

Hao-Jie Lu

List of Publications by Year in descending order

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117
papers

3,189
citations

172457

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189892

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120
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120
docs citations

120
times ranked

3816
citing authors

#	ARTICLE	IF	CITATIONS
1	Tailor-Made Magnetic Fe ₃ O ₄ @mTiO ₂ Microspheres with a Tunable Mesoporous Anatase Shell for Highly Selective and Effective Enrichment of Phosphopeptides. ACS Nano, 2012, 6, 3179-3188.	14.6	283
2	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. Nature Biomedical Engineering, 2019, 3, 306-317.	22.5	279
3	Ti ⁴⁺ -Immobilized Magnetic Composite Microspheres for Highly Selective Enrichment of Phosphopeptides. Advanced Functional Materials, 2013, 23, 107-115.	14.9	107
4	CARM1 Methylates GAPDH to Regulate Glucose Metabolism and Is Suppressed in Liver Cancer. Cell Reports, 2018, 24, 3207-3223.	6.4	96
5	Highly Efficient Enrichment Method for Glycopeptide Analyses: Using Specific and Nonspecific Nanoparticles Synergistically. Analytical Chemistry, 2014, 86, 2057-2064.	6.5	87
6	An Accessible Protocol for Solid-Phase Extraction of N-Linked Glycopeptides through Reductive Amination by Amine-Functionalized Magnetic Nanoparticles. Analytical Chemistry, 2013, 85, 5535-5541.	6.5	84
7	Tandem 18O Stable Isotope Labeling for Quantification of N-Glycoproteome. Journal of Proteome Research, 2010, 9, 227-236.	3.7	73
8	Par complex cluster formation mediated by phase separation. Nature Communications, 2020, 11, 2266.	12.8	73
9	Fishing the PTM proteome with chemical approaches using functional solid phases. Chemical Society Reviews, 2015, 44, 8260-8287.	38.1	70
10	Revealing the Dynamics of the 20 S Proteasome Phosphoproteome. Molecular and Cellular Proteomics, 2008, 7, 2073-2089.	3.8	69
11	ZnO~Poly(methyl methacrylate) Nanobeads for Enriching and Desalting Low-Abundant Proteins Followed by Directly MALDI-TOF MS Analysis. Analytical Chemistry, 2008, 80, 6758-6763.	6.5	61
12	CaCO ₃ ~Poly(methyl methacrylate) Nanoparticles for Fast Enrichment of Low-Abundance Peptides Followed by CaCO ₃ -Core Removal for MALDI-TOF MS Analysis. Angewandte Chemie - International Edition, 2006, 45, 3345-3349.	13.8	58
13	Highly Selective and Ultra Fast Solid-Phase Extraction of N-Glycoproteome by Oxime Click Chemistry Using Aminoxy-Functionalized Magnetic Nanoparticles. Analytical Chemistry, 2014, 86, 7920-7924.	6.5	54
14	Novel Proteomic Strategy Reveal Combined $\hat{\pm}^1$ Antitrypsin and Cathepsin D as Biomarkers for Colorectal Cancer Early Screening. Journal of Proteome Research, 2010, 9, 4701-4709.	3.7	53
15	Template-free synthesis of uniform magnetic mesoporous TiO ₂ nanospindles for highly selective enrichment of phosphopeptides. Materials Horizons, 2014, 1, 439.	12.2	53
16	Mass spectrometry-based N-glycoproteomics for cancer biomarker discovery. Clinical Proteomics, 2014, 11, 18.	2.1	51
17	Multi-targeted interference-free determination of ten $\hat{\pm}^2$ -blockers in human urine and plasma samples by alternating trilinear decomposition algorithm-assisted liquid chromatography~mass spectrometry in full scan mode: Comparison with multiple reaction monitoring. Analytica Chimica Acta, 2014, 848, 10-24.	5.4	45
18	Expanding Radical SAM Chemistry by Using Radical Addition Reactions and SAM Analogues. Angewandte Chemie - International Edition, 2016, 55, 11845-11848.	13.8	44

