

Mingliang Ye

List of Publications by Year in descending order

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246
papers

10,973
citations

30070
54
h-index

45317
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.	3.7	356
2	Monolithic stationary phases for liquid chromatography and capillary electrochromatography. <i>Journal of Chromatography A</i> , 2002, 954, 5-32.	3.7	353
3	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013, 8, 461-480.	12.0	340
4	A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . <i>Nature Communications</i> , 2012, 3, 1112.	12.8	324
5	Recent development of monolithic stationary phases with emphasis on microscale chromatographic separation. <i>Journal of Chromatography A</i> , 2008, 1184, 369-392.	3.7	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.	3.7	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.	3.8	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.	2.4	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.	2.2	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.	3.7	164
11	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	3.8	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.	6.5	150
13	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , 2016, 12, 959-966.	8.0	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.	8.0	139
15	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , 2007, 28, 2201-2215.	2.4	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.	6.5	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.	3.7	132
18	Method Development of Efficient Protein Extraction in Bone Tissue for Proteome Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 2287-2294.	3.7	128

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19	Development of phosphopeptide enrichment techniques for phosphoproteome analysis. <i>Analyst</i> , The, 2008, 133, 1128.	3.5	114
20	Capillary Trap Column with Strong Cation-Exchange Monolith for Automated Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 2007, 79, 6599-6606.	6.5	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.	5.6	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.	5.4	105
23	Capillary Electrochromatography for Separation of Peptides Driven with Electrophoretic Mobility on Monolithic Column. <i>Analytical Chemistry</i> , 2001, 73, 4918-4923.	6.5	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.	2.4	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.	3.7	99
26	CE-Microreactor-CE-MS/MS for Protein Analysis. <i>Analytical Chemistry</i> , 2007, 79, 2230-2238.	6.5	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.	2.4	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.	6.5	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.	6.5	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.	3.7	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.	12.4	91
32	Global Screening of CK2 Kinase Substrates by an Integrated Phosphoproteomics Workflow. <i>Scientific Reports</i> , 2013, 3, 3460.	3.3	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.	3.7	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.	3.7	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.	8.0	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.	3.7	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.	3.8	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.	3.7	74
39	Fe ³⁺ immobilized metal affinity chromatography with silica monolithic capillary column for phosphoproteome analysis. <i>Proteomics</i> , 2007, 7, 351-360.	2.2	73
40	Comparative proteomic analysis of <i>Rhodospiridium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009, 26, 553-566.	1.7	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.	5.4	72
42	Hydrogen bond based smart polymer for highly selective and tunable capture of multiply phosphorylated peptides. <i>Nature Communications</i> , 2017, 8, 461.	12.8	71
