Liang Li

List of Publications by Year
in descending order

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		22099	23472
235	14,466	59	111
papers	citations	h-index	g-index

667	667	667	16153
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	HMDB: the Human Metabolome Database. Nucleic Acids Research, 2007, 35, D521-D526.	6.5	2,563
2	HMDB: a knowledgebase for the human metabolome. Nucleic Acids Research, 2009, 37, D603-D610.	6.5	1,649
3	Differential ¹²C-/¹³C-Isotope Dansylation Labeling and Fast Liquid Chromatography/Mass Spectrometry for Absolute and Relative Quantification of the Metabolome. Analytical Chemistry, 2009, 81, 3919-3932.	3.2	345
4	Definitions of terms relating to mass spectrometry (IUPAC Recommendations 2013). Pure and Applied Chemistry, 2013, 85, 1515-1609.	0.9	305
5	Detection of High Molecular Weight Narrow Polydisperse Polymers up to 1.5 Million Daltons by MALDI Mass Spectrometry. Analytical Chemistry, 1996, 68, 2721-2725.	3.2	251
6	Sample normalization methods in quantitative metabolomics. Journal of Chromatography A, 2016, 1430, 80-95.	1.8	211
7	High-Resolution Matrix-Assisted Laser Desorption/Ionization in a Linear Time-of-Flight Mass Spectrometer. Analytical Chemistry, 1995, 67, 1950-1954.	3.2	194
8	Two-Layer Sample Preparation:Â A Method for MALDI-MS Analysis of Complex Peptide and Protein Mixtures. Analytical Chemistry, 1999, 71, 1087-1091.	3.2	185
9	MyCompoundID: Using an Evidence-Based Metabolome Library for Metabolite Identification. Analytical Chemistry, 2013, 85, 3401-3408.	3.2	185
10	Investigation of spectral reproducibility in direct analysis of bacteria proteins by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 1998, 12, 456-464.	0.7	179
11	High-Performance Isotope Labeling for Profiling Carboxylic Acid-Containing Metabolites in Biofluids by Mass Spectrometry. Analytical Chemistry, 2010, 82, 8789-8793.	3.2	161
12	Stable-Isotope Dimethylation Labeling Combined with LCâˆ’ESI MS for Quantification of Amine-Containing Metabolites in Biological Samples. Analytical Chemistry, 2007, 79, 8631-8638.	3.2	156
13	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 1. Sample Preparation and Desorption/Ionization Issues. Analytical Chemistry, 1997, 69, 4169-4175.	3.2	150
14	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 2. Instrumental Issues. Analytical Chemistry, 1997, 69, 4176-4183.	3.2	148
15	Microwave-assisted acid hydrolysis of proteins combined with liquid chromatography MALDI MS/MS for protein identification. Journal of the American Society for Mass Spectrometry, 2005, 16, 471-481.	1.2	140
16	A New Segmented Virus Associated with Human Febrile Illness in China. New England Journal of Medicine, 2019, 380, 2116-2125.	13.9	138
17	Micro-Scale Frontal Affinity Chromatography with Mass Spectrometric Detection: A New Method for the Screening of Compound Libraries. Angewandte Chemie - International Edition, 1998, 37, 3383-3387.	7.2	129
18	Characterization of Human Tear Proteome Using Multiple Proteomic Analysis Techniques. Journal of Proteome Research, 2005, 4, 2052-2061.	1.8	129

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19	Confocal Fluorescence Microscopic Imaging for Investigating the Analyte Distribution in MALDI Matrices. Analytical Chemistry, 1996, 68, 2494-2500.	3.2	127
20	Protein sequencing by mass analysis of polypeptide ladders after controlled protein hydrolysis. Nature Biotechnology, 2004, 22, 1291-1296.	9.4	118
21	Monocyte lipid rafts contain proteins implicated in vesicular trafficking and phagosome formation. Proteomics, 2003, 3, 536-548.	1.3	117
