

Ying Ge

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136
papers

5,567
citations

37
h-index

71
g-index

147
ext. papers

6,700
ext. citations

6.9
avg, IF

5.77
L-index

#	Paper	IF	Citations
136	Top down characterization of larger proteins (45 kDa) by electron capture dissociation mass spectrometry. <i>Journal of the American Chemical Society</i> , 2002 , 124, 672-8	16.4	336
135	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, 750-61	18	329
134	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
133	Activated ion electron capture dissociation for mass spectral sequencing of larger (42 kDa) proteins. <i>Analytical Chemistry</i> , 2000 , 72, 4778-84	7.8	292
132	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, 1774-9	11.5	232
131	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, 245-9	3.5	207
130	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	16.7	207
129	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, 4054-65	5.6	141
128	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137
127	Top-down proteomics in health and disease: challenges and opportunities. <i>Proteomics</i> , 2014 , 14, 1195-2108	10.8	135
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, 12658-63	11.5	131
125	Top-Down Proteomics: Ready for Prime Time?. <i>Analytical Chemistry</i> , 2018 , 90, 110-127	7.8	116
124	Comprehensive analysis of protein modifications by top-down mass spectrometry. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 711		105
123	MASH Suite Pro: A Comprehensive Software Tool for Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 703-14	7.6	95
122	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, 1838-49	7.6	90
121	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, 2752-64	7.6	81
120	Augmented phosphorylation of cardiac troponin I in hypertensive heart failure. <i>Journal of Biological Chemistry</i> , 2012 , 287, 848-57	5.4	79

119	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	7.8	78
118	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e18003614.8	4.8	77
117	In vivo 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, 8161-70	3.2	75
116	Top down characterization of secreted proteins from Mycobacterium tuberculosis by electron capture dissociation mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003 , 14, 253-61	3.5	70
115	Online Hydrophobic Interaction Chromatography-Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2016 , 88, 1885-91	7.8	68
114	Top-down Proteomics: Technology Advancements and Applications to Heart Diseases. <i>Expert Review of Proteomics</i> , 2016 , 13, 717-30	4.2	66
113	Middle-down mass spectrometry enables characterization of branched ubiquitin chains. <i>Biochemistry</i> , 2014 , 53, 4979-89	3.2	61
112	AMP-activated protein kinase phosphorylates cardiac troponin I and alters contractility of murine ventricular myocytes. <i>Circulation Research</i> , 2012 , 110, 1192-201	15.7	59
111	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, 464-70	3.5	58
110	Specific enrichment of phosphoproteins using functionalized multivalent nanoparticles. <i>Journal of the American Chemical Society</i> , 2015 , 137, 2432-5	16.4	54
109	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, 940-8	3.5	54
108	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	7.8	52
107	New mass-spectrometry-compatible degradable surfactant for tissue proteomics. <i>Journal of Proteome Research</i> , 2015 , 14, 1587-99	5.6	48
106	Effective protein separation by coupling hydrophobic interaction and reverse phase chromatography for top-down proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 7899-906	7.8	45
105	PP2A-BSholoenzyme substrate recognition, regulation and role in cytokinesis. <i>Cell Discovery</i> , 2017 , 3, 17027	22.3	44
104	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, 203-12	3.5	43
103	Top-down targeted proteomics for deep sequencing of tropomyosin isoforms. <i>Journal of Proteome Research</i> , 2013 , 12, 187-98	5.6	40
102	Comprehensive mass spectrometric mapping of the hydroxylated amino acid residues of the α (V) collagen chain. <i>Journal of Biological Chemistry</i> , 2012 , 287, 40598-610	5.4	39