43	Separation of acidic compounds by strong anion-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000, 887, 223-231.	3.7	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.	3.7	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.	6.5	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.	6.5	65
47	Separation of peptides by strong cation-exchange capillary electrochromatography. <i>Journal of Chromatography A</i> , 2000, 869, 385-394.	3.7	64
48	Efficient enrichment of glycopeptides using metal-organic frameworks by hydrophilic interaction chromatography. <i>Analyst</i> , 2014, 139, 4987-4993.	3.5	62
49	WIDENING THE BOTTLENECK OF PHOSPHOPROTEOMICS: EVOLVING STRATEGIES FOR PHOSPHOPEPTIDE ENRICHMENT. <i>Mass Spectrometry Reviews</i> , 2021, 40, 309-333.	5.4	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.	2.4	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.	6.5	57
52	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , 2014, 110, 145-154.	2.4	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.	6.5	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.	3.7	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.	3.8	55
56	Study of physically adsorbed stationary phases for open tubular capillary electrochromatography. <i>Electrophoresis</i> , 1999, 20, 2891-2897.	2.4	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.	2.4	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.	2.4	54
59	Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysis—A review. <i>Analytica Chimica Acta</i> , 2007, 598, 193-204.	5.4	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.	2.4	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.	21.0	52
62	Recent progress in polar stationary phases for CEC. <i>Electrophoresis</i> , 2007, 28, 148-163.	2.4	50
63	Perspectives of Comprehensive Phosphoproteome Analysis Using Shotgun Strategy. <i>Analytical Chemistry</i> , 2011, 83, 8078-8085.	6.5	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.	5.8	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.	3.7	49
66	Technologies and methods for sample pretreatment in efficient proteome and peptidome analysis. <i>Proteomics</i> , 2008, 8, 686-705.	2.2	49
67	Recent advances in mass spectrometry-based peptidome analysis. <i>Expert Review of Proteomics</i> , 2009, 6, 433-447.	3.0	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.	6.5	48
69	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2007, 26, 80-84.	11.4	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.	3.7	47
71	Solvent-Induced Protein Precipitation for Drug Target Discovery on the Proteomic Scale. <i>Analytical Chemistry</i> , 2020, 92, 1363-1371.	6.5	47
72	Capture and Dimethyl Labeling of Glycopeptides on Hydrazide Beads for Quantitative Glycoproteomics Analysis. <i>Analytical Chemistry</i> , 2012, 84, 8452-8456.	6.5	45

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73	Recent advances in methods for the analysis of protein oâ€glycosylation at proteome level. Journal of Separation Science, 2018, 41, 248-261.	2.5	44
74	Integration of covalent organic frameworks into hydrophilic membrane with hierarchical porous structure for fast adsorption of metal ions. Journal of Hazardous Materials, 2021, 407, 124390.	12.4	44
75	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . FEMS Yeast Research, 2011, 11, 42-51.	2.3	43
76	Capillary Electrochromatography Using a Strong Cation-Exchange Column with a Dynamically Modified Cationic Surfactant. Analytical Chemistry, 2000, 72, 616-621.	6.5	42
77	Comprehensive Peptidome Analysis of Mouse Livers by Size Exclusion Chromatography Prefractionation and NanoLCâ€MS/MS Identification. Journal of Proteome Research, 2007, 6, 801-808.	3.7	42
78	An immobilized titanium (IV) ion affinity chromatography adsorbent for solid phase extraction of phosphopeptides for phosphoproteome analysis. Journal of Chromatography A, 2017, 1498, 22-28.	3.7	42
79	Functional Nanochannels for Sensing Tyrosine Phosphorylation. Journal of the American Chemical Society, 2020, 142, 16324-16333.	13.7	42
