

Zhijie Wu

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

469
citations

840585

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h-index

887953

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17
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17
docs citations

17
times ranked

530
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of a Two-Dimensional Liquid Chromatography-Mass Spectrometry Platform for Simultaneous Multi-Attribute Characterization of Adeno-Associated Viruses. <i>Analytical Chemistry</i> , 2022, 94, 3219-3226.	3.2	15
2	Top-Down Proteomics Reveals Myofilament Proteoform Heterogeneity among Various Rat Skeletal Muscle Tissues. <i>Journal of Proteome Research</i> , 2020, 19, 446-454.	1.8	13
3	Nanoproteomics enables proteoform-resolved analysis of low-abundance proteins in human serum. <i>Nature Communications</i> , 2020, 11, 3903.	5.8	43
4	MASH Explorer: A Universal Software Environment for Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3867-3876.	1.8	62
5	Rapid Analysis of Reduced Antibody Drug Conjugate by Online LC-MS/MS with Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 15096-15103.	3.2	8
6	Enhancing Top-Down Proteomics Data Analysis by Combining Deconvolution Results through a Machine Learning Strategy. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1104-1113.	1.2	19
7	Analysis of cardiac troponin proteoforms by top-down mass spectrometry. <i>Methods in Enzymology</i> , 2019, 626, 347-374.	0.4	10
8	Bridged Hybrid Monolithic Column Coupled to High-Resolution Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2019, 91, 1743-1747.	3.2	28
9	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085.	1.3	9
10	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	1.3	147
11	Reproducible large-scale synthesis of surface silanized nanoparticles as an enabling nanoproteomics platform: Enrichment of the human heart phosphoproteome. <i>Nano Research</i> , 2019, 12, 1473-1481.	5.8	22
12	Comprehensive Characterization of the Recombinant Catalytic Subunit of cAMP-Dependent Protein Kinase by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2561-2570.	1.2	10
13	Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018, 90, 4935-4939.	3.2	17
14	Temperature-sensitive sarcomeric protein post-translational modifications revealed by top-down proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 122, 11-22.	0.9	19
15	Complete Characterization of Cardiac Myosin Heavy Chain (223 kDa) Enabled by Size-Exclusion Chromatography and Middle-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 4922-4930.	3.2	28
16	Side-chain-to-tail cyclization of ribosomally derived peptides promoted by aryl and alkyl amino-functionalized unnatural amino acids. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 5803-5812.	1.5	14