101	Proteomics in heart failure: top-down or bottom-up?. <i>Pflugers Archiv European Journal of Physiology</i> , 2014 , 466, 1199-209	4.6	37
100	Purification and high-resolution top-down mass spectrometric characterization of human salivary α -amylase. <i>Analytical Chemistry</i> , 2012 , 84, 3339-46	7.8	37
99	A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019 , 16, 417-420	21.6	36
98	Online Hydrophobic Interaction Chromatography-Mass Spectrometry for the Analysis of Intact Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018 , 90, 7135-7138	7.8	36
97	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, 2706-16	5.6	35
96	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	3.5	34
95	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, 8818-27	5.4	34
94	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, 2156-67	5.4	34
93	An Unbiased Proteomics Method to Assess the Maturation of Human Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Circulation Research</i> , 2019 , 125, 936-953	15.7	33
92	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	3.5	32
91	Phosphorylation, but not alternative splicing or proteolytic degradation, is conserved in human and mouse cardiac troponin T. <i>Biochemistry</i> , 2011 , 50, 6081-92	3.2	31
90	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	11.5	31
89	Blackbody infrared radiative dissociation of larger (42 kDa) multiply charged proteins. <i>International Journal of Mass Spectrometry</i> , 2001 , 210-211, 203-214	1.9	30
88	Higher-order structural characterisation of native proteins and complexes by top-down mass spectrometry. <i>Chemical Science</i> , 2020 , 11, 12918-12936	9.4	30
87	Detection of four oxidation sites in viral prolyl-4-hydroxylase by top-down mass spectrometry. <i>Protein Science</i> , 2003 , 12, 2320-6	6.3	28
86	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
85	Ultrahigh pressure fast size exclusion chromatography for top-down proteomics. <i>Proteomics</i> , 2013 , 13, 2563-6	4.8	27
84	Top-down proteomics: challenges, innovations, and applications in basic and clinical research. <i>Expert Review of Proteomics</i> , 2020 , 17, 719-733	4.2	27

83	Comprehensive characterization of monoclonal antibody by Fourier transform ion cyclotron resonance mass spectrometry. <i>MAbs</i> , 2019 , 11, 106-115	6.6	27
82	Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains in Cellulo. <i>Analytical Chemistry</i> , 2017 , 89, 4428-4434	7.8	26
81	Coupling functionalized cobalt ferrite nanoparticle enrichment with online LC/MS/MS for top-down phosphoproteomics. <i>Chemical Science</i> , 2017 , 8, 4306-4311	9.4	25
80	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
79	Top-down mass spectrometry of cardiac myofilament proteins in health and disease. <i>Proteomics - Clinical Applications</i> , 2014 , 8, 554-68	3.1	24
78	Nanoproteomics enables proteoform-resolved analysis of low-abundance proteins in human serum. <i>Nature Communications</i> , 2020 , 11, 3903	17.4	24
77	MASH Explorer: A Universal Software Environment for Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2020 , 19, 3867-3876	5.6	24
76	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	7.6	23
75	Novel Strategies to Address the Challenges in Top-Down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1278-1294	3.5	23
74	Alpha1 catalytic subunit of AMPK modulates contractile function of cardiomyocytes through phosphorylation of troponin I. <i>Life Sciences</i> , 2014 , 98, 75-82	6.8	22
73	A preferred AMPK phosphorylation site adjacent to the inhibitory loop of cardiac and skeletal troponin I. <i>Protein Science</i> , 2011 , 20, 894-907	6.3	22
72	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	3.5	21
71	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, 102-12	5.8	21
70	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	3.5	21
69	Epigenetic Priming of Human Pluripotent Stem Cell-Derived Cardiac Progenitor Cells Accelerates Cardiomyocyte Maturation. <i>Stem Cells</i> , 2019 , 37, 910-923	5.8	20
68	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	5.8	19
67	Effective top-down LC/MS+ method for assessing actin isoforms as a potential cardiac disease marker. <i>Analytical Chemistry</i> , 2015 , 87, 8399-8406	7.8	19
66	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	1.9	19

