

Liang Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6867983/publications.pdf>

Version: 2024-02-01

235
papers

14,466
citations

22132

59
h-index

23514

111
g-index

667
all docs

667
docs citations

667
times ranked

16153
citing authors

#	ARTICLE	IF	CITATIONS
1	HMDB: the Human Metabolome Database. <i>Nucleic Acids Research</i> , 2007, 35, D521-D526.	6.5	2,563
2	HMDB: a knowledgebase for the human metabolome. <i>Nucleic Acids Research</i> , 2009, 37, D603-D610.	6.5	1,649
3	Differential ¹² C-/ ¹³ C-Isotope Dansylation Labeling and Fast Liquid Chromatography/Mass Spectrometry for Absolute and Relative Quantification of the Metabolome. <i>Analytical Chemistry</i> , 2009, 81, 3919-3932.	3.2	345
4	Definitions of terms relating to mass spectrometry (IUPAC Recommendations 2013). <i>Pure and Applied Chemistry</i> , 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. <i>Analytical Chemistry</i> , 1996, 68, 2721-2725.	3.2	251
6	Sample normalization methods in quantitative metabolomics. <i>Journal of Chromatography A</i> , 2016, 1430, 80-95.	1.8	211
7	High-Resolution Matrix-Assisted Laser Desorption/Ionization in a Linear Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 1995, 67, 1950-1954.	3.2	194
8	Two-Layer Sample Preparation: A Method for MALDI-MS Analysis of Complex Peptide and Protein Mixtures. <i>Analytical Chemistry</i> , 1999, 71, 1087-1091.	3.2	185
9	MyCompoundID: Using an Evidence-Based Metabolome Library for Metabolite Identification. <i>Analytical Chemistry</i> , 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. <i>Rapid Communications in Mass Spectrometry</i> , 1998, 12, 456-464.	0.7	179
11	High-Performance Isotope Labeling for Profiling Carboxylic Acid-Containing Metabolites in Biofluids by Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 8789-8793.	3.2	161
12	Stable-Isotope Dimethylation Labeling Combined with LC ⁺ ESI MS for Quantification of Amine-Containing Metabolites in Biological Samples. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 1997, 69, 4176-4183.	3.2	148
15	Microwave-assisted acid hydrolysis of proteins combined with liquid chromatography MALDI MS/MS for protein identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 471-481.	1.2	140
16	A New Segmented Virus Associated with Human Febrile Illness in China. <i>New England Journal of Medicine</i> , 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. <i>Angewandte Chemie - International Edition</i> , 1998, 37, 3383-3387.	7.2	129
18	Characterization of Human Tear Proteome Using Multiple Proteomic Analysis Techniques. <i>Journal of Proteome Research</i> , 2005, 4, 2052-2061.	1.8	129

#	ARTICLE	IF	CITATIONS
19	Confocal Fluorescence Microscopic Imaging for Investigating the Analyte Distribution in MALDI Matrices. <i>Analytical Chemistry</i> , 1996, 68, 2494-2500.	3.2	127
20	Protein sequencing by mass analysis of polypeptide ladders after controlled protein hydrolysis. <i>Nature Biotechnology</i> , 2004, 22, 1291-1296.	9.4	118
21	Monocyte lipid rafts contain proteins implicated in vesicular trafficking and phagosome formation. <i>Proteomics</i> , 2003, 3, 536-548.	1.3	117
22	Comparison of SDS- and methanol-assisted protein solubilization and digestion methods for <i>Escherichia coli</i> membrane proteome analysis by 2-D LC-MS/MS. <i>Proteomics</i> , 2007, 7, 484-493.	1.3	117
23	IsoMS: Automated Processing of LC-MS Data Generated by a Chemical Isotope Labeling Metabolomics Platform. <i>Analytical Chemistry</i> , 2014, 86, 4675-4679.	3.2	111
24	A multiomics approach to heterogeneity in Alzheimer's disease: focused review and roadmap. <i>Brain</i> , 2020, 143, 1315-1331.	3.7	106
25	Differential Dimethyl Labeling of N-Termini of Peptides after Guanidination for Proteome Analysis. <i>Journal of Proteome Research</i> , 2005, 4, 2099-2108.	1.8	103
26	DnsID in MyCompoundID for Rapid Identification of Dansylated Amine- and Phenol-Containing Metabolites in LC-MS-Based Metabolomics. <i>Analytical Chemistry</i> , 2015, 87, 9838-9845.	3.2	103
27	Altered Gut Microbial Metabolites in Amnesic Mild Cognitive Impairment and Alzheimer's Disease: Signals in Host-Microbe Interplay. <i>Nutrients</i> , 2021, 13, 228.	1.7	103
28	Detection and identification of low-mass peptides and proteins from solvent suspensions of <i>Escherichia coli</i> by high performance liquid chromatography fractionation and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Proteomics</i> , 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. <i>Analytical Chemistry</i> , 2012, 84, 10723-10731.	3.2	95
33	Development of a Universal Metabolome-Standard Method for Long-Term LC-MS Metabolome Profiling and Its Application for Bladder Cancer Urine-Metabolite-Biomarker Discovery. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 2015, 87, 10619-10626.	3.2	93
35	Chemical derivatization in LC-MS-based metabolomics study. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 131, 115988.	5.8	88
36	Analysis of Single Mammalian Cell Lysates by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1996, 118, 11662-11663.	6.6	88

