

David C Schriemer

List of Publications by Year in descending order

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79
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citations

101384

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86
all docs

86
docs citations

86
times ranked

4684
citing authors

#	ARTICLE	IF	CITATIONS
1	Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain. <i>ELife</i> , 2022, 11, .	2.8	7
2	IMProv: A Resource for Cross-link-Driven Structure Modeling that Accommodates Protein Dynamics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100139.	2.5	6
3	Improving Spectral Validation Rates in Hydrogen-Deuterium Exchange Data Analysis. <i>Analytical Chemistry</i> , 2021, 93, 4246-4254.	3.2	16
4	The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. <i>Structure</i> , 2021, 29, 467-478.e6.	1.6	9
5	Correlation between Labeling Yield and Surface Accessibility in Covalent Labeling Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 207-216.	1.2	8
6	The substrate specificity of the human TRAPPII complex's Rab-guanine nucleotide exchange factor activity. <i>Communications Biology</i> , 2020, 3, 735.	2.0	16
7	A substrate binding model for the KEOPS tRNA modifying complex. <i>Nature Communications</i> , 2020, 11, 6233.	5.8	21
8	Harmonizing structural mass spectrometry analyses in the mass spec studio. <i>Journal of Proteomics</i> , 2020, 225, 103844.	1.2	7
9	Dipeptidase-1 Is an Adhesion Receptor for Neutrophil Recruitment in Lungs and Liver. <i>Cell</i> , 2019, 178, 1205-1221.e17.	13.5	80
10	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	9.0	452
11	SSEThread: Integrative threading of the DNA-PKcs sequence based on data from chemical cross-linking and hydrogen deuterium exchange. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 147, 92-102.	1.4	8
12	A microtubule crosslinking protocol for integrative structural modeling activities. <i>Analytical Biochemistry</i> , 2019, 586, 113416.	1.1	4
13	Quantitative Analysis of Protein Covalent Labeling Mass Spectrometry Data in the Mass Spec Studio. <i>Analytical Chemistry</i> , 2019, 91, 8492-8499.	3.2	15
14	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
15	Photo-Cross-Linking Mass Spectrometry and Integrative Modeling Enables Rapid Screening of Antigen Interactions Involving Bacterial Transferrin Receptors. <i>Journal of Proteome Research</i> , 2019, 18, 934-946.	1.8	20
16	The CHD6 chromatin remodeler is an oxidative DNA damage response factor. <i>Nature Communications</i> , 2019, 10, 241.	5.8	45
17	Simultaneous Proteoform Analysis of Histones H3 and H4 with a Simplified Middle-Down Proteomics Method. <i>Analytical Chemistry</i> , 2018, 90, 3083-3090.	3.2	17
18	Lysine Propionylation To Boost Sequence Coverage and Enable a "Silent SILAC" Strategy for Relative Protein Quantification. <i>Analytical Chemistry</i> , 2018, 90, 9077-9084.	3.2	5

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19	Novel Allosteric Pathway of Eg5 Regulation Identified through Multivariate Statistical Analysis of Hydrogen-Exchange Mass Spectrometry (HX-MS) Ligand Screening Data. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 428-437.	2.5	12
20	Nanospray HX-MS configuration for structural interrogation of large protein systems. <i>Analyst</i> , The, 2017, 142, 904-910.	1.7	19
21	Structural and functional characterization of the PNKP-XRCC4-LigIV DNA repair complex. <i>Nucleic Acids Research</i> , 2017, 45, 6238-6251.	6.5	39
22	Neprosin, a Selective Prolyl Endoprotease for Bottom-up Proteomics and Histone Mapping. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1162-1171.	2.5	34
23	Amino Acid Insertion Frequencies Arising from Photoproducts Generated Using Aliphatic Diazirines. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2011-2021.	1.2	42
24	Supporting metabolomics with adaptable software: design architectures for the end-user. <i>Current Opinion in Biotechnology</i> , 2017, 43, 110-117.	3.3	10
25	Lactoferrin binding protein B a bi-functional bacterial receptor protein. <i>PLoS Pathogens</i> , 2017, 13, e1006244.	2.1	27
26	High Sensitivity Crosslink Detection Coupled With Integrative Structure Modeling in the Mass Spec Studio. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3071-3080.	2.5	41
27	Carnivorous Nutrition in Pitcher Plants (<i>Nepenthes</i> spp.) via an Unusual Complement of Endogenous Enzymes. <i>Journal of Proteome Research</i> , 2016, 15, 3108-3117.	1.8	51
28	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. <i>Scientific Reports</i> , 2016, 6, 30980.	1.6	54
29	MS ² for high performance conformational analysis of complex protein states. <i>Protein Science</i> , 2015, 24, 1313-1324.	3.1	8
30	A Hypothesis-Directed Approach to the Targeted Development of a Multiplexed Proteomic Biomarker Assay for Cancer. <i>Cancer Informatics</i> , 2015, 14, CIN.S24388.	0.9	2
31	A robust capillary liquid chromatography/tandem mass spectrometry method for quantitation of neuromodulatory endocannabinoids. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 1889-1897.	0.7	39
32	Recombinant Nepenthesin II for Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 6681-6687.	3.2	54
33	Toward Standardizing Deuterium Content Reporting in Hydrogen Exchange-MS. <i>Analytical Chemistry</i> , 2014, 86, 11962-11965.	3.2	8
34	Tracking Allosteric Propagation with HX-MS. <i>Structure</i> , 2014, 22, 512-514.	1.6	1
35	Expression and characterization of plant aspartic protease nepenthesin-1 from <i>Nepenthes gracilis</i> . <i>Protein Expression and Purification</i> , 2014, 95, 121-128.	0.6	33
36	Nucleotide Exchange in Dimeric MCAK Induces Longitudinal and Lateral Stress at Microtubule Ends to Support Depolymerization. <i>Structure</i> , 2014, 22, 1173-1183.	1.6	12

