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List of Publications by Year
in descending order

134 papers	7,848 citations	57758 44 h-index	58581 82 g-index
147 all docs	147 docs citations	147 times ranked	6770 citing authors

#	Article	IF	Citations
1	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	8.0	580
2	Cardiac Repair in a Porcine Model of Acute Myocardial Infarction with Human Induced Pluripotent Stem Cell-Derived Cardiovascular Cells. Cell Stem Cell, 2014, 15, 750-761.	11.1	407
3	Top Down Characterization of Larger Proteins (45 kDa) by Electron Capture Dissociation Mass Spectrometry. Journal of the American Chemical Society, 2002, 124, 672-678.	13.7	357
4	Large Cardiac Muscle Patches Engineered From Human Induced-Pluripotent Stem Cellâ€"Derived Cardiac Cells Improve Recovery From Myocardial Infarction in Swine. Circulation, 2018, 137, 1712-1730.	1.6	332
5	Activated Ion Electron Capture Dissociation for Mass Spectral Sequencing of Larger (42 kDa) Proteins. Analytical Chemistry, 2000, 72, 4778-4784.	6.5	321
6	Top-down mass spectrometry of a 29-kDa protein for characterization of any posttranslational modification to within one residue. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1774-1779.	7.1	248
7	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. Nature Methods, 2019, 16, 587-594.	19.0	241
8	Electron capture dissociation of gaseous multiply charged ions by Fourier-transform ion cyclotron resonance. Journal of the American Society for Mass Spectrometry, 2001, 12, 245-249.	2.8	226
9	Topâ€down proteomics in health and disease: Challenges and opportunities. Proteomics, 2014, 14, 1195-1210.	2.2	169
10	Top-Down Quantitative Proteomics Identified Phosphorylation of Cardiac Troponin I as a Candidate Biomarker for Chronic Heart Failure. Journal of Proteome Research, 2011, 10, 4054-4065.	3.7	166
11	Top-Down Proteomics: Ready for Prime Time?. Analytical Chemistry, 2018, 90, 110-127.	6.5	159
12	Identification and Quantification of Proteoforms by Mass Spectrometry. Proteomics, 2019, 19, e1800361.	2.2	147
13	Top-down high-resolution mass spectrometry of cardiac myosin binding protein C revealed that truncation alters protein phosphorylation state. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12658-12663.	7.1	141
14	Comprehensive Analysis of Protein Modifications by Top-Down Mass Spectrometry. Circulation: Cardiovascular Genetics, 2011, 4, 711-711.	5.1	126
15	MASH Suite Pro: A Comprehensive Software Tool for Top-Down Proteomics. Molecular and Cellular Proteomics, 2016, 15, 703-714.	3.8	111
16	Top-Down Proteomics of Large Proteins up to 223 kDa Enabled by Serial Size Exclusion Chromatography Strategy. Analytical Chemistry, 2017, 89, 5467-5475.	6.5	108
17	The Human Proteoform Project: Defining the human proteome. Science Advances, 2021, 7, eabk0734.	10.3	106
18	Unraveling Molecular Complexity of Phosphorylated Human Cardiac Troponin I by Top Down Electron Capture Dissociation/Electron Transfer Dissociation Mass Spectrometry. Molecular and Cellular Proteomics, 2008, 7, 1838-1849.	3.8	104

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19	Novel Strategies to Address the Challenges in Top-Down Proteomics. Journal of the American Society for Mass Spectrometry, 2021, 32, 1278-1294.	2.8	102
20	Top-down Proteomics Reveals Concerted Reductions in Myofilament and Z-disc Protein Phosphorylation after Acute Myocardial Infarction. Molecular and Cellular Proteomics, 2014, 13, 2752-2764.	3.8	96
21	Augmented Phosphorylation of Cardiac Troponin I in Hypertensive Heart Failure*. Journal of Biological Chemistry, 2012, 287, 848-857.	3.4	88
22	Top-down Proteomics: Technology Advancements and Applications to Heart Diseases. Expert Review of Proteomics, 2016, 13, 717-730.	3.0	84
