

Tao Liu

List of Publications by Year in descending order

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125
papers

12,907
citations

28274

55
h-index

27406

106
g-index

133
all docs

133
docs citations

133
times ranked

15920
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
2	Reversed-phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. <i>Proteomics</i> , 2011, 11, 2019-2026.	2.2	564
3	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
4	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
5	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
6	Human Plasma N-Glycoproteome Analysis by Immunoaffinity Subtraction, Hydrazide Chemistry, and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 2070-2080.	3.7	394
7	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography-mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	12.0	377
8	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
9	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1690-1704.	3.8	323
10	Probability-Based Evaluation of Peptide and Protein Identifications from Tandem Mass Spectrometry and SEQUEST Analysis: The Human Proteome. <i>Journal of Proteome Research</i> , 2005, 4, 53-62.	3.7	320
11	Advances and Challenges in Liquid Chromatography-Mass Spectrometry-based Proteomics Profiling for Clinical Applications. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1727-1744.	3.8	309
12	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
13	Utilizing Human Blood Plasma for Proteomic Biomarker Discovery. <i>Journal of Proteome Research</i> , 2005, 4, 1073-1085.	3.7	288
14	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
15	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
16	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15395-15400.	7.1	211
17	Evaluation of Multiprotein Immunoaffinity Subtraction for Plasma Proteomics and Candidate Biomarker Discovery Using Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2167-2174.	3.8	197
18	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189

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19	Advancing the sensitivity of selected reaction monitoring-based targeted quantitative proteomics. <i>Proteomics</i> , 2012, 12, 1074-1092.	2.2	186
20	Enhanced Detection of Low Abundance Human Plasma Proteins Using a Tandem IgY12-SuperMix Immunoaffinity Separation Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1963-1973.	3.8	183
21	Establishing the Proteome of Normal Human Cerebrospinal Fluid. <i>PLoS ONE</i> , 2010, 5, e10980.	2.5	183
22	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
23	Advances in targeted proteomics and applications to biomedical research. <i>Proteomics</i> , 2016, 16, 2160-2182.	2.2	175
24	Liquid Chromatography-Mass Spectrometry-based Quantitative Proteomics. <i>Journal of Biological Chemistry</i> , 2011, 286, 25443-25449.	3.4	171
25	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
26	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	3.8	156
27	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. <i>Analytical Chemistry</i> , 2019, 91, 13119-13127.	6.5	156
28	Head-to-Head Comparison of Serum Fractionation Techniques. <i>Journal of Proteome Research</i> , 2007, 6, 828-836.	3.7	152
29	High-Throughput Comparative Proteome Analysis Using a Quantitative Cysteiny-peptide Enrichment Technology. <i>Analytical Chemistry</i> , 2004, 76, 5345-5353.	6.5	142
30	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	3.8	142
31	Quantitative proteomics analysis of adsorbed plasma proteins classifies nanoparticles with different surface properties and size. <i>Proteomics</i> , 2011, 11, 4569-4577.	2.2	135
32	Resin-assisted enrichment of thiols as a general strategy for proteomic profiling of cysteine-based reversible modifications. <i>Nature Protocols</i> , 2014, 9, 64-75.	12.0	131
33	Characterization of the Mouse Brain Proteome Using Global Proteomic Analysis Complemented with Cysteiny-peptide Enrichment. <i>Journal of Proteome Research</i> , 2006, 5, 361-369.	3.7	126
34	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	19.0	126
35	An Improved Boosting to Amplify Signal with Isobaric Labeling (iBASIL) Strategy for Precise Quantitative Single-cell Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 828-838.	3.8	121
36	Investigating the correspondence between transcriptomic and proteomic expression profiles using coupled cluster models. <i>Bioinformatics</i> , 2008, 24, 2894-2900.	4.1	117

