

Ying Ge

List of Publications by Year in descending order

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134
papers

7,848
citations

66250

44
h-index

66518

82
g-index

147
all docs

147
docs citations

147
times ranked

7548
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Fourierâ€transform ion cyclotron resonance mass spectrometry for characterizing proteoforms. <i>Mass Spectrometry Reviews</i> , 2022, 41, 158-177. | 2.8 | 12 |
| 2 | RBM20 phosphorylation and its role in nucleocytoplasmic transport and cardiac pathogenesis. <i>FASEB Journal</i> , 2022, 36, e22302. | 0.2 | 10 |
| 3 | Segmental Bronchial Allergen Challenge Elicits Distinct Metabolic Phenotypes in Allergic Asthma. <i>Metabolites</i> , 2022, 12, 381. | 1.3 | 2 |
| 4 | One-Pot Exosome Proteomics Enabled by a Photocleavable Surfactant. <i>Analytical Chemistry</i> , 2022, 94, 7164-7168. | 3.2 | 9 |
| 5 | Airway fibrin formation cascade in allergic asthma exacerbation: implications for inflammation and remodeling. <i>Clinical Proteomics</i> , 2022, 19, 15. | 1.1 | 3 |
| 6 | <i>Rbm20</i> ablation is associated with changes in the expression of titin-interacting and metabolic proteins. <i>Molecular Omics</i> , 2022, 18, 627-634. | 1.4 | 2 |
| 7 | Intact Protein Mass Spectrometry for Therapeutic Protein Quantitation, Pharmacokinetics, and Biotransformation in Preclinical and Clinical Studies: An Industry Perspective. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1886-1900. | 1.2 | 19 |
| 8 | Ultrahigh-Resolution Mass Spectrometry-Based Platform for Plasma Metabolomics Applied to Type 2 Diabetes Research. <i>Journal of Proteome Research</i> , 2021, 20, 463-473. | 1.8 | 15 |
| 9 | Systemic Metabolic Alterations Correlate with Islet-Level Prostaglandin E2 Production and Signaling Mechanisms That Predict β^2 -Cell Dysfunction in a Mouse Model of Type 2 Diabetes. <i>Metabolites</i> , 2021, 11, 58. | 1.3 | 16 |
| 10 | Stable Picodisc Assemblies from Saposin Proteins and Branched Detergents. <i>Biochemistry</i> , 2021, 60, 1108-1119. | 1.2 | 2 |
| 11 | Discovery of RSV-Induced BRD4 Protein Interactions Using Native Immunoprecipitation and Parallel Accumulationâ€Serial Fragmentation (PASEF) Mass Spectrometry. <i>Viruses</i> , 2021, 13, 454. | 1.5 | 20 |
| 12 | Novel Strategies to Address the Challenges in Top-Down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1278-1294. | 1.2 | 102 |
| 13 | Human Islet Expression Levels of Prostaglandin E ₂ Synthetic Enzymes, But Not Prostaglandin EP3 Receptor, Are Positively Correlated with Markers of β^2 -Cell Function and Mass in Nondiabetic Obesity. <i>ACS Pharmacology and Translational Science</i> , 2021, 4, 1338-1348. | 2.5 | 10 |
| 14 | High-Throughput Multi-attribute Analysis of Antibody-Drug Conjugates Enabled by Trapped Ion Mobility Spectrometry and Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 10013-10021. | 3.2 | 29 |
| 15 | Structural O-Glycoform Heterogeneity of the SARS-CoV-2 Spike Protein Receptor-Binding Domain Revealed by Top-Down Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2021, 143, 12014-12024. | 6.6 | 48 |
| 16 | Ultrafast and Reproducible Proteomics from Small Amounts of Heart Tissue Enabled by Azo and timsTOF Pro. <i>Journal of Proteome Research</i> , 2021, 20, 4203-4211. | 1.8 | 34 |
| 17 | Multiomics Method Enabled by Sequential Metabolomics and Proteomics for Human Pluripotent Stem-Cell-Derived Cardiomyocytes. <i>Journal of Proteome Research</i> , 2021, 20, 4646-4654. | 1.8 | 10 |
| 18 | Functionally Integrated Top-Down Proteomics for Standardized Assessment of Human Induced Pluripotent Stem Cell-Derived Engineered Cardiac Tissues. <i>Journal of Proteome Research</i> , 2021, 20, 1424-1433. | 1.8 | 14 |

