

Mingliang Ye

List of Publications by Year in descending order

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246
papers

10,973
citations

30047

54
h-index

45285

90
g-index

249
all docs

249
docs citations

249
times ranked

9844
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	Monolithic stationary phases for liquid chromatography and capillary electrochromatography. <i>Journal of Chromatography A</i> , 2002, 954, 5-32.	1.8	353
3	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013, 8, 461-480.	5.5	340
4	A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . <i>Nature Communications</i> , 2012, 3, 1112.	5.8	324
5	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
6	Specific Phosphopeptide Enrichment with Immobilized Titanium Ion Affinity Chromatography Adsorbent for Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 3957-3967.	1.8	239
7	Immobilized Zirconium Ion Affinity Chromatography for Specific Enrichment of Phosphopeptides in Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1656-1665.	2.5	228
8	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
9	Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. <i>Proteomics</i> , 2008, 8, 1346-1361.	1.3	192
10	Zirconium Phosphonate-Modified Porous Silicon for Highly Specific Capture of Phosphopeptides and MALDI-TOF MS Analysis. <i>Journal of Proteome Research</i> , 2006, 5, 2431-2437.	1.8	164
11	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	2.5	161
12	Profiling of Endogenous Serum Phosphorylated Peptides by Titanium (IV) Immobilized Mesoporous Silica Particles Enrichment and MALDI-TOFMS Detection. <i>Analytical Chemistry</i> , 2009, 81, 94-104.	3.2	150
13	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , 2016, 12, 959-966.	3.9	141
14	Fabrication of Hydrazone-Linked Covalent Organic Frameworks Using Alkyl Amine as Building Block for High Adsorption Capacity of Metal Ions. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 11706-11714.	4.0	139
15	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , 2007, 28, 2201-2215.	1.3	137
16	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
17	Synthesis and characterization of a new boronate affinity monolithic capillary for specific capture of cis-diol-containing compounds. <i>Journal of Chromatography A</i> , 2009, 1216, 4768-4774.	1.8	132
18	Method Development of Efficient Protein Extraction in Bone Tissue for Proteome Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 2287-2294.	1.8	128

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19	Development of phosphopeptide enrichment techniques for phosphoproteome analysis. <i>Analyst</i> , The, 2008, 133, 1128.	1.7	114
20	Capillary Trap Column with Strong Cation-Exchange Monolith for Automated Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 2007, 79, 6599-6606.	3.2	113
21	Facile synthesis of zwitterionic polymer-coated core-shell magnetic nanoparticles for highly specific capture of N-linked glycopeptides. <i>Nanoscale</i> , 2015, 7, 3100-3108.	2.8	106
22	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
23	Capillary Electrochromatography for Separation of Peptides Driven with Electrophoretic Mobility on Monolithic Column. <i>Analytical Chemistry</i> , 2001, 73, 4918-4923.	3.2	103
24	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. <i>Journal of Proteomics</i> , 2013, 78, 486-498.	1.2	103
25	Added Value for Tandem Mass Spectrometry Shotgun Proteomics Data Validation through Isoelectric Focusing of Peptides. <i>Journal of Proteome Research</i> , 2005, 4, 2273-2282.	1.8	99
26	CE-Microreactor-CE-MS/MS for Protein Analysis. <i>Analytical Chemistry</i> , 2007, 79, 2230-2238.	3.2	96
27	On-line protein digestion and peptide mapping by capillary electrophoresis with post-column labeling for laser-induced fluorescence detection. <i>Electrophoresis</i> , 2004, 25, 1319-1326.	1.3	95
28	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
29	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
30	Development of Efficient Protein Extraction Methods for Shotgun Proteome Analysis of Formalin-Fixed Tissues. <i>Journal of Proteome Research</i> , 2007, 6, 1038-1047.	1.8	92
31	Construction of hierarchically porous monoliths from covalent organic frameworks (COFs) and their application for bisphenol A removal. <i>Journal of Hazardous Materials</i> , 2018, 355, 145-153.	6.5	91
32	Global Screening of CK2 Kinase Substrates by an Integrated Phosphoproteomics Workflow. <i>Scientific Reports</i> , 2013, 3, 3460.	1.6	89
33	Optimized Peptide Separation and Identification for Mass Spectrometry Based Proteomics via Free-Flow Electrophoresis. <i>Journal of Proteome Research</i> , 2006, 5, 2241-2249.	1.8	88
34	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
35	Tailor-Made Stable Zr(IV)-Based Metal-Organic Frameworks for Laser Desorption/Ionization Mass Spectrometry Analysis of Small Molecules and Simultaneous Enrichment of Phosphopeptides. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 20292-20300.	4.0	84
36	Coupling the Immobilized Trypsin Microreactor of Monolithic Capillary with ¹⁵ N-RPLC-MS/MS for Shotgun Proteome Analysis. <i>Journal of Proteome Research</i> , 2006, 5, 422-428.	1.8	82

