

# Liang Li

## List of Publications by Citations

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244  
papers

11,630  
citations

54  
h-index

102  
g-index

667  
ext. papers

13,182  
ext. citations

6.1  
avg, IF

6.5  
L-index

#	Paper	IF	Citations
244	HMDB: the Human Metabolome Database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D521-6	20.1	2021
243	HMDB: a knowledgebase for the human metabolome. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D603-10	20.1	1431
242	Differential <sup>12</sup> C-/ <sup>13</sup> C-isotope dansylation labeling and fast liquid chromatography/mass spectrometry for absolute and relative quantification of the metabolome. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 3919-32	7.8	301
241	Definitions of terms relating to mass spectrometry (IUPAC Recommendations 2013). <i>Pure and Applied Chemistry</i> , <b>2013</b> , 85, 1515-1609	2.1	238
240	Detection of High Molecular Weight Narrow Polydisperse Polymers up to 1.5 Million Daltons by MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , <b>1996</b> , 68, 2721-5	7.8	225
239	High-resolution matrix-assisted laser desorption/ionization in a linear time-of-flight mass spectrometer. <i>Analytical Chemistry</i> , <b>1995</b> , 67, 1950-4	7.8	178
238	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> , <b>1998</b> , 12, 456-64	2.2	167
237	Two-layer sample preparation: a method for MALDI-MS analysis of complex peptide and protein mixtures. <i>Analytical Chemistry</i> , <b>1999</b> , 71, 1087-91	7.8	167
236	Sample normalization methods in quantitative metabolomics. <i>Journal of Chromatography A</i> , <b>2016</b> , 1430, 80-95	4.5	158
235	MyCompoundID: using an evidence-based metabolome library for metabolite identification. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 3401-8	7.8	143
234	High-performance isotope labeling for profiling carboxylic acid-containing metabolites in biofluids by mass spectrometry. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 8789-93	7.8	140
233	Stable-isotope dimethylation labeling combined with LC-ESI MS for quantification of amine-containing metabolites in biological samples. <i>Analytical Chemistry</i> , <b>2007</b> , 79, 8631-8	7.8	139
232	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> , <b>1997</b> , 69, 4169-4175	7.8	137
231	Mass Discrimination in the Analysis of Polydisperse Polymers by MALDI Time-of-Flight Mass Spectrometry. 2. Instrumental Issues. <i>Analytical Chemistry</i> , <b>1997</b> , 69, 4176-4183	7.8	137
230	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> , <b>2005</b> , 16, 471-81 <sup>3.5</sup>	7.5	127
229	Confocal Fluorescence Microscopic Imaging for Investigating the Analyte Distribution in MALDI Matrices. <i>Analytical Chemistry</i> , <b>1996</b> , 68, 2494-500	7.8	118
228	Characterization of human tear proteome using multiple proteomic analysis techniques. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 2052-61	5.6	117

227	Micro-Scale Frontal Affinity Chromatography with Mass Spectrometric Detection: A New Method for the Screening of Compound Libraries. <i>Angewandte Chemie - International Edition</i> , <b>1998</b> , 37, 3383-3387	16.4	112
226	Monocyte lipid rafts contain proteins implicated in vesicular trafficking and phagosome formation. <i>Proteomics</i> , <b>2003</b> , 3, 536-48	4.8	111
225	Protein sequencing by mass analysis of polypeptide ladders after controlled protein hydrolysis. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1291-6	44.5	109
224	Comparison of SDS- and methanol-assisted protein solubilization and digestion methods for Escherichia coli membrane proteome analysis by 2-D LC-MS/MS. <i>Proteomics</i> , <b>2007</b> , 7, 484-493	4.8	107
223	Differential dimethyl labeling of N-termini of peptides after guanidination for proteome analysis. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 2099-108	5.6	99
222	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> , <b>2004</b> , 4, 3156-66	4.8	96
221	Detection and identification of low-mass peptides and proteins from solvent suspensions of Escherichia coli by high performance liquid chromatography fractionation and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>1999</b> , 13, 73-8	2.2	90
220	IsoMS: automated processing of LC-MS data generated by a chemical isotope labeling metabolomics platform. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 4675-9	7.8	86
219	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> , <b>2004</b> , 18, 889-96	2.2	82
218	MyCompoundID MS/MS Search: Metabolite Identification Using a Library of Predicted Fragment-Ion-Spectra of 383,830 Possible Human Metabolites. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 10619-26	7.8	78
217	DnsID in MyCompoundID for rapid identification of dansylated amine- and phenol-containing metabolites in LC-MS-based metabolomics. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 9838-45	7.8	78
216	Analysis of Single Mammalian Cell Lysates by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , <b>1996</b> , 118, 11662-11663	16.4	78
215	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> , <b>2014</b> , 86, 6540-7	7.8	76
214	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> , <b>2012</b> , 84, 10723-31	7.8	76
213	Protein concentration and enzyme digestion on microbeads for MALDI-TOF peptides mass mapping of proteins from dilute solutions. <i>Analytical Chemistry</i> , <b>2000</b> , 72, 3355-62	7.8	76
212	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> , <b>1998</b> , 9, 275-81	3.5	74
211	Development of mass spectrometry-based shotgun method for proteome analysis of 500 to 5000 cancer cells. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 2262-71	7.8	70
210	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> , <b>2008</b> , 80, 4696-710	7.8	70