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|----|--|-----|-----------|
| 19 | Proteomic Analysis of the Functional Inward Rectifier Potassium Channel (Kir) 2.1 Reveals Several Novel Phosphorylation Sites. <i>Biochemistry</i> , 2021, 60, 3292-3301. | 1.2 | 5 |
| 20 | The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021, 7, eabk0734. | 4.7 | 106 |
| 21 | 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 |
| 22 | Photocleavable Surfactant-Enabled Extracellular Matrix Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 15693-15698. | 3.2 | 24 |
| 23 | Top-Down Proteomics of Endogenous Membrane Proteins Enabled by Cloud Point Enrichment and Multidimensional Liquid Chromatography-MS Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 15726-15735. | 3.2 | 24 |
| 24 | Top-down proteomics: challenges, innovations, and applications in basic and clinical research. <i>Expert Review of Proteomics</i> , 2020, 17, 719-733. | 1.3 | 70 |
| 25 | Nanoproteomics enables proteoform-resolved analysis of low-abundance proteins in human serum. <i>Nature Communications</i> , 2020, 11, 3903. | 5.8 | 43 |
| 26 | 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 |
| 27 | MASH Explorer: A Universal Software Environment for Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3867-3876. | 1.8 | 62 |
| 28 | 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 |
| 29 | Chemical Control of Quorum Sensing in <i>E. coli</i> : Identification of Small Molecule Modulators of SdiA and Mechanistic Characterization of a Covalent Inhibitor. <i>ACS Infectious Diseases</i> , 2020, 6, 3092-3103. | 1.8 | 13 |
| 30 | Distinct hypertrophic cardiomyopathy genotypes result in convergent sarcomeric proteoform profiles revealed by top-down proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24691-24700. | 3.3 | 67 |
| 31 | GRK5 Controls SAP97-Dependent Cardiotoxic β_1 Adrenergic Receptor-CaMKII Signaling in Heart Failure. <i>Circulation Research</i> , 2020, 127, 796-810. | 2.0 | 16 |
| 32 | 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 |
| 33 | High-Throughput Proteomics Enabled by a Photocleavable Surfactant. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 8406-8410. | 7.2 | 37 |
| 34 | High-Throughput Proteomics Enabled by a Photocleavable Surfactant. <i>Angewandte Chemie</i> , 2020, 132, 8484-8488. | 1.6 | 14 |
| 35 | MS-Derived Isotopic Fine Structure Reveals Forazoline A as a Thioketone-Containing Marine-Derived Natural Product. <i>Organic Letters</i> , 2020, 22, 1275-1279. | 2.4 | 12 |
| 36 | Higher-order structural characterisation of native proteins and complexes by top-down mass spectrometry. <i>Chemical Science</i> , 2020, 11, 12918-12936. | 3.7 | 81 |

