

Fang-Jun Wang

List of Publications by Year in descending order

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128
papers

4,766
citations

94381

37
h-index

110317

64
g-index

138
all docs

138
docs citations

138
times ranked

6037
citing authors

#	ARTICLE	IF	CITATIONS
1	Glycoproteomics Analysis of Human Liver Tissue by Combination of Multiple Enzyme Digestion and Hydrazide Chemistry. <i>Journal of Proteome Research</i> , 2009, 8, 651-661.	1.8	356
2	Recent development of monolithic stationary phases with emphasis on microscale chromatographic separation. <i>Journal of Chromatography A</i> , 2008, 1184, 369-392.	1.8	251
3	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , 2014, 96, 253-262.	1.2	209
4	Reversed-Phase-Reversed-Phase Liquid Chromatography Approach with High Orthogonality for Multidimensional Separation of Phosphopeptides. <i>Analytical Chemistry</i> , 2010, 82, 53-56.	3.2	135
5	ZnAl ₂ O ₃ -Hydrothermalite-Supported Au ₂₅ Nanoclusters as Precatalysts for Chemoselective Hydrogenation of β -Nitrostyrene. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 2709-2713.	7.2	127
6	One-Pot Process for Fabrication of Organic-Silica Hybrid Monolithic Capillary Columns Using Organic Monomer and Alkoxysilane. <i>Analytical Chemistry</i> , 2009, 81, 3529-3536.	3.2	126
7	Highly Efficient Extraction of Serum Peptides by Ordered Mesoporous Carbon. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 12218-12221.	7.2	118
8	Capillary Trap Column with Strong Cation-Exchange Monolith for Automated Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 2007, 79, 6599-6606.	3.2	113
9	Preparation of monodisperse immobilized Ti ⁴⁺ affinity chromatography microspheres for specific enrichment of phosphopeptides. <i>Analytica Chimica Acta</i> , 2009, 636, 34-41.	2.6	105
10	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
11	Gold Nanorod Photothermal Therapy Alters Cell Junctions and Actin Network in Inhibiting Cancer Cell Collective Migration. <i>ACS Nano</i> , 2018, 12, 9279-9290.	7.3	105
12	Novel Features of Eukaryotic Photosystem II Revealed by Its Crystal Structure Analysis from a Red Alga. <i>Journal of Biological Chemistry</i> , 2016, 291, 5676-5687.	1.6	100
13	Synthesis of branched PEG brushes hybrid hydrophilic magnetic nanoparticles for the selective enrichment of N-linked glycopeptides. <i>Chemical Communications</i> , 2012, 48, 8138.	2.2	99
14	Centrifugation Assisted Microreactor Enables Facile Integration of Trypsin Digestion, Hydrophilic Interaction Chromatography Enrichment, and On-Column Deglycosylation for Rapid and Sensitive N-Glycoproteome Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5146-5153.	3.2	95
15	Coupling Strong Anion-Exchange Monolithic Capillary with MALDI-TOF MS for Sensitive Detection of Phosphopeptides in Protein Digest. <i>Analytical Chemistry</i> , 2010, 82, 2907-2915.	3.2	93
16	Peptide profiling and the bioactivity character of yogurt in the simulated gastrointestinal digestion. <i>Journal of Proteomics</i> , 2016, 141, 24-46.	1.2	90
17	Enrichment and separation techniques for large-scale proteomics analysis of the protein post-translational modifications. <i>Journal of Chromatography A</i> , 2014, 1372, 1-17.	1.8	86
18	Comprehensive Mapping of Protein N-Glycosylation in Human Liver by Combining Hydrophilic Interaction Chromatography and Hydrazide Chemistry. <i>Journal of Proteome Research</i> , 2014, 13, 1713-1721.	1.8	74

