

Tao Liu

List of Publications by Year in descending order

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125
papers

12,907
citations

28242

55
h-index

27389

106
g-index

133
all docs

133
docs citations

133
times ranked

15920
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass spectrometry-based targeted proteomics for analysis of protein mutations. <i>Mass Spectrometry Reviews</i> , 2023, 42, 796-821.	2.8	19
2	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.	1.2	2
3	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.	1.9	1
4	Determining protein polarization proteome-wide using physical dissection of individual Stentor coeruleus cells. <i>Current Biology</i> , 2022, , .	1.8	4
5	Internal Standard Triggered-Parallel Reaction Monitoring Mass Spectrometry Enables Multiplexed Quantification of Candidate Biomarkers in Plasma. <i>Analytical Chemistry</i> , 2022, 94, 9540-9547.	3.2	11
6	Mass Spectrometry-Based for Analysis of. <i>Methods in Molecular Biology</i> , 2021, 2259, 247-257.	0.4	0
7	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.	7.7	189
8	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. <i>Communications Biology</i> , 2021, 4, 265.	2.0	46
9	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
10	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	7.7	62
11	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
12	Facile One-Pot Nanoproteomics for Label-Free Proteome Profiling of 50-1000 Mammalian Cells. <i>Journal of Proteome Research</i> , 2021, 20, 4452-4461.	1.8	12
13	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	13.5	236
14	Pan-cancer proteogenomic investigations identify post-transcriptional kinase targets. <i>Communications Biology</i> , 2021, 4, 1112.	2.0	5
15	Evaluating the Performance of 193 nm Ultraviolet Photodissociation for Tandem Mass Tag Labeled Peptides. <i>Journal of Analytical Chemistry and Chemical Analysis</i> , 2021, 2, 140-155.	0.8	3
16	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. <i>Nature Communications</i> , 2021, 12, 6246.	5.8	76
17	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100171.	2.5	9
18	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273

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19	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
20	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	2.9	83
21	Proteomic Analysis of Exosomes for Discovery of Protein Biomarkers for Prostate and Bladder Cancer. <i>Cancers</i> , 2020, 12, 2335.	1.7	44
22	Proteomic Tissue-Based Classifier for Early Prediction of Prostate Cancer Progression. <i>Cancers</i> , 2020, 12, 1268.	1.7	8
23	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.	1.1	16
24	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.	3.2	105
25	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
26	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
27	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.	2.5	121
28	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	3.3	46
29	Carrier-assisted One-pot Sample Preparation for Targeted Proteomics Analysis of Small Numbers of Human Cells. <i>Journal of Visualized Experiments</i> , 2020, , .	0.2	3
30	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.	1.6	15
31	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. <i>Analytical Chemistry</i> , 2019, 91, 11606-11613.	3.2	22
32	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
33	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. <i>Analytical Chemistry</i> , 2019, 91, 13119-13127.	3.2	156
34	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	2.5	14
35	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.	2.5	25
36	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.	3.2	36

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37	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1607-1618.	2.5	18
38	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
39	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.	3.2	86
40	Carrier-Assisted Single-Tube Processing Approach for Targeted Proteomics Analysis of Low Numbers of Mammalian Cells. <i>Analytical Chemistry</i> , 2019, 91, 1441-1451.	3.2	24
41	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.	2.3	11
42	iTRAQ-based quantitative proteomics reveals the neuroprotection of rhubarb in experimental intracerebral hemorrhage. <i>Journal of Ethnopharmacology</i> , 2019, 232, 244-254.	2.0	25
43	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. <i>Journal of Proteome Research</i> , 2019, 18, 694-699.	1.8	11
44	Inhibition of interleukin-1 receptor-associated kinase-1 is a therapeutic strategy for acute myeloid leukemia subtypes. <i>Leukemia</i> , 2018, 32, 2374-2387.	3.3	43
45	Targeted Quantification of Phosphorylation Dynamics in the Context of EGFR-MAPK Pathway. <i>Analytical Chemistry</i> , 2018, 90, 5256-5263.	3.2	39
46	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.	1.2	31
47	Quantitative proteomic analysis of intracerebral hemorrhage in rats with a focus on brain energy metabolism. <i>Brain and Behavior</i> , 2018, 8, e01130.	1.0	19
48	Characterization of the Ovarian Tumor Peptidome. <i>Vitamins and Hormones</i> , 2018, 107, 515-531.	0.7	5
49	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.	5.5	377
50	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.	3.2	38
51	Residual tissue repositories as a resource for population-based cancer proteomic studies. <i>Clinical Proteomics</i> , 2018, 15, 26.	1.1	32
52	Facile carrier-assisted targeted mass spectrometric approach for proteomic analysis of low numbers of mammalian cells. <i>Communications Biology</i> , 2018, 1, 103.	2.0	21
53	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.	3.2	21
54	Targeted proteomic assays for quantitation of proteins identified by proteogenomic analysis of ovarian cancer. <i>Scientific Data</i> , 2017, 4, 170091.	2.4	29