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37	Octadecylated Silica Monolith Capillary Column with Integrated Nanoelectrospray Ionization Emitter for Highly Efficient Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 454-461.	2.5	78
38	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
39	Fe ³⁺ immobilized metal affinity chromatography with silica monolithic capillary column for phosphoproteome analysis. <i>Proteomics</i> , 2007, 7, 351-360.	1.3	73
40	Comparative proteomic analysis of <i>Rhodospiridium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009, 26, 553-566.	0.8	72
41	One-pot synthesis of magnetic colloidal nanocrystal clusters coated with chitosan for selective enrichment of glycopeptides. <i>Analytica Chimica Acta</i> , 2014, 841, 99-105.	2.6	72
42	Hydrogen bond based smart polymer for highly selective and tunable capture of multiply phosphorylated peptides. <i>Nature Communications</i> , 2017, 8, 461.	5.8	71
43	Separation of acidic compounds by strong anion-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000, 887, 223-231.	1.8	68
44	Enrichment of Phosphopeptides by Fe ³⁺ -Immobilized Mesoporous Nanoparticles of MCM-41 for MALDI and Nano-LC-MS/MS Analysis. <i>Journal of Proteome Research</i> , 2006, 5, 3114-3124.	1.8	67
45	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
46	Dendritic Mesoporous Silica Nanoparticles with Abundant Ti ⁴⁺ for Phosphopeptide Enrichment from Cancer Cells with 96% Specificity. <i>Analytical Chemistry</i> , 2018, 90, 7617-7625.	3.2	65
47	Separation of peptides by strong cation-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000, 869, 385-394.	1.8	64
48	Efficient enrichment of glycopeptides using metal-organic frameworks by hydrophilic interaction chromatography. <i>Analyst</i> , 2014, 139, 4987-4993.	1.7	62
49	WIDENING THE BOTTLENECK OF PHOSPHOPROTEOMICS: EVOLVING STRATEGIES FOR PHOSPHOPEPTIDE ENRICHMENT. <i>Mass Spectrometry Reviews</i> , 2021, 40, 309-333.	2.8	62
50	Phosphoproteome analysis of human liver tissue by long gradient nanoflow LC coupled with multiple stage MS analysis. <i>Electrophoresis</i> , 2010, 31, 1080-1089.	1.3	61
51	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
52	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , 2014, 110, 145-154.	1.2	57
53	Facile Fabrication of Biomimetic Chitosan Membrane with Honeycomb-Like Structure for Enrichment of Glycosylated Peptides. <i>Analytical Chemistry</i> , 2019, 91, 2985-2993.	3.2	56
54	Selective on-line serum peptide extraction and multidimensional separation by coupling a restricted-access material-based capillary trap column with nanoliquid chromatography-tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2009, 1216, 5377-5384.	1.8	55