23	Online Hydrophobic Interaction Chromatographyâ€"Mass Spectrometry for Top-Down Proteomics. Analytical Chemistry, 2016, 88, 1885-1891.	6.5	83
24	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. Biochemistry, 2009, 48, 8161-8170.	2.5	82
25	A photocleavable surfactant for top-down proteomics. Nature Methods, 2019, 16, 417-420.	19.0	82
26	Higher-order structural characterisation of native proteins and complexes by top-down mass spectrometry. Chemical Science, 2020, 11, 12918-12936.	7.4	81
27	Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains. Biochemistry, 2014, 53, 4979-4989.	2.5	79
28	Top down characterization of secreted proteins from Mycobacterium tuberculosis by electron capture dissociation mass spectrometry. Journal of the American Society for Mass Spectrometry, 2003, 14, 253-261.	2.8	76
29	AMP-Activated Protein Kinase Phosphorylates Cardiac Troponin I and Alters Contractility of Murine Ventricular Myocytes. Circulation Research, 2012, 110, 1192-1201.	4.5	70
30	Top-down proteomics: challenges, innovations, and applications in basic and clinical research. Expert Review of Proteomics, 2020, 17, 719-733.	3.0	70
31	PP2A-Bâ€² holoenzyme substrate recognition, regulation and role in cytokinesis. Cell Discovery, 2017, 3, 17027.	6.7	68
32	MASH Suite: A User-Friendly and Versatile Software Interface for High-Resolution Mass Spectrometry Data Interpretation and Visualization. Journal of the American Society for Mass Spectrometry, 2014, 25, 464-470.	2.8	67
33	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2020, 31, 1783-1802.	2.8	67
34	Distinct hypertrophic cardiomyopathy genotypes result in convergent sarcomeric proteoform profiles revealed by top-down proteomics. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24691-24700.	7.1	67
35	New Mass-Spectrometry-Compatible Degradable Surfactant for Tissue Proteomics. Journal of Proteome Research, 2015, 14, 1587-1599.	3.7	66
36	Three Dimensional Liquid Chromatography Coupling Ion Exchange Chromatography/Hydrophobic Interaction Chromatography/Reverse Phase Chromatography for Effective Protein Separation in Top-Down Proteomics. Analytical Chemistry, 2015, 87, 5363-5371.	6.5	64

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37	MASH Explorer: A Universal Software Environment for Top-Down Proteomics. Journal of Proteome Research, 2020, 19, 3867-3876.	3.7	62
38	Specific Enrichment of Phosphoproteins Using Functionalized Multivalent Nanoparticles. Journal of the American Chemical Society, 2015, 137, 2432-2435.	13.7	61
39	Deciphering modifications in swine cardiac troponin I by top-down high-resolution tandem mass spectrometry. Journal of the American Society for Mass Spectrometry, 2010, 21, 940-948.	2.8	59
40	An Unbiased Proteomics Method to Assess the Maturation of Human Pluripotent Stem Cellâ€"Derived Cardiomyocytes. Circulation Research, 2019, 125, 936-953.	4.5	59
41	A five-level classification system for proteoform identifications. Nature Methods, 2019, 16, 939-940.	19.0	55
42	Online Hydrophobic Interaction Chromatographyâ€"Mass Spectrometry for the Analysis of Intact Monoclonal Antibodies. Analytical Chemistry, 2018, 90, 7135-7138.	6.5	53
43	Effective Protein Separation by Coupling Hydrophobic Interaction and Reverse Phase Chromatography for Top-down Proteomics. Analytical Chemistry, 2014, 86, 7899-7906.	6.5	52
44	Comprehensive characterization of monoclonal antibody by Fourier transform ion cyclotron resonance mass spectrometry. MAbs, 2019, 11, 106-115.	5.2	50
45	Structural O-Glycoform Heterogeneity of the SARS-CoV-2 Spike Protein Receptor-Binding Domain Revealed by Top-Down Mass Spectrometry. Journal of the American Chemical Society, 2021, 143, 12014-12024.	13.7	48
