

Mingliang Ye

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238
papers

8,963
citations

51
h-index

84
g-index

249
ext. papers

10,145
ext. citations

6.4
avg, IF

6.02
L-index

#	Paper	IF	Citations
238	Monolithic stationary phases for liquid chromatography and capillary electrochromatography. <i>Journal of Chromatography A</i> , 2002 , 954, 5-32	4.5	332
237	Glycoproteomics analysis of human liver tissue by combination of multiple enzyme digestion and hydrazide chemistry. <i>Journal of Proteome Research</i> , 2009 , 8, 651-61	5.6	305
236	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013 , 8, 461-80	18.8	270
235	A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . <i>Nature Communications</i> , 2012 , 3, 1112	17.4	244
234	Recent development of monolithic stationary phases with emphasis on microscale chromatographic separation. <i>Journal of Chromatography A</i> , 2008 , 1184, 369-92	4.5	242
233	Specific phosphopeptide enrichment with immobilized titanium ion affinity chromatography adsorbent for phosphoproteome analysis. <i>Journal of Proteome Research</i> , 2008 , 7, 3957-67	5.6	221
232	Immobilized zirconium ion affinity chromatography for specific enrichment of phosphopeptides in phosphoproteome analysis. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1656-65	7.6	220
231	Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. <i>Proteomics</i> , 2008 , 8, 1346-61	4.8	180
230	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , 2014 , 96, 253-62	3.9	166
229	Zirconium phosphonate-modified porous silicon for highly specific capture of phosphopeptides and MALDI-TOF MS analysis. <i>Journal of Proteome Research</i> , 2006 , 5, 2431-7	5.6	154
228	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	7.8	141
227	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , 2007 , 28, 2201-15	3.6	132
226	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, 4768-74	4.5	128
225	Systematic analysis of protein phosphorylation networks from phosphoproteomic data. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1070-83	7.6	123
224	Reversed-phase-reversed-phase liquid chromatography approach with high orthogonality for multidimensional separation of phosphopeptides. <i>Analytical Chemistry</i> , 2010 , 82, 53-6	7.8	120
223	Development of phosphopeptide enrichment techniques for phosphoproteome analysis. <i>Analyst</i> , 2008 , 133, 1128-38	5	112
222	Capillary trap column with strong cation-exchange monolith for automated shotgun proteome analysis. <i>Analytical Chemistry</i> , 2007 , 79, 6599-606	7.8	107

221	Method development of efficient protein extraction in bone tissue for proteome analysis. <i>Journal of Proteome Research</i> , 2007 , 6, 2287-94	5.6	103
220	Preparation of monodisperse immobilized Ti(4+) affinity chromatography microspheres for specific enrichment of phosphopeptides. <i>Analytica Chimica Acta</i> , 2009 , 636, 34-41	6.6	99
219	Facile synthesis of zwitterionic polymer-coated core-shell magnetic nanoparticles for highly specific capture of N-linked glycopeptides. <i>Nanoscale</i> , 2015 , 7, 3100-8	7.7	95
218	Capillary electrochromatography for separation of peptides driven with electrophoretic mobility on monolithic column. <i>Analytical Chemistry</i> , 2001 , 73, 4918-23	7.8	95
217	CE-microreactor-CE-MS/MS for protein analysis. <i>Analytical Chemistry</i> , 2007 , 79, 2230-8	7.8	91
216	Added value for tandem mass spectrometry shotgun proteomics data validation through isoelectric focusing of peptides. <i>Journal of Proteome Research</i> , 2005 , 4, 2273-82	5.6	91
215	On-line protein digestion and peptide mapping by capillary electrophoresis with post-column labeling for laser-induced fluorescence detection. <i>Electrophoresis</i> , 2004 , 25, 1319-26	3.6	90
214	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , 2016 , 12, 959-966	11.7	88
213	Coupling strong anion-exchange monolithic capillary with MALDI-TOF MS for sensitive detection of phosphopeptides in protein digest. <i>Analytical Chemistry</i> , 2010 , 82, 2907-15	7.8	87
212	Development of efficient protein extraction methods for shotgun proteome analysis of formalin-fixed tissues. <i>Journal of Proteome Research</i> , 2007 , 6, 1038-47	5.6	85
211	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, 5146-53	7.8	84
210	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. <i>Journal of Proteomics</i> , 2013 , 78, 486-98	3.9	79
209	Coupling the immobilized trypsin microreactor of monolithic capillary with muRPLC-MS/MS for shotgun proteome analysis. <i>Journal of Proteome Research</i> , 2006 , 5, 422-8	5.6	79
208	Optimized peptide separation and identification for mass spectrometry based proteomics via free-flow electrophoresis. <i>Journal of Proteome Research</i> , 2006 , 5, 2241-9	5.6	78
207	Octadecylated silica monolith capillary column with integrated nanoelectrospray ionization emitter for highly efficient proteome analysis. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 454-61	7.6	75
206	Enrichment and separation techniques for large-scale proteomics analysis of the protein post-translational modifications. <i>Journal of Chromatography A</i> , 2014 , 1372C, 1-17	4.5	72
205	Fe ³⁺ immobilized metal affinity chromatography with silica monolithic capillary column for phosphoproteome analysis. <i>Proteomics</i> , 2007 , 7, 351-60	4.8	72
204	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	9.5	71