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19	Advancements in mass spectrometry-based glycoproteomics and glycomics. <i>National Science Review</i> , 2016, 3, 345-364.	9.5	43
20	VHL deficiency augments anthracycline sensitivity of clear cell renal cell carcinomas by down-regulating ALDH2. <i>Nature Communications</i> , 2017, 8, 15337.	12.8	43
21	Duplex Stable Isotope Labeling (DuSIL) for Simultaneous Quantitation and Distinction of Sialylated and Neutral N-Glycans by MALDI-MS. <i>Analytical Chemistry</i> , 2018, 90, 10442-10449.	6.5	39
22	Ligand-free strategy for ultrafast and highly selective enrichment of glycopeptides using Ag-coated magnetic nanoarchitectures. <i>Journal of Materials Chemistry</i> , 2012, 22, 23981.	6.7	34
23	Fluorinated Carbon Tag Derivatization Combined with Fluorous Solid-Phase Extraction: A New Method for the Highly Sensitive and Selective Mass Spectrometric Analysis of Glycans. <i>Analytical Chemistry</i> , 2015, 87, 5125-5131.	6.5	34
24	Hyperplex-MRM: A Hybrid Multiple Reaction Monitoring Method Using mTRAQ/iTRAQ Labeling for Multiplex Absolute Quantification of Human Colorectal Cancer Biomarker. <i>Journal of Proteome Research</i> , 2013, 12, 3912-3919.	3.7	33
25	Stable Isotope Sequential Derivatization for Linkage-Specific Analysis of Sialylated N-Glycan Isomers by MS. <i>Analytical Chemistry</i> , 2019, 91, 15993-16001.	6.5	32
26	Chemical labeling for fine mapping of IgG N-glycosylation by ETD-MS. <i>Chemical Science</i> , 2019, 10, 9302-9307.	7.4	32
27	Glycan reductive isotope-coded amino acid labeling (GRIAL) for mass spectrometry-based quantitative N-glycomics. <i>Chemical Communications</i> , 2015, 51, 772-775.	4.1	31
28	Identification of Palmitoylated Transitional Endoplasmic Reticulum ATPase by Proteomic Technique and Pan Antipalmitoylation Antibody. <i>Journal of Proteome Research</i> , 2016, 15, 956-962.	3.7	31
29	Ultradeep Palmitoylomics Enabled by Dithiodipyridine-Functionalized Magnetic Nanoparticles. <i>Analytical Chemistry</i> , 2018, 90, 6161-6168.	6.5	31
30	Advances in sample preparation strategies for MS-based qualitative and quantitative N-glycomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 99, 34-46.	11.4	31
31	Integrated Pipeline of Isotopic Labeling and Selective Enriching for Quantitative Analysis of <i>N</i> -Glycome by Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 1486-1493.	6.5	30
32	Affinity Purification of the Hepatitis C Virus Replicase Identifies Valosin-Containing Protein, a Member of the ATPases Associated with Diverse Cellular Activities Family, as an Active Virus Replication Modulator. <i>Journal of Virology</i> , 2016, 90, 9953-9966.	3.4	29
33	The kinase CK1 ϵ controls the antiviral immune response by phosphorylating the signaling adaptor TRAF3. <i>Nature Immunology</i> , 2016, 17, 397-405.	14.5	29
34	A novel quantitative proteomics workflow by isobaric terminal labeling. <i>Journal of Proteomics</i> , 2012, 75, 5797-5806.	2.4	28
35	Quantitative analysis of site-specific α -N-glycans on sera haptoglobin β chain in liver diseases. <i>Acta Biochimica Et Biophysica Sinica</i> , 2013, 45, 1021-1029.	2.0	28
36	Highly Selective and Large Scale Mass Spectrometric Analysis of 4-Hydroxynonenal Modification via Fluorous Derivatization and Fluorous Solid-Phase Extraction. <i>Analytical Chemistry</i> , 2017, 89, 3093-3100.	6.5	28

