

Qibin Zhang

List of Publications by Year in descending order

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69
papers

2,917
citations

186209

28
h-index

175177

52
g-index

69
all docs

69
docs citations

69
times ranked

4530
citing authors

#	ARTICLE	IF	CITATIONS
1	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. <i>PLoS Pathogens</i> , 2010, 6, e1000719.	2.1	361
2	A Perspective on the Maillard Reaction and the Analysis of Protein Glycation by Mass Spectrometry: Probing the Pathogenesis of Chronic Disease. <i>Journal of Proteome Research</i> , 2009, 8, 754-769.	1.8	319
3	Enrichment and Analysis of Nonenzymatically Glycated Peptides: A Boronate Affinity Chromatography Coupled with Electron-Transfer Dissociation Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2323-2330.	1.8	147
4	Comprehensive untargeted lipidomic analysis using core-shell C30 particle column and high field orbitrap mass spectrometer. <i>Journal of Chromatography A</i> , 2016, 1440, 123-134.	1.8	117
5	Proteomic Profiling of Nonenzymatically Glycated Proteins in Human Plasma and Erythrocyte Membranes. <i>Journal of Proteome Research</i> , 2008, 7, 2025-2032.	1.8	103
6	Comprehensive Identification of Glycated Peptides and Their Glycation Motifs in Plasma and Erythrocytes of Control and Diabetic Subjects. <i>Journal of Proteome Research</i> , 2011, 10, 3076-3088.	1.8	92
7	Serum proteomics reveals systemic dysregulation of innate immunity in type 1 diabetes. <i>Journal of Experimental Medicine</i> , 2013, 210, 191-203.	4.2	91
8	A Method for Selective Enrichment and Analysis of Nitrotyrosine-Containing Peptides in Complex Proteome Samples. <i>Journal of Proteome Research</i> , 2007, 6, 2257-2268.	1.8	88
9	A reversed-phase capillary ultra-performance liquid chromatography-mass spectrometry (UPLC-MS) method for comprehensive top-down/bottom-up lipid profiling. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 2923-2933.	1.9	86
10	Application of electron transfer dissociation mass spectrometry in analyses of non-enzymatically glycated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 661-666.	0.7	78
11	Future of liquid chromatography-mass spectrometry in metabolic profiling and metabolomic studies for biomarker discovery. <i>Biomarkers in Medicine</i> , 2007, 1, 159-185.	0.6	78
12	Independent Generation of 5-(2-Deoxycytidinyl)methyl Radical and the Formation of a Novel Cross-Link Lesion between 5-Methylcytosine and Guanine. <i>Journal of the American Chemical Society</i> , 2003, 125, 12795-12802.	6.6	71
13	Improved Methods for the Enrichment and Analysis of Glycated Peptides. <i>Analytical Chemistry</i> , 2008, 80, 9822-9829.	3.2	65
14	Generation of 5-(2'-deoxycytidyl)methyl radical and the formation of intrastrand cross-link lesions in oligodeoxyribonucleotides. <i>Nucleic Acids Research</i> , 2005, 33, 1593-1603.	6.5	62
15	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	2.4	62
16	Characterization of intact N- and O-linked glycopeptides using higher energy collisional dissociation. <i>Analytical Biochemistry</i> , 2014, 452, 96-102.	1.1	56
17	Fragmentation of protonated ions of peptides containing cysteine, cysteine sulfinic acid, and cysteine sulfonic acid. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 697-702.	1.2	48
18	Capillary LC Coupled with High-Mass Measurement Accuracy Mass Spectrometry for Metabolic Profiling. <i>Analytical Chemistry</i> , 2007, 79, 6081-6093.	3.2	47

