

Wei-Jun Qian

List of Publications by Year in descending order

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Version: 2024-02-01

231
papers

14,174
citations

17776

65
h-index

30277

107
g-index

247
all docs

247
docs citations

247
times ranked

18484
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	Exploratory study reveals far reaching systemic and cellular effects of verapamil treatment in subjects with type 1 diabetes. <i>Nature Communications</i> , 2022, 13, 1159.	5.8	28
4	Multi-Site Observational Study to Assess Biomarkers for Susceptibility or Resilience to Chronic Pain: The Acute to Chronic Pain Signatures (A2CPS) Study Protocol. <i>Frontiers in Medicine</i> , 2022, 9, 849214.	1.2	4
5	Hanging drop sample preparation improves sensitivity of spatial proteomics. <i>Lab on A Chip</i> , 2022, 22, 2869-2877.	3.1	12
6	Regulation of hyperoxia-induced neonatal lung injury via post-translational cysteine redox modifications. <i>Redox Biology</i> , 2022, 55, 102405.	3.9	4
7	Characterization of cellular oxidative stress response by stoichiometric redox proteomics. <i>American Journal of Physiology - Cell Physiology</i> , 2021, 320, C182-C194.	2.1	23
8	Proteomic Approaches for Advancing the Understanding and Application of Oleaginous Bacteria for Bioconversion of Lignin to Lipids. <i>ACS Symposium Series</i> , 2021, , 61-96.	0.5	3
9	Enhancement of polyhydroxyalkanoate production by co-feeding lignin derivatives with glycerol in <i>Pseudomonas putida</i> KT2440. <i>Biotechnology for Biofuels</i> , 2021, 14, 11.	6.2	28
10	Defective insulin receptor signaling in hPSCs skews pluripotency and negatively perturbs neural differentiation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100495.	1.6	2
11	Lipid production from non-sugar compounds in pretreated lignocellulose hydrolysates by <i>Rhodococcus jostii</i> RHA1. <i>Biomass and Bioenergy</i> , 2021, 145, 105970.	2.9	6
12	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. <i>Communications Biology</i> , 2021, 4, 265.	2.0	46
13	New Insights Into the Biology of Protein O-GlcNAcylation: Approaches and Observations. <i>Frontiers in Aging</i> , 2021, 1, .	1.2	17
14	Stoichiometric Thiol Redox Proteomics for Quantifying Cellular Responses to Perturbations. <i>Antioxidants</i> , 2021, 10, 499.	2.2	19
15	Proteomic Profiling of the Substantia Nigra to Identify Determinants of Lewy Body Pathology and Dopaminergic Neuronal Loss. <i>Journal of Proteome Research</i> , 2021, 20, 2266-2282.	1.8	10
16	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021, 20, 2780-2795.	1.8	36
17	A Comprehensive Urine Proteome Database Generated From Patients With Various Renal Conditions and Prostate Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 548212.	1.2	18
18	Assessment of TMT Labeling Efficiency in Large-Scale Quantitative Proteomics: The Critical Effect of Sample pH. <i>ACS Omega</i> , 2021, 6, 12660-12666.	1.6	11