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55	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
56	Study of physically adsorbed stationary phases for open tubular capillary electrochromatography. <i>Electrophoresis</i> , 1999, 20, 2891-2897.	1.3	54
57	Separation of basic, acidic and neutral compounds by capillary electrochromatography using uncharged monolithic capillary columns modified with anionic and cationic surfactants. <i>Electrophoresis</i> , 2001, 22, 544-551.	1.3	54
58	Separation of enantiomers by nanoliquid chromatography and capillary electrochromatography using a bonded cellulose trisphenylcarbamate stationary phase. <i>Electrophoresis</i> , 2002, 23, 1246-1254.	1.3	54
59	Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysis—A review. <i>Analytica Chimica Acta</i> , 2007, 598, 193-204.	2.6	54
60	Large-pore mesoporous SBA-15 silica particles with submicrometer size as stationary phases for high-speed CEC separation. <i>Electrophoresis</i> , 2006, 27, 742-748.	1.3	52
61	Challenges and Advances in the Fabrication of Monolithic Bioseparation Materials and their Applications in Proteomics Research. <i>Advanced Materials</i> , 2019, 31, e1902023.	11.1	52
62	Recent progress in polar stationary phases for CEC. <i>Electrophoresis</i> , 2007, 28, 148-163.	1.3	50
63	Perspectives of Comprehensive Phosphoproteome Analysis Using Shotgun Strategy. <i>Analytical Chemistry</i> , 2011, 83, 8078-8085.	3.2	50
64	Proteomics analysis reveals the defense priming effect of chitosan oligosaccharides in Arabidopsis-Pst DC3000 interaction. <i>Plant Physiology and Biochemistry</i> , 2020, 149, 301-312.	2.8	50
65	Post-column fluorescence derivatization of proteins and peptides in capillary electrophoresis with a sheath flow reactor and 488 nm argon ion laser excitation. <i>Journal of Chromatography A</i> , 2004, 1022, 201-206.	1.8	49
66	Technologies and methods for sample pretreatment in efficient proteome and peptidome analysis. <i>Proteomics</i> , 2008, 8, 686-705.	1.3	49
67	Recent advances in mass spectrometry-based peptidome analysis. <i>Expert Review of Proteomics</i> , 2009, 6, 433-447.	1.3	49
68	In-Depth Analysis of Glycoprotein Sialylation in Serum Using a Dual-Functional Material with Superior Hydrophilicity and Switchable Surface Charge. <i>Analytical Chemistry</i> , 2017, 89, 3966-3972.	3.2	48
69	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2007, 26, 80-84.	5.8	47
70	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
71	Solvent-Induced Protein Precipitation for Drug Target Discovery on the Proteomic Scale. <i>Analytical Chemistry</i> , 2020, 92, 1363-1371.	3.2	47
72	Capture and Dimethyl Labeling of Glycopeptides on Hydrazide Beads for Quantitative Glycoproteomics Analysis. <i>Analytical Chemistry</i> , 2012, 84, 8452-8456.	3.2	45

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73	Recent advances in methods for the analysis of protein N-glycosylation at proteome level. <i>Journal of Separation Science</i> , 2018, 41, 248-261.	1.3	44
74	Integration of covalent organic frameworks into hydrophilic membrane with hierarchical porous structure for fast adsorption of metal ions. <i>Journal of Hazardous Materials</i> , 2021, 407, 124390.	6.5	44
75	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011, 11, 42-51.	1.1	43
76	Capillary Electrochromatography Using a Strong Cation-Exchange Column with a Dynamically Modified Cationic Surfactant. <i>Analytical Chemistry</i> , 2000, 72, 616-621.	3.2	42
77	Comprehensive Peptidome Analysis of Mouse Livers by Size Exclusion Chromatography Prefractionation and NanoLC-MS/MS Identification. <i>Journal of Proteome Research</i> , 2007, 6, 801-808.	1.8	42
78	An immobilized titanium (IV) ion affinity chromatography adsorbent for solid phase extraction of phosphopeptides for phosphoproteome analysis. <i>Journal of Chromatography A</i> , 2017, 1498, 22-28.	1.8	42
79	Functional Nanochannels for Sensing Tyrosine Phosphorylation. <i>Journal of the American Chemical Society</i> , 2020, 142, 16324-16333.	6.6	42
80	Highly Efficient Release of Glycopeptides from Hydrazide Beads by Hydroxylamine Assisted PNGase F Deglycosylation for N-Glycoproteome Analysis. <i>Analytical Chemistry</i> , 2015, 87, 10199-10204.	3.2	41
81	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae <i>Dunaliella salina</i> Revealed by Quantitative Proteomics and Phosphoproteomics. <i>Frontiers in Plant Science</i> , 2017, 8, 810.	1.7	41
82	Automatic Validation of Phosphopeptide Identifications by the MS2/MS3 Target-Decoy Search Strategy. <i>Journal of Proteome Research</i> , 2008, 7, 1640-1649.	1.8	40
83	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , 2011, 32, 4085-4095.	5.7	40
84	Site-specific characterization of cell membrane N-glycosylation with integrated hydrophilic interaction chromatography solid phase extraction and LC-MS/MS. <i>Journal of Proteomics</i> , 2014, 103, 194-203.	1.2	40
85	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. <i>Oncotarget</i> , 2016, 7, 25315-25327.	0.8	40
86	Characterization of small-molecule-biomacromolecule interactions: From simple to complex. <i>TrAC - Trends in Analytical Chemistry</i> , 2005, 24, 810-825.	5.8	39
87	Facile Preparation of Titanium(IV)-Immobilized Hierarchically Porous Hybrid Monoliths. <i>Analytical Chemistry</i> , 2017, 89, 4655-4662.	3.2	39
88	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome analysis by using a strong cation exchange trap column. <i>Proteomics</i> , 2007, 7, 528-539.	1.3	38
89	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
90	Antibody-Free Approach for the Global Analysis of Protein Methylation. <i>Analytical Chemistry</i> , 2016, 88, 11319-11327.	3.2	38