22	Comparison of SDS- and methanol-assisted protein solubilization and digestion methods forEscherichia colimembrane proteome analysis by 2-D LC-MS/MS. Proteomics, 2007, 7, 484-493.	1.3	117
23	IsoMS: Automated Processing of LC-MS Data Generated by a Chemical Isotope Labeling Metabolomics Platform. Analytical Chemistry, 2014, 86, 4675-4679.	3.2	111
24	A multiomics approach to heterogeneity in Alzheimerâ€™s disease: focused review and roadmap. Brain, 2020, 143, 1315-1331.	3.7	106
25	Differential Dimethyl Labeling of N-Termini of Peptides after Guanidination for Proteome Analysis. Journal of Proteome Research, 2005, 4, 2099-2108.	1.8	103
26	DnsID in MyCompoundID for Rapid Identification of Dansylated Amine- and Phenol-Containing Metabolites in LCâ€“MS-Based Metabolomics. Analytical Chemistry, 2015, 87, 9838-9845.	3.2	103
27	Altered Gut Microbial Metabolites in Amnestic Mild Cognitive Impairment and Alzheimerâ€™s Disease: Signals in Hostâ€“Microbe Interplay. Nutrients, 2021, 13, 228.	1.7	103
28	Detection and identification of low-mass peptides and proteins from solvent suspensions ofEscherichia coli by high performance liquid chromatography fractionation and matrix-assisted laser desorption/ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 1999, 13, 73-78.	0.7	101
29	Effects of common surfactants on protein digestion and matrix-assisted laser desorption/ionization mass spectrometric analysis of the digested peptides using two-layer sample preparation. Rapid Communications in Mass Spectrometry, 2004, 18, 889-896.	0.7	101
30	Metabolomic Coverage of Chemical-Group-Submetabolome Analysis: Group Classification and Four-Channel Chemical Isotope Labeling LC-MS. Analytical Chemistry, 2019, 91, 12108-12115.	3.2	100
31	Lipid raft proteomics: Analysis of in-solution digest of sodium dodecyl sulfate-solubilized lipid raft proteins by liquid chromatography-matrix-assisted laser desorption/ionization tandem mass spectrometry. Proteomics, 2004, 4, 3156-3166.	1.3	99
32	Determination of Total Concentration of Chemically Labeled Metabolites as a Means of Metabolome Sample Normalization and Sample Loading Optimization in Mass Spectrometry-Based Metabolomics. Analytical Chemistry, 2012, 84, 10723-10731.	3.2	95
33	Development of a Universal Metabolome-Standard Method for Long-Term LCâ€“MS Metabolome Profiling and Its Application for Bladder Cancer Urine-Metabolite-Biomarker Discovery. Analytical Chemistry, 2014, 86, 6540-6547.	3.2	93
34	MyCompoundID MS/MS Search: Metabolite Identification Using a Library of Predicted Fragment-Ion-Spectra of 383,830 Possible Human Metabolites. Analytical Chemistry, 2015, 87, 10619-10626.	3.2	93
35	Chemical derivatization in LC-MS-based metabolomics study. TrAC - Trends in Analytical Chemistry, 2020, 131, 115988.	5.8	88
36	Analysis of Single Mammalian Cell Lysates by Mass Spectrometry. Journal of the American Chemical Society, 1996, 118, 11662-11663.	6.6	88

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37	Development of High-Performance Chemical Isotope Labeling LCâ€"MS for Profiling the Carbonyl Submetabolome. Analytical Chemistry, 2017, 89, 6758-6765.	3.2	85
38	Analysis of the accuracy of determining average molecular weights of narrow polydispersity polymers by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Journal of the American Society for Mass Spectrometry, 1998, 9, 275-281.	1.2	83
39	Protein Concentration and Enzyme Digestion on Microbeads for MALDI-TOF Peptide Mass Mapping of Proteins from Dilute Solutions. Analytical Chemistry, 2000, 72, 3355-3362.	3.2	82