#	ARTICLE	IF	CITATIONS
37	Development of High-Performance Chemical Isotope Labeling LC-MS for Profiling the Carbonyl Submetabolome. <i>Analytical Chemistry</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 2015, 87, 1306-1313.	3.2	80
41	Proteome of the Escherichia coli envelope and technological challenges in membrane proteome analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008, 1778, 1698-1713.	1.4	79
42	Development of Mass Spectrometry-Based Shotgun Method for Proteome Analysis of 500 to 5000 Cancer Cells. <i>Analytical Chemistry</i> , 2010, 82, 2262-2271.	3.2	76
43	Time-Lag Focusing MALDI Time-of-Flight Mass Spectrometry for Polymer Characterization: Oligomer Resolution, Mass Accuracy, and Average Weight Information. <i>Analytical Chemistry</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 88-93.	1.2	75
45	Exploring the Precursor Ion Exclusion Feature of Liquid Chromatography-Electrospray Ionization Quadrupole Time-of-Flight Mass Spectrometry for Improving Protein Identification in Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 2008, 80, 4696-4710.	3.2	75
46	Development of Isotope Labeling LC-MS for Human Salivary Metabolomics and Application to Profiling Metabolome Changes Associated with Mild Cognitive Impairment. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Journal of Biological Chemistry</i> , 2007, 282, 6292-6299.	1.6	73
49	High-Performance Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry for Exosome Metabolomics. <i>Analytical Chemistry</i> , 2018, 90, 8314-8319.	3.2	72
50	Microbial metabolites in the marine carbon cycle. <i>Nature Microbiology</i> , 2022, 7, 508-523.	5.9	71
51	Proteome Profile of Cytosolic Component of Zebrafish Liver Generated by LC-ESI MS/MS Combined with Trypsin Digestion and Microwave-Assisted Acid Hydrolysis. <i>Journal of Proteome Research</i> , 2007, 6, 263-272.	1.8	69
52	Profiling novel metabolic biomarkers for Parkinson's disease using in-depth metabolomic analysis. <i>Movement Disorders</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 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. <i>Analytical Chemistry</i> , 2017, 89, 11664-11671.	3.2	67

#	ARTICLE	IF	CITATIONS
55	Development of High-Performance Chemical Isotope Labeling LC-MS for Profiling the Human Fecal Metabolome. <i>Analytical Chemistry</i> , 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. <i>Journal of Hazardous Materials</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1055-1063.	1.2	64
58	Liquid Chromatography MALDI MS/MS for Membrane Proteome Analysis. <i>Journal of Proteome Research</i> , 2004, 3, 719-727.	1.8	64
59	Quantitative Metabolome Analysis Based on Chromatographic Peak Reconstruction in Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 7011-7016.	3.2	63
60	Quantitative Proteome Analysis Using Differential Stable Isotopic Labeling and Microbore LC-MALDI MS and MS/MS. <i>Journal of Proteome Research</i> , 2005, 4, 734-742.	1.8	62
61	Metabolomics Analyses of Saliva Detect Novel Biomarkers of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 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. <i>Journal of Proteome Research</i> , 2003, 2, 543-552.	1.8	60
64	Nanoliter Chemistry Combined with Mass Spectrometry for Peptide Mapping of Proteins from Single Mammalian Cell Lysates. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 2016, 88, 2637-2644.	3.2	57
67	Laser desorption ionization and MALDI time-of-flight mass spectrometry for low molecular mass polyethylene analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1186-1192.	1.2	56
68	Ultra-high performance liquid chromatography tandem mass spectrometry for comprehensive analysis of urinary acylcarnitines. <i>Analytica Chimica Acta</i> , 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. <i>Analytical Chemistry</i> , 2009, 81, 1049-1060.	3.2	54
70	Matrix-assisted laser desorption ionization time-of-flight mass spectrometry for the analysis of polydienes. <i>Journal of the American Society for Mass Spectrometry</i> , 1997, 8, 1220-1229.	1.2	51
71	Combining Liquid Chromatography with MALDI Mass Spectrometry Using a Heated Droplet Interface. <i>Analytical Chemistry</i> , 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. <i>Analytical Chemistry</i> , 2013, 85, 11532-11539.	3.2	49