203	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, 20292-300	9.5	66
202	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, 3114-24	5.6	65
201	Separation of acidic compounds by strong anion-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000 , 887, 223-31	4.5	65
200	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, 3007-15	7.8	62
199	Comparative proteomic analysis of <i>Rhodospiridium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009 , 26, 553-66	3.4	62
198	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, 1713-21	5.6	61
197	Global screening of CK2 kinase substrates by an integrated phosphoproteomics workflow. <i>Scientific Reports</i> , 2013 , 3, 3460	4.9	61
196	Separation of peptides by strong cation-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000 , 869, 385-94	4.5	61
195	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	6.6	60
194	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	12.8	60
193	Phosphoproteome analysis of human liver tissue by long-gradient nanoflow LC coupled with multiple stage MS analysis. <i>Electrophoresis</i> , 2010 , 31, 1080-9	3.6	57
192	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , 2014 , 110, 145-54	3.9	54
191	Efficient enrichment of glycopeptides using metal-organic frameworks by hydrophilic interaction chromatography. <i>Analyst, The</i> , 2014 , 139, 4987-93	5	54
190	Dendritic Mesoporous Silica Nanoparticles with Abundant Ti for Phosphopeptide Enrichment from Cancer Cells with 96% Specificity. <i>Analytical Chemistry</i> , 2018 , 90, 7617-7625	7.8	53
189	Hydrogen bond based smart polymer for highly selective and tunable capture of multiply phosphorylated peptides. <i>Nature Communications</i> , 2017 , 8, 461	17.4	51
188	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, 7755-62	7.8	51
187	Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysis--a review. <i>Analytica Chimica Acta</i> , 2007 , 598, 193-204	6.6	51
186	Study of physically absorbed stationary phases for open tubular capillary electrochromatography. <i>Electrophoresis</i> , 1999 , 20, 2891-7	3.6	51