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19	Comparative proteomic analysis of <i>Rhodospiridium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009, 26, 553-566.	0.8	72
20	Oncogenic AURKA-enhanced N6-methyladenosine modification increases DROSHA mRNA stability to transactivate STC1 in breast cancer stem-like cells. <i>Cell Research</i> , 2021, 31, 345-361.	5.7	68
21	A Fully Automated System with Online Sample Loading, Isotope Dimethyl Labeling and Multidimensional Separation for High-Throughput Quantitative Proteome Analysis. <i>Analytical Chemistry</i> , 2010, 82, 3007-3015.	3.2	66
22	Multi-hierarchical profiling the structure-activity relationships of engineered nanomaterials at nano-bio interfaces. <i>Nature Communications</i> , 2018, 9, 4416.	5.8	61
23	Biflavones from <i>Ginkgo biloba</i> as inhibitors of human thrombin. <i>Bioorganic Chemistry</i> , 2019, 92, 103199.	2.0	61
24	Improvement of the Quantification Accuracy and Throughput for Phosphoproteome Analysis by a Pseudo Triplex Stable Isotope Dimethyl Labeling Approach. <i>Analytical Chemistry</i> , 2011, 83, 7755-7762.	3.2	57
25	Development of Glycoprotein Capture-Based Label-Free Method for the High-throughput Screening of Differential Glycoproteins in Hepatocellular Carcinoma. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006445.	2.5	55
26	Monolithic Capillary Column Based Glycoproteomic Reactor for High-Sensitive Analysis of N-Glycoproteome. <i>Analytical Chemistry</i> , 2013, 85, 2847-2852.	3.2	53
27	Five-plex isotope dimethyl labeling for quantitative proteomics. <i>Chemical Communications</i> , 2014, 50, 1708.	2.2	51
28	Perspectives of Comprehensive Phosphoproteome Analysis Using Shotgun Strategy. <i>Analytical Chemistry</i> , 2011, 83, 8078-8085.	3.2	50
29	Facile preparation of ordered mesoporous silica-carbon composite nanoparticles for glycan enrichment. <i>Chemical Communications</i> , 2013, 49, 5162.	2.2	49
30	Improve the Coverage for the Analysis of Phosphoproteome of HeLa Cells by a Tandem Digestion Approach. <i>Journal of Proteome Research</i> , 2012, 11, 2828-2837.	1.8	47
31	Capture and Dimethyl Labeling of Glycopeptides on Hydrazide Beads for Quantitative Glycoproteomics Analysis. <i>Analytical Chemistry</i> , 2012, 84, 8452-8456.	3.2	45
32	Unusual zymogen activation patterns in the protein corona of Ca-zeolites. <i>Nature Catalysis</i> , 2021, 4, 607-614.	16.1	44
33	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011, 11, 42-51.	1.1	43
34	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012, 2, 5.	1.9	43
35	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , 2011, 32, 4085-4095.	5.7	40
36	ZnAl-Hydrothermalite-Supported Au ₂₅ Nanoclusters as Precatalysts for Chemoselective Hydrogenation of 3-Nitrostyrene. <i>Angewandte Chemie</i> , 2017, 129, 2753-2757.	1.6	40