40	Counting Missing Values in a Metabolite-Intensity Data Set for Measuring the Analytical Performance of a Metabolomics Platform. Analytical Chemistry, 2015, 87, 1306-1313.	3.2	80
41	Proteome of the Escherichia coli envelope and technological challenges in membrane proteome analysis. Biochimica Et Biophysica Acta - Biomembranes, 2008, 1778, 1698-1713.	1.4	79
42	Development of Mass Spectrometry-Based Shotgun Method for Proteome Analysis of 500 to 5000 Cancer Cells. Analytical Chemistry, 2010, 82, 2262-2271.	3.2	76
43	Time-Lag Focusing MALDI Time-of-Flight Mass Spectrometry for Polymer Characterization:Â Oligomer Resolution, Mass Accuracy, and Average Weight Information. Analytical Chemistry, 1997, 69, 2734-2741.	3.2	75
44	Discerning matrix-cluster peaks in matrix-assisted laser desorption/ionization time-of-flight mass spectra of dilute peptide mixtures. Journal of the American Society for Mass Spectrometry, 2000, 11, 88-93.	1.2	75
45	Exploring the Precursor Ion Exclusion Feature of Liquid Chromatographyâ^'Electrospray Ionization Quadrupole Time-of-Flight Mass Spectrometry for Improving Protein Identification in Shotgun Proteome Analysis. Analytical Chemistry, 2008, 80, 4696-4710.	3.2	75
46	Development of Isotope Labeling LCâ€"MS for Human Salivary Metabolomics and Application to Profiling Metabolome Changes Associated with Mild Cognitive Impairment. Analytical Chemistry, 2012, 84, 10802-10811.	3.2	75
47	Chemical Isotope Labeling LC-MS for High Coverage and Quantitative Profiling of the Hydroxyl Submetabolome in Metabolomics. Analytical Chemistry, 2016, 88, 10617-10623.	3.2	74
48	Mitogen-activated Protein Kinase-dependent Activation of the Na+/H+ Exchanger Is Mediated through Phosphorylation of Amino Acids Ser770 and Ser771. Journal of Biological Chemistry, 2007, 282, 6292-6299.	1.6	73
49	High-Performance Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry for Exosome Metabolomics. Analytical Chemistry, 2018, 90, 8314-8319.	3.2	72
50	Microbial metabolites in the marine carbon cycle. Nature Microbiology, 2022, 7, 508-523.	5.9	71
51	Proteome Profile of Cytosolic Component of Zebrafish Liver Generated by LCâ^'ESI MS/MS Combined with Trypsin Digestion and Microwave-Assisted Acid Hydrolysis. Journal of Proteome Research, 2007, 6, 263-272.	1.8	69
52	Profiling novel metabolic biomarkers for Parkinson's disease using inâ€depth metabolomic analysis. Movement Disorders, 2017, 32, 1720-1728.	2.2	69
53	Lithium and transition metal ions enable low energy collision-induced dissociation of polyglycols in electrospray ionization mass spectrometry. Journal of the American Society for Mass Spectrometry, 2001, 12, 832-839.	1.2	67
54	Metabolomics of Small Numbers of Cells: Metabolomic Profiling of 100, 1000, and 10000 Human Breast Cancer Cells. Analytical Chemistry, 2017, 89, 11664-11671.	3.2	67

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55	Development of High-Performance Chemical Isotope Labeling LCâ€“MS for Profiling the Human Fecal Metabolome. Analytical Chemistry, 2015, 87, 829-836.	3.2	66
56	Toxicity mechanisms of polystyrene microplastics in marine mussels revealed by high-coverage quantitative metabolomics using chemical isotope labeling liquid chromatography mass spectrometry. Journal of Hazardous Materials, 2021, 417, 126003.	6.5	66
57	Detection of 25,000 molecules of Substance P by MALDI-TOF mass spectrometry and investigations into the fundamental limits of detection in MALDI. Journal of the American Society for Mass Spectrometry, 2001, 12, 1055-1063.	1.2	64
58	Liquid Chromatography MALDI MS/MS for Membrane Proteome Analysis. Journal of Proteome Research, 2004, 3, 719-727.	1.8	64