#	ARTICLE	IF	CITATIONS
73	Qualitative Metabolome Analysis of Human Cerebrospinal Fluid by ¹³ C-/ ¹² C-Isotope Dansylation Labeling Combined with Liquid Chromatography Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 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 Alzheimer's Disease. <i>Journal of Proteome Research</i> , 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. <i>Macromolecular Rapid Communications</i> , 1996, 17, 59-64.	2.0	47
76	Dansylhydrazine Isotope Labeling LC-MS for Comprehensive Carboxylic Acid Submetabolome Profiling. <i>Analytical Chemistry</i> , 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. <i>Zebrafish</i> , 2009, 6, 229-238.	0.5	45
78	Reactions of atomic transition-metal ions with long-chain alkanes. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 367-375.	1.2	43
79	Distinctive Metabolomics Patterns Associated With Insulin Resistance and Type 2 Diabetes Mellitus. <i>Frontiers in Molecular Biosciences</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 55-60.	1.2	42
81	Evaluating and minimizing batch effects in metabolomics. <i>Mass Spectrometry Reviews</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 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. <i>Analytica Chimica Acta</i> , 2011, 698, 36-43.	2.6	41
84	Liquid-liquid extraction combined with differential isotope dimethylaminophenacyl labeling for improved metabolomic profiling of organic acids. <i>Analytica Chimica Acta</i> , 2013, 803, 97-105.	2.6	41
85	Comprehensive and Quantitative Profiling of the Human Sweat Submetabolome Using High-Performance Chemical Isotope Labeling LC-MS. <i>Analytical Chemistry</i> , 2016, 88, 7378-7386.	3.2	41
86	Three-layer matrix/sample preparation method for MALDI MS analysis of low nanomolar protein samples. <i>Journal of the American Society for Mass Spectrometry</i> , 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. <i>Macromolecules</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 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, LC-MALDI MS and MS/MS. <i>Journal of Proteome Research</i> , 2005, 4, 1419-1426.	1.8	39
90	High glucose promotes gastric cancer chemoresistance in vivo and in vitro. <i>Molecular Medicine Reports</i> , 2015, 12, 843-850.	1.1	39

#	ARTICLE	IF	CITATIONS
91	Parallel Metabolomic Profiling of Cerebrospinal Fluid and Serum for Identifying Biomarkers of Injury Severity after Acute Human Spinal Cord Injury. <i>Scientific Reports</i> , 2016, 6, 38718.	1.6	38
92	Development of Isotope Labeling Liquid Chromatography–Mass Spectrometry for Metabolic Profiling of Bacterial Cells and Its Application for Bacterial Differentiation. <i>Analytical Chemistry</i> , 2013, 85, 5755-5763.	3.2	37
93	Combining Avidin–Biotin Chemistry with Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 1996, 68, 3382-3387.	3.2	36
94	Ion-pairing reversed-phase liquid chromatography fractionation in combination with isotope labeling reversed-phase liquid chromatography–mass spectrometry for comprehensive metabolome profiling. <i>Journal of Chromatography A</i> , 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. <i>Cell Reports</i> , 2014, 7, 565-574.	2.9	36
96	Elevated acetyl–CoA by amino acid recycling fuels microalgal neutral lipid accumulation in exponential growth phase for biofuel production. <i>Plant Biotechnology Journal</i> , 2017, 15, 497-509.	4.1	36
97	Nanoliter Solvent Extraction Combined with Microspot MALDI TOF Mass Spectrometry for the Analysis of Hydrophobic Biomolecules. <i>Analytical Chemistry</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 2105-2116.	1.2	35
99	Dexamethasone-Induced Perturbations in Tissue Metabolomics Revealed by Chemical Isotope Labeling LC-MS Analysis. <i>Metabolites</i> , 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. <i>Journal of Proteome Research</i> , 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. <i>Analytical Chemistry</i> , 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. <i>Analytica Chimica Acta</i> , 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. <i>Analytica Chimica Acta</i> , 2012, 750, 161-172.	2.6	32
104	Nonocclusive Sweat Collection Combined with Chemical Isotope Labeling LC–MS for Human Sweat Metabolomics and Mapping the Sweat Metabolomes at Different Skin Locations. <i>Analytical Chemistry</i> , 2017, 89, 7847-7851.	3.2	32
105	Photo-induced dissociation of electrospray generated ions in an ion trap/time-of-flight mass spectrometer. <i>Review of Scientific Instruments</i> , 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. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 782, 317-329.	1.2	31
107	Simple and Robust Two-Layer Matrix/Sample Preparation Method for MALDI MS/MS Analysis of Peptides. <i>Journal of Proteome Research</i> , 2005, 4, 1709-1716.	1.8	30
108	Chronic inhibition of farnesyl pyrophosphate synthase attenuates cardiac hypertrophy and fibrosis in spontaneously hypertensive rats. <i>Biochemical Pharmacology</i> , 2010, 79, 399-406.	2.0	30