80	Highly Efficient Release of Glycopeptides from Hydrazide Beads by Hydroxylamine Assisted PNGase F Deglycosylation for N-Glycoproteome Analysis. Analytical Chemistry, 2015, 87, 10199-10204.	6.5	41
81	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae <i>Dunaliella salina</i> Revealed by Quantitative Proteomics and Phosphoproteomics. Frontiers in Plant Science, 2017, 8, 810.	3.6	41
82	Automatic Validation of Phosphopeptide Identifications by the MS2/MS3 Target-Decoy Search Strategy. Journal of Proteome Research, 2008, 7, 1640-1649.	3.7	40
83	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. Biomaterials, 2011, 32, 4085-4095.	11.4	40
84	Site-specific characterization of cell membrane N-glycosylation with integrated hydrophilic interaction chromatography solid phase extraction and LCâ€MS/MS. Journal of Proteomics, 2014, 103, 194-203.	2.4	40
85	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. Oncotarget, 2016, 7, 25315-25327.	1.8	40
86	Characterization of small-moleculeâ€biomacromolecule interactions: From simple to complex. TrAC - Trends in Analytical Chemistry, 2005, 24, 810-825.	11.4	39
87	Facile Preparation of Titanium(IV)-Immobilized Hierarchically Porous Hybrid Monoliths. Analytical Chemistry, 2017, 89, 4655-4662.	6.5	39
88	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome analysis by using a strong cation exchange trap column. Proteomics, 2007, 7, 528-539.	2.2	38
89	Phosphoric acid functionalized mesoporous organo-silica (EPO) as the adsorbent for in situ enrichment and isotope labeling of endogenous phosphopeptides. Chemical Communications, 2012, 48, 961-963.	4.1	38
90	Antibody-Free Approach for the Global Analysis of Protein Methylation. Analytical Chemistry, 2016, 88, 11319-11327.	6.5	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.	6.5	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.	2.5	37
93	SIRT5 Promotes Hepatocellular Carcinoma Progression by Regulating Mitochondrial Apoptosis. <i>Journal of Cancer</i> , 2019, 10, 3871-3882.	2.5	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.	6.5	36
95	Synthesis and Characterization of Hydrazide-Linked and Amide-Linked Organic Polymers. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 32060-32067.	8.0	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.	2.5	35
97	Online Multidimensional Separation with Biphasic Monolithic Capillary Column for Shotgun Proteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 306-310.	3.7	35
98	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , 2015, 114, 226-233.	2.4	35
99	Effects of organic modifiers on solute retention and electrokinetic migrations in micellar electrokinetic capillary chromatography. <i>Electrophoresis</i> , 1999, 20, 2898-2908.	2.4	34
100	Isobaric cross-sequence labeling of peptides by using site-selective N-terminus dimethylation. <i>Chemical Communications</i> , 2012, 48, 6265.	4.1	34
101	Strategies for large-scale analysis of non-histone protein methylation by LC-MS/MS. <i>Analyst</i> , The, 2017, 142, 3536-3548.	3.5	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.	6.5	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.	12.8	34
104	Specific capture of phosphopeptides by Zr ⁴⁺ -modified monolithic capillary column. <i>Journal of Separation Science</i> , 2007, 30, 2917-2923.	2.5	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.	3.7	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.	9.0	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.	2.8	32
108	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , 2015, 5, 10164.	3.3	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.	2.4	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.	6.5	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.	4.6	31
112	An overview on enrichment methods for cell surface proteome profiling. <i>Journal of Separation Science</i> , 2020, 43, 292-312.	2.5	31
113	A simple integrated system for rapid analysis of sialicâ€“acidâ€“containing <i><scp>N</scp></i>-glycopeptides from human serum. <i>Proteomics</i> , 2013, 13, 1306-1313.	2.2	30