59	Quantitative Metabolome Analysis Based on Chromatographic Peak Reconstruction in Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. Analytical Chemistry, 2015, 87, 7011-7016.	3.2	63
60	Quantitative Proteome Analysis Using Differential Stable Isotopic Labeling and Microbore LCâˆ'MALDI MS and MS/MS. Journal of Proteome Research, 2005, 4, 734-742.	1.8	62
61	Metabolomics Analyses of Saliva Detect Novel Biomarkers of Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2018, 65, 1401-1416.	1.2	62
62	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for polymer analysis: solvent effect in sample preparation. Journal of the American Society for Mass Spectrometry, 1998, 9, 1303-1310.	1.2	61
63	Development and Applications of In-Gel CNBr/Tryptic Digestion Combined with Mass Spectrometry for the Analysis of Membrane Proteins. Journal of Proteome Research, 2003, 2, 543-552.	1.8	60
64	Nanoliter Chemistry Combined with Mass Spectrometry for Peptide Mapping of Proteins from Single Mammalian Cell Lysates. Analytical Chemistry, 1998, 70, 5344-5347.	3.2	59
65	Two-Layer Sample Preparation Method for MALDI Mass Spectrometric Analysis of Protein and Peptide Samples Containing Sodium Dodecyl Sulfate. Analytical Chemistry, 2001, 73, 2968-2975.	3.2	58
66	Differential Isotope Labeling of 38 Dietary Polyphenols and Their Quantification in Urine by Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry. Analytical Chemistry, 2016, 88, 2637-2644.	3.2	57
67	Laser desorption ionization and MALDI time-of-flight mass spectrometry for low molecular mass polyethylene analysis. Journal of the American Society for Mass Spectrometry, 2001, 12, 1186-1192.	1.2	56
68	Ultra-high performance liquid chromatography tandem mass spectrometry for comprehensive analysis of urinary acylcarnitines. Analytica Chimica Acta, 2011, 689, 77-84.	2.6	56
69	Off-Line Two-Dimensional Liquid Chromatography with Maximized Sample Loading to Reversed-Phase Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometry for Shotgun Proteome Analysis. Analytical Chemistry, 2009, 81, 1049-1060.	3.2	54
70	Matrix-assisted laser desorption ionization time-of-flight mass spectrometry for the analysis of polydienes. Journal of the American Society for Mass Spectrometry, 1997, 8, 1220-1229.	1.2	51
71	Combining Liquid Chromatography with MALDI Mass Spectrometry Using a Heated Droplet Interface. Analytical Chemistry, 2004, 76, 992-1001.	3.2	51
72	5-Diethylamino-naphthalene-1-sulfonyl Chloride (DensCl): A Novel Triplex Isotope Labeling Reagent for Quantitative Metabolome Analysis by Liquid Chromatography Mass Spectrometry. Analytical Chemistry, 2013, 85, 11532-11539.	3.2	49

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73	Qualitative Metabolome Analysis of Human Cerebrospinal Fluid by¹³C-/¹²C-Isotope Dansylation Labeling Combined with Liquid Chromatography Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2011, 22, 339-347.	1.2	48
74	Development of Isotope Labeling Liquid Chromatography Mass Spectrometry for Mouse Urine Metabolomics: Quantitative Metabolomic Study of Transgenic Mice Related to Alzheimerâ€™s Disease. Journal of Proteome Research, 2014, 13, 4457-4469.	1.8	48
75	Characterization of pyrene end-labeled poly(ethylene glycol) by high resolution MALDI time-of-flight mass spectrometry. Macromolecular Rapid Communications, 1996, 17, 59-64.	2.0	47
76	Dansylhydrazine Isotope Labeling LC-MS for Comprehensive Carboxylic Acid Submetabolome Profiling. Analytical Chemistry, 2018, 90, 13514-13522.	3.2	46
77	Large-Scale Proteome Profile of the Zebrafish (<i>Danio rerio</i>) Gill for Physiological and Biomarker Discovery Studies. Zebrafish, 2009, 6, 229-238.	0.5	45