#	ARTICLE	IF	CITATIONS
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. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1573-1587.	1.2	30
110	Nanoflow LC-MS for High-Performance Chemical Isotope Labeling Quantitative Metabolomics. <i>Analytical Chemistry</i> , 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. <i>Journal of Chromatography A</i> , 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. <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Analytical Chemistry</i> , 2000, 72, 3847-3852.	3.2	29
114	Comparative Proteomic and Metabolomic Analysis of <i>Staphylococcus warneri</i> SG1 Cultured in the Presence and Absence of Butanol. <i>Journal of Proteome Research</i> , 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. <i>Scientific Reports</i> , 2016, 6, 32272.	1.6	29
116	Dansylation isotope labeling liquid chromatography mass spectrometry for parallel profiling of human urinary and fecal submetabolomes. <i>Analytica Chimica Acta</i> , 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. <i>Analytica Chimica Acta</i> , 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. <i>Analytical Chemistry</i> , 2014, 86, 3568-3574.	3.2	28
119	Overcoming Sample Matrix Effect in Quantitative Blood Metabolomics Using Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 9424-9431.	3.2	28
120	Brain Transforming Growth Factor- β 2 Resists Hypertension Via Regulating Microglial Activation. <i>Stroke</i> , 2017, 48, 2557-2564.	1.0	28
121	MALDI Mass Spectrometry Combined with Avidin-Biotin Chemistry for Analysis of Protein Modifications. <i>Analytical Chemistry</i> , 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. <i>Analytica Chimica Acta</i> , 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. <i>Analytical Chemistry</i> , 2002, 74, 1729-1736.	3.2	26
124	β -Catenin, a Sox2 binding partner, regulates the DNA binding and transcriptional activity of Sox2 in breast cancer cells. <i>Cellular Signalling</i> , 2014, 26, 492-501.	1.7	26
125	Development and characterization of an electrospray ionization ion trap/linear time-of-flight mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 1997, 8, 1085-1093.	1.2	25
126	Alzheimer's Biomarkers From Multiple Modalities Selectively Discriminate Clinical Status: Relative Importance of Salivary Metabolomics Panels, Genetic, Lifestyle, Cognitive, Functional Health and Demographic Risk Markers. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 296.	1.7	25

#	ARTICLE	IF	CITATIONS
127	Metabolomic profile overlap in prototypical autoimmune humoral disease: a comparison of myasthenia gravis and rheumatoid arthritis. <i>Metabolomics</i> , 2020, 16, 10.	1.4	25
128	Microwave-Assisted Protein Solubilization for Mass Spectrometry-Based Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 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 CO ₂ laser. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 1805-1811.	0.7	23
130	Effect of 2MEGA Labeling on Membrane Proteome Analysis Using LC-ESI QTOF MS. <i>Journal of Proteome Research</i> , 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. <i>Analytica Chimica Acta</i> , 2018, 1037, 97-106.	2.6	23
132	Metabolomics Distinguishes DOCK8 Deficiency from Atopic Dermatitis: Towards a Biomarker Discovery. <i>Metabolites</i> , 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. <i>Rapid Communications in Mass Spectrometry</i> , 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. <i>Journal of Diabetes Research</i> , 2015, 2015, 1-11.	1.0	22
135	Metabolomic analysis of oxidative stress: Superoxide dismutase mutation and paraquat induced stress in <i>Drosophila melanogaster</i> . <i>Free Radical Biology and Medicine</i> , 2017, 113, 323-334.	1.3	21
136	Development of a NanoLC-MS workflow for high-sensitivity global lipidomic analysis. <i>Analytica Chimica Acta</i> , 2020, 1139, 88-99.	2.6	21
137	Nanoliter Sample Handling Combined with Microspot MALDI-MS for Detection of Gel-Separated Phosphoproteins. <i>Journal of Proteome Research</i> , 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. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1596-1605.	1.2	19
139	Hydrolysis enhances bioavailability of proanthocyanidin-derived metabolites and improves β -cell function in glucose intolerant rats. <i>Journal of Nutritional Biochemistry</i> , 2015, 26, 850-859.	1.9	19
140	Development of versatile isotopic labeling reagents for profiling the amine submetabolome by liquid chromatography-mass spectrometry. <i>Analytica Chimica Acta</i> , 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. <i>EBioMedicine</i> , 2016, 8, 331-340.	2.7	19
142	High-Performance Chemical Isotope Labeling Liquid Chromatography-Mass Spectrometry for Profiling the Metabolomic Reprogramming Elicited by Ammonium Limitation in Yeast. <i>Journal of Proteome Research</i> , 2016, 15, 1602-1612.	1.8	19
143	Dansylation Metabolite Assay: A Simple and Rapid Method for Sample Amount Normalization in Metabolomics. <i>Analytical Chemistry</i> , 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 LC-MS. <i>Journal of Proteomics</i> , 2015, 118, 130-139.	1.2	18