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37	Phosphoric acid functionalized mesoporous organo-silica (EPO) as the adsorbent for in situ enrichment and isotope labeling of endogenous phosphopeptides. <i>Chemical Communications</i> , 2012, 48, 961-963.	2.2	38
38	Separation of intact proteins by using polyhedral oligomeric silsesquioxane based hybrid monolithic capillary columns. <i>Journal of Chromatography A</i> , 2013, 1317, 138-147.	1.8	38
39	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , 2017, 89, 1469-1476.	3.2	38
40	Online Multidimensional Separation with Biphasic Monolithic Capillary Column for Shotgun Proteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 306-310.	1.8	35
41	Development of a combined chemical and enzymatic approach for the mass spectrometric identification and quantification of aberrant N-glycosylation. <i>Journal of Proteomics</i> , 2012, 75, 1666-1674.	1.2	35
42	Magnetic nanoparticles coated with maltose-functionalized polyethyleneimine for highly efficient enrichment of N-glycopeptides. <i>Journal of Chromatography A</i> , 2015, 1425, 213-220.	1.8	35
43	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2015, 114, 226-233.	1.2	35
44	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012, 48, 6265.	2.2	34
45	Proteomic reactors and their applications in biology. <i>FEBS Journal</i> , 2011, 278, 3796-3806.	2.2	33
46	High-Sensitivity N-Glycoproteomic Analysis of Mouse Brain Tissue by Protein Extraction with a Mild Detergent of N-Dodecyl β -D-Maltoside. <i>Analytical Chemistry</i> , 2015, 87, 2054-2057.	3.2	32
47	Functionalizing with glycopeptide dendrimers significantly enhances the hydrophilicity of the magnetic nanoparticles. <i>Chemical Communications</i> , 2015, 51, 4093-4096.	2.2	32
48	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , 2015, 5, 10164.	1.6	32
49	Comprehensive proteome quantification reveals NgBR as a new regulator for epithelial-mesenchymal transition of breast tumor cells. <i>Journal of Proteomics</i> , 2015, 112, 38-52.	1.2	32
50	Real-Time Tracking the Synthesis and Degradation of Albumin in Complex Biological Systems with a near-Infrared Fluorescent Probe. <i>Analytical Chemistry</i> , 2017, 89, 9884-9891.	3.2	32
51	Improved Recovery and Identification of Membrane Proteins from Rat Hepatic Cells using a Centrifugal Proteomic Reactor. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.008425.	2.5	31
52	A simple integrated system for rapid analysis of sialic acid-containing N-glycopeptides from human serum. <i>Proteomics</i> , 2013, 13, 1306-1313.	1.3	30
53	Analytical Aspects of Proteomics: 2009-2010. <i>Analytical Chemistry</i> , 2011, 83, 4407-4426.	3.2	28
54	Selective capture of phosphopeptides by hierarchical Ti-aluminophosphate-5 molecular sieves. <i>Chemical Communications</i> , 2012, 48, 1802.	2.2	26

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55	Large-Scale Quantification of Single Amino-Acid Variations by a Variation-Associated Database Search Strategy. <i>Journal of Proteome Research</i> , 2014, 13, 241-248.	1.8	26
56	Isolation and characterization of PSI-LHCI super-complex and their sub-complexes from a red alga <i>Cyanidioschyzon merolae</i> . <i>Photosynthesis Research</i> , 2017, 133, 201-214.	1.6	26
57	Comprehensive and Reliable Phosphorylation Site Mapping of Individual Phosphoproteins by Combination of Multiple Stage Mass Spectrometric Analysis with a Target-Decoy Database Search. <i>Analytical Chemistry</i> , 2009, 81, 5794-5805.	3.2	25
58	Preparation of capillary hybrid monolithic column with sulfonate strong cation exchanger for proteome analysis. <i>Journal of Chromatography A</i> , 2012, 1256, 136-143.	1.8	25
59	Preparation of a butyl-silica hybrid monolithic column with a process for bioseparation by capillary liquid chromatography. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 2265-2271.	1.9	24
60	C ₁ N and N ₂ H Bond Metathesis Reactions Mediated by Carbon Dioxide. <i>ChemSusChem</i> , 2015, 8, 2066-2072.	3.6	24
61	Probing the Lysine Proximal Microenvironments within Membrane Protein Complexes by Active Dimethyl Labeling and Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 12060-12065.	3.2	24
62	Large-Scale Proteome Quantification of Hepatocellular Carcinoma Tissues by a Three-Dimensional Liquid Chromatography Strategy Integrated with Sample Preparation. <i>Journal of Proteome Research</i> , 2014, 13, 3645-3654.	1.8	22
63	Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. <i>Journal of Chromatography A</i> , 2007, 1171, 56-62.	1.8	21
64	Reductive methylation labeling, from quantitative to structural proteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 118, 771-778.	5.8	21
65	Prediction of ligand modulation patterns on membrane receptors via lysine reactivity profiling. <i>Chemical Communications</i> , 2019, 55, 4311-4314.	2.2	20
66	Comprehensive analysis of the N and C terminus of endogenous serum peptides reveals a highly conserved cleavage site pattern derived from proteolytic enzymes. <i>Protein and Cell</i> , 2012, 3, 669-674.	4.8	19
67	Enhancing the performance of LC-MS for intact protein analysis by counteracting the signal suppression effects of trifluoroacetic acid during electrospray. <i>Chemical Communications</i> , 2015, 51, 14758-14760.	2.2	19
68	Protein digestomic analysis reveals the bioactivity of deer antler velvet in simulated gastrointestinal digestion. <i>Food Research International</i> , 2017, 96, 182-190.	2.9	19
69	Probing the Proteomics Dark Regions by VAILase Cleavage at Aliphatic Amino Acids. <i>Analytical Chemistry</i> , 2020, 92, 2770-2777.	3.2	19
70	Highly efficient N-glycoproteomic sample preparation by combining C18 and graphitized carbon adsorbents. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 3103-3109.	1.9	18
71	Proteomic analysis reveals the protective effects of emodin on severe acute pancreatitis induced lung injury by inhibiting neutrophil proteases activity. <i>Journal of Proteomics</i> , 2020, 220, 103760.	1.2	18
72	Inactivating SARS-CoV-2 by electrochemical oxidation. <i>Science Bulletin</i> , 2021, 66, 720-726.	4.3	18