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19	Independent Generation of the 5-Hydroxy-5,6-dihydrothymidin-6-yl Radical and Its Reactivity in Dinucleoside Monophosphates. <i>Journal of the American Chemical Society</i> , 2004, 126, 13287-13297.	6.6	45
20	Gangliosides are essential endosomal receptors for quasi-enveloped and naked hepatitis A virus. <i>Nature Microbiology</i> , 2020, 5, 1069-1078.	5.9	45
21	Recognition and Incision of Oxidative Intrastrand Cross-Link Lesions by UvrABC Nuclease. <i>Biochemistry</i> , 2006, 45, 10739-10746.	1.2	44
22	Off-line mixed-mode liquid chromatography coupled with reversed phase high performance liquid chromatography-high resolution mass spectrometry to improve coverage in lipidomics analysis. <i>Analytica Chimica Acta</i> , 2017, 954, 140-150.	2.6	39
23	Perturbations in the lipid profile of individuals with newly diagnosed type 1 diabetes mellitus: Lipidomics analysis of a Diabetes Antibody Standardization Program sample subset. <i>Clinical Biochemistry</i> , 2010, 43, 948-956.	0.8	38
24	Ozone-induced dissociation on a traveling wave high-resolution mass spectrometer for determination of double bond position in lipids. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 1415-1423.	0.7	38
25	Temporal expression profiling of plasma proteins reveals oxidative stress in early stages of Type 1 Diabetes progression. <i>Journal of Proteomics</i> , 2018, 172, 100-110.	1.2	36
26	Analysis of non-enzymatically glycosylated peptides: neutral-loss-triggered MS ³ versus multi-stage activation tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 3027-3034.	0.7	35
27	Metabolomic response of human skin tissue to low dose ionizing radiation. <i>Molecular BioSystems</i> , 2012, 8, 1979.	2.9	31
28	Carbohydrate intake attenuates post-exercise plasma levels of cytochrome P450-generated oxylipins. <i>PLoS ONE</i> , 2019, 14, e0213676.	1.1	31
29	Combined Pulsed-Q Dissociation and Electron Transfer Dissociation for Identification and Quantification of iTRAQ-Labeled Phosphopeptides. <i>Analytical Chemistry</i> , 2009, 81, 4137-4143.	3.2	30
30	Structural Analysis of Unsaturated Glycosphingolipids Using Shotgun Ozone-Induced Dissociation Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2330-2343.	1.2	29
31	A statistical analysis of the effects of urease pre-treatment on the measurement of the urinary metabolome by gas chromatography-mass spectrometry. <i>Metabolomics</i> , 2014, 10, 897-908.	1.4	28
32	Serum Proteome Profiles in Stricturing Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1935-1941.	0.9	28
33	Online 2D-LC-MS/MS Platform for Analysis of Glycated Proteome. <i>Analytical Chemistry</i> , 2018, 90, 1081-1086.	3.2	28
34	Comprehensive analysis of oxylipins in human plasma using reversed-phase liquid chromatography-triple quadrupole mass spectrometry with heatmap-assisted selection of transitions. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 367-385.	1.9	28
35	Simultaneous determination of tryptophan and its 31 catabolites in mouse tissues by polarity switching UHPLC-SRM-MS. <i>Analytica Chimica Acta</i> , 2018, 1037, 200-210.	2.6	27
36	Blueberry and/or Banana Consumption Mitigate Arachidonic, Cytochrome P450 Oxylipin Generation During Recovery From 75-Km Cycling: A Randomized Trial. <i>Frontiers in Nutrition</i> , 2020, 7, 121.	1.6	25

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37	The Reactivity of the 5-Hydroxy-5,6-dihydrothymidin-6-yl Radical in Oligodeoxyribonucleotides. <i>Chemical Research in Toxicology</i> , 2005, 18, 1897-1906.	1.7	22
38	Type 1 diabetes cadaveric human pancreata exhibit a unique exocrine tissue proteomic profile. <i>Proteomics</i> , 2016, 16, 1432-1446.	1.3	21
39	Isobaric Labeling of Intact Gangliosides toward Multiplexed LC-MS/MS-Based Quantitative Analysis. <i>Analytical Chemistry</i> , 2018, 90, 2578-2586.	3.2	21
40	Recent advances in the mass spectrometric analysis of glycosphingolipidome – A review. <i>Analytica Chimica Acta</i> , 2020, 1132, 134-155.	2.6	21
41	Temporal profiles of plasma proteome during childhood development. <i>Journal of Proteomics</i> , 2017, 152, 321-328.	1.2	20
42	Proteomic profiling of human islets collected from frozen pancreata using laser capture microdissection. <i>Journal of Proteomics</i> , 2017, 150, 149-159.	1.2	18
43	Accurate mass and retention time library of serum lipids for type 1 diabetes research. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 5937-5949.	1.9	18
44	Activation of PPAR α -catalase pathway reverses alcoholic liver injury via upregulating NAD synthesis and accelerating alcohol clearance. <i>Free Radical Biology and Medicine</i> , 2021, 174, 249-263.	1.3	17
45	Application of High-Resolution ¹ H MAS NMR Spectroscopy to the Analysis of Intact Bones from Mice Exposed to Gamma Radiation. <i>Radiation Research</i> , 2009, 172, 607-616.	0.7	14
46	Formation of dehydroalanine from mimosine and cysteine: artifacts in gas chromatography/mass spectrometry based metabolomics. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 2561-2564.	0.7	14
47	Simultaneous quantification of free fatty acids and acylcarnitines in plasma samples using dansylhydrazine labeling and liquid chromatography-triple quadrupole mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 2841-2849.	1.9	14
48	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
49	Glycated Plasma Proteins as More Sensitive Markers for Glycemic Control in Type 1 Diabetes. <i>Proteomics - Clinical Applications</i> , 2020, 14, 1900104.	0.8	13
50	Human GDPD3 overexpression promotes liver steatosis by increasing lysophosphatidic acid production and fatty acid uptake. <i>Journal of Lipid Research</i> , 2020, 61, 1075-1086.	2.0	13
51	Isobaric Labeling-Based LC-MS/MS Strategy for Comprehensive Profiling of Human Pancreatic Tissue Proteome. <i>Methods in Molecular Biology</i> , 2017, 1788, 215-224.	0.4	10
52	Orthogonal Method for Double-Bond Placement via Ozone-Induced Dissociation Mass Spectrometry (OzID-MS). <i>Journal of Natural Products</i> , 2019, 82, 3421-3431.	1.5	10
53	Differential Isotope Labeling by Permethylated and Reversed-Phase Liquid Chromatography-Mass Spectrometry for Relative Quantification of Intact Neutral Glycolipids in Mammalian Cells. <i>Analytical Chemistry</i> , 2019, 91, 9673-9681.	3.2	8
54	Pancreatic Tissue Proteomics Unveils Key Proteins, Pathways, and Networks Associated with Type 1 Diabetes. <i>Proteomics - Clinical Applications</i> , 2020, 14, e2000053.	0.8	8