#	ARTICLE	IF	CITATIONS
145	Matrix effect on chemical isotope labeling and its implication in metabolomic sample preparation for quantitative metabolomics. <i>Metabolomics</i> , 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. <i>Scientific Reports</i> , 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. <i>Journal of Separation Science</i> , 1995, 7, 603-610.	1.0	17
148	Laser-induced surface ionization in a time-of-flight mass spectrometer. <i>Review of Scientific Instruments</i> , 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. <i>Journal of Proteome Research</i> , 2009, 8, 3403-3414.	1.8	17
150	Accurate Mass Measurement of Oligonucleotides Using a Time-lag Focusing Matrix-assisted Laser Desorption/Ionization Time-of-flight Mass Spectrometer. , 1996, 10, 1792-1796.		16
151	Metabolomic profiling of bronchoalveolar lavage fluids by isotope labeling liquid chromatography mass spectrometry: a promising approach to studying experimental asthma. <i>Metabolomics</i> , 2014, 10, 1305-1317.	1.4	16
152	Downregulation of PDCD4 by miR-21 suppresses tumor transformation and proliferation in a nude mouse renal cancer model. <i>Oncology Letters</i> , 2017, 14, 3371-3378.	0.8	16
153	Lipidome Alterations Induced by Cystic Fibrosis, CFTR Mutation, and Lung Function. <i>Journal of Proteome Research</i> , 2021, 20, 549-564.	1.8	16
154	Obesity Connected Metabolic Changes in Type 2 Diabetic Patients Treated With Metformin. <i>Frontiers in Pharmacology</i> , 2020, 11, 616157.	1.6	16
155	Metabolomic and Immunological Profiling of Respiratory Syncytial Virus Infection after Intranasal Immunization with a Subunit Vaccine Candidate. <i>Journal of Proteome Research</i> , 2019, 18, 1145-1161.	1.8	15
156	Controlling Preanalytical Process in High-Coverage Quantitative Metabolomics: Spot-Sample Collection for Mouse Urine and Fecal Metabolome Profiling. <i>Analytical Chemistry</i> , 2019, 91, 4958-4963.	3.2	15
157	Distinctive metabolic profiles between Cystic Fibrosis mutational subclasses and lung function. <i>Metabolomics</i> , 2021, 17, 4.	1.4	15
158	Metabolomic study of stress responses leading to plant resistance in mandarin fruit mediated by preventive applications of <i>Bacillus subtilis</i> cyclic lipopeptides. <i>Postharvest Biology and Technology</i> , 2019, 156, 110946.	2.9	14
159	Effects of Freeze-Thaw Cycles of Blood Samples on High-Coverage Quantitative Metabolomics. <i>Analytical Chemistry</i> , 2020, 92, 9265-9272.	3.2	14
160	Comprehensive Serum Lipidomics for Detecting Incipient Dementia in Parkinson's Disease. <i>Journal of Proteome Research</i> , 2021, 20, 4053-4067.	1.8	14
161	Liquid chromatography electrospray ionization and matrix-assisted laser desorption ionization tandem mass spectrometry for the analysis of lipid raft proteome of monocytes. <i>Analytica Chimica Acta</i> , 2008, 627, 82-90.	2.6	13
162	Proteome Profile of Human Breast Cancer Tissue Generated by LC-ESI-MS/MS Combined with Sequential Protein Precipitation and Solubilization. <i>Journal of Proteome Research</i> , 2008, 7, 3583-3590.	1.8	13