114	A New Searching Strategy for the Identification of O-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2019, 91, 3852-3859.	6.5	30
115	Facile preparation of bifunctional adsorbents for efficiently enriching N-glycopeptides and phosphopeptides. <i>Analytica Chimica Acta</i> , 2021, 1144, 111-120.	5.4	29
116	Capillary electrochromatography with a silica column with a dynamically modified cationic surfactant. <i>Journal of Chromatography A</i> , 1999, 855, 137-145.	3.7	28
117	Capillary electrochromatography with physically and dynamically absorbed stationary phases. <i>Electrophoresis</i> , 2000, 21, 4073-4095.	2.4	28
118	Sensitive profiling of cell surface proteome by using an optimized biotinylation method. <i>Journal of Proteomics</i> , 2019, 196, 33-41.	2.4	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.	2.5	27
120	Enrichment of peptides from plasma for peptidome analysis using multiwalled carbon nanotubes. <i>Journal of Separation Science</i> , 2007, 30, 930-943.	2.5	27
121	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 6247-6256.	3.7	27
122	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 9307-9314.	6.5	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.	5.5	27
124	Determination of CK2 Specificity and Substrates by Proteome-Derived Peptide Libraries. <i>Journal of Proteome Research</i> , 2013, 12, 3813-3821.	3.7	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.	3.7	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.	3.7	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.	5.4	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.	6.5	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.	3.7	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.	6.7	25
131	Antibiotic-Like Activity of Atomic Layer Boron Nitride for Combating Resistant Bacteria. <i>ACS Nano</i> , 2022, 16, 7674-7688.	14.6	25
132	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. <i>BMC Bioinformatics</i> , 2007, 8, 323.	2.6	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.	3.7	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.	3.7	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.	3.7	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.	5.4	23
137	Protein digestion priority is independent of protein abundances. <i>Nature Methods</i> , 2014, 11, 220-222.	19.0	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.	5.5	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.	5.9	22
140	Enantiomer separation by strong anion-exchange capillary electrochromatography with dynamically modified sulfated β -cyclodextrin. <i>Electrophoresis</i> , 2001, 22, 518-525.	2.4	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.	3.7	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.	3.7	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.	3.7	21
144	Sol-gel preparation of titanium (IV)-immobilized hierarchically porous organosilica hybrid monoliths. <i>Analytica Chimica Acta</i> , 2019, 1046, 199-207.	5.4	21

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145	Comparative evaluation of MAX-Ti ₃ AlC ₂ and MXene-Ti ₃ C ₂ as affinity chromatographic materials for highly selective enrichment of phosphopeptides. <i>Nanoscale</i> , 2021, 13, 2923-2930.	5.6	21
146	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, 1769-1775.	1.5	20
147	Integration of Cell Lysis, Protein Extraction, and Digestion into One Step for Ultrafast Sample Preparation for Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2014, 86, 6786-6791.	6.5	20
148	Thiol-radical-mediated polymerization for preparation of POSS-containing polyacrylate monoliths in capillary liquid chromatography. <i>Talanta</i> , 2018, 190, 62-69.	5.5	20
149	Modification-free approaches to screen drug targets at proteome level. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 124, 115574.	11.4	20
150	Protein digestomic analysis reveals the bioactivity of deer antler velvet in simulated gastrointestinal digestion. <i>Food Research International</i> , 2017, 96, 182-190.	6.2	19