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91	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , 2017, 89, 1469-1476.	3.2	38
92	Preparation and evaluation of rigid porous polyacrylamide-based strong cation-exchange monolithic columns for capillary electrochromatography. <i>Journal of Separation Science</i> , 2007, 30, 2986-2992.	1.3	37
93	SIRT5 Promotes Hepatocellular Carcinoma Progression by Regulating Mitochondrial Apoptosis. <i>Journal of Cancer</i> , 2019, 10, 3871-3882.	1.2	37
94	Preparation of Polypropylene Spin Tips Filled with Immobilized Titanium(IV) Ion Monolithic Adsorbent for Robust Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2016, 88, 5058-5064.	3.2	36
95	Synthesis and Characterization of Hydrazide-Linked and Amide-Linked Organic Polymers. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 32060-32067.	4.0	36
96	Selective extraction of peptides in acidic human plasma by porous silica nanoparticles for peptidome analysis with 2D LC-MS/MS. <i>Journal of Separation Science</i> , 2007, 30, 2204-2209.	1.3	35
97	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
98	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2015, 114, 226-233.	1.2	35
99	Effects of organic modifiers on solute retention and electrokinetic migrations in micellar electrokinetic capillary chromatography. <i>Electrophoresis</i> , 1999, 20, 2898-2908.	1.3	34
100	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012, 48, 6265.	2.2	34
101	Strategies for large-scale analysis of non-histone protein methylation by LC-MS/MS. <i>Analyst</i> , 2017, 142, 3536-3548.	1.7	34
102	Dual-Functional Titanium(IV) Immobilized Metal Affinity Chromatography Approach for Enabling Large-Scale Profiling of Protein Mannose-6-Phosphate Glycosylation and Revealing Its Predominant Substrates. <i>Analytical Chemistry</i> , 2019, 91, 11589-11597.	3.2	34
103	Glyco-Decipher enables glycan database-independent peptide matching and in-depth characterization of site-specific N-glycosylation. <i>Nature Communications</i> , 2022, 13, 1900.	5.8	34
104	Specific capture of phosphopeptides by Zr ⁴⁺ -modified monolithic capillary column. <i>Journal of Separation Science</i> , 2007, 30, 2917-2923.	1.3	33
105	Facile preparation of polysaccharide functionalized macroporous adsorption resin for highly selective enrichment of glycopeptides. <i>Journal of Chromatography A</i> , 2017, 1498, 72-79.	1.8	33
106	One-step preparation of phosphate-rich carbonaceous spheres via a hydrothermal approach for phosphopeptide analysis. <i>Green Chemistry</i> , 2019, 21, 2052-2060.	4.6	33
107	Study of competitive binding of enantiomers to protein by affinity capillary electrochromatography. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2002, 27, 651-660.	1.4	32
108	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