78	Reactions of atomic transition-metal ions with long-chain alkanes. Journal of the American Society for Mass Spectrometry, 2001, 12, 367-375.	1.2	43
79	Distinctive Metabolomics Patterns Associated With Insulin Resistance and Type 2 Diabetes Mellitus. Frontiers in Molecular Biosciences, 2020, 7, 609806.	1.6	43
80	Application of an integrated matrix-assisted laser desorption/ionization time-of-flight, electrospray ionization mass spectrometry and tandem mass spectrometry approach to characterizing complex polyol mixtures. Journal of the American Society for Mass Spectrometry, 2001, 12, 55-60.	1.2	42
81	Evaluating and minimizing batch effects in metabolomics. Mass Spectrometry Reviews, 2022, 41, 421-442.	2.8	42
82	Observation of sodium gel-induced protein modifications in dodecylsulfate polyacrylamide gel electrophoresis and its implications for accurate molecular weight determination of gel-separated proteins by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Journal of the American Society for Mass Spectrometry, 1999, 10, 512-520.	1.2	41
83	Comparison of surfactant-assisted shotgun methods using acid-labile surfactants and sodium dodecyl sulfate for membrane proteome analysis. Analytica Chimica Acta, 2011, 698, 36-43.	2.6	41
84	Liquidâ€"liquid extraction combined with differential isotope dimethylaminophenacyl labeling for improved metabolomic profiling of organic acids. Analytica Chimica Acta, 2013, 803, 97-105.	2.6	41
85	Comprehensive and Quantitative Profiling of the Human Sweat Submetabolome Using High-Performance Chemical Isotope Labeling LCâ€"MS. Analytical Chemistry, 2016, 88, 7378-7386.	3.2	41
86	Three-layer matrix/sample preparation method for MALDI MS analysis of low nanomolar protein samples. Journal of the American Society for Mass Spectrometry, 2006, 17, 780-785.	1.2	40
87	Analysis of Structurally Complex Polymers by Time-Lag Focusing Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry. Macromolecules, 1997, 30, 1955-1963.	2.2	39
88	Characterization of poly(ethylene glycol) esters using low energy collision-induced dissociation in electrospray ionization mass spectrometry. Journal of the American Society for Mass Spectrometry, 2002, 13, 888-897.	1.2	39
89	Identification and Quantification of Differentially Expressed Proteins in E-Cadherin Deficient SCC9 Cells and SCC9 Transfectants Expressing E-Cadherin by Dimethyl Isotope Labeling, LCâ˜'MALDI MS and MS/MS. Journal of Proteome Research, 2005, 4, 1419-1426.	1.8	39
90	High glucose promotes gastric cancer chemoresistance in vivo and in vitro. Molecular Medicine Reports, 2015, 12, 843-850.	1.1	39

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91	Parallel Metabolomic Profiling of Cerebrospinal Fluid and Serum for Identifying Biomarkers of Injury Severity after Acute Human Spinal Cord Injury. Scientific Reports, 2016, 6, 38718.	1.6	38
92	Development of Isotope Labeling Liquid Chromatographyâ€“Mass Spectrometry for Metabolic Profiling of Bacterial Cells and Its Application for Bacterial Differentiation. Analytical Chemistry, 2013, 85, 5755-5763.	3.2	37
93	Combining Avidinâˆ’Biotin Chemistry with Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. Analytical Chemistry, 1996, 68, 3382-3387.	3.2	36
94	Ion-pairing reversed-phase liquid chromatography fractionation in combination with isotope labeling reversed-phase liquid chromatographyâ€“mass spectrometry for comprehensive metabolome profiling. Journal of Chromatography A, 2011, 1218, 3689-3694.	1.8	36
95	Rewiring AMPK and Mitochondrial Retrograde Signaling for Metabolic Control of Aging and Histone Acetylation in Respiratory-Defective Cells. Cell Reports, 2014, 7, 565-574.	2.9	36