151	Chemoenzymatic Approach for the Proteomics Analysis of Mucin-Type Core-1 O-Glycosylation in Human Serum. <i>Analytical Chemistry</i> , 2018, 90, 12714-12722.	6.5	19
152	Proteomics analysis of site-specific glycoforms by a virtual multistage mass spectrometry method. <i>Analytica Chimica Acta</i> , 2019, 1070, 60-68.	5.4	19
153	Probing the Proteomics Dark Regions by VAILase Cleavage at Aliphatic Amino Acids. <i>Analytical Chemistry</i> , 2020, 92, 2770-2777.	6.5	19
154	Characterization of a small-molecule inhibitor targeting NEMO/IKK β to suppress colorectal cancer growth. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 71.	17.1	19
155	A bead-based approach for large-scale identification of in vitro kinase substrates. <i>Proteomics</i> , 2011, 11, 4632-4637.	2.2	18
156	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.	5.4	18
157	Synthesis of polymeric monoliths via thiol-maleimide polymerization reaction for highly efficient chromatographic separation. <i>Journal of Chromatography A</i> , 2017, 1514, 72-79.	3.7	18
158	One-Step SH2 Superbinder-Based Approach for Sensitive Analysis of Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , 2019, 18, 1870-1879.	3.7	18
159	Highly Efficient Enrichment of <i>O</i> -GlcNAc Glycopeptides Based on Chemical Oxidation and Reversible Hydrazone Chemistry. <i>Analytical Chemistry</i> , 2021, 93, 16618-16627.	6.5	18
160	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.	3.6	17
161	Targeting the EphB4 receptor tyrosine kinase sensitizes HER2-positive breast cancer cells to Lapatinib. <i>Cancer Letters</i> , 2020, 475, 53-64.	7.2	17
162	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , 2008, 31, 2589-2597.	2.5	16

#	ARTICLE	IF	CITATIONS
163	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, 1879-1887.	2.5	16
164	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, 9830-9837.	6.5	16
165	Highly Efficient Analysis of Glycoprotein Sialylation in Human Serum by Simultaneous Quantification of Glycosites and Site-Specific Glycoforms. <i>Journal of Proteome Research</i> , 2019, 18, 3439-3446.	3.7	16
166	Matrix Thermal Shift Assay for Fast Construction of Multidimensional Ligand-Target Space. <i>Analytical Chemistry</i> , 2022, 94, 6482-6490.	6.5	16
167	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , 2008, 8, 3094-3104.	2.2	15
168	Improvement of proteome coverage using hydrophobic monolithic columns in shotgun proteome analysis. <i>Journal of Chromatography A</i> , 2009, 1216, 3887-3894.	3.7	15
169	Classification Filtering Strategy to Improve the Coverage and Sensitivity of Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2010, 82, 6168-6175.	6.5	15
170	A new method for quantitative analysis of cell surface glycoproteome. <i>Proteomics</i> , 2012, 12, 3328-3337.	2.2	15
171	Biphasic Affinity Chromatographic Approach for Deep Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 2405-2410.	6.5	15
172	GALNT6 promotes invasion and metastasis of human lung adenocarcinoma cells through O-glycosylating chaperone protein GRP78. <i>Cell Death and Disease</i> , 2020, 11, 352.	6.3	15
173	Automated Intact Glycopeptide Enrichment Method Facilitating Highly Reproducible Analysis of Serum Site-Specific N-Glycoproteome. <i>Analytical Chemistry</i> , 2021, 93, 7473-7480.	6.5	15
174	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, 134-142.	3.7	14
175	N-Terminal Labeling of Peptides by Trypsin-Catalyzed Ligation for Quantitative Proteomics. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 9205-9209.	13.8	14
176	Sensitive Approaches for the Assay of the Global Protein Tyrosine Phosphorylation in Complex Samples Using a Mutated SH2 Domain. <i>Analytical Chemistry</i> , 2017, 89, 2304-2311.	6.5	14
177	Pseudotargeted MS Method for the Sensitive Analysis of Protein Phosphorylation in Protein Complexes. <i>Analytical Chemistry</i> , 2018, 90, 6214-6221.	6.5	14