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73	Phosphoproteome analysis of an early onset mouse model (<sc>T</sc><sc>CRND</sc>8) of <sc>A</sc> Alzheimer's disease reveals temporal changes in neuronal and glia signaling pathways. Proteomics, 2013, 13, 1292-1305.	1.3	17
74	Small-Molecule Antagonist Targeting Exportin-1 via Rational Structure-Based Discovery. Journal of Medicinal Chemistry, 2020, 63, 3881-3895.	2.9	17
75	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. Journal of Separation Science, 2008, 31, 2589-2597.	1.3	16
76	Fractionation of phosphopeptides on strong anion-exchange capillary trap column for large-scale phosphoproteome analysis of microgram samples. Journal of Separation Science, 2010, 33, 1879-1887.	1.3	16
77	Improvement of proteome coverage using hydrophobic monolithic columns in shotgun proteome analysis. Journal of Chromatography A, 2009, 1216, 3887-3894.	1.8	15
78	Modulating the selectivity of affinity absorbents to multi-phosphopeptides by a competitive substitution strategy. Journal of Chromatography A, 2016, 1461, 35-41.	1.8	15
79	Probing conformational hotspots for the recognition and intervention of protein complexes by lysine reactivity profiling. Chemical Science, 2021, 12, 1451-1457.	3.7	15
80	Combination of online enzyme digestion with stable isotope labeling for high-throughput quantitative proteome analysis. Proteomics, 2012, 12, 3129-3137.	1.3	14
81	N-terminal Labeling of Peptides by Trypsin-Catalyzed Ligation for Quantitative Proteomics. Angewandte Chemie - International Edition, 2013, 52, 9205-9209.	7.2	14
82	Global Quantification of Intact Proteins via Chemical Isotope Labeling and Mass Spectrometry. Journal of Proteome Research, 2019, 18, 2185-2194.	1.8	14
83	Quantitative Lysine Reactivity Profiling Reveals Conformational Inhibition Dynamics and Potency of Aurora A Kinase Inhibitors. Analytical Chemistry, 2019, 91, 13222-13229.	3.2	13
84	Integration of monolithic frit into the particulate capillary (IMFPC) column in shotgun proteome analysis. Analytica Chimica Acta, 2009, 652, 324-330.	2.6	12
85	<i>In Situ</i> Sample Processing Approach (ISPA) for Comprehensive Quantitative Phosphoproteome Analysis. Journal of Proteome Research, 2014, 13, 3896-3904.	1.8	12
86	Phosphorylation of PP1 Regulator Sds22 by PLK1 Ensures Accurate Chromosome Segregation. Journal of Biological Chemistry, 2016, 291, 21123-21136.	1.6	12
87	Detecting Proteins Glycosylation by a Homogeneous Reaction System with Zwitterionic Gold Nanoclusters. Analytical Chemistry, 2017, 89, 4339-4343.	3.2	12
88	Highly efficient artificial blood coagulation shortcut confined on Ca-zeolite surface. Nano Research, 2021, 14, 3309-3318.	5.8	12
89	A one-step approach for preparation of an octadecyl-silica hybrid monolithic column via a non-hydrolytic sol-gel (NHSG) method. RSC Advances, 2013, 3, 22160.	1.7	11
90	A six-plex proteome quantification strategy reveals the dynamics of protein turnover. Scientific Reports, 2013, 3, 1827.	1.6	11