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37	Quantitative proteomics identifies altered O-GlcNAcylation of structural, synaptic and memory-associated proteins in Alzheimer's disease. <i>Journal of Pathology</i> , 2017, 243, 78-88.	4.5	105
38	Automated Coupling of Nanodroplet Sample Preparation with Liquid Chromatography-Mass Spectrometry for High-Throughput Single-Cell Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 10588-10596.	6.5	105
39	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1060-1071.	3.8	104
40	Distinct Cerebrospinal Fluid Proteomes Differentiate Post-Treatment Lyme Disease from Chronic Fatigue Syndrome. <i>PLoS ONE</i> , 2011, 6, e17287.	2.5	103
41	Accurate Mass Measurements in Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3621-3653.	47.7	102
42	Boosting to Amplify Signal with Isobaric Labeling (BASIL) Strategy for Comprehensive Quantitative Phosphoproteomic Characterization of Small Populations of Cells. <i>Analytical Chemistry</i> , 2019, 91, 5794-5801.	6.5	86
43	Quantitative Analysis of Human Immunodeficiency Virus Type 1-Infected CD4 + Cell Proteome: Dysregulated Cell Cycle Progression and Nuclear Transport Coincide with Robust Virus Production. <i>Journal of Virology</i> , 2007, 81, 7571-7583.	3.4	84
44	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
45	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. <i>Nature Communications</i> , 2021, 12, 6246.	12.8	76
46	Simple Sodium Dodecyl Sulfate-Assisted Sample Preparation Method for LC-MS-Based Proteomics Applications. <i>Analytical Chemistry</i> , 2012, 84, 2862-2867.	6.5	74
47	Spatial mapping of the neurite and soma proteomes reveals a functional Cdc42/Rac regulatory network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1931-1936.	7.1	73
48	Mass spectrometry for translational proteomics: progress and clinical implications. <i>Genome Medicine</i> , 2012, 4, 63.	8.2	71
49	Systematic Optimization of Long Gradient Chromatography Mass Spectrometry for Deep Analysis of Brain Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 829-838.	3.7	71
50	Targeted Quantification of Low ng/mL Level Proteins in Human Serum without Immunoaffinity Depletion. <i>Journal of Proteome Research</i> , 2013, 12, 3353-3361.	3.7	68
51	Improved proteome coverage by using high efficiency cysteinyl peptide enrichment: The human mammary epithelial cell proteome. <i>Proteomics</i> , 2005, 5, 1263-1273.	2.2	65
52	Mapping N-Linked Glycosylation Sites in the Secretome and Whole Cells of <i>Aspergillus niger</i> Using Hydrazide Chemistry and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 143-156.	3.7	62
53	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. <i>Proteomics</i> , 2014, 14, 2719-2730.	2.2	62
54	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	16.8	62

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55	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ^{18}O -Labeled δ -Universal Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	3.7	59
56	A Highly Sensitive Targeted Mass Spectrometric Assay for Quantification of AGR2 Protein in Human Urine and Serum. <i>Journal of Proteome Research</i> , 2014, 13, 875-882.	3.7	59
57	Determination of Burn Patient Outcome by Large-Scale Quantitative Discovery Proteomics. <i>Critical Care Medicine</i> , 2013, 41, 1421-1434.	0.9	55
58	Blood Peptidome-Degradome Profile of Breast Cancer. <i>PLoS ONE</i> , 2010, 5, e13133.	2.5	54
59	The clinical impact of recent advances in LC-MS for cancer biomarker discovery and verification. <i>Expert Review of Proteomics</i> , 2016, 13, 99-114.	3.0	50
60	Enhanced Sensitivity for Selected Reaction Monitoring Mass Spectrometry-based Targeted Proteomics Using a Dual Stage Electrodynamical Ion Funnel Interface. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S9.	3.8	49
61	Contributions of immunoaffinity chromatography to deep proteome profiling of human biofluids. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1021, 57-68.	2.3	47
62	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	6.5	46
63	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. <i>Communications Biology</i> , 2021, 4, 265.	4.4	46
64	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
65	Proteomic Analysis of Exosomes for Discovery of Protein Biomarkers for Prostate and Bladder Cancer. <i>Cancers</i> , 2020, 12, 2335.	3.7	44
66	Capillary Electrophoresis-Electrospray Mass Spectrometry for the Characterization of High-Mannose-Type N-Glycosylation and Differential Oxidation in Glycoproteins by Charge Reversal and Protease/Glycosidase Digestion. <i>Analytical Chemistry</i> , 2001, 73, 5875-5885.	6.5	43
67	Strategy for Degradome-Peptidomic Analysis of Human Blood Plasma. <i>Journal of Proteome Research</i> , 2010, 9, 2339-2346.	3.7	43
68	Analysis of serum total and free PSA using immunoaffinity depletion coupled to SRM: correlation with clinical immunoassay tests. <i>Journal of Proteomics</i> , 2012, 75, 4747-4757.	2.4	43
69	Inhibition of interleukin-1 receptor-associated kinase-1 is a therapeutic strategy for acute myeloid leukemia subtypes. <i>Leukemia</i> , 2018, 32, 2374-2387.	7.2	43
70	A Systematic Analysis of a Deep Mouse Epididymal Sperm Proteome. <i>Biology of Reproduction</i> , 2012, 87, 141.	2.7	41
71	Long-Gradient Separations Coupled with Selected Reaction Monitoring for Highly Sensitive, Large Scale Targeted Protein Quantification in a Single Analysis. <i>Analytical Chemistry</i> , 2013, 85, 9196-9203.	6.5	41
72	Targeted Quantification of Phosphorylation Dynamics in the Context of EGFR-MAPK Pathway. <i>Analytical Chemistry</i> , 2018, 90, 5256-5263.	6.5	39