185	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, 544-51	3.6	50
184	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	7.6	49
183	Recent progress in polar stationary phases for CEC. <i>Electrophoresis</i> , 2007 , 28, 148-63	3.6	48
182	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, 5377-84	4.5	47
181	Technologies and methods for sample pretreatment in efficient proteome and peptidome analysis. <i>Proteomics</i> , 2008 , 8, 686-705	4.8	47
180	Large-pore mesoporous SBA-15 silica particles with submicrometer size as stationary phases for high-speed CEC separation. <i>Electrophoresis</i> , 2006 , 27, 742-8	3.6	47
179	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, 201-6	4.5	46
178	Separation of enantiomers by nanoliquid chromatography and capillary electrochromatography using a bonded cellulose trisphenylcarbamate stationary phase. <i>Electrophoresis</i> , 2002 , 23, 1246-54	3.6	46
177	Perspectives of comprehensive phosphoproteome analysis using shotgun strategy. <i>Analytical Chemistry</i> , 2011 , 83, 8078-85	7.8	45
176	Improve the coverage for the analysis of phosphoproteome of HeLa cells by a tandem digestion approach. <i>Journal of Proteome Research</i> , 2012 , 11, 2828-37	5.6	44
175	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2007 , 26, 80-84	14.6	44
174	Recent advances in mass spectrometry-based peptidome analysis. <i>Expert Review of Proteomics</i> , 2009 , 6, 433-47	4.2	42
173	Capture and dimethyl labeling of glycopeptides on hydrazide beads for quantitative glycoproteomics analysis. <i>Analytical Chemistry</i> , 2012 , 84, 8452-6	7.8	40
172	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011 , 11, 42-51	3.1	40
171	Capillary electrochromatography using a strong cation-exchange column with a dynamically modified cationic surfactant. <i>Analytical Chemistry</i> , 2000 , 72, 616-21	7.8	40
170	Facile Fabrication of Biomimetic Chitosan Membrane with Honeycomb-Like Structure for Enrichment of Glycosylated Peptides. <i>Analytical Chemistry</i> , 2019 , 91, 2985-2993	7.8	39
169	Highly Efficient Release of Glycopeptides from Hydrazide Beads by Hydroxylamine Assisted PNGase F Deglycosylation for N-Glycoproteome Analysis. <i>Analytical Chemistry</i> , 2015 , 87, 10199-204	7.8	39
168	Automatic validation of phosphopeptide identifications by the MS2/MS3 target-decoy search strategy. <i>Journal of Proteome Research</i> , 2008 , 7, 1640-9	5.6	39

167	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	3.9	36
166	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, 961-3	5.8	36
165	Comprehensive peptidome analysis of mouse livers by size exclusion chromatography prefractionation and nanoLC-MS/MS identification. <i>Journal of Proteome Research</i> , 2007 , 6, 801-8	5.6	36
164	Preparation and evaluation of rigid porous polyacrylamide-based strong cation-exchange monolithic columns for capillary electrochromatography. <i>Journal of Separation Science</i> , 2007 , 30, 2986-92	3.4	35
163	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	4.8	35
162	Characterization of small-moleculeBiomacromolecule interactions: From simple to complex. <i>TrAC - Trends in Analytical Chemistry</i> , 2005 , 24, 810-825	14.6	35
161	Challenges and Advances in the Fabrication of Monolithic Bioseparation Materials and their Applications in Proteomics Research. <i>Advanced Materials</i> , 2019 , 31, e1902023	24	34
160	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , 2011 , 32, 4085-95	15.6	34
159	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	7.8	33
158	Effects of organic modifiers on solute retention and electrokinetic migrations in micellar electrokinetic capillary chromatography. <i>Electrophoresis</i> , 1999 , 20, 2898-908	3.6	33
157	Selective extraction of peptides in acidic human plasma by porous silica nanoparticles for peptidome analysis with 2-D LC-MS/MS. <i>Journal of Separation Science</i> , 2007 , 30, 2204-9	3.4	32
156	Recent advances in methods for the analysis of protein o-glycosylation at proteome level. <i>Journal of Separation Science</i> , 2018 , 41, 248-261	3.4	31
155	Online multidimensional separation with biphasic monolithic capillary column for shotgun proteome analysis. <i>Journal of Proteome Research</i> , 2008 , 7, 306-10	5.6	31
154	Specific capture of phosphopeptides by Zr ⁴⁺ -modified monolithic capillary column. <i>Journal of Separation Science</i> , 2007 , 30, 2917-23	3.4	31
153	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. <i>Oncotarget</i> , 2016 , 7, 25315-27	3.3	31
152	Preparation of Polypropylene Spin Tips Filled with Immobilized Titanium(IV) Ion Monolithic Adsorbent for Robust Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2016 , 88, 5058-64	7.8	31
151	Facile preparation of polysaccharide functionalized macroporous adsorption resin for highly selective enrichment of glycopeptides. <i>Journal of Chromatography A</i> , 2017 , 1498, 72-79	4.5	30
150	Facile Preparation of Titanium(IV)-Immobilized Hierarchically Porous Hybrid Monoliths. <i>Analytical Chemistry</i> , 2017 , 89, 4655-4662	7.8	29