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19	Repetitive diacetyl vapor exposure promotes ubiquitin proteasome stress and precedes bronchiolitis obliterans pathology. <i>Archives of Toxicology</i> , 2021, 95, 2469-2483.	1.9	8
20	Enhanced epithelial sodium channel activity in neonatal Scnn1b mouse lung attenuates high oxygen-induced lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 321, L29-L41.	1.3	4
21	Altered β^2 -Cell Prohormone Processing and Secretion in Type 1 Diabetes. <i>Diabetes</i> , 2021, 70, 1038-1050.	0.3	28
22	Resin-Assisted Capture Coupled with Isobaric Tandem Mass Tag Labeling for Multiplexed Quantification of Protein Thiol Oxidation. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	3
23	Tutorial: best practices and considerations for mass-spectrometry-based protein biomarker discovery and validation. <i>Nature Protocols</i> , 2021, 16, 3737-3760.	5.5	110
24	Fate, cytotoxicity and cellular metabolomic impact of ingested nanoscale carbon dots using simulated digestion and a triculture small intestinal epithelial model. <i>NanoImpact</i> , 2021, 23, 100349.	2.4	10
25	Endurance Training Reprograms The White Adipose Tissue Proteome Of Rats In A Sex-specific Manner. <i>Medicine and Science in Sports and Exercise</i> , 2021, 53, 119-120.	0.2	0
26	A Sweet H ₂ S/H ₂ O ₂ Dual Release System and Specific Protein S-Persulfidation Mediated by Thioglucose/Glucose Oxidase. <i>Journal of the American Chemical Society</i> , 2021, 143, 13325-13332.	6.6	23
27	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
28	Defining the Dynamic Regulation of O-GlcNAc Proteome in the Mouse Cortex--the O-GlcNAcylation of Synaptic and Trafficking Proteins Related to Neurodegenerative Diseases. <i>Frontiers in Aging</i> , 2021, 2, .	1.2	10
29	Elamipretide (SS-31) treatment attenuates age-associated post-translational modifications of heart proteins. <i>GeroScience</i> , 2021, 43, 2395-2412.	2.1	17
30	Mass spectrometry-based direct detection of multiple types of protein thiol modifications in pancreatic beta cells under endoplasmic reticulum stress. <i>Redox Biology</i> , 2021, 46, 102111.	3.9	27
31	Comprehensive Proteomics Analysis of Stressed Human Islets Identifies GDF15 as a Target for Type 1 Diabetes Intervention. <i>Cell Metabolism</i> , 2020, 31, 363-374.e6.	7.2	78
32	Evaluation of the cytotoxic and cellular proteome impacts of food-grade TiO ₂ (E171) using simulated gastrointestinal digestions and a tri-culture small intestinal epithelial model. <i>NanoImpact</i> , 2020, 17, 100202.	2.4	30
33	A proteome-wide assessment of the oxidative stress paradigm for metal and metal-oxide nanomaterials in human macrophages. <i>NanoImpact</i> , 2020, 17, 100194.	2.4	29
34	Protein thiol oxidation in the rat lung following e-cigarette exposure. <i>Redox Biology</i> , 2020, 37, 101758.	3.9	16
35	Stoichiometric quantification of the thiol redox proteome of macrophages reveals subcellular compartmentalization and susceptibility to oxidative perturbations. <i>Redox Biology</i> , 2020, 36, 101649.	3.9	34
36	Receptor-Driven ERK Pulses Reconfigure MAPK Signaling and Enable Persistence of Drug-Adapted BRAF-Mutant Melanoma Cells. <i>Cell Systems</i> , 2020, 11, 478-494.e9.	2.9	71