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73	Improved Sensitivity and Separations for Phosphopeptides using Online Liquid Chromatography Coupled with Structures for Lossless Ion Manipulations Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 10889-10896.	6.5	38
74	Network Analysis of Epidermal Growth Factor Signaling Using Integrated Genomic, Proteomic and Phosphorylation Data. <i>PLoS ONE</i> , 2012, 7, e34515.	2.5	37
75	Gray Matter Is Targeted in First-Attack Multiple Sclerosis. <i>PLoS ONE</i> , 2013, 8, e66117.	2.5	36
76	Automated Nanoflow Two-Dimensional Reversed-Phase Liquid Chromatography System Enables In-Depth Proteome and Phosphoproteome Profiling of Nanoscale Samples. <i>Analytical Chemistry</i> , 2019, 91, 9707-9715.	6.5	36
77	Sensitive Targeted Quantification of ERK Phosphorylation Dynamics and Stoichiometry in Human Cells without Affinity Enrichment. <i>Analytical Chemistry</i> , 2015, 87, 1103-1110.	6.5	32
78	Residual tissue repositories as a resource for population-based cancer proteomic studies. <i>Clinical Proteomics</i> , 2018, 15, 26.	2.1	32
79	Towards Discovery and Targeted Peptide Biomarker Detection Using nanoESI-TIMS-TOF MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 817-826.	2.8	31
80	Expediting SRM Assay Development for Large-Scale Targeted Proteomics Experiments. <i>Journal of Proteome Research</i> , 2014, 13, 4479-4487.	3.7	29
81	Simultaneous Proteomic Discovery and Targeted Monitoring using Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3694-3705.	3.8	29
82	Targeted proteomic assays for quantitation of proteins identified by proteogenomic analysis of ovarian cancer. <i>Scientific Data</i> , 2017, 4, 170091.	5.3	29
83	Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.	3.7	26
84	An Integrative Analysis of Tumor Proteomic and Phosphoproteomic Profiles to Examine the Relationships Between Kinase Activity and Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S26-S36.	3.8	25
85	iTRAQ-based quantitative proteomics reveals the neuroprotection of rhubarb in experimental intracerebral hemorrhage. <i>Journal of Ethnopharmacology</i> , 2019, 232, 244-254.	4.1	25
86	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. <i>Molecular Oncology</i> , 2014, 8, 1169-1180.	4.6	24
87	Carrier-Assisted Single-Tube Processing Approach for Targeted Proteomics Analysis of Low Numbers of Mammalian Cells. <i>Analytical Chemistry</i> , 2019, 91, 1441-1451.	6.5	24
88	Analytical platform evaluation for quantification of ERG in prostate cancer using protein and mRNA detection methods. <i>Journal of Translational Medicine</i> , 2015, 13, 54.	4.4	23
89	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. <i>Analytical Chemistry</i> , 2019, 91, 11606-11613.	6.5	22
90	Deep-Dive Targeted Quantification for Ultrasensitive Analysis of Proteins in Nondepleted Human Blood Plasma/Serum and Tissues. <i>Analytical Chemistry</i> , 2017, 89, 9139-9146.	6.5	21

