

Ziqing Lin

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,435
citations

331538

21
h-index

345118

36
g-index

38
all docs

38
docs citations

38
times ranked

1806
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of chiral normal-phase liquid chromatography as a secondary tier in pharmaceutical chiral screening strategy. <i>Journal of Chromatography A</i> , 2022, 1672, 463053.	1.8	2
2	High-molecular weight impurity screening by size-exclusion chromatography on a reversed-phase column. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 196, 113908.	1.4	2
3	Evaluation of a polysaccharide-based chiral reversed-phase liquid chromatography screen strategy in pharmaceutical analysis. <i>Journal of Chromatography A</i> , 2021, 1645, 462085.	1.8	10
4	A generic liquid chromatography-mass spectrometry method for monitoring bis(pinacolato)diboron mutagenic impurity in pharmaceutical compounds. <i>Journal of Chromatography Open</i> , 2021, 1, 100009.	0.8	1
5	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
6	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.	1.2	67
7	Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2019, 91, 11661-11669.	3.2	22
8	An Unbiased Proteomics Method to Assess the Maturation of Human Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Circulation Research</i> , 2019, 125, 936-953.	2.0	59
9	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	9.0	241
10	High-Precision Quantitation of Biofluid Samples Using Direct Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2019, 91, 6986-6990.	3.2	14
11	A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019, 16, 417-420.	9.0	82
12	A Top-Down Proteomics Platform Coupling Serial Size Exclusion Chromatography and Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 3835-3844.	3.2	37
13	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. <i>Nature Communications</i> , 2019, 10, 5612.	5.8	15
14	Comprehensive characterization of monoclonal antibody by Fourier transform ion cyclotron resonance mass spectrometry. <i>MAbs</i> , 2019, 11, 106-115.	2.6	50
15	Deletion of Enigma Homologue from the Z-disc slows tension development kinetics in mouse myocardium. <i>Journal of General Physiology</i> , 2019, 151, 670-679.	0.9	6
16	Simultaneous Quantification of Protein Expression and Modifications by Top-down Targeted Proteomics: A Case of the Sarcomeric Subproteome. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 594-605.	2.5	27
17	Comprehensive Characterization of Swine Cardiac Troponin T Proteoforms by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1284-1294.	1.2	15
18	Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018, 90, 4935-4939.	3.2	17

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19	Novel Sarcopenia-related Alterations in Sarcomeric Protein Post-translational Modifications (PTMs) in Skeletal Muscles Identified by Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 134-145.	2.5	36
20	Top-Down Proteomics: Ready for Prime Time?. <i>Analytical Chemistry</i> , 2018, 90, 110-127.	3.2	159
21	Online Hydrophobic Interaction Chromatography–Mass Spectrometry for the Analysis of Intact Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 7135-7138.	3.2	53
22	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
23	In-capillary microextraction for direct mass spectrometry analysis of biological samples. <i>Talanta</i> , 2018, 189, 451-457.	2.9	15
24	Distinct sequences and post-translational modifications in cardiac atrial and ventricular myosin light chains revealed by top-down mass spectrometry. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 107, 13-21.	0.9	28
25	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
26	Coupling functionalized cobalt ferrite nanoparticle enrichment with online LC/MS/MS for top-down phosphoproteomics. <i>Chemical Science</i> , 2017, 8, 4306-4311.	3.7	34
27	Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2017, 13, 1267-1273.	3.9	28
28	The Impact of Phosphorylation on Electron Capture Dissociation of Proteins: A Top-Down Perspective. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1805-1814.	1.2	9
29	Paper-capillary spray for direct mass spectrometry analysis of biofluid samples. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 1385-1390.	1.9	37
30	Comprehensive analysis of tropomyosin isoforms in skeletal muscles by top-down proteomics. <i>Journal of Muscle Research and Cell Motility</i> , 2016, 37, 41-52.	0.9	29
31	Gas-phase reactions of cyclopropenylidene with protonated alkyl amines. <i>Analyst, The</i> , 2016, 141, 2412-2417.	1.7	7
32	Real-Time Sample Analysis Using a Sampling Probe and Miniature Mass Spectrometer. <i>Analytical Chemistry</i> , 2015, 87, 8867-8873.	3.2	37
33	Development of a Mass Spectrometry Sampling Probe for Chemical Analysis in Surgical and Endoscopic Procedures. <i>Analytical Chemistry</i> , 2013, 85, 11843-11850.	3.2	31
34	In situ arsenic speciation on solid surfaces by desorption electrospray ionization tandem mass spectrometry. <i>Analyst, The</i> , 2010, 135, 1268.	1.7	18
35	Rapid screening of active ingredients in drugs by mass spectrometry with low-temperature plasma probe. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 591-599.	1.9	72
36	Real-time monitoring of chemical reactions by mass spectrometry utilizing a low-temperature plasma probe. <i>Analyst, The</i> , 2009, 134, 1863.	1.7	65

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37	Versatile Platform Employing Desorption Electrospray Ionization Mass Spectrometry for High-Throughput Analysis. <i>Analytical Chemistry</i> , 2008, 80, 6131-6136.	3.2	47