#	ARTICLE	IF	CITATIONS
163	Strategy of using microsome-based metabolite production to facilitate the identification of endogenous metabolites by liquid chromatography mass spectrometry. <i>Analytica Chimica Acta</i> , 2011, 685, 36-44.	2.6	13
164	Chemical-Vapor-Assisted Electrospray Ionization for Increasing Analyte Signals in Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 331-335.	3.2	13
165	Surface Analysis of Bulk Polymers Using Laser-Induced Photoelectron Ionization with Laser Desorption in a Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 1996, 68, 250-256.	3.2	12
166	Investigation of the applicability of a sequential digestion protocol using trypsin and leucine aminopeptidase M for protein identification by matrix-assisted laser desorption/ionization - time of flight mass spectrometry. <i>Proteomics</i> , 2001, 1, 987-1000.	1.3	12
167	Limited proteolysis combined with isotope labeling and quantitative LC-MALDI MS for monitoring protein conformational changes: a study on calcium-binding sites of cardiac Troponin C. <i>Analytica Chimica Acta</i> , 2005, 534, 3-10.	2.6	12
168	A study of reproducibility of guanidination ¹⁸ dimethylation labeling and liquid chromatography matrix-assisted laser desorption ionization mass spectrometry for relative proteome quantification. <i>Analytica Chimica Acta</i> , 2007, 585, 219-226.	2.6	12
169	MMP ² inhibits PCSK9 ⁹ induced degradation of the LDL receptor in Hepa1 ^{1c7} cells. <i>FEBS Letters</i> , 2015, 589, 490-496.	1.3	12
170	Structure and proteolytic susceptibility of the inhibitory C-terminal tail of cardiac troponin I. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 661-671.	1.1	12
171	Beyond the antibodies: serum metabolomic profiling of myasthenia gravis. <i>Metabolomics</i> , 2019, 15, 109.	1.4	11
172	MSC-triggered metabolomic alterations in liver-resident immune cells isolated from CCl4-induced mouse ALI model. <i>Experimental Cell Research</i> , 2019, 383, 111511.	1.2	11
173	Comprehensive Lipidomic and Metabolomic Analysis for Studying Metabolic Changes in Lung Tissue Induced by a Vaccine against Respiratory Syncytial Virus. <i>ACS Infectious Diseases</i> , 2020, 6, 2130-2142.	1.8	11
174	Tissue Lipidomic Alterations Induced by Prolonged Dexamethasone Treatment. <i>Journal of Proteome Research</i> , 2021, 20, 1558-1570.	1.8	11
175	Cerebrospinal Fluid Metabolomics After Natural Product Treatment in an Experimental Model of Cerebral Ischemia. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 670-680.	1.0	10
176	Impact of Oxygen Concentration on Metabolic Profile of Human Placenta-Derived Mesenchymal Stem Cells As Determined by Chemical Isotope Labeling LC ¹⁸ MS. <i>Journal of Proteome Research</i> , 2018, 17, 1866-1878.	1.8	10
177	Chemical Isotope Labeling LC-MS for Human Blood Metabolome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1730, 213-225.	0.4	10
178	Dissociation of protonated phenylthiohydantoin-amino acids and phenylthiocarbamoyl-dipeptides. <i>Journal of Mass Spectrometry</i> , 1998, 33, 543-553.	0.7	9
179	Fragmentation of protonated dansyl-labeled amines for structural analysis of amine-containing metabolites. <i>International Journal of Mass Spectrometry</i> , 2012, 316-318, 292-299.	0.7	9
180	Development of microwave-assisted acid hydrolysis of proteins using a commercial microwave reactor and its combination with LC ¹⁸ MS for protein full-sequence analysis. <i>Talanta</i> , 2014, 129, 290-295.	2.9	9

#	ARTICLE	IF	CITATIONS
181	Development of chemical isotope labeling liquid chromatography mass spectrometry for silkworm hemolymph metabolomics. <i>Analytica Chimica Acta</i> , 2016, 942, 1-11.	2.6	9
182	Targeting amine- and phenol-containing metabolites in urine by dansylation isotope labeling and liquid chromatography mass spectrometry for evaluation of bladder cancer biomarkers. <i>Journal of Food and Drug Analysis</i> , 2019, 27, 460-474.	0.9	9
183	Activation of the Na ⁺ /H ⁺ exchanger in isolated cardiomyocytes through \hat{I}^2 -Raf dependent pathways. Role of Thr653 of the cytosolic tail. <i>Journal of Molecular and Cellular Cardiology</i> , 2016, 99, 65-75.	0.9	8
184	Reversible Covalent Reaction of Levosimendan with Cardiac Troponin C <i>in Vitro</i> and <i>in Situ</i> . <i>Biochemistry</i> , 2018, 57, 2256-2265.	1.2	8
185	The effect of using silicon based diffusion pump fluid on spectral quality in an electrospray ionization ion trap/time-of-flight mass spectrometer. <i>Review of Scientific Instruments</i> , 1997, 68, 3252-3253.	0.6	7
186	Quantitative proteomic analysis of HER2 normal and overexpressing MCF-7 breast cancer cells revealed proteomic changes accompanied with HER2 gene amplification. <i>Journal of Proteomics</i> , 2013, 91, 200-209.	1.2	7
187	Automation of dimethylation after guanidination labeling chemistry and its compatibility with common buffers and surfactants for mass spectrometry-based shotgun quantitative proteome analysis. <i>Analytica Chimica Acta</i> , 2013, 788, 81-88.	2.6	7
188	Impact of Low-Intensity Pulsed Ultrasound on Transcript and Metabolite Abundance in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2017, 16, 2975-2982.	1.8	7
189	The Impact of GFP Reporter Gene Transduction and Expression on Metabolomics of Placental Mesenchymal Stem Cells Determined by UHPLC-Q/TOF-MS. <i>Stem Cells International</i> , 2017, 2017, 1-12.	1.2	7
190	Bretschneider solution-induced alterations in the urine metabolome in cardiac surgery patients. <i>Scientific Reports</i> , 2018, 8, 17774.	1.6	7
191	Metabolic profiling associated with autophagy of human placenta-derived mesenchymal stem cells by chemical isotope labeling LC-MS. <i>Experimental Cell Research</i> , 2018, 372, 52-60.	1.2	7
192	Comprehensive Metabolomic Comparison of Five Cereal Vinegars Using Non-Targeted and Chemical Isotope Labeling LC-MS Analysis. <i>Metabolites</i> , 2022, 12, 427.	1.3	7
193	High-Coverage Quantitative Metabolomics of Human Urine: Effects of Freeze-Thaw Cycles on the Urine Metabolome and Biomarker Discovery. <i>Analytical Chemistry</i> , 2022, 94, 9880-9887.	3.2	7
194	Benefit of microwave-assisted acid hydrolysis of proteins for mass spectrometric profiling of the human heart tissue proteome. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2779-2783.	0.7	6
195	Microwave-assisted acid hydrolysis of proteins combined with peptide fractionation and mass spectrometry analysis for characterizing protein terminal sequences. <i>Journal of Proteomics</i> , 2014, 100, 68-78.	1.2	6
196	High-performance isotope-labeling liquid chromatography mass spectrometry for investigating the effect of drinking Goji tea on urine metabolome profiling. <i>Science China Chemistry</i> , 2014, 57, 678-685.	4.2	6
197	Chemical isotope labeling liquid chromatography mass spectrometry for investigating acute dietary effects of cow milk consumption on human urine metabolome. <i>Journal of Food and Drug Analysis</i> , 2019, 27, 565-574.	0.9	6
198	Retention time shift analysis and correction in chemical isotope labeling liquid chromatography/mass spectrometry for metabolome analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8643.	0.7	6