65	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, 1272-80	6.3	19
64	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734	14.3	19
63	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	7.8	19
62	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	7.8	18
61	Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2017 , 13, 1267-1273	11.7	18
60	The impact of antibody selection on the detection of cardiac troponin I. <i>Clinica Chimica Acta</i> , 2013 , 420, 82-8	6.2	17
59	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	16.4	17
58	Bridged Hybrid Monolithic Column Coupled to High-Resolution Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2019 , 91, 1743-1747	7.8	16
57	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	5.6	16
56	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	7.6	16
55	High-Throughput Proteomics Enabled by a Photocleavable Surfactant. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 8406-8410	16.4	15
54	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	10	14
53	Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018 , 90, 4935-4939	7.8	14
52	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	5.2	13
51	High throughput screening of disulfide-containing proteins in a complex mixture. <i>Proteomics</i> , 2013 , 13, 3256-60	4.8	13
50	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	5.6	12
49	Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2019 , 91, 11661-11669	7.8	12
48	High-Throughput Proteomics Enabled by a Photocleavable Surfactant. <i>Angewandte Chemie</i> , 2020 , 132, 8484-8488	3.6	12

47	Nonenzymatic Polymerization of Ubiquitin: Single-Step Synthesis and Isolation of Discrete Ubiquitin Oligomers. <i>Angewandte Chemie</i> , 2012 , 124, 13262-13265	3.6	11
46	Quantitative proteomics reveals differential regulation of protein expression in recipient myocardium after trilineage cardiovascular cell transplantation. <i>Proteomics</i> , 2015 , 15, 2560-7	4.8	10
45	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	3.5	9
44	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	3.5	9
43	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, 220-32	3.5	9
42	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	3.5	9
41	Temperature-sensitive sarcomeric protein post-translational modifications revealed by top-down proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2018 , 122, 11-22	5.8	8
40	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019 , 91, 10937-10942	7.8	8
39	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	3.5	8
38	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	5.6	8
37	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, 1970085	4.8	7
36	The Human Proteoform Project: A Plan to Define the Human Proteome		7
35	Discovery of RSV-Induced BRD4 Protein Interactions Using Native Immunoprecipitation and Parallel Accumulation-Serial Fragmentation (PASEF) Mass Spectrometry. <i>Viruses</i> , 2021 , 13,	6.2	7
34	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. <i>Nature Communications</i> , 2019 , 10, 5612	17.4	7
33	Top-Down Proteomics Reveals Myofilament Proteoform Heterogeneity among Various Rat Skeletal Muscle Tissues. <i>Journal of Proteome Research</i> , 2020 , 19, 446-454	5.6	7
32	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	5.6	7
31	Photocleavable Surfactant-Enabled Extracellular Matrix Proteomics. <i>Analytical Chemistry</i> , 2020 , 92, 15693-15698	3.8	7
30	Dissecting human skeletal muscle troponin proteoforms by top-down mass spectrometry. <i>Journal of Muscle Research and Cell Motility</i> , 2015 , 36, 169-81	3.5	5

