

Jared B Shaw

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,811
citations

236912

25
h-index

289230

40
g-index

41
all docs

41
docs citations

41
times ranked

2145
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced Top-Down Protein Characterization with Electron Capture Dissociation and Cyclic Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 3888-3896.	6.5	14
2	Improved Protein and PTM Characterization with a Practical Electron-Based Fragmentation on Q-TOF Instruments. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2081-2091.	2.8	14
3	Proteo-Genomic Analysis Identifies Two Major Sites of Vulnerability on Ebolavirus Glycoprotein for Neutralizing Antibodies in Convalescent Human Plasma. <i>Frontiers in Immunology</i> , 2021, 12, 706757.	4.8	4
4	Tunable Heteroassembly of a Plant Pseudoenzyme-Enzyme Complex. <i>ACS Chemical Biology</i> , 2021, 16, 2315-2325.	3.4	13
5	Evaluating the Performance of 193 nm Ultraviolet Photodissociation for Tandem Mass Tag Labeled Peptides. <i>Analytica—A Journal of Analytical Chemistry and Chemical Analysis</i> , 2021, 2, 140-155.	1.7	3
6	Charge Movement and Structural Changes in the Gas-Phase Unfolding of Multimeric Protein Complexes Captured by Native Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 1788-1795.	6.5	31
7	Direct Determination of Antibody Chain Pairing by Top-down and Middle-down Mass Spectrometry Using Electron Capture Dissociation and Ultraviolet Photodissociation. <i>Analytical Chemistry</i> , 2020, 92, 766-773.	6.5	50
8	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	2.8	67
9	Antifungal symbiotic peptide NCR044 exhibits unique structure and multifaceted mechanisms of action that confer plant protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16043-16054.	7.1	36
10	Rapid and Simultaneous Characterization of Drug Conjugation in Heavy and Light Chains of a Monoclonal Antibody Revealed by High-Resolution Ion Mobility Separations in SLIM. <i>Analytical Chemistry</i> , 2020, 92, 5004-5012.	6.5	21
11	Single-Cell Metabolic Profiling: Metabolite Formulas from Isotopic Fine Structures in Heterogeneous Plant Cell Populations. <i>Analytical Chemistry</i> , 2020, 92, 7289-7298.	6.5	37
12	Siderophore profiling of co-habiting soil bacteria by ultra-high resolution mass spectrometry. <i>Metallomics</i> , 2019, 11, 166-175.	2.4	19
13	Ambient Metabolic Profiling and Imaging of Biological Samples with Ultrahigh Molecular Resolution Using Laser Ablation Electrospray Ionization 21 Tesla FTICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 5028-5035.	6.5	40
14	High Speed Intact Protein Characterization Using 4X Frequency Multiplication, Ion Trap Harmonization, and 21 Tesla FTICR-MS. <i>Analytical Chemistry</i> , 2018, 90, 5557-5562.	6.5	23
15	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	3.7	35
16	Micronutrient metal speciation is controlled by competitive organic chelation in grassland soils. <i>Soil Biology and Biochemistry</i> , 2018, 120, 283-291.	8.8	31
17	Increasing the Separation Capacity of Intact Histone Proteoforms Chromatography Coupling Online Weak Cation Exchange-HILIC to Reversed Phase LC UVPD-HRMS. <i>Journal of Proteome Research</i> , 2018, 17, 3791-3800.	3.7	43
18	Sequencing Grade Tandem Mass Spectrometry for Top-Down Proteomics Using Hybrid Electron Capture Dissociation Methods in a Benchtop Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2018, 90, 10819-10827.	6.5	54

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19	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , 2018, 125, 290-299.	8.8	37
20	A unique deubiquitinase that deconjugates phosphoribosyl-linked protein ubiquitination. <i>Cell Research</i> , 2017, 27, 865-881.	12.0	70
21	Unambiguous identification and discovery of bacterial siderophores by direct injection 21 Tesla Fourier transform ion cyclotron resonance mass spectrometry. <i>Metallomics</i> , 2017, 9, 82-92.	2.4	21
22	Molecular Characterization of Organosulfur Compounds in Biodiesel and Diesel Fuel Secondary Organic Aerosol. <i>Environmental Science & Technology</i> , 2017, 51, 119-127.	10.0	74
23	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	19.0	126
24	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	62
25	21 Tesla Fourier Transform Ion Cyclotron Resonance Mass Spectrometer Greatly Expands Mass Spectrometry Toolbox. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1929-1936.	2.8	86
26	Vacuum Ultraviolet Photodissociation and Fourier Transform Ion Cyclotron Resonance (FT-ICR) Mass Spectrometry: Revisited. <i>Analytical Chemistry</i> , 2016, 88, 3019-3023.	6.5	29
27	High-Throughput Bioconjugation for Enhanced 193 nm Photodissociation via Droplet Phase Initiated Ion/Ion Chemistry Using a Front-End Dual Spray Reactor. <i>Analytical Chemistry</i> , 2015, 87, 9396-9402.	6.5	15
28	The first pilot project of the consortium for top-down proteomics: <sc>A</sc> status report. <i>Proteomics</i> , 2014, 14, 1130-1140.	2.2	90
29	Ultraviolet Photodissociation for Characterization of Whole Proteins on a Chromatographic Time Scale. <i>Analytical Chemistry</i> , 2014, 86, 2185-2192.	6.5	81
30	Comparison of MS/MS Methods for Characterization of DNA/Cisplatin Adducts. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 265-273.	2.8	17
31	Extending the Isotopically Resolved Mass Range of Orbitrap Mass Spectrometers. <i>Analytical Chemistry</i> , 2013, 85, 8313-8318.	6.5	22
32	Complete Protein Characterization Using Top-Down Mass Spectrometry and Ultraviolet Photodissociation. <i>Journal of the American Chemical Society</i> , 2013, 135, 12646-12651.	13.7	297
33	Concurrent Automated Sequencing of the Glycan and Peptide Portions of <i>O</i> -Linked Glycopeptide Anions by Ultraviolet Photodissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 9253-9261.	6.5	65
34	Activated Ion Negative Electron Transfer Dissociation of Multiply Charged Peptide Anions. <i>Analytical Chemistry</i> , 2013, 85, 4721-4728.	6.5	10
35	High-throughput Database Search and Large-scale Negative Polarity Liquid Chromatography-Tandem Mass Spectrometry with Ultraviolet Photodissociation for Complex Proteomic Samples. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2604-2614.	3.8	33
36	Systematic Comparison of Ultraviolet Photodissociation and Electron Transfer Dissociation for Peptide Anion Characterization. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1707-1715.	2.8	29

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37	Tyrosine sulfation in a Gram-negative bacterium. <i>Nature Communications</i> , 2012, 3, 1153.	12.8	63
38	Tyrosine Deprotonation Yields Abundant and Selective Backbone Cleavage in Peptide Anions upon Negative Electron Transfer Dissociation and Ultraviolet Photodissociation. <i>Journal of the American Chemical Society</i> , 2012, 134, 15624-15627.	13.7	9
39	Analysis of protein digests by transmission-mode desorption electrospray ionization mass spectrometry with ultraviolet photodissociation. <i>International Journal of Mass Spectrometry</i> , 2011, 308, 203-208.	1.5	7
40	Implementing Photodissociation in an Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1105-1108.	2.8	32