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37	ELISA-PLA: A novel hybrid platform for the rapid, highly sensitive and specific quantification of proteins and post-translational modifications. <i>Biosensors and Bioelectronics</i> , 2016, 80, 385-391.	10.1	27
38	Positive Enrichment of C-Terminal Peptides Using Oxazolone Chemistry and Biotinylation. <i>Analytical Chemistry</i> , 2015, 87, 9916-9922.	6.5	26
39	Reverse capture for selectively and sensitively revealing the N-glycome of serum exosomes. <i>Chemical Communications</i> , 2019, 55, 14339-14342.	4.1	26
40	A peptidic inhibitor for PD-1 palmitoylation targets its expression and functions. <i>RSC Chemical Biology</i> , 2021, 2, 192-205.	4.1	26
41	Facile Synthesis of Boronic Acid-Functionalized Magnetic Mesoporous Silica Nanocomposites for Highly Specific Enrichment of Glycopeptides. <i>Chinese Journal of Chemistry</i> , 2011, 29, 835-839.	4.9	25
42	Activated hepatic stellate cells promote epithelial-to-mesenchymal transition in hepatocellular carcinoma through transglutaminase 2-induced pseudohypoxia. <i>Communications Biology</i> , 2018, 1, 168.	4.4	25
43	On-plate enrichment methods for MALDI-MS analysis in proteomics. <i>Analytical Methods</i> , 2012, 4, 2622.	2.7	24
44	Metallic Element Chelated Tag Labeling (MeCTL) for Quantitation of N-Glycans in MALDI-MS. <i>Analytical Chemistry</i> , 2017, 89, 7470-7476.	6.5	24
45	MdFDIA: A Mass Defect Based Four-Plex Data-Independent Acquisition Strategy for Proteome Quantification. <i>Analytical Chemistry</i> , 2017, 89, 10248-10255.	6.5	24
46	In Vivo Termini Amino Acid Labeling for Quantitative Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6026-6033.	6.5	23
47	Highly specific enrichment of N-glycoproteome through a nonreductive amination reaction using Fe ₃ O ₄ @SiO ₂ -aniline nanoparticles. <i>Chemical Communications</i> , 2015, 51, 5982-5985.	4.1	23
48	N-glycopeptide Signatures of IgA2 in Serum from Patients with Hepatitis B Virus-related Liver Diseases. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2262-2272.	3.8	23
49	Fluorous Solid-Phase Extraction Technique Based on Nanographite Fluoride. <i>Analytical Chemistry</i> , 2017, 89, 4566-4572.	6.5	21
50	PLC β 2 negatively regulates the inflammatory response to virus infection by inhibiting phosphoinositide-mediated activation of TAK1. <i>Nature Communications</i> , 2019, 10, 746.	12.8	20
51	A streamlined strategy for rapid and selective analysis of serum N-glycome. <i>Analytica Chimica Acta</i> , 2019, 1050, 80-87.	5.4	20
52	Specific Analysis of α -2,3-Sialylated N-Glycan Linkage Isomers by Microchip Capillary Electrophoresis-Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 5537-5546.	6.5	20
53	Quantification of N-glycosylation site occupancy status based on labeling/label-free strategies with LC-MS/MS. <i>Talanta</i> , 2017, 170, 509-513.	5.5	19
54	Palmitoylation of MDH2 by ZDHHC18 activates mitochondrial respiration and accelerates ovarian cancer growth. <i>Science China Life Sciences</i> , 2022, 65, 2017-2030.	4.9	19