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91	Facile carrier-assisted targeted mass spectrometric approach for proteomic analysis of low numbers of mammalian cells. <i>Communications Biology</i> , 2018, 1, 103.	4.4	21
92	Quantitative proteomic analysis of intracerebral hemorrhage in rats with a focus on brain energy metabolism. <i>Brain and Behavior</i> , 2018, 8, e01130.	2.2	19
93	Mass spectrometry-based targeted proteomics for analysis of protein mutations. <i>Mass Spectrometry Reviews</i> , 2023, 42, 796-821.	5.4	19
94	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1607-1618.	3.8	18
95	¹⁸ O-Labeled Proteome Reference as Global Internal Standards for Targeted Quantification by Selected Reaction Monitoring-Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.007302.	3.8	17
96	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. <i>Journal of Proteome Research</i> , 2017, 16, 4523-4530.	3.7	17
97	Analysis of recombinant and modified proteins by capillary zone electrophoresis coupled with electrospray ionization tandem mass spectrometry. <i>Journal of Chromatography A</i> , 1999, 855, 695-707.	3.7	16
98	Detection of Head and Neck Cancer Based on Longitudinal Changes in Serum Protein Abundance. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1665-1672.	2.5	16
99	The Use of a Quantitative Cysteinyl-Peptide Enrichment Technology for High-Throughput Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2007, 359, 107-124.	0.9	16
100	Human adipose tissue- and umbilical cord-derived stem cells: which is a better alternative to treat spinal cord injury?. <i>Neural Regeneration Research</i> , 2020, 15, 2306.	3.0	15
101	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	3.8	14
102	Multiplexed targeted mass spectrometry assays for prostate cancer-associated urinary proteins. <i>Oncotarget</i> , 2017, 8, 101887-101898.	1.8	14
103	Proteomic approaches for site-specific <i>O</i> -GlcNAcylation analysis. <i>Bioanalysis</i> , 2014, 6, 2571-2580.	1.5	13
104	Proteome and transcriptome profiles of a Her2/Neu-driven mouse model of breast cancer. <i>Proteomics - Clinical Applications</i> , 2011, 5, 179-188.	1.6	12
105	Facile One-Pot Nanoproteomics for Label-Free Proteome Profiling of 50–1000 Mammalian Cells. <i>Journal of Proteome Research</i> , 2021, 20, 4452-4461.	3.7	12
106	Application of free-flow electrophoresis to the purification of trichosanthin from a crude product of acetone fractional precipitation. <i>Electrophoresis</i> , 1998, 19, 1097-1103.	2.4	11
107	Preconditioning in the Rhesus Macaque Induces a Proteomic Signature Following Cerebral Ischemia that Is Associated with Neuroprotection. <i>Translational Stroke Research</i> , 2019, 10, 440-448.	4.2	11
108	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. <i>Journal of Proteome Research</i> , 2019, 18, 694-699.	3.7	11

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109	Internal Standard Triggered-Parallel Reaction Monitoring Mass Spectrometry Enables Multiplexed Quantification of Candidate Biomarkers in Plasma. <i>Analytical Chemistry</i> , 2022, 94, 9540-9547.	6.5	11
110	Microscale depletion of high abundance proteins in human biofluids using IgY14 immunoaffinity resin: analysis of human plasma and cerebrospinal fluid. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 7117-7125.	3.7	10
111	An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2002-2008.	2.8	10
112	Large-Scale and Deep Quantitative Proteome Profiling Using Isobaric Labeling Coupled with Two-Dimensional LC-MS/MS. <i>Methods in Molecular Biology</i> , 2016, 1410, 237-247.	0.9	10
113	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100171.	3.8	9
114	Proteomic Tissue-Based Classifier for Early Prediction of Prostate Cancer Progression. <i>Cancers</i> , 2020, 12, 1268.	3.7	8
115	Quantification of mutant SPOP proteins in prostate cancer using mass spectrometry-based targeted proteomics. <i>Journal of Translational Medicine</i> , 2017, 15, 175.	4.4	5
116	Characterization of the Ovarian Tumor Peptidome. <i>Vitamins and Hormones</i> , 2018, 107, 515-531.	1.7	5
117	Pan-cancer proteogenomic investigations identify post-transcriptional kinase targets. <i>Communications Biology</i> , 2021, 4, 1112.	4.4	5
118	Determining protein polarization proteome-wide using physical dissection of individual Stentor coeruleus cells. <i>Current Biology</i> , 2022, , .	3.9	4
119	Carrier-assisted One-pot Sample Preparation for Targeted Proteomics Analysis of Small Numbers of Human Cells. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	3
120	Evaluating the Performance of 193 nm Ultraviolet Photodissociation for Tandem Mass Tag Labeled Peptides. <i>Analytical Chemistry and Chemical Analysis</i> , 2021, 2, 140-155.	1.7	3
121	Evaluation of Differential Peptide Loading on Tandem Mass Tag-Based Proteomic and Phosphoproteomic Data Quality. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 17-30.	2.8	2
122	Mass Spectrometry for Biomarker Development. <i>Biomarkers in Disease</i> , 2015, , 17-48.	0.1	1
123	Capecitabine Regulates HSP90AB1 Expression and Induces Apoptosis via Akt/SMARCC1/AP-1/ROS Axis in T Cells. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	4.0	1
124	Mass Spectrometry-Based for Analysis of. <i>Methods in Molecular Biology</i> , 2021, 2259, 247-257.	0.9	0
125	Mass Spectrometry for Biomarker Development. , 2014, , 1-25.		0