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55	Ganglioside isomer analysis using ion polarity switching liquid chromatography-tandem mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 3269-3279.	1.9	8
56	Structural analysis of N- and O-glycans using ZIC-HILIC/dialysis coupled to NMR detection. <i>Fungal Genetics and Biology</i> , 2014, 72, 207-215.	0.9	7
57	Fragmentation Behavior and Gas-Phase Structures of Cationized Glycosphingolipids in Ozone-Induced Dissociation Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1609-1620.	1.2	7
58	HLA Allele-Specific Quantitative Profiling of Type 1 Diabetic B Lymphocyte Immunopeptidome. <i>Journal of Proteome Research</i> , 2022, 21, 250-264.	1.8	7
59	LipidMiner: a software for automated identification and quantification of lipids from multiple liquid chromatography/mass spectrometry data files. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 981-985.	0.7	6
60	Synthesis, Purification, and Mass Spectrometric Characterization of Stable Isotope-Labeled Amadori-Glycated Phospholipids. <i>ACS Omega</i> , 2018, 3, 15725-15733.	1.6	5
61	A UPLC-MRM-MS method for comprehensive profiling of Amadori compound-modified phosphatidylethanolamines in human plasma. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 431-443.	1.9	5
62	Development of a fibrinogen-specific sandwich enzyme-linked immunosorbent assay microarray assay for distinguishing between blood plasma and serum samples. <i>Analytical Biochemistry</i> , 2011, 414, 99-102.	1.1	4
63	ROFI - The Use of Repeated Optimization for Feature Interpretation. , 2016, , .		3
64	Comprehensive Identification of Amadori Compound-Modified Phosphatidylethanolamines in Human Plasma. <i>Chemical Research in Toxicology</i> , 2019, 32, 1449-1457.	1.7	3
65	Label-Free LC-MS/MS Strategy for Comprehensive Proteomic Profiling of Human Islets Collected Using Laser Capture Microdissection from Frozen Pancreata. <i>Methods in Molecular Biology</i> , 2019, 1871, 253-264.	0.4	3
66	Comprehensive Quantification of Carboxymethyllysine-Modified Peptides in Human Plasma. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 744-752.	1.2	3
67	Pancreatic INS-1 β 2-Cell Response to Thapsigargin and Rotenone: A Comparative Proteomics Analysis Uncovers Key Pathways of β 2-Cell Dysfunction. <i>Chemical Research in Toxicology</i> , 2022, 35, 1080-1094.	1.7	3
68	Bayesian Posterior Integration for Classification of Mass Spectrometry Data. , 2017, , 203-211.		1
69	Quantification of Plasma Oxylipins Using Solid-Phase Extraction and Reversed-Phase Liquid Chromatography-Triple Quadrupole Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2306, 171-186.	0.4	1