209	Proteome of the Escherichia coli envelope and technological challenges in membrane proteome analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>2008</b> , 1778, 1698-713	3.8	68
208	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> , <b>2000</b> , 11, 88-93	3.5	67
207	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> , <b>2012</b> , 84, 10802-11	7.8	66
206	Time-lag focusing MALDI time-of-flight mass spectrometry for polymer characterization: oligomer resolution, mass accuracy, and average weight information. <i>Analytical Chemistry</i> , <b>1997</b> , 69, 2734-41	7.8	66
205	Development of High-Performance Chemical Isotope Labeling LC-MS for Profiling the Carbonyl Submetabolome. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 6758-6765	7.8	64
204	Mitogen-activated protein kinase-dependent activation of the Na <sup>+</sup> /H <sup>+</sup> exchanger is mediated through phosphorylation of amino acids Ser770 and Ser771. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 6292-9	5.4	64
203	A New Segmented Virus Associated with Human Febrile Illness in China. <i>New England Journal of Medicine</i> , <b>2019</b> , 380, 2116-2125	59.2	63
202	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> , <b>2007</b> , 6, 263-72	5.6	63
201	Counting missing values in a metabolite-intensity data set for measuring the analytical performance of a metabolomics platform. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 1306-13	7.8	61
200	Liquid chromatography MALDI MS/MS for membrane proteome analysis. <i>Journal of Proteome Research</i> , <b>2004</b> , 3, 719-27	5.6	60
199	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> , <b>2001</b> , 12, 832-9	3.5	59
198	Development of high-performance chemical isotope labeling LC-MS for profiling the human fecal metabolome. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 829-36	7.8	58
197	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> , <b>1998</b> , 9, 1303-10	3.5	58
196	Chemical Isotope Labeling LC-MS for High Coverage and Quantitative Profiling of the Hydroxyl Submetabolome in Metabolomics. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 10617-10623	7.8	58
195	Quantitative proteome analysis using differential stable isotopic labeling and microbore LC-MALDI MS and MS/MS. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 734-42	5.6	57
194	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> , <b>2001</b> , 12, 1055-1063	3.5	57
193	Metabolomics of Small Numbers of Cells: Metabolomic Profiling of 100, 1000, and 10000 Human Breast Cancer Cells. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 11664-11671	7.8	54
192	Quantitative Metabolome Analysis Based on Chromatographic Peak Reconstruction in Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 7011-6	7.8	54

191	Nanoliter chemistry combined with mass spectrometry for peptide mapping of proteins from single mammalian cell lysates. <i>Analytical Chemistry</i> , <b>1998</b> , 70, 5344-7	7.8	54
190	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> , <b>2001</b> , 12, 1186-92	3.5	52
189	Differential Isotope Labeling of 38 Dietary Polyphenols and Their Quantification in Urine by Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 2637-44	7.8	50
188	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> , <b>2009</b> , 81, 1049-60	7.8	50
187	Metabolomic Coverage of Chemical-Group-Submetabolome Analysis: Group Classification and Four-Channel Chemical Isotope Labeling LC-MS. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 12108-12115	7.8	48
186	Two-layer sample preparation method for MALDI mass spectrometric analysis of protein and peptide samples containing sodium dodecyl sulfate. <i>Analytical Chemistry</i> , <b>2001</b> , 73, 2968-75	7.8	48
185	High-Performance Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry for Exosome Metabolomics. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 8314-8319	7.8	47
184	Profiling novel metabolic biomarkers for Parkinson's disease using in-depth metabolomic analysis. <i>Movement Disorders</i> , <b>2017</b> , 32, 1720-1728	7	47
183	Combining liquid chromatography with MALDI mass spectrometry using a heated droplet interface. <i>Analytical Chemistry</i> , <b>2004</b> , 76, 992-1001	7.8	47
182	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> , <b>2013</b> , 85, 11532-9	7.8	45
181	Ultra-high performance liquid chromatography tandem mass spectrometry for comprehensive analysis of urinary acylcarnitines. <i>Analytica Chimica Acta</i> , <b>2011</b> , 689, 77-84	6.6	44
180	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> , <b>1997</b> , 8, 1220-1229	3.5	44
179	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> , <b>2003</b> , 2, 543-52	5.6	44
178	Qualitative metabolome analysis of human cerebrospinal fluid by <sup>13</sup> C/ <sup>12</sup> 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> , <b>2011</b> , 22, 339-47	3.5	43
177	Characterization of pyrene end-labeled poly(ethylene glycol) by high resolution MALDI time-of-flight mass spectrometry. <i>Macromolecular Rapid Communications</i> , <b>1996</b> , 17, 59-64	4.8	42
176	Large-scale proteome profile of the zebrafish ( <i>Danio rerio</i> ) gill for physiological and biomarker discovery studies. <i>Zebrafish</i> , <b>2009</b> , 6, 229-38	2	41
175	A multiomics approach to heterogeneity in Alzheimer's disease: focused review and roadmap. <i>Brain</i> , <b>2020</b> , 143, 1315-1331	11.2	40
174	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> , <b>2001</b> , 12, 55-60	3.5	39