#	ARTICLE	IF	CITATIONS
199	Endoplasmic reticulum stress/XBP1 promotes airway mucin secretion under the influence of neutrophil elastase. <i>International Journal of Molecular Medicine</i> , 2021, 47, .	1.8	6
200	Metabolomics Profiling of Cystic Renal Disease towards Biomarker Discovery. <i>Biology</i> , 2021, 10, 770.	1.3	6
201	Quantitative Metabolomic Profiling Using Dansylation Isotope Labeling and Liquid Chromatography Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2014, 1198, 127-136.	0.4	6
202	Development of a High-Coverage Quantitative Metabolome Analysis Method Using Four-Channel Chemical Isotope Labeling LC-MS for Analyzing High-Salt Fermented Food. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 8827-8837.	2.4	6
203	Differential isotope dansylation labeling combined with liquid chromatography mass spectrometry for quantification of intact and N-terminal truncated proteins. <i>Analytica Chimica Acta</i> , 2013, 792, 79-85.	2.6	5
204	In-Gel Microwave-Assisted Acid Hydrolysis of Proteins Combined with Liquid Chromatography Tandem Mass Spectrometry for Mapping Protein Sequences. <i>Analytical Chemistry</i> , 2014, 86, 600-607.	3.2	5
205	Identification of ABC transporters acting in vitamin B 12 metabolism in <i>Caenorhabditis elegans</i> . <i>Molecular Genetics and Metabolism</i> , 2017, 122, 160-171.	0.5	5
206	Mass Accuracy Check Using Common Background Peaks for Improving Metabolome Data Quality in Chemical Isotope Labeling LC-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1733-1741.	1.2	5
207	Development of a matrix-assisted laser desorption ionization mass spectrometric method for rapid process-monitoring of phthalocyanine compounds. <i>Analytica Chimica Acta</i> , 2012, 736, 69-77.	2.6	4
208	Thioimidate Bond Formation between Cardiac Troponin C and Nitrile-containing Compounds. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1007-1012.	1.3	4
209	High-Coverage Metabolome Analysis Reveals Significant Diet Effects of Autoclaved and Irradiated Feed on Mouse Fecal and Urine Metabolomics. <i>Molecular Nutrition and Food Research</i> , 2021, 65, 2100110.	1.5	4
210	Evidence for copurification of micronuclei in sucrose density gradient-enriched plasma membranes from cell lines. <i>Analytical Biochemistry</i> , 2010, 396, 69-75.	1.1	3
211	Macroporous reversed-phase separation of proteins combined with reversed-phase separation of phosphopeptides and tandem mass spectrometry for profiling the phosphoproteome of MDA-MB-231 cells. <i>Electrophoresis</i> , 2014, 35, 3479-3486.	1.3	3
212	The Biochemical Markers Associated with the Occurrence of Coronary Spasm. <i>BioMed Research International</i> , 2019, 2019, 1-8.	0.9	3
213	Chemical Isotope Labeling LC-MS for Metabolomics. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1280, 1-18.	0.8	3
214	Normalization of Samples of Limited Amounts in Quantitative Metabolomics Using Liquid Chromatography Fluorescence Detection with Dansyl Labeling of Metabolites. <i>Analytical Chemistry</i> , 2021, 93, 3418-3425.	3.2	3
215	Investigation of spectral reproducibility in direct analysis of bacteria proteins by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1998, 12, 456-464.	0.7	3
216	A Dual Ionization Source with Laser Desorption Sample Introduction in a Time-of-Flight Mass Spectrometer. <i>Instrumentation Science and Technology</i> , 1995, 23, 317-328.	0.9	2