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91	In-situ generation and global property profiling of metal nanoclusters by ultraviolet laser dissociation-mass spectrometry. <i>Science China Chemistry</i> , 2022, 65, 1196-1203.	4.2	11
92	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , 2013, 78, 389-397.	1.2	10
93	Enhancing the Mass Spectrometry Sensitivity for Oligonucleotide Detection by Organic Vapor Assisted Electrospray. <i>Analytical Chemistry</i> , 2017, 89, 10256-10263.	3.2	10
94	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome and peptide profiling analysis by using a monolithic analytical capillary column. <i>Electrophoresis</i> , 2008, 29, 1612-1618.	1.3	9
95	Water-soluble Au nanoclusters for multiplexed mass spectrometry imaging. <i>Chemical Communications</i> , 2017, 53, 12688-12691.	2.2	9
96	Characterization and manipulation of the photosystem II-semiconductor interfacial molecular interactions in solar-to-chemical energy conversion. <i>Journal of Energy Chemistry</i> , 2022, 70, 437-443.	7.1	9
97	Single-Atom Pt ⁺ Derived from the Laser Dissociation of a Platinum Cluster: Insights into Nonoxidative Alkane Conversion. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 5987-5991.	2.1	8
98	Elucidating the Molecular Mechanism of Dynamic Photodamage of Photosystem II Membrane Protein Complex by Integrated Proteomics Strategy. <i>CCS Chemistry</i> , 2022, 4, 182-193.	4.6	8
99	Comprehensive proteomic analysis of sea cucumbers (<i>Stichopus japonicus</i>) in thermal processing by HPLC-MS/MS. <i>Food Chemistry</i> , 2022, 373, 131368.	4.2	8
100	Motif-dependent immune co-receptor interactome profiling by photoaffinity chemical proteomics. <i>Cell Chemical Biology</i> , 2022, 29, 1024-1036.e5.	2.5	8
101	Differential analysis of N-glycoproteome between hepatocellular carcinoma and normal human liver tissues by combination of multiple protease digestion and solid phase based labeling. <i>Clinical Proteomics</i> , 2014, 11, 26.	1.1	7
102	Inhibition of human thrombin by the constituents of licorice: inhibition kinetics and mechanistic insights through <i>in vitro</i> and <i>in silico</i> studies. <i>RSC Advances</i> , 2020, 10, 3626-3635.	1.7	7
103	Improving the performance of proteomic analysis via VAILase cleavage and 193-nm ultraviolet photodissociation. <i>Analytica Chimica Acta</i> , 2021, 1155, 338340.	2.6	7
104	Reversed Phase Monolithic Column Based Enzyme Reactor for Protein Analysis. <i>Chinese Journal of Analytical Chemistry</i> , 2013, 41, 10-14.	0.9	6
105	Elucidating the various multi-phosphorylation statuses of protein functional regions by 193-nm ultraviolet photodissociation. <i>Chinese Chemical Letters</i> , 2018, 29, 694-698.	4.8	6
106	Chloride-Mediated Peroxide-Free Photochemical Oxidation of Proteins (PPOP) in Mass Spectrometry-Based Structural Analysis. <i>Analytical Chemistry</i> , 2022, 94, 1135-1142.	3.2	6
107	High specific phosphopeptides enrichment by titanium silicalite with post-treatment of desilication. <i>Analytical Methods</i> , 2013, 5, 2939.	1.3	5
108	Electrospray ionization in concentrated acetonitrile vapor improves the performance of mass spectrometry for proteomic analyses. <i>Journal of Chromatography A</i> , 2017, 1483, 101-109.	1.8	5

