

# 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  | Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.  | 9.0 | 241       |
| 2  | Top-Down Proteomics: Ready for Prime Time?. <i>Analytical Chemistry</i> , 2018, 90, 110-127.  | 3.2 | 159       |
| 3  | A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019, 16, 417-420.   | 9.0 | 82        |
| 4  | 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        |
| 5  | 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        |
| 6  | Real-time monitoring of chemical reactions by mass spectrometry utilizing a low-temperature plasma probe. <i>Analyst</i> , 2009, 134, 1863.   | 1.7 | 65        |
| 7  | 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        |
| 8  | Online Hydrophobic Interaction Chromatography-Mass Spectrometry for the Analysis of Intact Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 7135-7138.  | 3.2 | 53        |
| 9  | Comprehensive characterization of monoclonal antibody by Fourier transform ion cyclotron resonance mass spectrometry. <i>MAbs</i> , 2019, 11, 106-115.  | 2.6 | 50        |
| 10 | Versatile Platform Employing Desorption Electrospray Ionization Mass Spectrometry for High-Throughput Analysis. <i>Analytical Chemistry</i> , 2008, 80, 6131-6136.  | 3.2 | 47        |
| 11 | Real-Time Sample Analysis Using a Sampling Probe and Miniature Mass Spectrometer. <i>Analytical Chemistry</i> , 2015, 87, 8867-8873.  | 3.2 | 37        |
| 12 | Paper-capillary spray for direct mass spectrometry analysis of biofluid samples. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 1385-1390.  | 1.9 | 37        |
| 13 | 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        |
| 14 | 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        |
| 15 | 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        |
| 16 | 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        |
| 17 | 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        |
| 18 | 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        |

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|----|--|-----|-----------|
| 19 | 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        |
| 20 | Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2017, 13, 1267-1273.  | 3.9 | 28        |
| 21 | 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        |
| 22 | Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2019, 91, 11661-11669.   | 3.2 | 22        |
| 23 | 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        |
| 24 | In situ arsenic speciation on solid surfaces by desorption electrospray ionization tandem mass spectrometry. <i>Analyst, The</i> , 2010, 135, 1268.  | 1.7 | 18        |
| 25 | Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018, 90, 4935-4939.  | 3.2 | 17        |
| 26 | 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        |
| 27 | In-capillary microextraction for direct mass spectrometry analysis of biological samples. <i>Talanta</i> , 2018, 189, 451-457.   | 2.9 | 15        |
| 28 | 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        |
| 29 | High-Precision Quantitation of Biofluid Samples Using Direct Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2019, 91, 6986-6990.  | 3.2 | 14        |
| 30 | 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        |
| 31 | 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        |
| 32 | 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         |
| 33 | Gas-phase reactions of cyclopropenylidene with protonated alkyl amines. <i>Analyst, The</i> , 2016, 141, 2412-2417.  | 1.7 | 7         |
| 34 | 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         |
| 35 | 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         |
| 36 | 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         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 37 | 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         |