David C Schriemer

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4886149/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain. ELife, 2022, 11, .	6.0	7
2	IMProv: A Resource for Cross-link-Driven Structure Modeling that Accommodates Protein Dynamics. Molecular and Cellular Proteomics, 2021, 20, 100139.	3.8	6
3	Improving Spectral Validation Rates in Hydrogen–Deuterium Exchange Data Analysis. Analytical Chemistry, 2021, 93, 4246-4254.	6.5	16
4	The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. Structure, 2021, 29, 467-478.e6.	3.3	9
5	Correlation between Labeling Yield and Surface Accessibility in Covalent Labeling Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2020, 31, 207-216.	2.8	8
6	The substrate specificity of the human TRAPPII complex's Rab-guanine nucleotide exchange factor activity. Communications Biology, 2020, 3, 735.	4.4	16
7	A substrate binding model for the KEOPS tRNA modifying complex. Nature Communications, 2020, 11, 6233.	12.8	21
8	Harmonizing structural mass spectrometry analyses in the mass spec studio. Journal of Proteomics, 2020, 225, 103844.	2.4	7
9	Dipeptidase-1 Is an Adhesion Receptor for Neutrophil Recruitment in Lungs and Liver. Cell, 2019, 178, 1205-1221.e17.	28.9	80
10	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
11	SSEThread: Integrative threading of the DNA-PKcs sequence based on data from chemical cross-linking and hydrogen deuterium exchange. Progress in Biophysics and Molecular Biology, 2019, 147, 92-102.	2.9	8
12	A microtubule crosslinking protocol for integrative structural modeling activities. Analytical Biochemistry, 2019, 586, 113416.	2.4	4
13	Quantitative Analysis of Protein Covalent Labeling Mass Spectrometry Data in the Mass Spec Studio. Analytical Chemistry, 2019, 91, 8492-8499.	6.5	15
14	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	6.5	100
15	Photo-Cross-Linking Mass Spectrometry and Integrative Modeling Enables Rapid Screening of Antigen Interactions Involving Bacterial Transferrin Receptors. Journal of Proteome Research, 2019, 18, 934-946.	3.7	20
16	The CHD6 chromatin remodeler is an oxidative DNA damage response factor. Nature Communications, 2019, 10, 241.	12.8	45
17	Simultaneous Proteoform Analysis of Histones H3 and H4 with a Simplified Middle-Down Proteomics Method. Analytical Chemistry, 2018, 90, 3083-3090.	6.5	17
18	Lysine Propionylation To Boost Sequence Coverage and Enable a "Silent SILAC―Strategy for Relative Protein Quantification. Analytical Chemistry, 2018, 90, 9077-9084.	6.5	5

#	Article	IF	CITATIONS
19	Novel Allosteric Pathway of Eg5 Regulation Identified through Multivariate Statistical Analysis of Hydrogen-Exchange Mass Spectrometry (HX-MS) Ligand Screening Data. Molecular and Cellular Proteomics, 2017, 16, 428-437.	3.8	12
20	Nanospray HX-MS configuration for structural interrogation of large protein systems. Analyst, The, 2017, 142, 904-910.	3.5	19
21	Structural and functional characterization of the PNKP–XRCC4–LigIV DNA repair complex. Nucleic Acids Research, 2017, 45, 6238-6251.	14.5	39
22	Neprosin, a Selective Prolyl Endoprotease for Bottom-up Proteomics and Histone Mapping. Molecular and Cellular Proteomics, 2017, 16, 1162-1171.	3.8	34
23	Amino Acid Insertion Frequencies Arising from Photoproducts Generated Using Aliphatic Diazirines. Journal of the American Society for Mass Spectrometry, 2017, 28, 2011-2021.	2.8	42
24	Supporting metabolomics with adaptable software: design architectures for the end-user. Current Opinion in Biotechnology, 2017, 43, 110-117.	6.6	10
25	Lactoferrin binding protein B – a bi-functional bacterial receptor protein. PLoS Pathogens, 2017, 13, e1006244.	4.7	27
26	High Sensitivity Crosslink Detection Coupled With Integrative Structure Modeling in the Mass Spec Studio. Molecular and Cellular Proteomics, 2016, 15, 3071-3080.	3.8	41
27	Carnivorous Nutrition in Pitcher Plants (<i>Nepenthes</i> spp.) via an Unusual Complement of Endogenous Enzymes. Journal of Proteome Research, 2016, 15, 3108-3117.	3.7	51
28	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. Scientific Reports, 2016, 6, 30980.	3.3	54
29	<scp>HXâ€MS</scp> 2 for high performance conformational analysis of complex protein states. Protein Science, 2015, 24, 1313-1324.	7.6	8
30	A Hypothesis-Directed Approach to the Targeted Development of a Multiplexed Proteomic Biomarker Assay for Cancer. Cancer Informatics, 2015, 14, CIN.S24388.	1.9	2
31	A robust capillary liquid chromatography/tandem mass spectrometry method for quantitation of neuromodulatory endocannabinoids. Rapid Communications in Mass Spectrometry, 2015, 29, 1889-1897.	1.5	39
32	Recombinant Nepenthesin II for Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2015, 87, 6681-6687.	6.5	54
33	Toward Standardizing Deuterium Content Reporting in Hydrogen Exchange-MS. Analytical Chemistry, 2014, 86, 11962-11965.	6.5	8
34	Tracking Allosteric Propagation with HX-MS. Structure, 2014, 22, 512-514.	3.3	1
35	Expression and characterization of plant aspartic protease nepenthesin-1 from Nepenthes gracilis. Protein Expression and Purification, 2014, 95, 121-128.	1.3	33
36	Nucleotide Exchange in Dimeric MCAK Induces Longitudinal and Lateral Stress at Microtubule Ends to Support Depolymerization. Structure, 2014, 22, 1173-1183.	3.3	12