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55	Site-Specific Quantification of Protein Palmitoylation by Cysteine-Stable Isotope Metabolic Labeling. <i>Analytical Chemistry</i> , 2018, 90, 10543-10550.	6.5	18
56	Approach for Identification and Quantification of C-Terminal Peptides: Incorporation of Isotopic Arginine Labeling Based on Oxazolone Chemistry. <i>Analytical Chemistry</i> , 2013, 85, 10745-10753.	6.5	17
57	Palmitoylation as a Signal for Delivery. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1248, 399-424.	1.6	17
58	Identification of Arsenic Direct-Binding Proteins in Acute Promyelocytic Leukaemia Cells. <i>International Journal of Molecular Sciences</i> , 2015, 16, 26871-26879.	4.1	16
59	In-Depth Analysis of C Terminomes Based on LysC Digestion and Site-Selective Dimethylation. <i>Analytical Chemistry</i> , 2019, 91, 6498-6506.	6.5	16
60	ITMSQ: A software tool for N- and C-terminal fragment ion pairs based isobaric tandem mass spectrometry quantification. <i>Proteomics</i> , 2015, 15, 3755-3764.	2.2	15
61	Relative Quantification of N-Glycopeptide Sialic Acid Linkage Isomers by Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 15617-15625.	6.5	15
62	Recent developments of nanoparticle-based enrichment methods for mass spectrometric analysis in proteomics. <i>Science China Chemistry</i> , 2010, 53, 695-703.	8.2	14
63	O-GlcNAcylation of MEK2 promotes the proliferation and migration of breast cancer cells. <i>Glycobiology</i> , 2021, 31, 571-581.	2.5	13
64	Selective Identification and Site-Specific Quantification of 4-Hydroxy-2-nonenal-Modified Proteins. <i>Analytical Chemistry</i> , 2019, 91, 5235-5243.	6.5	12
65	Dual isotopic labeling combined with fluoruous solid-phase extraction for simultaneous discovery of neutral/sialylated N-glycans as biomarkers for gastric cancer. <i>Analytica Chimica Acta</i> , 2020, 1104, 87-94.	5.4	12
66	A thiazolidine formation-based approach for ultrafast and highly efficient solid-phase extraction of N-Glycoproteome. <i>Analytica Chimica Acta</i> , 2020, 1100, 174-181.	5.4	12
67	Solving signal instability to maintain the second-order advantage in the resolution and determination of multi-analytes in complex systems by modeling liquid chromatography-mass spectrometry data using alternating trilinear decomposition method assisted with piecewise direct standardization. <i>Journal of Chromatography A</i> , 2015, 1407, 157-168.	3.7	11
68	Highly specific purification of N-glycans using phosphate-based derivatization as an affinity tag in combination with Ti4+-SPE enrichment for mass spectrometric analysis. <i>Analytica Chimica Acta</i> , 2016, 934, 145-151.	5.4	11
69	Isoelectric focusing array with immobilized pH gradient and dynamic scanning imaging for diabetes diagnosis. <i>Analytica Chimica Acta</i> , 2019, 1063, 178-186.	5.4	11
70	A practical approach to enrich intact tryptic N-glycopeptides through size exclusion chromatography and hydrophilicity (SELIC) using an acrylamide-agarose composite gel system. <i>Analytica Chimica Acta</i> , 2019, 1058, 107-116.	5.4	11
71	Comparative analysis of intact glycopeptides from mannose receptor among different breast cancer subtypes using mass spectrometry. <i>Talanta</i> , 2021, 223, 121676.	5.5	11
72	Fast Discrimination of Sialylated N-Glycan Linkage Isomers with One-Step Derivatization by Microfluidic Capillary Electrophoresis-Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 4666-4676.	6.5	11