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37	Mass Spec Studio for Integrative Structural Biology. <i>Structure</i> , 2014, 22, 1538-1548.	1.6	86
38	Peptideâ€“Column Interactions and Their Influence on Back Exchange Rates in Hydrogen/Deuterium Exchange-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1006-1015.	1.2	51
39	Nepenthesin from Monkey Cups for Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 464-472.	2.5	54
40	Platform Dependencies in Bottom-up Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 539-548.	2.5	34
41	Steric and allosteric factors prevent simultaneous binding of transferrin-binding proteins A and B to transferrin. <i>Biochemical Journal</i> , 2012, 444, 189-197.	1.7	5
42	Low-dose laulimalide represents a novel molecular probe for investigating microtubule organization. <i>Cell Cycle</i> , 2012, 11, 3045-3054.	1.3	11
43	High-Resolution Mapping of Carbene-Based Protein Footprints. <i>Analytical Chemistry</i> , 2012, 84, 4411-4418.	3.2	57
44	Probing protein interactions with hydrogen/deuterium exchange and mass spectrometryâ€“A review. <i>Analytica Chimica Acta</i> , 2012, 721, 7-21.	2.6	142
45	Assembly of Ebola Virus Matrix Protein VP40 Is Regulated by Latch-Like Properties of N and C Terminal Tails. <i>PLoS ONE</i> , 2012, 7, e39978.	1.1	19
46	Mass Spectrometry of Laser-Initiated Carbene Reactions for Protein Topographic Analysis. <i>Analytical Chemistry</i> , 2011, 83, 2913-2920.	3.2	56
47	MRM methods for high precision shift measurements in H/DX-MS. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 26-35.	0.7	8
48	XRCC4 Protein Interactions with XRCC4-like Factor (XLF) Create an Extended Grooved Scaffold for DNA Ligation and Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2011, 286, 32638-32650.	1.6	151
49	Conserved Interaction between Transferrin and Transferrin-binding Proteins from Porcine Pathogens. <i>Journal of Biological Chemistry</i> , 2011, 286, 21353-21360.	1.6	18
50	Structural Variations within the Transferrin Binding Site on Transferrin-binding Protein B, TbpB. <i>Journal of Biological Chemistry</i> , 2011, 286, 12683-12692.	1.6	42
51	Rheostatic control of tryptic digestion in a microscale fluidic system. <i>Analytica Chimica Acta</i> , 2010, 657, 53-59.	2.6	10
52	Discovery and Characterization of the Laulimalide-Microtubule Binding Mode by Mass Shift Perturbation Mapping. <i>Chemistry and Biology</i> , 2010, 17, 725-734.	6.2	111
53	Hydra: software for tailored processing of H/D exchange data from MS or tandem MS analyses. <i>BMC Bioinformatics</i> , 2009, 10, 162.	1.2	70
54	Surrogate H/D Detection Strategy for Protein Conformational Analysis Using MS/MS Data. <i>Analytical Chemistry</i> , 2009, 81, 7900-7907.	3.2	17

