse distance constraints from disulfide bonds and chemical cross-linking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3409-3427.	2.6	29
105	A Capillary Monolithic Trypsin Reactor for Efficient Protein Digestion <i>in Online and Offline Coupling to ESI and MALDI Mass Spectrometry</i> . <i>Analytical Chemistry</i> , 2010, 82, 1434-1443.	6.5	79
106	Cleavable Cross-Linker for Protein Structure Analysis: Reliable Identification of Cross-Linking Products by Tandem MS. <i>Analytical Chemistry</i> , 2010, 82, 6958-6968.	6.5	211
107	Recombinant Expression, in Vitro Refolding, and Biophysical Characterization of the Human Glucagon-like Peptide-1 Receptor. <i>Biochemistry</i> , 2010, 49, 7956-7965.	2.5	23
108	A Novel Disulfide Pattern in Laminin-Type Epidermal Growth Factor-like (LE) Modules of Laminin β ²¹ and β ³¹ Chains. <i>Biochemistry</i> , 2010, 49, 8359-8366.	2.5	10

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109	Recombinant production of bioactive human TNF- α by SUMO-fusion system " High yields from shake-flask culture. <i>Protein Expression and Purification</i> , 2010, 72, 238-243.	1.3	18
110	Separate Elements within a Single IQ-like Motif in Adenylyl Cyclase Type 8 Impart Ca ²⁺ /Calmodulin Binding and Autoinhibition. <i>Journal of Biological Chemistry</i> , 2009, 284, 15573-15588.	3.4	15
111	Immobilized monolithic enzyme reactors for application in proteomics and pharmaceuticals. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 1583-1588.	3.7	21
112	Heterobifunctional isotope-labeled amine-reactive photo-cross-linker for structural investigation of proteins by matrix-assisted laser desorption/ionization tandem time-of-flight and electrospray ionization LTQ-Orbitrap mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 2811-2818.	1.5	37
113	Structural Insights into the Calmodulin~Munc13 Interaction Obtained by Cross-Linking and Mass Spectrometry. <i>Biochemistry</i> , 2009, 48, 5908-5921.	2.5	65
114	An Innovative Method To Study Target Protein~Drug Interactions by Mass Spectrometry. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 2875-2879.	6.4	23
115	Structural and Biophysical Characterization of the Proteins Interacting with the Herpes Simplex Virus 1 Origin of Replication. <i>Journal of Biological Chemistry</i> , 2009, 284, 16343-16353.	3.4	12
116	Chances and pitfalls of chemical cross-linking with amine-reactive N-hydroxysuccinimide esters. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 392, 305-312.	3.7	232
117	Determination of disulfide bond patterns in laminin β 1 chain N-terminal domains by nano-high-performance liquid chromatography/matrix-assisted laser desorption/ionization time-of-flight/time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 1933-1940.	1.5	16
118	Expression and purification of the ligand-binding domain of peroxisome proliferator-activated receptor alpha (PPAR α). <i>Protein Expression and Purification</i> , 2008, 62, 185-189.	1.3	10
119	Isotope-Labeled Photoaffinity Reagents and Mass Spectrometry To Identify Protein~Ligand Interactions. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 660-662.	13.8	41
120	Investigation of Protein~Ligand Interactions by Mass Spectrometry. <i>ChemMedChem</i> , 2007, 2, 425-431.	3.2	38
121	Annexin A2/P11 interaction: New insights into annexin A2 tetramer structure by chemical crosslinking, high-resolution mass spectrometry, and computational modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 254-269.	2.6	39
122	Isotope-labeled cross-linkers and fourier transform ion cyclotron resonance mass spectrometry for structural analysis of a protein/peptide complex. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1100-1113.	2.8	72
123	Chemical cross-linking and mass spectrometry to map three-dimensional protein structures and protein~protein interactions. <i>Mass Spectrometry Reviews</i> , 2006, 25, 663-682.	5.4	589
124	Mapping Protein Interfaces by Chemical Cross-Linking and Fourier Transform Ion Cyclotron Resonance Mass Spectrometry: Application to a Calmodulin/Adenylyl Cyclase 8 Peptide Complex. <i>European Journal of Mass Spectrometry</i> , 2005, 11, 525-534.	1.0	45
125	Mapping protein interfaces by a trifunctional cross-linker combined with MALDI-TOF and ESI-FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 1921-1931.	2.8	81
126	Chemical cross-linking and FTICR mass spectrometry for protein structure characterization. <i>Analytical and Bioanalytical Chemistry</i> , 2005, 381, 44-47.	3.7	25

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127	Chemical Cross-Linking and High-Performance Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Protein Interaction Analysis: Application to a Calmodulin/Target Peptide Complex. <i>Analytical Chemistry</i> , 2005, 77, 495-503.	6.5	70
128	Mapping the Topology and Determination of a Low-Resolution Three-Dimensional Structure of the Calmodulin-Melittin Complex by Chemical Cross-Linking and High-Resolution FTICRMS: Direct Demonstration of Multiple Binding Modes. <i>Biochemistry</i> , 2004, 43, 4703-4715.	2.5	103
129	Mapping spatial proximities of sulfhydryl groups in proteins using a fluorogenic cross-linker and mass spectrometry. <i>Analytical Biochemistry</i> , 2004, 331, 27-32.	2.4	16
130	Evaluation of the metal binding properties of a histidine-rich fusogenic peptide by electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2003, 38, 1150-1159.	1.6	13
131	Chemical cross-linking and mass spectrometry for mapping three-dimensional structures of proteins and protein complexes. <i>Journal of Mass Spectrometry</i> , 2003, 38, 1225-1237.	1.6	250
132	Mapping low-resolution three-dimensional protein structures using chemical cross-linking and Fourier transform ion-cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 2005-2014.	1.5	80
133	Mapping Protein Interfaces with a Fluorogenic Cross-Linker and Mass Spectrometry: Application to Nebulin-Calmodulin Complexes. <i>Biochemistry</i> , 2001, 40, 7903-7913.	2.5	68
134	Chemical Cross-Linking and Mass Spectrometry for Investigation of Protein-Protein Interactions. , 0, , 83-107.		3