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37	Near-Single-Cell Proteomics Profiling of the Proximal Tubular and Glomerulus of the Normal Human Kidney. <i>Frontiers in Medicine</i> , 2020, 7, 499.	1.2	12
38	Cytotoxicity and cellular proteome impact of cellulose nanocrystals using simulated digestion and an in vitro small intestinal epithelium cellular model. <i>NanoImpact</i> , 2020, 20, 100269.	2.4	10
39	Proteomic Tissue-Based Classifier for Early Prediction of Prostate Cancer Progression. <i>Cancers</i> , 2020, 12, 1268.	1.7	8
40	Block Design with Common Reference Samples Enables Robust Large-Scale Label-Free Quantitative Proteome Profiling. <i>Journal of Proteome Research</i> , 2020, 19, 2863-2872.	1.8	10
41	Development of Multiplexed Immuno-N-Terminomics to Reveal the Landscape of Proteolytic Processing in Early Embryogenesis of <i>Drosophila melanogaster</i> . <i>Analytical Chemistry</i> , 2020, 92, 4926-4934.	3.2	7
42	Accurate Identification of Deamidation and Citrullination from Global Shotgun Proteomics Data Using a Dual-Search Delta Score Strategy. <i>Journal of Proteome Research</i> , 2020, 19, 1863-1872.	1.8	16
43	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	13.5	147
44	Nitrate bioreduction dynamics in hyporheic zone sediments under cyclic changes of chemical compositions. <i>Journal of Hydrology</i> , 2020, 585, 124836.	2.3	3
45	Oxidative Stress and Redox Modifications in Nanomaterial-Cellular Interactions. <i>Molecular and Integrative Toxicology</i> , 2020, , 127-148.	0.5	5
46	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
47	Late-life restoration of mitochondrial function reverses cardiac dysfunction in old mice. <i>ELife</i> , 2020, 9, .	2.8	68
48	Meta-analysis of peptides to detect protein significance. <i>Statistics and Its Interface</i> , 2020, 13, 465-474.	0.2	0
49	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
50	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
51	The role of proteomics in assessing beta-cell dysfunction and death in type 1 diabetes. <i>Expert Review of Proteomics</i> , 2019, 16, 569-582.	1.3	8
52	Response to Comment on Sims et al. Proinsulin Secretion Is a Persistent Feature of Type 1 Diabetes. <i>Diabetes Care</i> 2019;42:258-264. <i>Diabetes Care</i> , 2019, 42, e85-e86.	4.3	5
53	Increased β -cell proliferation before immune cell invasion prevents progression of type 1 diabetes. <i>Nature Metabolism</i> , 2019, 1, 509-518.	5.1	38
54	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

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55	Architecture and subunit arrangement of native AMPA receptors elucidated by cryo-EM. <i>Science</i> , 2019, 364, 355-362.	6.0	134
56	Discovery of potential pathways for biological conversion of poplar wood into lipids by co-fermentation of <i>Rhodococci</i> strains. <i>Biotechnology for Biofuels</i> , 2019, 12, 60.	6.2	69
57	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
58	Improving mitochondrial function with SS-31 reverses age-related redox stress and improves exercise tolerance in aged mice. <i>Free Radical Biology and Medicine</i> , 2019, 134, 268-281.	1.3	101
59	Proinsulin Secretion Is a Persistent Feature of Type 1 Diabetes. <i>Diabetes Care</i> , 2019, 42, 258-264.	4.3	82
60	Stable Acinar Progenitor Cell Model Identifies Treacle-Dependent Radioresistance. <i>Radiation Research</i> , 2019, 192, 135.	0.7	4
61	Abstract 3165: Identification of candidate biomarkers for aggressive prostate cancer using targeted proteomics and FFPE tissue samples with outcomes data. , 2019, , .		0
62	Abstract LB-B09: ERK pulses drive non-genetic resistance in drug-adapted BRAFV600Emelanoma cells. , 2019, , .		0
63	Nanodroplet processing platform for deep and quantitative proteome profiling of 10 ⁴ -100 mammalian cells. <i>Nature Communications</i> , 2018, 9, 882.	5.8	384
64	Targeted Quantification of Phosphorylation Dynamics in the Context of EGFR-MAPK Pathway. <i>Analytical Chemistry</i> , 2018, 90, 5256-5263.	3.2	39
65	Subnanogram proteomics: Impact of LC column selection, MS instrumentation and data analysis strategy on proteome coverage for trace samples. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 4-10.	0.7	67
66	Genomics and biochemistry investigation on the metabolic pathway of milled wood and alkali lignin-derived aromatic metabolites of <i>Comamonas serinivorans</i> SP-35. <i>Biotechnology for Biofuels</i> , 2018, 11, 338.	6.2	39
67	Reversal of age related post-translational modifications improves mitochondrial and skeletal muscle function through redox dependent mechanisms. <i>Free Radical Biology and Medicine</i> , 2018, 128, S124.	1.3	0
68	Insulin receptor-mediated signaling regulates pluripotency markers and lineage differentiation. <i>Molecular Metabolism</i> , 2018, 18, 153-163.	3.0	18
69	Nanoproteomics comes of age. <i>Expert Review of Proteomics</i> , 2018, 15, 865-871.	1.3	42
70	Fatiguing contractions increase protein S-glutathionylation occupancy in mouse skeletal muscle. <i>Redox Biology</i> , 2018, 17, 367-376.	3.9	68
71	Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1864-1874.	2.5	105
72	Urinary Virome Perturbations in Kidney Transplantation. <i>Frontiers in Medicine</i> , 2018, 5, 72.	1.2	12