178	Theoretical study of the separation mechanism of ionizable compounds in capillary electrochromatography. <i>Science in China Series B: Chemistry</i> , 1999, 42, 639-648.	0.8	13
179	Analysis of the human urine endogenous peptides by nanoparticle extraction and mass spectrometry identification. <i>Analytica Chimica Acta</i> , 2014, 829, 40-47.	5.4	13
180	Mitotic Protein CSPP1 Interacts with CENP-H Protein to Coordinate Accurate Chromosome Oscillation in Mitosis. <i>Journal of Biological Chemistry</i> , 2015, 290, 27053-27066.	3.4	13

#	ARTICLE	IF	CITATIONS
181	Amine Chemistry Method for Selective Enrichment of N-Linked Glycopeptides for Glycoproteomics Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 3892-3899.	3.7	13
182	SH2 Superbinder Modified Monolithic Capillary Column for the Sensitive Analysis of Protein Tyrosine Phosphorylation. <i>Journal of Proteome Research</i> , 2018, 17, 243-251.	3.7	13
183	A new chromatographic approach to analyze methylproteome with enhanced lysine methylation identification performance. <i>Analytica Chimica Acta</i> , 2019, 1068, 111-119.	5.4	13
184	One-step synthesis of hydrophilic microspheres for highly selective enrichment of N-linked glycopeptides. <i>Analytica Chimica Acta</i> , 2020, 1130, 91-99.	5.4	13
185	Glycoproteomics Analysis Reveals Differential Expression of Site-Specific Glycosylation in Human Milk Whey during Lactation. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 6690-6700.	5.2	13
186	Precipitate-Supported Thermal Proteome Profiling Coupled with Deep Learning for Comprehensive Screening of Drug Target Proteins. <i>ACS Chemical Biology</i> , 2022, 17, 252-262.	3.4	13
187	Integration of monolithic frit into the particulate capillary (IMFPC) column in shotgun proteome analysis. <i>Analytica Chimica Acta</i> , 2009, 652, 324-330.	5.4	12
188	<i>In Situ</i> Sample Processing Approach (iSPA) for Comprehensive Quantitative Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 3896-3904.	3.7	12
189	Identification of phosphopeptides with unknown cleavage specificity by a de novo sequencing assisted database search strategy. <i>Proteomics</i> , 2014, 14, 2410-2416.	2.2	12
190	Specific Enrichment of Peptides with N-Terminal Serine/Threonine by a Solid-Phase Capture-Release Approach for Efficient Proteomics Analysis. <i>Analytical Chemistry</i> , 2015, 87, 11353-11360.	6.5	12
191	Selective Enrichment of Cysteine-Containing Phosphopeptides for Subphosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 5341-5347.	3.7	12
192	Highly Efficient Enrichment of O-GalNAc Glycopeptides by Using Immobilized Metal Ion Affinity Chromatography. <i>Analytical Chemistry</i> , 2021, 93, 7579-7587.	6.5	12
193	Separation of 4-dimethylamino-6-(4-methoxy-1-naphthyl)-1,3,5-triazine-2-hydrazine derivatives of carbonyl compounds by reversed-phase capillary electrochromatography. <i>Electrophoresis</i> , 2001, 22, 1298-1304.	2.4	11
194	In vivo protein allylation to capture protein methylation candidates. <i>Chemical Communications</i> , 2016, 52, 6689-6692.	4.1	11
195	Enzyme Kinetics for Complex System Enables Accurate Determination of Specificity Constants of Numerous Substrates in a Mixture by Proteomics Platform. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 135-145.	3.8	11
196	An integrated strategy for high-sensitive and multi-level glycoproteome analysis from low micrograms of protein samples. <i>Journal of Chromatography A</i> , 2019, 1600, 46-54.	3.7	11
197	Microparticle-Assisted Precipitation Screening Method for Robust Drug Target Identification. <i>Analytical Chemistry</i> , 2020, 92, 13912-13921.	6.5	11
198	Rapid Enzyme-Mediated Biotinylation for Cell Surface Proteome Profiling. <i>Analytical Chemistry</i> , 2021, 93, 4542-4551.	6.5	11

#	ARTICLE	IF	CITATIONS
199	Mechanical stress induced protein precipitation method for drug target screening. <i>Analytica Chimica Acta</i> , 2021, 1168, 338612.	5.4	11
200	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , 2013, 78, 389-397.	2.4	10