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55	Structural Mass Spectrometry of the $\alpha\beta$ -Tubulin Dimer Supports a Revised Model of Microtubule Assembly. <i>Biochemistry</i> , 2009, 48, 4858-4870.	1.2	43
56	Integrating Accelerated Tryptic Digestion into Proteomics Workflows. <i>Methods in Molecular Biology</i> , 2009, 492, 241-254.	0.4	4
57	A Unique Mode of Microtubule Stabilization Induced by Peloruside A. <i>Journal of Molecular Biology</i> , 2008, 378, 1016-1030.	2.0	110
58	Restraining Expansion of the Peak Envelope in H/D Exchange-MS and Its Application in Detecting Perturbations of Protein Structure/Dynamics. <i>Analytical Chemistry</i> , 2008, 80, 7004-7011.	3.2	43
59	Detection and Identification of Sub-nanogram Levels of Protein in a NanoLC-Trypsin-MS System. <i>Journal of Proteome Research</i> , 2006, 5, 1959-1966.	1.8	73
60	Quantitating the Statistical Distribution of Deuterium Incorporation To Extend the Utility of H/D Exchange MS Data. <i>Analytical Chemistry</i> , 2006, 78, 207-214.	3.2	50
61	Emerging challenges in ligand discovery: new opportunities for chromatographic assay. <i>Expert Review of Proteomics</i> , 2005, 2, 891-900.	1.3	5
62	High-Throughput Screening for Enzyme Inhibitors Using Frontal Affinity Chromatography with Liquid Chromatography and Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 6125-6133.	3.2	69
63	Blending Protein Separation and Peptide Analysis through Real-Time Proteolytic Digestion. <i>Analytical Chemistry</i> , 2005, 77, 1572-1579.	3.2	188
64	Peer Reviewed: Biosensor Alternative: Frontal Affinity Chromatography. <i>Analytical Chemistry</i> , 2004, 76, 440 A-448 A.	3.2	56
65	Frontal affinity chromatography—mass spectrometry assay technology for multiple stages of drug discovery: applications of a chromatographic biosensor. <i>Analytical Biochemistry</i> , 2003, 319, 1-12.	1.1	69
66	On-column digestion of proteins in aqueous-organic solvents. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 1044-1050.	0.7	103
67	Hydrogen/Deuterium Exchange Mass Spectrometry of Actin in Various Biochemical Contexts. <i>Journal of Molecular Biology</i> , 2003, 334, 373-385.	2.0	26
68	Micro-Scale Frontal Affinity Chromatography with Mass Spectrometric Detection: A New Method for the Screening of Compound Libraries. <i>Angewandte Chemie - International Edition</i> , 1998, 37, 3383-3387.	7.2	129
69	MALDI Mass Spectrometry Combined with Avidin-Biotin Chemistry for Analysis of Protein Modifications. <i>Analytical Chemistry</i> , 1998, 70, 1569-1575.	3.2	27
70	Analysis of Structurally Complex Polymers by Time-Lag Focusing Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry. <i>Macromolecules</i> , 1997, 30, 1955-1963.	2.2	39
71	Time-Lag Focusing MALDI Time-of-Flight Mass Spectrometry for Polymer Characterization: Oligomer Resolution, Mass Accuracy, and Average Weight Information. <i>Analytical Chemistry</i> , 1997, 69, 2734-2741.	3.2	75
72	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 1. Sample Preparation and Desorption/Ionization Issues. <i>Analytical Chemistry</i> , 1997, 69, 4169-4175.	3.2	150

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73	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 2. Instrumental Issues. Analytical Chemistry, 1997, 69, 4176-4183.	3.2	148
74	Matrix-assisted laser desorption ionization time-of-flight mass spectrometry for the analysis of polydienes. Journal of the American Society for Mass Spectrometry, 1997, 8, 1220-1229.	1.2	51
75	Surface Analysis of Bulk Polymers Using Laser-Induced Photoelectron Ionization with Laser Desorption in a Time-of-Flight Mass Spectrometer. Analytical Chemistry, 1996, 68, 250-256.	3.2	12
76	Detection of High Molecular Weight Narrow Polydisperse Polymers up to 1.5 Million Daltons by MALDI Mass Spectrometry. Analytical Chemistry, 1996, 68, 2721-2725.	3.2	251
77	Combining Avidin-Biotin Chemistry with Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. Analytical Chemistry, 1996, 68, 3382-3387.	3.2	36
78	Laser-Induced surface ionization in a time-of-flight mass spectrometer. Review of Scientific Instruments, 1995, 66, 55-62.	0.6	17
79	A Dual Ionization Source with Laser Desorption Sample Introduction in a Time-of-Flight Mass Spectrometer. Instrumentation Science and Technology, 1995, 23, 317-328.	0.9	2