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73	Nanowell-mediated two-dimensional liquid chromatography enables deep proteome profiling of <1000 mammalian cells. <i>Chemical Science</i> , 2018, 9, 6944-6951.	3.7	33
74	Serum biomarkers for diagnosis and prediction of type 1 diabetes. <i>Translational Research</i> , 2018, 201, 13-25.	2.2	42
75	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
76	Mass spectrometry-based proteomics for system-level characterization of biological responses to engineered nanomaterials. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 6067-6077.	1.9	22
77	Abstract 2573: Selection of candidate biomarkers for aggressive prostate cancer based on targeted proteomics. , 2018, .		0
78	Biodegradation of alkaline lignin by <i>Bacillus ligniniphilus</i> L1. <i>Biotechnology for Biofuels</i> , 2017, 10, 44.	6.2	129
79	Targeted quantification of functional enzyme dynamics in environmental samples for microbially mediated biogeochemical processes. <i>Environmental Microbiology Reports</i> , 2017, 9, 512-521.	1.0	16
80	Quantitative proteomic characterization of redox-dependent post-translational modifications on protein cysteines. <i>Molecular BioSystems</i> , 2017, 13, 816-829.	2.9	52
81	An alpha-synuclein MRM assay with diagnostic potential for Parkinson's disease and monitoring disease progression. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1700045.	0.8	9
82	S-Nitrosylation inhibits the kinase activity of tomato phosphoinositide-dependent kinase 1 (PDK1). <i>Journal of Biological Chemistry</i> , 2017, 292, 19743-19751.	1.6	22
83	Functional Enzyme-Based Approach for Linking Microbial Community Functions with Biogeochemical Process Kinetics. <i>Environmental Science & Technology</i> , 2017, 51, 11848-11857.	4.6	27
84	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
85	Targeted proteomic assays for quantitation of proteins identified by proteogenomic analysis of ovarian cancer. <i>Scientific Data</i> , 2017, 4, 170091.	2.4	29
86	Advances in microscale separations towards nanoproteomics applications. <i>Journal of Chromatography A</i> , 2017, 1523, 40-48.	1.8	43
87	LC-SRM-Based Targeted Quantification of Urinary Protein Biomarkers. <i>Methods in Molecular Biology</i> , 2017, 1788, 145-156.	0.4	4
88	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
89	Fatiguing Contractions Induce Acute Redox Signaling in Mouse Muscle. <i>Free Radical Biology and Medicine</i> , 2017, 112, 191-192.	1.3	3
90	Optimization for Peptide Sample Preparation for Urine Peptidomics. <i>Methods in Molecular Biology</i> , 2017, 1788, 63-72.	0.4	5