#	ARTICLE	IF	CITATIONS
217	Identification and Quantification of Differentially Expressed Proteins in E-Cadherin Deficient SCC9 Cells and SCC9 Transfectants Expressing E-Cadherin by Dimethyl Isotope Labeling, LC-MALDI MS and MS/MSJ. <i>Proteome Res.</i> 2005,4, 1419-1426. <i>Journal of Proteome Research</i> , 2005, 4, 1872-1872.	1.8	2
218	Improving accuracy of peak-pair intensity ratio measurement in differential chemical isotope labeling LC-MS for quantitative metabolomics. <i>International Journal of Mass Spectrometry</i> , 2018, 434, 202-208.	0.7	2
219	MALDI-MS for Polymer Characterization. , 0, , 245-297.		1
220	Analytical performance of reciprocal isotope labeling of proteome digests for quantitative proteomics and its application for comparative studies of aerobic and anaerobic <i>Escherichia coli</i> proteomes. <i>Analytica Chimica Acta</i> , 2013, 795, 25-35.	2.6	1
221	Microbore liquid chromatography ultraviolet detection for quantification of total peptide amount and its application for assessing sample quality in shotgun proteome analysis of hundreds of cells. <i>Journal of Chromatography A</i> , 2014, 1338, 51-57.	1.8	1
222	Characterizing the effects of hypoxia on the metabolic profiles of mesenchymal stromal cells derived from three tissue sources using chemical isotope labeling liquid chromatography-mass spectrometry. <i>Cell and Tissue Research</i> , 2020, 380, 79-91.	1.5	1
223	High tolerance to instrument drifts by differential chemical isotope labeling LC-MS: A case study of the effect of LC leak in long-term sample runs on quantitative metabolome analysis. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4589.	0.7	1
224	High-coverage quantitative liver metabolomics using perfused and non-perfused liver tissues. <i>Analytica Chimica Acta</i> , 2021, 1153, 338300.	2.6	1
225	Metabolic profile of irradiated whole blood by chemical isotope-labeling liquid chromatography-mass spectrometry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 204, 114247.	1.4	1
226	Investigation of spectral reproducibility in direct analysis of bacteria proteins by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. , 1998, 12, 456.		1
227	Detection and identification of low-mass peptides and proteins from solvent suspensions of <i>Escherichia coli</i> by high performance liquid chromatography fractionation and matrix-assisted laser desorption/ionization mass spectrometry. , 1999, 13, 73.		1
228	Detection and identification of low-mass peptides and proteins from solvent suspensions of <i>Escherichia coli</i> by high performance liquid chromatography fractionation and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1999, 13, 73-78.	0.7	1
229	Liquid Chromatography MALDI MS/MS for Membrane Proteome Analysis. <i>Methods in Molecular Biology</i> , 2009, 528, 295-310.	0.4	1
230	Development of a method for dansylation of metabolites using organic solvent-compatible buffer systems for amine/phenol submetabolome analysis. <i>Analytica Chimica Acta</i> , 2022, 1189, 339218.	2.6	1
231	Potential Urinary Biomarkers of Young Adults With Short-Term Co-Exposure to Particulate Matter and Bioaerosols in a Time Course Identified by an Unbiased Metabolomic Approach With Gas/Liquid Chromatography-Mass Spectroscopy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
232	Non-surgical management of an abrupt cavitation and large oval-shaped lung abscess secondary to acute thromboembolic pulmonary infarction: a case report. <i>Journal of International Medical Research</i> , 2021, 49, 030006052110316.	0.4	0
233	Comprehensive proteome profile of the zebrafish (<i>Danio rerio</i>) gill: applications to physiological and biomarker discovery studies. <i>FASEB Journal</i> , 2009, 23, 629.4.	0.2	0
234	Chemical Analysis. , 0, , 301-305.		0

#	ARTICLE	IF	CITATIONS
235	Metabolomics of Small Numbers of Cells Using Chemical Isotope Labeling Combined with Nanoflow LC-MS. <i>Neuromethods</i> , 2021, , 49-60.	0.2	0