46	Comprehensive Mass Spectrometric Mapping of the Hydroxylated Amino Acid residues of the Î±1(V) Collagen Chain. Journal of Biological Chemistry, 2012, 287, 40598-40610.	3.4	47
47	Single amino acid sequence polymorphisms in rat cardiac troponin revealed by topâ€"down tandem mass spectrometry. Journal of Muscle Research and Cell Motility, 2008, 29, 203-212.	2.0	46
48	Proteomics in heart failure: top-down or bottom-up?. Pflugers Archiv European Journal of Physiology, 2014, 466, 1199-1209.	2.8	46
49	Top-down Targeted Proteomics for Deep Sequencing of Tropomyosin Isoforms. Journal of Proteome Research, 2013, 12, 187-198.	3.7	45
50	Top-Down Targeted Proteomics Reveals Decrease in Myosin Regulatory Light-Chain Phosphorylation That Contributes to Sarcopenic Muscle Dysfunction. Journal of Proteome Research, 2016, 15, 2706-2716.	3.7	43
51	Nanoproteomics enables proteoform-resolved analysis of low-abundance proteins in human serum. Nature Communications, 2020, 11, 3903.	12.8	43
52	Purification and High-Resolution Top-Down Mass Spectrometric Characterization of Human Salivary Î±-Amylase. Analytical Chemistry, 2012, 84, 3339-3346.	6.5	42
53	Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains in Cellulo. Analytical Chemistry, 2017, 89, 4428-4434.	6.5	41
54	In-depth proteomic analysis of human tropomyosin by top-down mass spectrometry. Journal of Muscle Research and Cell Motility, 2013, 34, 199-210.	2.0	40

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55	Myocardial Infarction-induced N-terminal Fragment of Cardiac Myosin-binding Protein C (cMyBP-C) Impairs Myofilament Function in Human Myocardium. Journal of Biological Chemistry, 2014, 289, 8818-8827.	3.4	39
56	Generation and Functional Characterization of Knock-in Mice Harboring the Cardiac Troponin I-R21C Mutation Associated with Hypertrophic Cardiomyopathy. Journal of Biological Chemistry, 2012, 287, 2156-2167.	3.4	38
57	A Top-Down Proteomics Platform Coupling Serial Size Exclusion Chromatography and Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 2019, 91, 3835-3844.	6.5	37
58	Highâ€Throughput Proteomics Enabled by a Photocleavable Surfactant. Angewandte Chemie - International Edition, 2020, 59, 8406-8410.	13.8	37
59	Novel Sarcopenia-related Alterations in Sarcomeric Protein Post-translational Modifications (PTMs) in Skeletal Muscles Identified by Top-down Proteomics. Molecular and Cellular Proteomics, 2018, 17, 134-145.	3.8	36
60	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
61	Phosphorylation, but Not Alternative Splicing or Proteolytic Degradation, Is Conserved in Human and Mouse Cardiac Troponin T. Biochemistry, 2011, 50, 6081-6092.	2.5	34
62	Coupling functionalized cobalt ferrite nanoparticle enrichment with online LC/MS/MS for top-down phosphoproteomics. Chemical Science, 2017, 8, 4306-4311.	7.4	34
63	Ultrafast and Reproducible Proteomics from Small Amounts of Heart Tissue Enabled by Azo and timsTOF Pro. Journal of Proteome Research, 2021, 20, 4203-4211.	3.7	34
64	Blackbody infrared radiative dissociation of larger (42 kDa) multiply charged proteins. International Journal of Mass Spectrometry, 2001, 210-211, 203-214.	1.5	32
65	Detection of four oxidation sites in viral prolyl-4-hydroxylase by top-down mass spectrometry. Protein Science, 2009, 12, 2320-2326.	7.6	32
66	Ultrahigh pressure fast size exclusion chromatography for top-down proteomics. Proteomics, 2013, 13, 2563-2566.	2.2	31
67	Epigenetic Priming of Human Pluripotent Stem Cell-Derived Cardiac Progenitor Cells Accelerates Cardiomyocyte Maturation. Stem Cells, 2019, 37, 910-923.	3.2	30
68	Comprehensive analysis of tropomyosin isoforms in skeletal muscles by top-down proteomics. Journal of Muscle Research and Cell Motility, 2016, 37, 41-52.	2.0	29