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91	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
92	Multiplexed targeted mass spectrometry assays for prostate cancer-associated urinary proteins. <i>Oncotarget</i> , 2017, 8, 101887-101898.	0.8	14
93	Abstract 226: Verification of prostate cancer genomics biomarker candidates at protein level using PRISM-SRM. , 2017, , .		0
94	Advances in targeted proteomics and applications to biomedical research. <i>Proteomics</i> , 2016, 16, 2160-2182.	1.3	175
95	S&T-10 PROSTATE CANCER DIAGNOSIS BY MULTIPLE SECRETED PROTEIN BIOMARKERS IN VOIDED URINE. <i>Journal of Urology</i> , 2016, 195, .	0.2	0
96	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
97	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. <i>Science Signaling</i> , 2016, 9, rs6.	1.6	119
98	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
99	SerpinB1 Promotes Pancreatic β Cell Proliferation. <i>Cell Metabolism</i> , 2016, 23, 194-205.	7.2	177
100	9-Fluorenylmethyl (Fm) Disulfides: Biomimetic Precursors for Persulfides. <i>Organic Letters</i> , 2016, 18, 904-907.	2.4	65
101	Mining the human urine proteome for monitoring renal transplant injury. <i>Kidney International</i> , 2016, 89, 1244-1252.	2.6	80
102	SNaPP: Simplified Nanoproteomics Platform for Reproducible Global Proteomic Analysis of Nanogram Protein Quantities. <i>Endocrinology</i> , 2016, 157, 1307-1314.	1.4	48
103	The current state of the art of quantitative phosphoproteomics and its applications to diabetes research. <i>Expert Review of Proteomics</i> , 2016, 13, 421-433.	1.3	26
104	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69.	1.5	187
105	Quantitative Profiling of Protein S-Glutathionylation Reveals Redox-Dependent Regulation of Macrophage Function during Nanoparticle-Induced Oxidative Stress. <i>ACS Nano</i> , 2016, 10, 524-538.	7.3	77
106	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
107	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016, 1410, 223-236.	0.4	33
108	An efficient method for native protein purification in the selected range from prostate cancer tissue digests. <i>Chinese Clinical Oncology</i> , 2016, 5, 78-78.	0.4	4

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109	Abstract 3872: Quantification of mutant SPOP proteins in prostate cancer using targeted proteomics. , 2016, , .		0
110	The Measurement of Reversible Redox Dependent Post-translational Modifications and Their Regulation of Mitochondrial and Skeletal Muscle Function. <i>Frontiers in Physiology</i> , 2015, 6, 347.	1.3	46
111	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
112	Preserved DNA Damage Checkpoint Pathway Protects against Complications in Long-Standing Type 1 Diabetes. <i>Cell Metabolism</i> , 2015, 22, 239-252.	7.2	40
113	Compensatory Islet Response to Insulin Resistance Revealed by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 3111-3122.	1.8	22
114	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
115	Abstract 1818: Analytical platform evaluation for quantification of ERG oncoprotein in prostate cancer using protein and mRNA detection methods. , 2015, , .		0
116	High and Low Doses of Ionizing Radiation Induce Different Secretome Profiles in a Human Skin Model. <i>PLoS ONE</i> , 2014, 9, e92332.	1.1	13
117	Proteomic approaches for site-specific <i>O</i>-GlcNAcylation analysis. <i>Bioanalysis</i> , 2014, 6, 2571-2580.	0.6	13
118	Proteome-wide Light/Dark Modulation of Thiol Oxidation in Cyanobacteria Revealed by Quantitative Site-specific Redox Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3270-3285.	2.5	75
119	Detecting differential protein expression in large-scale population proteomics. <i>Bioinformatics</i> , 2014, 30, 2741-2746.	1.8	17
120	A Method to Determine Lysine Acetylation Stoichiometries. <i>International Journal of Proteomics</i> , 2014, 2014, 1-8.	2.0	33
121	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. <i>Molecular Oncology</i> , 2014, 8, 1169-1180.	2.1	24
122	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
123	Proteomic identification and quantification of S-glutathionylation in mouse macrophages using resin-assisted enrichment and isobaric labeling. <i>Free Radical Biology and Medicine</i> , 2014, 67, 460-470.	1.3	91
124	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
125	Expediting SRM Assay Development for Large-Scale Targeted Proteomics Experiments. <i>Journal of Proteome Research</i> , 2014, 13, 4479-4487.	1.8	29
126	Brain Insulin Lowers Circulating BCAA Levels by Inducing Hepatic BCAA Catabolism. <i>Cell Metabolism</i> , 2014, 20, 898-909.	7.2	124