201	Quantitative proteomic and phosphoproteomic studies reveal novel 5-fluorouracil resistant targets in hepatocellular carcinoma. <i>Journal of Proteomics</i> , 2019, 208, 103501.	2.4	10
202	Fast fabrication of a hybrid monolithic column containing cyclic and aliphatic hydrophobic ligands via photo-initiated thiol-ene polymerization. <i>Journal of Separation Science</i> , 2019, 42, 1332-1340.	2.5	10
203	Profiling of Endogenously Intact N-Linked and O-Linked Glycopeptides from Human Serum Using an Integrated Platform. <i>Journal of Proteome Research</i> , 2020, 19, 1423-1434.	3.7	10
204	Separation of acidic and neutral compounds by strong anion-exchange capillary electrochromatography dynamically modified with sodium dodecylsulfate. <i>Chromatographia</i> , 2001, 53, 425-430.	1.3	9
205	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.	2.4	9
206	Trypsin-Catalyzed N-Terminal Labeling of Peptides with Stable Isotope-Coded Affinity Tags for Proteome Analysis. <i>Analytical Chemistry</i> , 2014, 86, 1170-1177.	6.5	9
207	A bead-based cleavage method for large-scale identification of protease substrates. <i>Scientific Reports</i> , 2016, 6, 22645.	3.3	9
208	The divide and conquer strategies for deep phosphoproteomics analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 105, 282-291.	11.4	9
209	Highly Efficient Identification of O-GalNAc Glycosylation by an Acid-Assisted Glycoform Simplification Approach. <i>Proteomics</i> , 2018, 18, e1800042.	2.2	9
210	Fast fabrication and modification of polyoctahedral silsesquioxane-containing monolithic columns via two-step photo-initiated reactions and their application in proteome analysis of tryptic digests. <i>Talanta</i> , 2020, 209, 120526.	5.5	9
211	Analysis of therapeutic monoclonal antibody glycoforms by mass spectrometry for pharmacokinetics study. <i>Talanta</i> , 2017, 165, 664-670.	5.5	8
212	Caffeic acid phenethyl ester (CAPE) revisited: Covalent modulation of XPO1/CRM1 activities and implication for its mechanism of action. <i>Chemical Biology and Drug Design</i> , 2017, 89, 655-662.	3.2	8
213	Palladium catalyst imbedded in polymers of intrinsic microporosity for the Suzuki-Miyaura coupling reaction. <i>RSC Advances</i> , 2018, 8, 35205-35210.	3.6	8
214	A Simplified Thermal Proteome Profiling Approach to Screen Protein Targets of a Ligand. <i>Proteomics</i> , 2020, 20, e1900372.	2.2	8
215	Selective enrichment of N-terminal proline peptides via hydrazide chemistry for proteomics analysis. <i>Analytica Chimica Acta</i> , 2021, 1142, 48-55.	5.4	8
216	Casein Kinase 2 interacts with human mitogen- and stress-activated protein kinase MSK1 and phosphorylates it at Multiple sites. <i>BMB Reports</i> , 2009, 42, 840-845.	2.4	8

#	ARTICLE	IF	CITATIONS
217	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.	2.1	7
218	One-Pot Preparation of Macroporous Organic-Silica Monolith for the Organic-Oil-Water Separation. <i>ChemistrySelect</i> , 2017, 2, 4538-4544.	1.5	7
219	Thiol-ene polymerization for hierarchically porous hybrid materials by adding degradable polycaprolactone for adsorption of bisphenol A. <i>Journal of Hazardous Materials</i> , 2019, 367, 465-472.	12.4	7
220	Atomically Precise Structure Determination of Porous Organic Cage from Ab Initio PXRD Structure Analysis: Its Molecular Click Postfunctionalization and CO ₂ Capture Application. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 17815-17823.	8.0	7
221	An efficient approach based on basic strong cation exchange chromatography for enriching methylated peptides with high specificity for methylproteomics analysis. <i>Analytica Chimica Acta</i> , 2021, 1161, 338467.	5.4	6
222	MS-Decipher: a user-friendly proteome database search software with an emphasis on deciphering the spectra of O-linked glycopeptides. <i>Bioinformatics</i> , 2022, 38, 1911-1919.	4.1	6
223	Endo-M Mediated Chemoenzymatic Approach Enables Reversible Glycopeptide Labeling for <i>O</i> -GlcNAcylation Analysis. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	6