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109	Identification of pyridoxal phosphate-modified proteins using mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 195-200.	0.7	5
110	Photochemical bromination and iodination of peptides and proteins by photoexcitation of aqueous halides. <i>Chemical Communications</i> , 2021, 57, 11972-11975.	2.2	5
111	6-Shogaol Inhibits Oxidative Stress-Induced Rat Vascular Smooth Muscle Cell Apoptosis by Regulating OXR1-p53 Axis. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 808162.	1.6	5
112	The interfacial interactions of nanomaterials with human serum albumin. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 4677-4684.	1.9	5
113	Specific mixing facilitates the comparative quantification of phosphorylation sites with significant dysregulations. <i>Analytica Chimica Acta</i> , 2017, 950, 129-137.	2.6	4
114	Lysine reactivity profiling reveals molecular insights into human serum albumin-small-molecule drug interactions. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7431-7440.	1.9	4
115	Self-Adaptable Quinone-Quinol Exchange Mechanism of Photosystem II. <i>Journal of Physical Chemistry B</i> , 2018, 122, 10478-10489.	1.2	3
116	Elucidating the molecular mechanisms of perfluorooctanoic acid-serum protein interactions by structural mass spectrometry. <i>Chemosphere</i> , 2021, , 132945.	4.2	3
117	Emerging investigator series: long-term exposure of amorphous silica nanoparticles disrupts the lysosomal and cholesterol homeostasis in macrophages. <i>Environmental Science: Nano</i> , 2022, 9, 105-117.	2.2	3
118	A strategy with label-free quantification of the targeted peptides for quantitative peptidome analysis of human serum. <i>Science China Chemistry</i> , 2010, 53, 759-767.	4.2	2
119	Nano LC-MS Based Proteomic Analysis as a Predicting Approach to Study Cellular Responses of Carbon Nanotubes. <i>Journal of Nanoscience and Nanotechnology</i> , 2016, 16, 2350-2359.	0.9	2
120	Profiling the short-lived cationic species generated during catalytic dehydration of short-chain alcohols. <i>Communications Chemistry</i> , 2018, 1, .	2.0	2
121	High-performance micro/nanoplastics characterization by MALDI-FTICR mass spectrometry. <i>Chemosphere</i> , 2022, 307, 135601.	4.2	2
122	Enrichment of peptides containing consensus sequence by an enzymatic approach for targeted analysis of proteins. <i>Proteomics</i> , 2011, 11, 3578-3581.	1.3	1
123	Analysis of oligonucleotides by ion-pair reversed-phase liquid chromatography coupled with positive mode electrospray ionization mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 4167-4173.	1.9	1
124	Size-Selective VAILase Proteolysis Provides Dynamic Insights into Protein Structures. <i>Analytical Chemistry</i> , 2021, 93, 10653-10660.	3.2	1
125	Large-Scale Proteome and Phosphoproteome Quantification by Using Dimethylation Isotope Labeling. <i>Springer Theses</i> , 2014, , 67-94.	0.0	0
126	Development of Polymer-Based Hydrophobic Monolithic Columns and Their Applications in Proteome Analysis. <i>Springer Theses</i> , 2014, , 35-65.	0.0	0

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127	Applications of Monolithic Column and Isotope Dimethylation Labeling in Shotgun Proteome Analysis. Springer Theses, 2014, , .	0.0	0
128	Catalyst-free Photochemical Bromination of Unprotected Aromatic Amino Acid Derivatives by Using a Rotating Ultraviolet Photoreactor. Chemical Research in Chinese Universities, 0, , 1.	1.3	0