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73	High-throughput site-specific <i>N</i> -glycoproteomics reveals glyco-signatures for liver disease diagnosis. <i>National Science Review</i> , 2023, 10, .	9.5	11
74	Expanding Radical SAM Chemistry by Using Radical Addition Reactions and SAM Analogues. <i>Angewandte Chemie</i> , 2016, 128, 12024-12027.	2.0	10
75	A novel triplex isobaric termini labeling quantitative approach for simultaneously supplying three quantitative sources. <i>Analytica Chimica Acta</i> , 2018, 1001, 70-77.	5.4	10
76	Rapid and Easy Enrichment Strategy for Naturally Acetylated N Termini Based on LysN Digestion and Amine-Reactive Resin Capture. <i>Analytical Chemistry</i> , 2020, 92, 8315-8322.	6.5	10
77	Fabrication of Alkoxyamine-Functionalized Magnetic Core-Shell Microspheres via Reflux Precipitation Polymerization for Glycopeptide Enrichment. <i>Polymers</i> , 2016, 8, 74.	4.5	9
78	Site-Specific Quantification of Protein Ubiquitination on MS2 Fragment Ion Level via Isobaric Peptide Labeling. <i>Analytical Chemistry</i> , 2017, 89, 11468-11475.	6.5	9
79	Discover the <i>Post-translational</i> Modification Proteome Using Mass Spectrometry. <i>Chinese Journal of Chemistry</i> , 2021, 39, 550-558.	4.9	9
80	Linkage-selective derivatization for glycosylation site- and glycoform-specific characterization of sialic acid isomers using mass spectrometry. <i>Chemical Communications</i> , 2021, 57, 9590-9593.	4.1	9
81	Progress of proteomics-driven precision medicine: From a glycosylation view. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, .	1.5	9
82	Diagnosis of thymic epithelial tumor subtypes by a quantitative proteomic approach. <i>Analyst, The</i> , 2018, 143, 2491-2500.	3.5	8
83	Selective Enrichment and Quantification of N-Terminal Glycine Peptides via Sortase A Mediated Ligation. <i>Analytical Chemistry</i> , 2018, 90, 14303-14308.	6.5	8
84	A barcode mode based on glycosylation sites of membrane type mannose receptor as a new potential diagnostic marker for breast cancer. <i>Talanta</i> , 2019, 191, 21-26.	5.5	8
85	SAPT, a Fast and Efficient Approach for Simultaneous Profiling of Protein N- and C-Terminome. <i>Analytical Chemistry</i> , 2021, 93, 10553-10560.	6.5	8
86	Nascent Proteome and Glycoproteome Reveal the Inhibition Role of ALG1 in Hepatocellular Carcinoma Cell Migration. <i>Phenomics</i> , 2022, 2, 230-241.	2.9	8
87	Mapping and analyzing the human liver proteome: progress and potential. <i>Expert Review of Proteomics</i> , 2016, 13, 833-843.	3.0	7
88	FluoroTRAQ: Quantitative Analysis of Protein S-Nitrosylation through Fluorous Solid-Phase Extraction Combining with iTRAQ by Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 15317-15322.	6.5	7
89	Progress in Research Methods for Protein Palmitoylation. <i>Chinese Journal of Analytical Chemistry</i> , 2014, 42, 616-622.	1.7	6
90	Global in vivo terminal amino acid labeling for exploring differential expressed proteins induced by dialyzed serum cultivation. <i>Analyst, The</i> , 2014, 139, 4497-4504.	3.5	6