#	Article	IF	CITATIONS
37	Mass Spec Studio for Integrative Structural Biology. Structure, 2014, 22, 1538-1548.	3.3	86
38	Peptide–Column Interactions and Their Influence on Back Exchange Rates in Hydrogen/Deuterium Exchange-MS. Journal of the American Society for Mass Spectrometry, 2013, 24, 1006-1015.	2.8	51
39	Nepenthesin from Monkey Cups for Hydrogen/Deuterium Exchange Mass Spectrometry. Molecular and Cellular Proteomics, 2013, 12, 464-472.	3.8	54
40	Platform Dependencies in Bottom-up Hydrogen/Deuterium Exchange Mass Spectrometry. Molecular and Cellular Proteomics, 2013, 12, 539-548.	3.8	34
41	Steric and allosteric factors prevent simultaneous binding of transferrin-binding proteins A and B to transferrin. Biochemical Journal, 2012, 444, 189-197.	3.7	5
42	Low-dose laulimalide represents a novel molecular probe for investigating microtubule organization. Cell Cycle, 2012, 11, 3045-3054.	2.6	11
43	High-Resolution Mapping of Carbene-Based Protein Footprints. Analytical Chemistry, 2012, 84, 4411-4418.	6.5	57
44	Probing protein interactions with hydrogen/deuterium exchange and mass spectrometry—A review. Analytica Chimica Acta, 2012, 721, 7-21.	5.4	142
45	Assembly of Ebola Virus Matrix Protein VP40 Is Regulated by Latch-Like Properties of N and C Terminal Tails. PLoS ONE, 2012, 7, e39978.	2.5	19
46	Mass Spectrometry of Laser-Initiated Carbene Reactions for Protein Topographic Analysis. Analytical Chemistry, 2011, 83, 2913-2920.	6.5	56
47	MRM methods for high precision shift measurements in H/DX-MS. International Journal of Mass Spectrometry, 2011, 302, 26-35.	1.5	8
48	XRCC4 Protein Interactions with XRCC4-like Factor (XLF) Create an Extended Grooved Scaffold for DNA Ligation and Double Strand Break Repair. Journal of Biological Chemistry, 2011, 286, 32638-32650.	3.4	151
49	Conserved Interaction between Transferrin and Transferrin-binding Proteins from Porcine Pathogens. Journal of Biological Chemistry, 2011, 286, 21353-21360.	3.4	18
50	Structural Variations within the Transferrin Binding Site on Transferrin-binding Protein B, TbpB. Journal of Biological Chemistry, 2011, 286, 12683-12692.	3.4	42
51	Rheostatic control of tryptic digestion in a microscale fluidic system. Analytica Chimica Acta, 2010, 657, 53-59.	5.4	10
52	Discovery and Characterization of the Laulimalide-Microtubule Binding Mode by Mass Shift Perturbation Mapping. Chemistry and Biology, 2010, 17, 725-734.	6.0	111
53	Hydra: software for tailored processing of H/D exchange data from MS or tandem MS analyses. BMC Bioinformatics, 2009, 10, 162.	2.6	70
54	Surrogate H/D Detection Strategy for Protein Conformational Analysis Using MS/MS Data. Analytical Chemistry, 2009, 81, 7900-7907.	6.5	17