149	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , 2017 , 89, 1469-1476	7.8	29
148	Antibody-Free Approach for the Global Analysis of Protein Methylation. <i>Analytical Chemistry</i> , 2016 , 88, 11319-11327	7.8	29
147	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	4.5	28
146	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , 2015 , 5, 10164	4.9	28
145	Synthesis and Characterization of Hydrazide-Linked and Amide-Linked Organic Polymers. <i>ACS Applied Materials & Interfaces</i> , 2016 , 8, 32060-32067	9.5	28
144	A simple integrated system for rapid analysis of sialic-acid-containing N-glycopeptides from human serum. <i>Proteomics</i> , 2013 , 13, 1306-13	4.8	28
143	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Revealed by Quantitative Proteomics and Phosphoproteomics. <i>Frontiers in Plant Science</i> , 2017 , 8, 810	6.2	28
142	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012 , 48, 6265-7	5.8	28
141	Study of competitive binding of enantiomers to protein by affinity capillary electrochromatography. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2002 , 27, 651-60	3.5	28
140	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2015 , 114, 226-33	3.9	27
139	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	3.9	27
138	Modeling and optimization for separation of ionic solutes in pressurized flow capillary electrochromatography. <i>Journal of Separation Science</i> , 2002 , 25, 416-426	3.4	27
137	Strategies for large-scale analysis of non-histone protein methylation by LC-MS/MS. <i>Analyst, The</i> , 2017 , 142, 3536-3548	5	26
136	Capillary electrochromatography with physically and dynamically absorbed stationary phases. <i>Electrophoresis</i> , 2000 , 21, 4073-95	3.6	26
135	Capillary electrochromatography with a silica column with a dynamically modified cationic surfactant. <i>Journal of Chromatography A</i> , 1999 , 855, 137-45	4.5	26
134	WIDENING THE BOTTLENECK OF PHOSPHOPROTEOMICS: EVOLVING STRATEGIES FOR PHOSPHOPEPTIDE ENRICHMENT. <i>Mass Spectrometry Reviews</i> , 2021 , 40, 309-333	11	26
133	SIRT5 Promotes Hepatocellular Carcinoma Progression by Regulating Mitochondrial Apoptosis. <i>Journal of Cancer</i> , 2019 , 10, 3871-3882	4.5	25
132	Enrichment of peptides from plasma for peptidome analysis using multiwalled carbon nanotubes. <i>Journal of Separation Science</i> , 2007 , 30, 930-43	3.4	25

131	Preparation of capillary hybrid monolithic column with sulfonate strong cation exchanger for proteome analysis. <i>Journal of Chromatography A</i> , 2012 , 1256, 136-43	4.5	24
130	Induction of predominant tenogenic phenotype in human dermal fibroblasts via synergistic effect of TGF- β and elongated cell shape. <i>American Journal of Physiology - Cell Physiology</i> , 2016 , 310, C357-72	5.4	23
129	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. <i>BMC Bioinformatics</i> , 2007 , 8, 323	3.6	23
128	Functional Nanochannels for Sensing Tyrosine Phosphorylation. <i>Journal of the American Chemical Society</i> , 2020 , 142, 16324-16333	16.4	23
127	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, 4673-81	5.6	22
126	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, 5794-805	7.8	22
125	ArMone: a software suite specially designed for processing and analysis of phosphoproteome data. <i>Journal of Proteome Research</i> , 2010 , 9, 2743-51	5.6	21
124	Solvent-Induced Protein Precipitation for Drug Target Discovery on the Proteomic Scale. <i>Analytical Chemistry</i> , 2020 , 92, 1363-1371	7.8	21
123	One-step preparation of phosphate-rich carbonaceous spheres via a hydrothermal approach for phosphopeptide analysis. <i>Green Chemistry</i> , 2019 , 21, 2052-2060	10	20
122	Large-scale quantification of single amino-acid variations by a variation-associated database search strategy. <i>Journal of Proteome Research</i> , 2014 , 13, 241-8	5.6	20
121	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, 191-5	6.2	20
120	Protein digestion priority is independent of protein abundances. <i>Nature Methods</i> , 2014 , 11, 220-2	21.6	20
119	Determination of CK2 specificity and substrates by proteome-derived peptide libraries. <i>Journal of Proteome Research</i> , 2013 , 12, 3813-21	5.6	20
118	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	4.5	20
117	Enantiomer separation by strong anion-exchange capillary electrochromatography with dynamically modified sulfated beta-cyclodextrin. <i>Electrophoresis</i> , 2001 , 22, 518-25	3.6	20
116	A New Searching Strategy for the Identification of O-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2019 , 91, 3852-3859	7.8	20
115	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	4.5	19
114	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	7.8	19