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127	Optimization for peptide sample preparation for urine peptidomics. <i>Clinical Proteomics</i> , 2014, 11, 7.	1.1	33
128	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 621-631.	2.5	73
129	Perturbations in the Urinary Exosome in Transplant Rejection. <i>Frontiers in Medicine</i> , 2014, 1, 57.	1.2	43
130	Abstract 2483: An antibody-independent, complementary SRM strategy for ultrasensitive and multiplexed quantification of cancer biomarker candidates. , 2014, , .		0
131	Liver-Derived Systemic Factors Drive β Cell Hyperplasia in Insulin-Resistant States. <i>Cell Reports</i> , 2013, 3, 968.	2.9	1
132	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	0.8	17
133	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
134	Liver-Derived Systemic Factors Drive β Cell Hyperplasia in Insulin-Resistant States. <i>Cell Reports</i> , 2013, 3, 401-410.	2.9	123
135	Impact of <i>alg3</i> gene deletion on growth, development, pigment production, protein secretion, and functions of recombinant <i>Trichoderma reesei</i> cellobiohydrolases in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2013, 61, 120-132.	0.9	25
136	Quantitative site-specific reactivity profiling of S-nitrosylation in mouse skeletal muscle using cysteinyl peptide enrichment coupled with mass spectrometry. <i>Free Radical Biology and Medicine</i> , 2013, 57, 68-78.	1.3	61
137	Evaluation of Selected Binding Domains for the Analysis of Ubiquitinated Proteomes. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1214-1223.	1.2	7
138	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
139	Resin-Assisted Enrichment of N-Terminal Peptides for Characterizing Proteolytic Processing. <i>Analytical Chemistry</i> , 2013, 85, 6826-6832.	3.2	24
140	Synthesis and Application of an Environmentally Insensitive Cy3-Based Arsenical Fluorescent Probe To Identify Adaptive Microbial Responses Involving Proximal Dithiol Oxidation. <i>Journal of the American Chemical Society</i> , 2013, 135, 3567-3575.	6.6	25
141	In-Source Fragmentation and the Sources of Partially Tryptic Peptides in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 910-916.	1.8	51
142	Antibody-free PRISM-SRM for multiplexed protein quantification: is this the new competition for immunoassays in bioanalysis?. <i>Bioanalysis</i> , 2013, 5, 267-269.	0.6	20
143	Determination of Burn Patient Outcome by Large-Scale Quantitative Discovery Proteomics. <i>Critical Care Medicine</i> , 2013, 41, 1421-1434.	0.4	55
144	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

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145	IgY14 and SuperMix immunoaffinity separations coupled with liquid chromatography-mass spectrometry for human plasma proteomics biomarker discovery. <i>Methods</i> , 2012, 56, 246-253.	1.9	57
146	Identification of phosphorylated butyrylcholinesterase in human plasma using immunoaffinity purification and mass spectrometry. <i>Analytica Chimica Acta</i> , 2012, 723, 68-75.	2.6	28
147	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
148	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
149	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
150	Advancing the sensitivity of selected reaction monitoring-based targeted quantitative proteomics. <i>Proteomics</i> , 2012, 12, 1074-1092.	1.3	186
151	Abstract 1268: Accurate measurement of serum total and free PSA using immunoaffinity depletion coupled to SRM: Correlation with clinical immunoassays. , 2012, , .		0
152	Unraveling pancreatic islet biology by quantitative proteomics. <i>Expert Review of Proteomics</i> , 2011, 8, 495-504.	1.3	12
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