224	High specific phosphopeptides enrichment by titanium silicalite with post-treatment of desilication. <i>Analytical Methods</i> , 2013, 5, 2939.	2.7	5
225	Highly Efficient Separation of Methylated Peptides Utilizing Selective Complexation between Lysine and 18-Crown-6. <i>Analytical Chemistry</i> , 2020, 92, 15663-15670.	6.5	5
226	Multi-histidine functionalized material for the specific enrichment of sialylated glycopeptides. <i>Journal of Chromatography A</i> , 2020, 1627, 461422.	3.7	5
227	Operative ubiquitin-specific protease 22 deubiquitination confers a more invasive phenotype to cholangiocarcinoma. <i>Cell Death and Disease</i> , 2021, 12, 678.	6.3	5
228	Mapping of phosphorylation sites in human MSK1 activated by a novel interaction with MRK ² . <i>Electrophoresis</i> , 2010, 31, 1283-1293.	2.4	4
229	Enrichment of Methylated Peptides Using an Antibody-free Approach for Global Methylproteomics Analysis. <i>Current Protocols in Protein Science</i> , 2018, 91, 14.18.1-14.18.14.	2.8	4
230	Integrated Microstructured Photonic Fiber as a Bifunctional Robust Frit and Efficient Electrospray Emitter of a Packed Column for Capillary Liquid Chromatography-Tandem Mass Spectrometry Analysis of Complex Biological Samples. <i>Analytical Chemistry</i> , 2020, 92, 2274-2282.	6.5	4
231	A Tyrosine Phosphoproteome Analysis Approach Enabled by Selective Dephosphorylation with Protein Tyrosine Phosphatase. <i>Analytical Chemistry</i> , 2022, 94, 4155-4164.	6.5	4
232	The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. <i>Proteomics</i> , 2015, 15, 3613-3616.	2.2	3
233	A New Workflow for the Analysis of Phosphosite Occupancy in Paired Samples by Integration of Proteomics and Phosphoproteomics Data Sets. <i>Journal of Proteome Research</i> , 2020, 19, 3807-3816.	3.7	3
234	A Mass-Spectrometry-Based Antibody-Free Approach Enables the Quantification of D-Dimer in Plasma. <i>Journal of Proteome Research</i> , 2020, 19, 3143-3152.	3.7	3

#	ARTICLE	IF	CITATIONS
235	Instance Based Algorithm for Posterior Probability Calculation by TargetâDecoy Strategy to Improve Protein Identifications. Analytical Chemistry, 2008, 80, 9326-9335.	6.5	2
236	A strategy with label-free quantification of the targeted peptides for quantitative peptidome analysis of human serum. Science China Chemistry, 2010, 53, 759-767.	8.2	2
237	Mirror-Cutting-Based Digestion Strategy Enables the <i>In-Depth</i> and Accuracy Characterization of N-Linked Protein Glycosylation. Journal of Proteome Research, 2021, 20, 4948-4958.	3.7	2
238	Proteome-Wide Deconvolution of Drug Targets and Binding Sites by Lysine Reactivity Profiling. Analytical Chemistry, 2022, 94, 3352-3359.	6.5	2
239	Enrichment of peptides containing consensus sequence by an enzymatic approach for targeted analysis of proteins. Proteomics, 2011, 11, 3578-3581.	2.2	1
240	Investigating the Relationship between the SubstratesâConsumption and Their Abundances in a Complex Enzymatic System. Analytical Chemistry, 2017, 89, 10644-10648.	6.5	1
241	Comparative proteomic analysis of protein methylation provides insight into the resistance of hepatocellular carcinoma to 5-fluorouracil. Journal of Proteomics, 2020, 219, 103738.	2.4	1
242	Chemical Depletion of Histidine-Containing Peptides Allows Identification of More Low-Abundance Methylation Sites from Proteome Samples. Journal of Proteome Research, 2021, 20, 2497-2505.	3.7	1
243	An antibodyâfree enrichment approach enabled by reductive glutaraldehydation for monomethyllysine proteome analysis. Proteomics, 2022, , 2100378.	2.2	1
244	Hanfa Zou, 1961â2016. Journal of Chromatography A, 2017, 1498, 2-7.	3.7	0
245	A chemoenzymatic approach enables the siteâspecific conjugation of recombinant proteins. Electrophoresis, 2019, 40, 2125-2128.	2.4	0
246	EndoâMediated Chemoenzymatic Approach Enables Reversible Glycopeptide Labeling for <i>O</i>-GlcNAcylation Analysis. Angewandte Chemie, 0, , .	2.0	0