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|----|---|-----|-----------|
| 37 | Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019, 91, 10937-10942. | 3.2 | 11 |
| 38 | Analysis of cardiac troponin proteoforms by top-down mass spectrometry. <i>Methods in Enzymology</i> , 2019, 626, 347-374. | 0.4 | 10 |
| 39 | Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2019, 91, 11661-11669. | 3.2 | 22 |
| 40 | A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940. | 9.0 | 55 |
| 41 | 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 |
| 42 | 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 |
| 43 | Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085. | 1.3 | 9 |
| 44 | Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594. | 9.0 | 241 |
| 45 | Epigenetic Priming of Human Pluripotent Stem Cell-Derived Cardiac Progenitor Cells Accelerates Cardiomyocyte Maturation. <i>Stem Cells</i> , 2019, 37, 910-923. | 1.4 | 30 |
| 46 | Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361. | 1.3 | 147 |
| 47 | 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 |
| 48 | Top-down Mass Spectrometry of Sarcomeric Protein Post-translational Modifications from Non-human Primate Skeletal Muscle. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2460-2469. | 1.2 | 26 |
| 49 | A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019, 16, 417-420. | 9.0 | 82 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | Comprehensive characterization of monoclonal antibody by Fourier transform ion cyclotron resonance mass spectrometry. <i>MAbs</i> , 2019, 11, 106-115. | 2.6 | 50 |
| 54 | 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 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | Harnessing the Power of Proteomics to Assess Drug Safety and Guide Clinical Trials. <i>Circulation</i> , 2018, 137, 1011-1014. | 1.6 | 5 |
| 57 | 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 |
| 58 | ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325. | 1.8 | 35 |
| 59 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214. | 3.9 | 580 |
| 60 | Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018, 90, 4935-4939. | 3.2 | 17 |
| 61 | 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 |
| 62 | Large Cardiac Muscle Patches Engineered From Human Induced-Pluripotent Stem Cell-Derived Cardiac Cells Improve Recovery From Myocardial Infarction in Swine. <i>Circulation</i> , 2018, 137, 1712-1730. | 1.6 | 332 |
| 63 | Top-Down Proteomics: Ready for Prime Time?. <i>Analytical Chemistry</i> , 2018, 90, 110-127. | 3.2 | 159 |
| 64 | Online Hydrophobic Interaction Chromatography-Mass Spectrometry for the Analysis of Intact Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 7135-7138. | 3.2 | 53 |
| 65 | The HCM-linked W792R mutation in cardiac myosin-binding protein C reduces C6 FnIII domain stability. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 314, H1179-H1191. | 1.5 | 19 |
| 66 | 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 |
| 67 | Characterization of TTN Novex Splicing Variants across Species and the Role of RBM20 in Novex-Specific Exon Splicing. <i>Genes</i> , 2018, 9, 86. | 1.0 | 7 |
| 68 | Z-band and M-band titin splicing and regulation by RNA binding motif 20 in striated muscles. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9986-9996. | 1.2 | 10 |
| 69 | Mass Spectrometry Analysis of RBM20 Phosphorylation and Its Role in Titin Splicing. <i>FASEB Journal</i> , 2018, 32, 791.13. | 0.2 | 0 |
| 70 | Top-Down Proteomics of Large Proteins up to 223 kDa Enabled by Serial Size Exclusion Chromatography Strategy. <i>Analytical Chemistry</i> , 2017, 89, 5467-5475. | 3.2 | 108 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | Quantitative Proteomics and Immunohistochemistry Reveal Insights into Cellular and Molecular Processes in the Infarct Border Zone One Month after Myocardial Infarction. <i>Journal of Proteome Research</i> , 2017, 16, 2101-2112. | 1.8 | 18 |
| 75 | Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains in Cellulo. <i>Analytical Chemistry</i> , 2017, 89, 4428-4434. | 3.2 | 41 |
| 76 | Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2017, 13, 1267-1273. | 3.9 | 28 |
| 77 | PP2A-B α holoenzyme substrate recognition, regulation and role in cytokinesis. <i>Cell Discovery</i> , 2017, 3, 17027. | 3.1 | 68 |
| 78 | Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry (UbiChEM-MS) Reveals Cell-Cycle Dependent Formation of Lys11/Lys48 Branched Ubiquitin Chains. <i>Journal of Proteome Research</i> , 2017, 16, 3363-3369. | 1.8 | 22 |
| 79 | 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 |
| 80 | Subunit-Specific Labeling of Ubiquitin Chains by Using Sortase: Insights into the Selectivity of Deubiquitinases. <i>ChemBioChem</i> , 2016, 17, 1525-1531. | 1.3 | 6 |
| 81 | Top-Down Targeted Proteomics Reveals Decrease in Myosin Regulatory Light-Chain Phosphorylation That Contributes to Sarcopenic Muscle Dysfunction. <i>Journal of Proteome Research</i> , 2016, 15, 2706-2716. | 1.8 | 43 |
| 82 | A Family of Photolabile Nitroveratryl-Based Surfactants That Self-Assemble into Photodegradable Supramolecular Structures. <i>Langmuir</i> , 2016, 32, 3963-3969. | 1.6 | 10 |
| 83 | 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 |
| 84 | Top-Down Proteomics. , 2016, , 187-212. | | 1 |
| 85 | Top-down Proteomics: Technology Advancements and Applications to Heart Diseases. <i>Expert Review of Proteomics</i> , 2016, 13, 717-730. | 1.3 | 84 |
| 86 | MASH Suite Pro: A Comprehensive Software Tool for Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 703-714. | 2.5 | 111 |
| 87 | Comprehensive Characterization of AMP-Activated Protein Kinase Catalytic Domain by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 220-232. | 1.2 | 9 |
| 88 | Online Hydrophobic Interaction Chromatography-Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2016, 88, 1885-1891. | 3.2 | 83 |
| 89 | Quantitative proteomics reveals differential regulation of protein expression in recipient myocardium after trilineage cardiovascular cell transplantation. <i>Proteomics</i> , 2015, 15, 2560-2567. | 1.3 | 12 |
| 90 | Specific Enrichment of Phosphoproteins Using Functionalized Multivalent Nanoparticles. <i>Journal of the American Chemical Society</i> , 2015, 137, 2432-2435. | 6.6 | 61 |