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55	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	9.0	126
56	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. <i>Journal of Proteome Research</i> , 2017, 16, 4523-4530.	1.8	17
57	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.	2.1	105
58	Quantification of mutant SPOP proteins in prostate cancer using mass spectrometry-based targeted proteomics. <i>Journal of Translational Medicine</i> , 2017, 15, 175.	1.8	5
59	Multiplexed targeted mass spectrometry assays for prostate cancer-associated urinary proteins. <i>Oncotarget</i> , 2017, 8, 101887-101898.	0.8	14
60	Advances in targeted proteomics and applications to biomedical research. <i>Proteomics</i> , 2016, 16, 2160-2182.	1.3	175
61	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.	2.5	29
62	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
63	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.	1.2	47
64	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.	2.5	104
65	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	1.8	44
66	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.	1.3	50
67	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.	0.4	10
68	An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2002-2008.	1.2	10
69	Sensitive Targeted Quantification of ERK Phosphorylation Dynamics and Stoichiometry in Human Cells without Affinity Enrichment. <i>Analytical Chemistry</i> , 2015, 87, 1103-1110.	3.2	32
70	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.	1.8	23
71	Mass Spectrometry for Biomarker Development. <i>Biomarkers in Disease</i> , 2015, , 17-48.	0.0	1
72	Systematic Optimization of Long Gradient Chromatography Mass Spectrometry for Deep Analysis of Brain Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 829-838.	1.8	71

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73	Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.	1.8	26
74	Proteomic approaches for site-specific <i>O</i> -GlcNAcylation analysis. <i>Bioanalysis</i> , 2014, 6, 2571-2580.	0.6	13
75	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. <i>Proteomics</i> , 2014, 14, 2719-2730.	1.3	62
76	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. <i>Molecular Oncology</i> , 2014, 8, 1169-1180.	2.1	24
77	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.	1.8	59
78	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.	5.5	131
79	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.	1.9	10
80	Expediting SRM Assay Development for Large-Scale Targeted Proteomics Experiments. <i>Journal of Proteome Research</i> , 2014, 13, 4479-4487.	1.8	29
81	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.	2.5	323
82	Mass Spectrometry for Biomarker Development. , 2014, , 1-25.		0
83	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.	3.2	41
84	Targeted Quantification of Low ng/mL Level Proteins in Human Serum without Immunoaffinity Depletion. <i>Journal of Proteome Research</i> , 2013, 12, 3353-3361.	1.8	68
85	Determination of Burn Patient Outcome by Large-Scale Quantitative Discovery Proteomics. <i>Critical Care Medicine</i> , 2013, 41, 1421-1434.	0.4	55
86	Gray Matter Is Targeted in First-Attack Multiple Sclerosis. <i>PLoS ONE</i> , 2013, 8, e66117.	1.1	36
87	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.	3.3	211
88	A Systematic Analysis of a Deep Mouse Epididymal Sperm Proteome ¹ . <i>Biology of Reproduction</i> , 2012, 87, 141.	1.2	41
89	Mass spectrometry for translational proteomics: progress and clinical implications. <i>Genome Medicine</i> , 2012, 4, 63.	3.6	71
90	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.	1.2	43