69	High-Throughput Multi-attribute Analysis of Antibody-Drug Conjugates Enabled by Trapped Ion Mobility Spectrometry and Top-Down Mass Spectrometry. Analytical Chemistry, 2021, 93, 10013-10021.	6.5	29
70	Distinct sequences and post-translational modifications in cardiac atrial and ventricular myosin light chains revealed by top-down mass spectrometry. Journal of Molecular and Cellular Cardiology, 2017, 107, 13-21.	1.9	28
71	Complete Characterization of Cardiac Myosin Heavy Chain (223 kDa) Enabled by Size-Exclusion Chromatography and Middle-Down Mass Spectrometry. Analytical Chemistry, 2017, 89, 4922-4930.	6.5	28
72	Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. Nature Chemical Biology, 2017, 13, 1267-1273.	8.0	28

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73	Bridged Hybrid Monolithic Column Coupled to High-Resolution Mass Spectrometry for Top-Down Proteomics. Analytical Chemistry, 2019, 91, 1743-1747.	6.5	28
74	Topâ€down mass spectrometry of cardiac myofilament proteins in health and disease. Proteomics - Clinical Applications, 2014, 8, 554-568.	1.6	27
75	Effective Top-Down LC/MS+ Method for Assessing Actin Isoforms as a Potential Cardiac Disease Marker. Analytical Chemistry, 2015, 87, 8399-8406.	6.5	27
76	Comprehensive assessment of chamber-specific and transmural heterogeneity in myofilament protein phosphorylation by top-down mass spectrometry. Journal of Molecular and Cellular Cardiology, 2015, 87, 102-112.	1.9	27
77	Simultaneous Quantification of Protein Expression and Modifications by Top-down Targeted Proteomics: A Case of the Sarcomeric Subproteome. Molecular and Cellular Proteomics, 2019, 18, 594-605.	3.8	27
78	Top-down Mass Spectrometry of Sarcomeric Protein Post-translational Modifications from Non-human Primate Skeletal Muscle. Journal of the American Society for Mass Spectrometry, 2019, 30, 2460-2469.	2.8	26
79	Alpha1 catalytic subunit of AMPK modulates contractile function of cardiomyocytes through phosphorylation of troponin I. Life Sciences, 2014, 98, 75-82.	4.3	24
80	Photocleavable Surfactant-Enabled Extracellular Matrix Proteomics. Analytical Chemistry, 2020, 92, 15693-15698.	6.5	24
81	Top-Down Proteomics of Endogenous Membrane Proteins Enabled by Cloud Point Enrichment and Multidimensional Liquid Chromatographyâ€"Mass Spectrometry. Analytical Chemistry, 2020, 92, 15726-15735.	6.5	24
82	A preferred AMPK phosphorylation site adjacent to the inhibitory loop of cardiac and skeletal troponin I. Protein Science, 2011, 20, 894-907.	7.6	23
83	Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry (UbiChEM-MS) Reveals Cell-Cycle Dependent Formation of Lys11/Lys48 Branched Ubiquitin Chains. Journal of Proteome Research, 2017, 16, 3363-3369.	3.7	22
84	Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. Analytical Chemistry, 2019, 91, 11661-11669.	6.5	22
85	Reproducible large-scale synthesis of surface silanized nanoparticles as an enabling nanoproteomics platform: Enrichment of the human heart phosphoproteome. Nano Research, 2019, 12, 1473-1481.	10.4	22
86	Top-down high-resolution electron capture dissociation mass spectrometry for comprehensive characterization of post-translational modifications in Rhesus monkey cardiac troponin I. International Journal of Mass Spectrometry, 2011, 305, 95-102.	1.5	21
87	Delineating Anopheles gambiae coactivator associated arginine methyltransferase 1 automethylation using topâ€"down high resolution tandem mass spectrometry. Protein Science, 2009, 18, 1272-1280.	7.6	20
88	Discovery of RSV-Induced BRD4 Protein Interactions Using Native Immunoprecipitation and Parallel Accumulationâ€"Serial Fragmentation (PASEF) Mass Spectrometry. Viruses, 2021, 13, 454.	3.3	20