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109	Comprehensive proteome quantification reveals NgBR as a new regulator for epithelialâ€“mesenchymal transition of breast tumor cells. <i>Journal of Proteomics</i> , 2015, 112, 38-52.	1.2	32
110	Dual-Functional Ti(IV)-IMAC Material Enables Simultaneous Enrichment and Separation of Diverse Glycopeptides and Phosphopeptides. <i>Analytical Chemistry</i> , 2021, 93, 8568-8576.	3.2	32
111	Induction of predominant tenogenic phenotype in human dermal fibroblasts via synergistic effect of TGF-Î² and elongated cell shape. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 310, C357-C372.	2.1	31
112	An overview on enrichment methods for cell surface proteome profiling. <i>Journal of Separation Science</i> , 2020, 43, 292-312.	1.3	31
113	A simple integrated system for rapid analysis of sialicâ€“acidâ€“containing N-glycopeptides from human serum. <i>Proteomics</i> , 2013, 13, 1306-1313.	1.3	30
114	A New Searching Strategy for the Identification of O-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2019, 91, 3852-3859.	3.2	30
115	Facile preparation of bifunctional adsorbents for efficiently enriching N-glycopeptides and phosphopeptides. <i>Analytica Chimica Acta</i> , 2021, 1144, 111-120.	2.6	29
116	Capillary electrochromatography with a silica column with a dynamically modified cationic surfactant. <i>Journal of Chromatography A</i> , 1999, 855, 137-145.	1.8	28
117	Capillary electrochromatography with physically and dynamically absorbed stationary phases. <i>Electrophoresis</i> , 2000, 21, 4073-4095.	1.3	28
118	Sensitive profiling of cell surface proteome by using an optimized biotinylation method. <i>Journal of Proteomics</i> , 2019, 196, 33-41.	1.2	28
119	Modeling and optimization for separation of ionic solutes in pressurized flow capillary electrochromatography. <i>Journal of Separation Science</i> , 2002, 25, 416-426.	1.3	27
120	Enrichment of peptides from plasma for peptidome analysis using multiwalled carbon nanotubes. <i>Journal of Separation Science</i> , 2007, 30, 930-943.	1.3	27
121	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 6247-6256.	1.9	27
122	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 9307-9314.	3.2	27
123	One-step fabrication of cinchona-based hybrid monolithic chiral stationary phases via photo-initiated thiol-ene polymerization for cLC enantioseparation. <i>Talanta</i> , 2019, 198, 432-439.	2.9	27
124	Determination of CK2 Specificity and Substrates by Proteome-Derived Peptide Libraries. <i>Journal of Proteome Research</i> , 2013, 12, 3813-3821.	1.8	26
125	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
126	Preparation and characterization of hydrophilic hybrid monoliths via thiol-ene click polymerization and their applications in chromatographic analysis and glycopeptides enrichment. <i>Journal of Chromatography A</i> , 2017, 1498, 37-45.	1.8	26

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127	Facile preparation of microporous organic polymers functionalized macroporous hydrophilic resin for selective enrichment of glycopeptides. <i>Analytica Chimica Acta</i> , 2018, 1030, 96-104.	2.6	26
128	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
129	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
130	One-Step Preparation of Zwitterionic-Rich Hydrophilic Hydrothermal Carbonaceous Materials for Enrichment of N-Glycopeptides. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 11511-11520.	3.2	25
131	Antibiotic-Like Activity of Atomic Layer Boron Nitride for Combating Resistant Bacteria. <i>ACS Nano</i> , 2022, 16, 7674-7688.	7.3	25
132	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. <i>BMC Bioinformatics</i> , 2007, 8, 323.	1.2	24
133	Fast preparation of hybrid monolithic columns via photo-initiated thiol-yne polymerization for capillary liquid chromatography. <i>Journal of Chromatography A</i> , 2018, 1538, 8-16.	1.8	24
134	Depletion of Acidic Phosphopeptides by SAX To Improve the Coverage for the Detection of Basophilic Kinase Substrates. <i>Journal of Proteome Research</i> , 2012, 11, 4673-4681.	1.8	23
135	Functionalization of hybrid monolithic columns via thiol-ene click reaction for proteomics analysis. <i>Journal of Chromatography A</i> , 2017, 1498, 29-36.	1.8	23
136	Preparation of epoxy-functionalized hierarchically porous hybrid monoliths via free radical polymerization and application in HILIC enrichment of glycopeptides. <i>Analytica Chimica Acta</i> , 2019, 1058, 97-106.	2.6	23
137	Protein digestion priority is independent of protein abundances. <i>Nature Methods</i> , 2014, 11, 220-222.	9.0	22
138	Analysis of the endogenous human serum peptides by on-line extraction with restricted-access material and HPLC-MS/MS identification. <i>Talanta</i> , 2014, 127, 191-195.	2.9	22
139	Porous styryl-linked polyhedral oligomeric silsesquioxane (POSS) polymers used as a support for platinum catalysts. <i>Materials Chemistry Frontiers</i> , 2019, 3, 851-859.	3.2	22
140	Enantiomer separation by strong anion-exchange capillary electrochromatography with dynamically modified sulfated β -cyclodextrin. <i>Electrophoresis</i> , 2001, 22, 518-525.	1.3	21
141	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
142	ArMone: A Software Suite Specially Designed for Processing and Analysis of Phosphoproteome Data. <i>Journal of Proteome Research</i> , 2010, 9, 2743-2751.	1.8	21
143	Facile preparation of multi-functionalized hybrid monoliths via two-step photo-initiated reactions for two-dimensional liquid chromatography-mass spectrometry. <i>Journal of Chromatography A</i> , 2017, 1524, 135-142.	1.8	21
144	Sol-gel preparation of titanium (IV)-immobilized hierarchically porous organosilica hybrid monoliths. <i>Analytica Chimica Acta</i> , 2019, 1046, 199-207.	2.6	21

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