96	Elevated acetylâ€•CoA by amino acid recycling fuels microalgal neutral lipid accumulation in exponential growth phase for biofuel production. Plant Biotechnology Journal, 2017, 15, 497-509.	4.1	36
97	Nanoliter Solvent Extraction Combined with Microspot MALDI TOF Mass Spectrometry for the Analysis of Hydrophobic Biomolecules. Analytical Chemistry, 2001, 73, 2929-2936.	3.2	35
98	A method for comprehensive analysis of urinary acylglycines by using ultra-performance liquid chromatography quadrupole linear ion trap mass spectrometry. Journal of the American Society for Mass Spectrometry, 2010, 21, 2105-2116.	1.2	35
99	Dexamethasone-Induced Perturbations in Tissue Metabolomics Revealed by Chemical Isotope Labeling LC-MS Analysis. Metabolites, 2020, 10, 42.	1.3	35
100	Integrated SDS Removal and Peptide Separation by Strong-Cation Exchange Liquid Chromatography for SDS-Assisted Shotgun Proteome Analysis. Journal of Proteome Research, 2012, 11, 818-828.	1.8	34
101	Development of Chemical Isotope Labeling LC-MS for Milk Metabolomics: Comprehensive and Quantitative Profiling of the Amine/Phenol Submetabolome. Analytical Chemistry, 2017, 89, 4435-4443.	3.2	34
102	Integrated analyses utilizing metabolomics and transcriptomics reveal perturbation of the polyamine pathway in oral cavity squamous cell carcinoma. Analytica Chimica Acta, 2019, 1050, 113-122.	2.6	34
103	Development of an isotope labeling ultra-high performance liquid chromatography mass spectrometric method for quantification of acylglycines in human urine. Analytica Chimica Acta, 2012, 750, 161-172.	2.6	32
104	Nonocclusive Sweat Collection Combined with Chemical Isotope Labeling LCâ€“MS for Human Sweat Metabolomics and Mapping the Sweat Metabolomes at Different Skin Locations. Analytical Chemistry, 2017, 89, 7847-7851.	3.2	32
105	Photo-induced dissociation of electrospray generated ions in an ion trap/time-of-flight mass spectrometer. Review of Scientific Instruments, 1999, 70, 4192-4199.	0.6	31
106	Low-mass proteome analysis based on liquid chromatography fractionation, nanoliter protein concentration/digestion, and microspot matrix-assisted laser desorption ionization mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 317-329.	1.2	31
107	Simple and Robust Two-Layer Matrix/Sample Preparation Method for MALDI MS/MS Analysis of Peptides. Journal of Proteome Research, 2005, 4, 1709-1716.	1.8	30
108	Chronic inhibition of farnesyl pyrophosphate synthase attenuates cardiac hypertrophy and fibrosis in spontaneously hypertensive rats. Biochemical Pharmacology, 2010, 79, 399-406.	2.0	30

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109	Reproducible microwave-assisted acid hydrolysis of proteins using a household microwave oven and its combination with LC-ESI MS/MS for mapping protein sequences and modifications. Journal of the American Society for Mass Spectrometry, 2010, 21, 1573-1587.	1.2	30
110	Nanoflow LCâ€“MS for High-Performance Chemical Isotope Labeling Quantitative Metabolomics. Analytical Chemistry, 2015, 87, 11468-11474.	3.2	30
111	Quantification of 38 dietary polyphenols in plasma by differential isotope labelling and liquid chromatography electrospray ionization tandem mass spectrometry. Journal of Chromatography A, 2018, 1558, 50-58.	1.8	30
112	Investigation of the quantitative capabilities of an electrospray ionization ion trap/linear time-of-flight mass spectrometer. Rapid Communications in Mass Spectrometry, 1998, 12, 695-700.	0.7	29