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91	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.	1.8	62
92	Simple Sodium Dodecyl Sulfate-Assisted Sample Preparation Method for LC-MS-Based Proteomics Applications. <i>Analytical Chemistry</i> , 2012, 84, 2862-2867.	3.2	74
93	Advancing the sensitivity of selected reaction monitoring-based targeted quantitative proteomics. <i>Proteomics</i> , 2012, 12, 1074-1092.	1.3	186
94	Network Analysis of Epidermal Growth Factor Signaling Using Integrated Genomic, Proteomic and Phosphorylation Data. <i>PLoS ONE</i> , 2012, 7, e34515.	1.1	37
95	Liquid Chromatography-Mass Spectrometry-based Quantitative Proteomics. <i>Journal of Biological Chemistry</i> , 2011, 286, 25443-25449.	1.6	171
96	Proteome and transcriptome profiles of a Her2/Neu-driven mouse model of breast cancer. <i>Proteomics - Clinical Applications</i> , 2011, 5, 179-188.	0.8	12
97	Reversed-phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. <i>Proteomics</i> , 2011, 11, 2019-2026.	1.3	564
98	Quantitative proteomics analysis of adsorbed plasma proteins classifies nanoparticles with different surface properties and size. <i>Proteomics</i> , 2011, 11, 4569-4577.	1.3	135
99	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.	2.5	17
100	Enhanced Sensitivity for Selected Reaction Monitoring Mass Spectrometry-based Targeted Proteomics Using a Dual Stage Electrodynamic Ion Funnel Interface. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S9.	2.5	49
101	Distinct Cerebrospinal Fluid Proteomes Differentiate Post-Treatment Lyme Disease from Chronic Fatigue Syndrome. <i>PLoS ONE</i> , 2011, 6, e17287.	1.1	103
102	Strategy for Degradomic-Peptidomic Analysis of Human Blood Plasma. <i>Journal of Proteome Research</i> , 2010, 9, 2339-2346.	1.8	43
103	Establishing the Proteome of Normal Human Cerebrospinal Fluid. <i>PLoS ONE</i> , 2010, 5, e10980.	1.1	183
104	Blood Peptidome-Degradome Profile of Breast Cancer. <i>PLoS ONE</i> , 2010, 5, e13133.	1.1	54
105	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled "Universal" Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	1.8	59
106	Investigating the correspondence between transcriptomic and proteomic expression profiles using coupled cluster models. <i>Bioinformatics</i> , 2008, 24, 2894-2900.	1.8	117
107	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.	3.3	73
108	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.	2.5	183

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109	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.	1.5	84
110	Accurate Mass Measurements in Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3621-3653.	23.0	102
111	Head-to-Head Comparison of Serum Fractionation Techniques. <i>Journal of Proteome Research</i> , 2007, 6, 828-836.	1.8	152
112	The Use of a Quantitative CysteinyI-Peptide Enrichment Technology for High-Throughput Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2007, 359, 107-124.	0.4	16
113	Characterization of the Mouse Brain Proteome Using Global Proteomic Analysis Complemented with CysteinyI-Peptide Enrichment. <i>Journal of Proteome Research</i> , 2006, 5, 361-369.	1.8	126
114	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.	2.5	197
115	Advances and Challenges in Liquid Chromatography-Mass Spectrometry-based Proteomics Profiling for Clinical Applications. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1727-1744.	2.5	309
116	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
117	Improved proteome coverage by using high efficiency cysteinyI peptide enrichment: The human mammary epithelial cell proteome. <i>Proteomics</i> , 2005, 5, 1263-1273.	1.3	65
118	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.	2.5	156
119	Utilizing Human Blood Plasma for Proteomic Biomarker Discovery. <i>Journal of Proteome Research</i> , 2005, 4, 1073-1085.	1.8	288
120	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.	1.8	320
121	Human Plasma N-Glycoproteome Analysis by Immunoaffinity Subtraction, Hydrazide Chemistry, and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 2070-2080.	1.8	394
122	High-Throughput Comparative Proteome Analysis Using a Quantitative CysteinyI-peptide Enrichment Technology. <i>Analytical Chemistry</i> , 2004, 76, 5345-5353.	3.2	142
123	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.	3.2	43
124	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.	1.8	16
125	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.	1.3	11