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|-----|--|-----|-----------|
| 91 | New Mass-Spectrometry-Compatible Degradable Surfactant for Tissue Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 1587-1599. | 1.8 | 66 |
| 92 | Dissecting human skeletal muscle troponin proteoforms by top-down mass spectrometry. <i>Journal of Muscle Research and Cell Motility</i> , 2015, 36, 169-181. | 0.9 | 7 |
| 93 | Effective Top-Down LC/MS+ Method for Assessing Actin Isoforms as a Potential Cardiac Disease Marker. <i>Analytical Chemistry</i> , 2015, 87, 8399-8406. | 3.2 | 27 |
| 94 | Three Dimensional Liquid Chromatography Coupling Ion Exchange Chromatography/Hydrophobic Interaction Chromatography/Reverse Phase Chromatography for Effective Protein Separation in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 5363-5371. | 3.2 | 64 |
| 95 | Comprehensive assessment of chamber-specific and transmural heterogeneity in myofilament protein phosphorylation by top-down mass spectrometry. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 87, 102-112. | 0.9 | 27 |
| 96 | Myocardial Infarction-induced N-terminal Fragment of Cardiac Myosin-binding Protein C (cMyBP-C) Impairs Myofilament Function in Human Myocardium. <i>Journal of Biological Chemistry</i> , 2014, 289, 8818-8827. | 1.6 | 39 |
| 97 | Cardiac Repair in a Porcine Model of Acute Myocardial Infarction with Human Induced Pluripotent Stem Cell-Derived Cardiovascular Cells. <i>Cell Stem Cell</i> , 2014, 15, 750-761. | 5.2 | 407 |
| 98 | Alpha1 catalytic subunit of AMPK modulates contractile function of cardiomyocytes through phosphorylation of troponin I. <i>Life Sciences</i> , 2014, 98, 75-82. | 2.0 | 24 |
| 99 | MASH Suite: A User-Friendly and Versatile Software Interface for High-Resolution Mass Spectrometry Data Interpretation and Visualization. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 464-470. | 1.2 | 67 |
| 100 | Top-down proteomics in health and disease: Challenges and opportunities. <i>Proteomics</i> , 2014, 14, 1195-1210. | 1.3 | 169 |
| 101 | Top-down Proteomics Reveals Concerted Reductions in Myofilament and Z-disc Protein Phosphorylation after Acute Myocardial Infarction. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2752-2764. | 2.5 | 96 |
| 102 | Top-down mass spectrometry of cardiac myofilament proteins in health and disease. <i>Proteomics - Clinical Applications</i> , 2014, 8, 554-568. | 0.8 | 27 |
| 103 | Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains. <i>Biochemistry</i> , 2014, 53, 4979-4989. | 1.2 | 79 |
| 104 | Effective Protein Separation by Coupling Hydrophobic Interaction and Reverse Phase Chromatography for Top-down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 7899-7906. | 3.2 | 52 |
| 105 | Proteomics in heart failure: top-down or bottom-up?. <i>Pflugers Archiv European Journal of Physiology</i> , 2014, 466, 1199-1209. | 1.3 | 46 |
| 106 | In-depth proteomic analysis of human tropomyosin by top-down mass spectrometry. <i>Journal of Muscle Research and Cell Motility</i> , 2013, 34, 199-210. | 0.9 | 40 |
| 107 | Ultrahigh pressure fast size exclusion chromatography for top-down proteomics. <i>Proteomics</i> , 2013, 13, 2563-2566. | 1.3 | 31 |
| 108 | Top-down Targeted Proteomics for Deep Sequencing of Tropomyosin Isoforms. <i>Journal of Proteome Research</i> , 2013, 12, 187-198. | 1.8 | 45 |