113	Structural Analysis of Polymer End Groups by Electrospray Ionization High-Energy Collision-Induced Dissociation Tandem Mass Spectrometry. Analytical Chemistry, 2000, 72, 3847-3852.	3.2	29
114	Comparative Proteomic and Metabolomic Analysis of Staphylococcus warneri SG1 Cultured in the Presence and Absence of Butanol. Journal of Proteome Research, 2013, 12, 4478-4489.	1.8	29
115	Metabolite Analysis and Histology on the Exact Same Tissue: Comprehensive Metabolomic Profiling and Metabolic Classification of Prostate Cancer. Scientific Reports, 2016, 6, 32272.	1.6	29
116	Dansylation isotope labeling liquid chromatography mass spectrometry for parallel profiling of human urinary and fecal submetabolomes. Analytica Chimica Acta, 2016, 903, 100-109.	2.6	29
117	Applying quantitative metabolomics based on chemical isotope labeling LC-MS for detecting potential milk adulterant in human milk. Analytica Chimica Acta, 2018, 1001, 78-85.	2.6	29
118	PEP Search in MyCompoundID: Detection and Identification of Dipeptides and Tripeptides Using Dimethyl Labeling and Hydrophilic Interaction Liquid Chromatography Tandem Mass Spectrometry. Analytical Chemistry, 2014, 86, 3568-3574.	3.2	28
119	Overcoming Sample Matrix Effect in Quantitative Blood Metabolomics Using Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. Analytical Chemistry, 2017, 89, 9424-9431.	3.2	28
120	Brain Transforming Growth Factor-Î² Resists Hypertension Via Regulating Microglial Activation. Stroke, 2017, 48, 2557-2564.	1.0	28
121	MALDI Mass Spectrometry Combined with Avidinâ^'Biotin Chemistry for Analysis of Protein Modifications. Analytical Chemistry, 1998, 70, 1569-1575.	3.2	27
122	Development of chemical isotope labeling LC-MS for tissue metabolomics and its application for brain and liver metabolome profiling in Alzheimer's disease mouse model. Analytica Chimica Acta, 2019, 1050, 95-104.	2.6	27
123	Ammonium Dodecyl Sulfate as an Alternative to Sodium Dodecyl Sulfate for Protein Sample Preparation with Improved Performance in MALDI Mass Spectrometry. Analytical Chemistry, 2002, 74, 1729-1736.	3.2	26
124	Î²-Catenin, a Sox2 binding partner, regulates the DNA binding and transcriptional activity of Sox2 in breast cancer cells. Cellular Signalling, 2014, 26, 492-501.	1.7	26
125	Development and characterization of an electrospray ionization ion trap/linear time-of-flight mass spectrometer. Journal of the American Society for Mass Spectrometry, 1997, 8, 1085-1093.	1.2	25
126	Alzheimerâ€™s Biomarkers From Multiple Modalities Selectively Discriminate Clinical Status: Relative Importance of Salivary Metabolomics Panels, Genetic, Lifestyle, Cognitive, Functional Health and Demographic Risk Markers. Frontiers in Aging Neuroscience, 2018, 10, 296.	1.7	25

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127	Metabolomic profile overlap in prototypical autoimmune humoral disease: a comparison of myasthenia gravis and rheumatoid arthritis. Metabolomics, 2020, 16, 10.	1.4	25
128	Microwave-Assisted Protein Solubilization for Mass Spectrometry-Based Shotgun Proteome Analysis. Analytical Chemistry, 2012, 84, 6181-6191.	3.2	24
129	Photoinduced dissociation of electrospray-generated ions in an ion trap/time-of-flight mass spectrometer using a pulsed CO2 laser. Rapid Communications in Mass Spectrometry, 2002, 16, 1805-1811.	0.7	23
130	Effect of 2MEGA Labeling on Membrane Proteome Analysis Using LC-ESI QTOF MS. Journal of Proteome Research, 2006, 5, 2567-2576.	1.8	23
131	Development of a simple and efficient method of harvesting and lysing adherent mammalian cells for chemical isotope labeling LC-MS-based cellular metabolomics. Analytica Chimica Acta, 2018, 1037, 97-106.	2.6	23