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91	Reductive Amination Combining Dimethylation for Quantitative Analysis of Early-Stage Glycated Proteins. <i>Analytical Chemistry</i> , 2018, 90, 3752-3758.	6.5	6
92	MdCDPM: A Mass Defect-Based Chemical-Directed Proteomics Method for Targeted Analysis of Intact Sialylglycopeptides. <i>Analytical Chemistry</i> , 2019, 91, 9986-9992.	6.5	6
93	Tracking Pathogen Infections by Time-Resolved Chemical Proteomics. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2235-2240.	13.8	6
94	Sol-gel-derived Poly(dimethylsiloxane) Enzymatic Reactor for Microfluidic Peptide Mapping. <i>Chinese Journal of Chemistry</i> , 2006, 24, 903-909.	4.9	5
95	HST-MRM-MS: A Novel High-Sample-Throughput Multiple Reaction Monitoring Mass Spectrometric Method for Multiplex Absolute Quantitation of Hepatocellular Carcinoma Serum Biomarker. <i>Journal of Proteome Research</i> , 2019, 18, 469-477.	3.7	5
96	Advances in Analysis of Linkage Isomers of Sialylated N-Glycans by Mass Spectrometry. <i>Acta Chimica Sinica</i> , 2021, 79, 705.	1.4	5
97	One step carboxyl group isotopic labeling for quantitative analysis of intact N-glycopeptides by mass spectrometry. <i>Chemical Communications</i> , 2021, 57, 4154-4157.	4.1	5
98	Analysis of Serum Paraoxonase 1 Using Mass Spectrometry and Lectin Immunoassay in Patients With Alpha-Fetoprotein Negative Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 651421.	2.8	5
99	Enhancing Comprehensive Analysis of Newly Synthesized Proteins Based on Cleavable Bioorthogonal Tagging. <i>Analytical Chemistry</i> , 2021, 93, 9408-9417.	6.5	5
100	Methodology for Detecting Protein Palmitoylation. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1248, 425-430.	1.6	5
101	Electrospray ionization fourier transform ion cyclotron resonance mass spectrometric study on sodium azide cluster ions. <i>Chinese Journal of Chemistry</i> , 2004, 22, 1164-1169.	4.9	4
102	Precisely designed rattle-type mTiO ₂ @P(NIPAM-co-MBA) microspheres with screening gel network for highly selective extraction of phosphopeptide. <i>RSC Advances</i> , 2014, 4, 42957-42964.	3.6	4
103	Glycan reductive amino acid coded affinity tagging (GRACAT) for highly specific analysis of N-glycome by mass spectrometry. <i>Analytica Chimica Acta</i> , 2019, 1089, 90-99.	5.4	4
104	Integrated Strategy for Discovery and Validation of Glycated Candidate Biomarkers for Hemodialysis Patients with Cardiovascular Complications. <i>Analytical Chemistry</i> , 2021, 93, 4398-4407.	6.5	4
105	Mass spectrometry-based analysis of IgG glycosylation and its applications. <i>International Journal of Mass Spectrometry</i> , 2022, 474, 116799.	1.5	4
106	Enhanced Ionization of Phosphatidylcholines during MALDI Mass Spectrometry Using DCTB as Matrix. <i>Chinese Journal of Chemistry</i> , 2012, 30, 2091-2096.	4.9	3
107	Mass defect-based carbonyl activated tags (mdCATs) for multiplex data-independent acquisition proteome quantification. <i>Chemical Communications</i> , 2021, 57, 737-740.	4.1	3
108	Comprehensive Profiling for Histone H4 of Human Liver Cells Using High Resolution LTQ-Orbitrap Mass Spectrometry. <i>Chinese Journal of Chemistry</i> , 2011, 29, 171-177.	4.9	2

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109	Sample preparation approaches for qualitative and quantitative analysis of lipid-derived electrophile modified proteomes by mass spectrometry. <i>Molecular Omics</i> , 2020, 16, 511-520.	2.8	2
110	Fractionation-free negative enriching for in-depth C-terminome analysis. <i>Chinese Chemical Letters</i> , 2021, , .	9.0	2
111	Specific and Reversible Enrichment of Early-Stage Glycated Proteome Based on Thiazolidine Chemistry and Palladium-Mediated Cleavage. <i>Analytical Chemistry</i> , 2022, 94, 5213-5220.	6.5	2
112	Direct digestion of living cells via a gel-based strategy for mass spectrometric analysis. <i>Chemical Communications</i> , 2017, 53, 1421-1424.	4.1	1
113	A Streamlined Sample Preparation Method for Mass Spectrometric Analysis. <i>Current Protocols in Cell Biology</i> , 2018, 78, 5.8.1-5.8.8.	2.3	1
114	A novel method for large-scale confirmation of protein structures and surface accessible modification sites. <i>Talanta</i> , 2020, 211, 120697.	5.5	1
115	Iterative Non- <i>m/z</i> -Sharing Rule for Confident and Sensitive Protein Identification of Non-shotgun Proteomics. <i>Chinese Journal of Chemistry</i> , 2009, 27, 331-337.	4.9	0
116	New lysine-acetylated proteins screened by immunoaffinity and liquid chromatography-mass spectrometry. <i>Science China Chemistry</i> , 2010, 53, 238-244.	8.2	0
117	Multiple technical routes to obtain a proteomics expression profile of French liver samples. <i>Analytical Methods</i> , 2014, 6, 2950-2958.	2.7	0