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|-----|--|-----|-----------|
| 109 | The impact of antibody selection on the detection of cardiac troponin I. <i>Clinica Chimica Acta</i> , 2013, 420, 82-88. | 0.5 | 18 |
| 110 | High throughput screening of disulfide-containing proteins in a complex mixture. <i>Proteomics</i> , 2013, 13, 3256-3260. | 1.3 | 15 |
| 111 | N-terminal region of cardiac myosin binding protein impairs myofilament function. <i>FASEB Journal</i> , 2013, 27, 921.7. | 0.2 | 0 |
| 112 | AMP-Activated Protein Kinase Phosphorylates Cardiac Troponin I and Alters Contractility of Murine Ventricular Myocytes. <i>Circulation Research</i> , 2012, 110, 1192-1201. | 2.0 | 70 |
| 113 | Generation and Functional Characterization of Knock-in Mice Harboring the Cardiac Troponin I-R21C Mutation Associated with Hypertrophic Cardiomyopathy. <i>Journal of Biological Chemistry</i> , 2012, 287, 2156-2167. | 1.6 | 38 |
| 114 | Comprehensive Mass Spectrometric Mapping of the Hydroxylated Amino Acid residues of the β 1(V) Collagen Chain. <i>Journal of Biological Chemistry</i> , 2012, 287, 40598-40610. | 1.6 | 47 |
| 115 | Augmented Phosphorylation of Cardiac Troponin I in Hypertensive Heart Failure*. <i>Journal of Biological Chemistry</i> , 2012, 287, 848-857. | 1.6 | 88 |
| 116 | Purification and High-Resolution Top-Down Mass Spectrometric Characterization of Human Salivary β -Amylase. <i>Analytical Chemistry</i> , 2012, 84, 3339-3346. | 3.2 | 42 |
| 117 | Top-Down Quantitative Proteomics Identified Phosphorylation of Cardiac Troponin I as a Candidate Biomarker for Chronic Heart Failure. <i>Journal of Proteome Research</i> , 2011, 10, 4054-4065. | 1.8 | 166 |
| 118 | Phosphorylation, but Not Alternative Splicing or Proteolytic Degradation, Is Conserved in Human and Mouse Cardiac Troponin T. <i>Biochemistry</i> , 2011, 50, 6081-6092. | 1.2 | 34 |
| 119 | Top-down high-resolution electron capture dissociation mass spectrometry for comprehensive characterization of post-translational modifications in Rhesus monkey cardiac troponin I. <i>International Journal of Mass Spectrometry</i> , 2011, 305, 95-102. | 0.7 | 21 |
| 120 | A preferred AMPK phosphorylation site adjacent to the inhibitory loop of cardiac and skeletal troponin I. <i>Protein Science</i> , 2011, 20, 894-907. | 3.1 | 23 |
| 121 | Comprehensive Analysis of Protein Modifications by Top-Down Mass Spectrometry. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 711-711. | 5.1 | 126 |
| 122 | Deciphering modifications in swine cardiac troponin I by top-down high-resolution tandem mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 940-948. | 1.2 | 59 |
| 123 | Delineating <i>Anopheles gambiae</i> coactivator associated arginine methyltransferase 1 automethylation using top-down high resolution tandem mass spectrometry. <i>Protein Science</i> , 2009, 18, 1272-1280. | 3.1 | 20 |
| 124 | <i>In Vivo</i> Phosphorylation Site Mapping in Mouse Cardiac Troponin I by High Resolution Top-Down Electron Capture Dissociation Mass Spectrometry: Ser22/23 Are the Only Sites Basally Phosphorylated. <i>Biochemistry</i> , 2009, 48, 8161-8170. | 1.2 | 82 |
| 125 | Detection of four oxidation sites in viral prolyl-4-hydroxylase by top-down mass spectrometry. <i>Protein Science</i> , 2009, 12, 2320-2326. | 3.1 | 32 |
| 126 | Top-down high-resolution mass spectrometry of cardiac myosin binding protein C revealed that truncation alters protein phosphorylation state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12658-12663. | 3.3 | 141 |

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|-----|--|-----|-----------|
| 127 | Single amino acid sequence polymorphisms in rat cardiac troponin revealed by top-down tandem mass spectrometry. <i>Journal of Muscle Research and Cell Motility</i> , 2008, 29, 203-212. | 0.9 | 46 |
| 128 | Unraveling Molecular Complexity of Phosphorylated Human Cardiac Troponin I by Top Down Electron Capture Dissociation/Electron Transfer Dissociation Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1838-1849. | 2.5 | 104 |
| 129 | Top down characterization of secreted proteins from <i>Mycobacterium tuberculosis</i> by electron capture dissociation mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 253-261. | 1.2 | 76 |
| 130 | Top-down mass spectrometry of a 29-kDa protein for characterization of any posttranslational modification to within one residue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1774-1779. | 3.3 | 248 |
| 131 | Top Down Characterization of Larger Proteins (45 kDa) by Electron Capture Dissociation Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2002, 124, 672-678. | 6.6 | 357 |
| 132 | Blackbody infrared radiative dissociation of larger (42 kDa) multiply charged proteins. <i>International Journal of Mass Spectrometry</i> , 2001, 210-211, 203-214. | 0.7 | 32 |
| 133 | Electron capture dissociation of gaseous multiply charged ions by Fourier-transform ion cyclotron resonance. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 245-249. | 1.2 | 226 |
| 134 | Activated Ion Electron Capture Dissociation for Mass Spectral Sequencing of Larger (42 kDa) Proteins. <i>Analytical Chemistry</i> , 2000, 72, 4778-4784. | 3.2 | 321 |