89	The HCM-linked W792R mutation in cardiac myosin-binding protein C reduces C6 FnIII domain stability. American Journal of Physiology - Heart and Circulatory Physiology, 2018, 314, H1179-H1191.	3.2	19
90	Temperature-sensitive sarcomeric protein post-translational modifications revealed by top-down proteomics. Journal of Molecular and Cellular Cardiology, 2018, 122, 11-22.	1.9	19

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91	Intact Protein Mass Spectrometry for Therapeutic Protein Quantitation, Pharmacokinetics, and Biotransformation in Preclinical and Clinical Studies: An Industry Perspective. Journal of the American Society for Mass Spectrometry, 2021, 32, 1886-1900.	2.8	19
92	Enhancing Top-Down Proteomics Data Analysis by Combining Deconvolution Results through a Machine Learning Strategy. Journal of the American Society for Mass Spectrometry, 2020, 31, 1104-1113.	2.8	19
93	The impact of antibody selection on the detection of cardiac troponin I. Clinica Chimica Acta, 2013, 420, 82-88.	1.1	18
94	Quantitative Proteomics and Immunohistochemistry Reveal Insights into Cellular and Molecular Processes in the Infarct Border Zone One Month after Myocardial Infarction. Journal of Proteome Research, 2017, 16, 2101-2112.	3.7	18
95	Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. Analytical Chemistry, 2018, 90, 4935-4939.	6.5	17
96	GRK5 Controls SAP97-Dependent Cardiotoxic Î² ₁ Adrenergic Receptor-CaMKII Signaling in Heart Failure. Circulation Research, 2020, 127, 796-810.	4.5	16
97	Systemic Metabolic Alterations Correlate with Islet-Level Prostaglandin E2 Production and Signaling Mechanisms That Predict Î²-Cell Dysfunction in a Mouse Model of Type 2 Diabetes. Metabolites, 2021, 11, 58.	2.9	16
98	High throughput screening of disulfideâ€containing proteins in a complex mixture. Proteomics, 2013, 13, 3256-3260.	2.2	15
99	Comprehensive Characterization of Swine Cardiac Troponin T Proteoforms by Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2018, 29, 1284-1294.	2.8	15
100	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. Nature Communications, 2019, 10, 5612.	12.8	15
101	Ultrahigh-Resolution Mass Spectrometry-Based Platform for Plasma Metabolomics Applied to Type 2 Diabetes Research. Journal of Proteome Research, 2021, 20, 463-473.	3.7	15
102	Highâ€Throughput Proteomics Enabled by a Photocleavable Surfactant. Angewandte Chemie, 2020, 132, 8484-8488.	2.0	14
103	Functionally Integrated Top-Down Proteomics for Standardized Assessment of Human Induced Pluripotent Stem Cell-Derived Engineered Cardiac Tissues. Journal of Proteome Research, 2021, 20, 1424-1433.	3.7	14
104	Top-Down Proteomics Reveals Myofilament Proteoform Heterogeneity among Various Rat Skeletal Muscle Tissues. Journal of Proteome Research, 2020, 19, 446-454.	3.7	13
105	Chemical Control of Quorum Sensing in E.Âcoli: Identification of Small Molecule Modulators of SdiA and Mechanistic Characterization of a Covalent Inhibitor. ACS Infectious Diseases, 2020, 6, 3092-3103.	3.8	13
106	Quantitative proteomics reveals differential regulation of protein expression in recipient myocardium after trilineage cardiovascular cell transplantation. Proteomics, 2015, 15, 2560-2567.	2.2	12
107	Fourierâ€transform ion cyclotron resonance mass spectrometry for characterizing proteoforms. Mass Spectrometry Reviews, 2022, 41, 158-177.	5.4	12
108	MS-Derived Isotopic Fine Structure Reveals Forazoline A as a Thioketone-Containing Marine-Derived Natural Product. Organic Letters, 2020, 22, 1275-1279.	4.6	12

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109	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. Analytical Chemistry, 2019, 91, 10937-10942.	6.5	11