#	Article	IF	CITATIONS
55	Structural Mass Spectrometry of the αβ-Tubulin Dimer Supports a Revised Model of Microtubule Assembly. Biochemistry, 2009, 48, 4858-4870.	2.5	43
56	Integrating Accelerated Tryptic Digestion into Proteomics Workflows. Methods in Molecular Biology, 2009, 492, 241-254.	0.9	4
57	A Unique Mode of Microtubule Stabilization Induced by Peloruside A. Journal of Molecular Biology, 2008, 378, 1016-1030.	4.2	110
58	Restraining Expansion of the Peak Envelope in H/D Exchange-MS and Its Application in Detecting Perturbations of Protein Structure/Dynamics. Analytical Chemistry, 2008, 80, 7004-7011.	6.5	43
59	Detection and Identification of Sub-nanogram Levels of Protein in a NanoLC-Trypsin-MS System. Journal of Proteome Research, 2006, 5, 1959-1966.	3.7	73
60	Quantitating the Statistical Distribution of Deuterium Incorporation To Extend the Utility of H/D Exchange MS Data. Analytical Chemistry, 2006, 78, 207-214.	6.5	50
61	Emerging challenges in ligand discovery: new opportunities for chromatographic assay. Expert Review of Proteomics, 2005, 2, 891-900.	3.0	5
62	High-Throughput Screening for Enzyme Inhibitors Using Frontal Affinity Chromatography with Liquid Chromatography and Mass Spectrometry. Analytical Chemistry, 2005, 77, 6125-6133.	6.5	69
63	Blending Protein Separation and Peptide Analysis through Real-Time Proteolytic Digestion. Analytical Chemistry, 2005, 77, 1572-1579.	6.5	188
64	Peer Reviewed: Biosensor Alternative: Frontal Affinity Chromatography. Analytical Chemistry, 2004, 76, 440 A-448 A.	6.5	56
65	Frontal affinity chromatography–mass spectrometry assay technology for multiple stages of drug discovery: applications of a chromatographic biosensor. Analytical Biochemistry, 2003, 319, 1-12.	2.4	69
66	On-column digestion of proteins in aqueous-organic solvents. Rapid Communications in Mass Spectrometry, 2003, 17, 1044-1050.	1.5	103
67	Hydrogen/Deuterium Exchange Mass Spectrometry of Actin in Various Biochemical Contexts. Journal of Molecular Biology, 2003, 334, 373-385.	4.2	26
68	Micro-Scale Frontal Affinity Chromatography with Mass Spectrometric Detection: A New Method for the Screening of Compound Libraries. Angewandte Chemie - International Edition, 1998, 37, 3383-3387.	13.8	129
69	MALDI Mass Spectrometry Combined with Avidinâ^Biotin Chemistry for Analysis of Protein Modifications. Analytical Chemistry, 1998, 70, 1569-1575.	6.5	27
70	Analysis of Structurally Complex Polymers by Time-Lag Focusing Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry. Macromolecules, 1997, 30, 1955-1963.	4.8	39
71	Time-Lag Focusing MALDI Time-of-Flight Mass Spectrometry for Polymer Characterization:Â Oligomer Resolution, Mass Accuracy, and Average Weight Information. Analytical Chemistry, 1997, 69, 2734-2741. –	6.5	75
72	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 1. Sample Preparation and Desorption/Ionization Issues. Analytical Chemistry, 1997, 69, 4169-4175.	6.5	150

#	Article	IF	CITATIONS
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.	6.5	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.	2.8	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.	6.5	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.	6.5	251
77	Combining Avidinâ^'Biotin Chemistry with Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. Analytical Chemistry, 1996, 68, 3382-3387.	6.5	36
78	Laserâ€induced surface ionization in a timeâ€ofâ€flight mass spectrometer. Review of Scientific Instruments, 1995, 66, 55-62.	1.3	17
79	A Dual Ionization Source with Laser Desorption Sample Introduction in a Time-of-Flight Mass	1.8	2