132	Metabolomics Distinguishes DOCK8 Deficiency from Atopic Dermatitis: Towards a Biomarker Discovery. Metabolites, 2019, 9, 274.	1.3	23
133	Effects of matrix-assisted laser desorption/ionization experimental conditions on quantitative compositional analysis of ethylene oxide/propylene oxide copolymers. Rapid Communications in Mass Spectrometry, 2000, 14, 2175-2181.	0.7	22
134	Alteration of Mevalonate Pathway in Proliferated Vascular Smooth Muscle from Diabetic Mice: Possible Role in High-Glucose-Induced Atherogenic Process. Journal of Diabetes Research, 2015, 2015, 1-11.	1.0	22
135	Metabolomic analysis of oxidative stress: Superoxide dismutase mutation and paraquat induced stress in Drosophila melanogaster. Free Radical Biology and Medicine, 2017, 113, 323-334.	1.3	21
136	Development of a NanoLC-MS workflow for high-sensitivity global lipidomic analysis. Analytica Chimica Acta, 2020, 1139, 88-99.	2.6	21
137	Nanoliter Sample Handling Combined with Microspot MALDIâ˜'MS for Detection of Gel-Separated Phosphoproteins. Journal of Proteome Research, 2005, 4, 515-522.	1.8	19
138	Microwave-assisted acid and base hydrolysis of intact proteins containing disulfide bonds for protein sequence analysis by mass spectrometry. Journal of the American Society for Mass Spectrometry, 2010, 21, 1596-1605.	1.2	19
139	Hydrolysis enhances bioavailability of proanthocyanidin-derived metabolites and improves Î²-cell function in glucose intolerant rats. Journal of Nutritional Biochemistry, 2015, 26, 850-859.	1.9	19
140	Development of versatile isotopic labeling reagents for profiling the amine submetabolome by liquid chromatographyâ€"mass spectrometry. Analytica Chimica Acta, 2015, 881, 107-116.	2.6	19
141	Cognitive Enhancement in Infants Associated with Increased Maternal Fruit Intake During Pregnancy: Results from a Birth Cohort Study with Validation in an Animal Model. EBioMedicine, 2016, 8, 331-340.	2.7	19
142	High-Performance Chemical Isotope Labeling Liquid Chromatographyâ€"Mass Spectrometry for Profiling the Metabolomic Reprogramming Elicited by Ammonium Limitation in Yeast. Journal of Proteome Research, 2016, 15, 1602-1612.	1.8	19
143	Dansylation Metabolite Assay: A Simple and Rapid Method for Sample Amount Normalization in Metabolomics. Analytical Chemistry, 2014, 86, 9428-9433.	3.2	18
144	Effects of sample injection amount and time-of-flight mass spectrometric detection dynamic range on metabolome analysis by high-performance chemical isotope labeling LCâ€"MS. Journal of Proteomics, 2015, 118, 130-139.	1.2	18

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145	Matrix effect on chemical isotope labeling and its implication in metabolomic sample preparation for quantitative metabolomics. Metabolomics, 2015, 11, 1733-1742.	1.4	18
146	Chemical Isotope Labeling LC-MS for Monitoring Disease Progression and Treatment in Animal Models: Plasma Metabolomics Study of Osteoarthritis Rat Model. Scientific Reports, 2017, 7, 40543.	1.6	18
147	Development of an ion trap / linear time-of-flight mass spectrometer with electrospray ionization for micro-column liquid chromatography detection. Journal of Separation Science, 1995, 7, 603-610.	1.0	17
148	Laserâ€induced surface ionization in a timeâ€ofâ€flight mass spectrometer. Review of Scientific Instruments, 1995, 66, 55-62.	0.6	17
149	Targeted Quantitative Mass Spectrometric Identification of Differentially Expressed Proteins between Bax-Expressing and Deficient Colorectal Carcinoma Cells. Journal of Proteome Research, 2009, 8, 3403-3414.	1.8	17
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