29	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	4.7	5
28	Analysis of cardiac troponin proteoforms by top-down mass spectrometry. <i>Methods in Enzymology</i> , 2019 , 626, 347-374	1.7	5
27	Top-Down Proteomics of Endogenous Membrane Proteins Enabled by Cloud Point Enrichment and Multidimensional Liquid Chromatography-Mass Spectrometry. <i>Analytical Chemistry</i> , 2020 , 92, 15726-15735	7.8	5
26	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	7.8	5
25	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	7.8	5
24	Subunit-Specific Labeling of Ubiquitin Chains by Using Sortase: Insights into the Selectivity of Deubiquitinases. <i>ChemBioChem</i> , 2016 , 17, 1525-31	3.8	5
23	A Family of Photolabile Nitroveratryl-Based Surfactants That Self-Assemble into Photodegradable Supramolecular Structures. <i>Langmuir</i> , 2016 , 32, 3963-9	4	5
22	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	3.5	5
21	Systemic Metabolic Alterations Correlate with Islet-Level Prostaglandin E Production and Signaling Mechanisms That Predict β Cell Dysfunction in a Mouse Model of Type 2 Diabetes. <i>Metabolites</i> , 2021 , 11,	5.6	5
20	GRK5 Controls SAP97-Dependent Cardiotoxic β Adrenergic Receptor-CaMKII Signaling in Heart Failure. <i>Circulation Research</i> , 2020 , 127, 796-810	15.7	4
19	MS-Derived Isotopic Fine Structure Reveals Forazoline A as a Thioketone-Containing Marine-Derived Natural Product. <i>Organic Letters</i> , 2020 , 22, 1275-1279	6.2	4
18	Characterization of TTN Novex Splicing Variants across Species and the Role of RBM20 in Novex-Specific Exon Splicing. <i>Genes</i> , 2018 , 9,	4.2	4
17	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	5.6	4
16	Chemical Control of Quorum Sensing in : Identification of Small Molecule Modulators of SdiA and Mechanistic Characterization of a Covalent Inhibitor. <i>ACS Infectious Diseases</i> , 2020 , 6, 3092-3103	5.5	3
15	Fourier-transform ion cyclotron resonance mass spectrometry for characterizing proteoforms. <i>Mass Spectrometry Reviews</i> , 2020 ,	11	3
14	Human Islet Expression Levels of Prostaglandin E Synthetic Enzymes, But Not Prostaglandin EP3 Receptor, Are Positively Correlated with Markers of β Cell Function and Mass in Nondiabetic Obesity. <i>ACS Pharmacology and Translational Science</i> , 2021 , 4, 1338-1348	5.9	2
13	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	3.4	2
12	RBM20 phosphorylation on serine/arginine domain is crucial to regulate pre-mRNA splicing and protein shuttling in the heart		1

11	Stable Picodisc Assemblies from Saposin Proteins and Branched Detergents. <i>Biochemistry</i> , 2021 , 60, 1108-1119	1	1
10	Structural O-Glycoform Heterogeneity of the SARS-CoV-2 Spike Protein Receptor-Binding Domain Revealed by Native Top-Down Mass Spectrometry 2021 ,	5.6	1
9	Top-Down Proteomics 2016 , 187-212	5.6	1
8	Multimics Method Enabled by Sequential Metabolomics and Proteomics for Human Pluripotent Stem-Cell-Derived Cardiomyocytes. <i>Journal of Proteome Research</i> , 2021 , 20, 4646-4654	5.6	1
7	Airway fibrin formation cascade in allergic asthma exacerbation: implications for inflammation and remodeling.. <i>Clinical Proteomics</i> , 2022 , 19, 15	5	1
6	Proteomic Analysis of the Functional Inward Rectifier Potassium Channel (Kir) 2.1 Reveals Several Novel Phosphorylation Sites. <i>Biochemistry</i> , 2021 , 60, 3292-3301	3.2	0
5	RBM20 phosphorylation and its role in nucleocytoplasmic transport and cardiac pathogenesis.. <i>FASEB Journal</i> , 2022 , 36, e22302	0.9	0
4	Segmental Bronchial Allergen Challenge Elicits Distinct Metabolic Phenotypes in Allergic Asthma. <i>Metabolites</i> , 2022 , 12, 381	5.6	0
3	Size Exclusion Chromatography Strategies and MASH Explorer for Large Proteoform Characterization. <i>Methods in Molecular Biology</i> , 2022 , 15-30	1.4	0
2	Mass Spectrometry Analysis of RBM20 Phosphorylation and Its Role in Titin Splicing. <i>FASEB Journal</i> , 2018 , 32, 791.13	0.9	
1	N-terminal region of cardiac myosin binding protein-C impairs myofilament function. <i>FASEB Journal</i> , 2013 , 27, 921.7	0.9	