113	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 6247-56	4.4	19
112	Iminodiacetic acid derivatized porous silicon as a matrix support for sample pretreatment and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 1769-75	2.2	19
111	Facile preparation of microporous organic polymers functionalized macroporous hydrophilic resin for selective enrichment of glycopeptides. <i>Analytica Chimica Acta</i> , 2018 , 1030, 96-104	6.6	19
110	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	8.3	17
109	Integration of cell lysis, protein extraction, and digestion into one step for ultrafast sample preparation for phosphoproteome analysis. <i>Analytical Chemistry</i> , 2014 , 86, 6786-91	7.8	17
108	Synthesis of polymeric monoliths via thiol-maleimide polymerization reaction for highly efficient chromatographic separation. <i>Journal of Chromatography A</i> , 2017 , 1514, 72-79	4.5	17
107	Preparation of open tubular capillary columns by in situ ring-opening polymerization and their applications in cLC-MS/MS analysis of tryptic digest. <i>Analytica Chimica Acta</i> , 2017 , 979, 58-65	6.6	16
106	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	6.6	16
105	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	4.5	16
104	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017 , 89, 9307-9314	7.8	16
103	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	12.8	16
102	Functionalization of hybrid monolithic columns via thiol-ene click reaction for proteomics analysis. <i>Journal of Chromatography A</i> , 2017 , 1498, 29-36	4.5	15
101	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	5.4	15
100	Thiol-radical-mediated polymerization for preparation of POSS-containing polyacrylate monoliths in capillary liquid chromatography. <i>Talanta</i> , 2018 , 190, 62-69	6.2	15
99	A bead-based approach for large-scale identification of in vitro kinase substrates. <i>Proteomics</i> , 2011 , 11, 4632-7	4.8	15
98	Classification filtering strategy to improve the coverage and sensitivity of phosphoproteome analysis. <i>Analytical Chemistry</i> , 2010 , 82, 6168-75	7.8	15
97	Fractionation of phosphopeptides on strong anion-exchange capillary trap column for large-scale phosphoproteome analysis of microgram samples. <i>Journal of Separation Science</i> , 2010 , 33, 1879-87	3.4	15
96	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , 2008 , 8, 3094-104	4.8	15

95	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	6.2	15
94	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	4.5	14
93	Au-cysteine modified macroporous adsorption resin: preparation and highly selective enrichment and identification of N-linked glycopeptides from the complex biological sample. <i>RSC Advances</i> , 2016 , 6, 113058-113065	3.7	14
92	High-throughput determination of the site-specific N-sialoglycan occupancy rates by differential oxidation of glycoproteins followed with quantitative glycoproteomics analysis. <i>Analytical Chemistry</i> , 2014 , 86, 9830-7	7.8	14
91	A new method for quantitative analysis of cell surface glycoproteome. <i>Proteomics</i> , 2012 , 12, 3328-37	4.8	14
90	Biological fingerprinting analysis of the interactome of a kinase inhibitor in human plasma by a chemiproteomic approach. <i>Journal of Chromatography A</i> , 2006 , 1134, 134-42	4.5	14
89	Amine Chemistry Method for Selective Enrichment of N-Linked Glycopeptides for Glycoproteomics Analysis. <i>Journal of Proteome Research</i> , 2015 , 14, 3892-9	5.6	13
88	An overview on enrichment methods for cell surface proteome profiling. <i>Journal of Separation Science</i> , 2020 , 43, 292-312	3.4	13
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