110	A Family of Photolabile Nitroveratryl-Based Surfactants That Self-Assemble into Photodegradable Supramolecular Structures. Langmuir, 2016, 32, 3963-3969.	3.5	10
111	Zâ€band and Mâ€band titin splicing and regulation by RNA binding motif 20 in striated muscles. Journal of Cellular Biochemistry, 2018, 119, 9986-9996.	2.6	10
112	Analysis of cardiac troponin proteoforms by top-down mass spectrometry. Methods in Enzymology, 2019, 626, 347-374.	1.0	10
113	Comprehensive Characterization of the Recombinant Catalytic Subunit of cAMP-Dependent Protein Kinase by Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 2561-2570.	2.8	10
114	Human Islet Expression Levels of Prostaglandin E₂ Synthetic Enzymes, But Not Prostaglandin EP3 Receptor, Are Positively Correlated with Markers of Î²-Cell Function and Mass in Nondiabetic Obesity. ACS Pharmacology and Translational Science, 2021, 4, 1338-1348.	4.9	10
115	Multiomics Method Enabled by Sequential Metabolomics and Proteomics for Human Pluripotent Stem-Cell-Derived Cardiomyocytes. Journal of Proteome Research, 2021, 20, 4646-4654.	3.7	10
116	RBM20 phosphorylation and its role in nucleocytoplasmic transport and cardiac pathogenesis. FASEB Journal, 2022, 36, e22302.	0.5	10
117	Comprehensive Characterization of AMP-Activated Protein Kinase Catalytic Domain by Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2016, 27, 220-232.	2.8	9
118	The Impact of Phosphorylation on Electron Capture Dissociation of Proteins: A Top-Down Perspective. Journal of the American Society for Mass Spectrometry, 2017, 28, 1805-1814.	2.8	9
119	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. Proteomics, 2019, 19, 1970085.	2.2	9
120	One-Pot Exosome Proteomics Enabled by a Photocleavable Surfactant. Analytical Chemistry, 2022, 94, 7164-7168.	6.5	9
121	Rapid Analysis of Reduced Antibody Drug Conjugate by Online LC-MS/MS with Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 2020, 92, 15096-15103.	6.5	8
122	Dissecting human skeletal muscle troponin proteoforms by top-down mass spectrometry. Journal of Muscle Research and Cell Motility, 2015, 36, 169-181.	2.0	7
123	Characterization of TTN Novex Splicing Variants across Species and the Role of RBM20 in Novex-Specific Exon Splicing. Genes, 2018, 9, 86.	2.4	7
124	Subunitâ€Specific Labeling of Ubiquitin Chains by Using Sortase: Insights into the Selectivity of Deubiquitinases. ChemBioChem, 2016, 17, 1525-1531.	2.6	6
125	Deletion of Enigma Homologue from the Z-disc slows tension development kinetics in mouse myocardium. Journal of General Physiology, 2019, 151, 670-679.	1.9	6
126	Harnessing the Power of Proteomics to Assess Drug Safety and Guide Clinical Trials. Circulation, 2018, 137, 1011-1014.	1.6	5

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127	Proteomic Analysis of the Functional Inward Rectifier Potassium Channel (Kir) 2.1 Reveals Several Novel Phosphorylation Sites. Biochemistry, 2021, 60, 3292-3301.	2.5	5
128	Airway fibrin formation cascade in allergic asthma exacerbation: implications for inflammation and remodeling. Clinical Proteomics, 2022, 19, 15.	2.1	3
129	Stable Picodisc Assemblies from Saposin Proteins and Branched Detergents. Biochemistry, 2021, 60, 1108-1119.	2.5	2
130	Segmental Bronchial Allergen Challenge Elicits Distinct Metabolic Phenotypes in Allergic Asthma. Metabolites, 2022, 12, 381.	2.9	2
131	Rbm20 ablation is associated with changes in the expression of titin-interacting and metabolic proteins. Molecular Omics, 2022, 18, 627-634.	2.8	2
132	Top-Down Proteomics. , 2016, , 187-212.		1
133	Nâ€terminal region of cardiac myosin binding proteinâ€C impairs myofilament function. FASEB Journal, 2013, 27, 921.7.	0.5	0
134	Mass Spectrometry Analysis of RBM20 Phosphorylation and Its Role in Titin Splicing. FASEB Journal, 2018, 32, 791.13.	0.5	0