173	Reactions of atomic transition-metal ions with long-chain alkanes. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2001</b> , 12, 367-75	3.5	39
172	Liquid-liquid extraction combined with differential isotope dimethylaminophenacyl labeling for improved metabolomic profiling of organic acids. <i>Analytica Chimica Acta</i> , <b>2013</b> , 803, 97-105	6.6	37
171	Comparison of surfactant-assisted shotgun methods using acid-labile surfactants and sodium dodecyl sulfate for membrane proteome analysis. <i>Analytica Chimica Acta</i> , <b>2011</b> , 698, 36-43	6.6	37
170	Analysis of Structurally Complex Polymers by Time-Lag Focusing Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry. <i>Macromolecules</i> , <b>1997</b> , 30, 1955-1963	5.5	37
169	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> , <b>2005</b> , 4, 1419-26	5.6	36
168	Observation of gel-induced protein modifications in sodium dodecylsulfate [corrected] 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 Proteome Research</i> , <b>2003</b> , 10, 512-20	3.5	36
167	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> , <b>2014</b> , 13, 4457-69	5.6	35
166	Development of isotope labeling liquid chromatography-mass spectrometry for metabolic profiling of bacterial cells and its application for bacterial differentiation. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 5755-63	7.8	35
165	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> , <b>2002</b> , 13, 888-97	3.5	35
164	Metabolomics Analyses of Saliva Detect Novel Biomarkers of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , <b>2018</b> , 65, 1401-1416	4.3	35
163	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> , <b>2006</b> , 17, 780-785	3.5	34
162	Combining avidin-biotin chemistry with matrix-assisted laser desorption/ionization mass spectrometry. <i>Analytical Chemistry</i> , <b>1996</b> , 68, 3382-7	7.8	34
161	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> , <b>2011</b> , 1218, 3689-94	4.5	32
160	Rewiring AMPK and mitochondrial retrograde signaling for metabolic control of aging and histone acetylation in respiratory-defective cells. <i>Cell Reports</i> , <b>2014</b> , 7, 565-574	10.6	31
159	Integrated SDS removal and peptide separation by strong-cation exchange liquid chromatography for SDS-assisted shotgun proteome analysis. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 818-28	5.6	31
158	Photo-induced dissociation of electrospray generated ions in an ion trap/time-of-flight mass spectrometer. <i>Review of Scientific Instruments</i> , <b>1999</b> , 70, 4192-4199	1.7	31
157	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> , <b>2010</b> , 21, 2105-16	3.5	30
156	Nanoliter solvent extraction combined with microspot MALDI TOF mass spectrometry for the analysis of hydrophobic biomolecules. <i>Analytical Chemistry</i> , <b>2001</b> , 73, 2929-36	7.8	30



155	Chemical derivatization in LC-MS-based metabolomics study. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2020</b> , 131, 115988	14.6	30
154	Comprehensive and Quantitative Profiling of the Human Sweat Submetabolome Using High-Performance Chemical Isotope Labeling LC-MS. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 7378-86	7.8	30
153	Elevated acetyl-CoA by amino acid recycling fuels microalgal neutral lipid accumulation in exponential growth phase for biofuel production. <i>Plant Biotechnology Journal</i> , <b>2017</b> , 15, 497-509	11.6	28
152	Chronic inhibition of farnesyl pyrophosphate synthase attenuates cardiac hypertrophy and fibrosis in spontaneously hypertensive rats. <i>Biochemical Pharmacology</i> , <b>2010</b> , 79, 399-406	6	28
151	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> , <b>2010</b> , 21, 1573-87	3.5	28
150	Simple and robust two-layer matrix/sample preparation method for MALDI MS/MS analysis of peptides. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 1709-16	5.6	27
149	Structural analysis of polymer end groups by electrospray ionization high-energy collision-induced dissociation tandem mass spectrometry. <i>Analytical Chemistry</i> , <b>2000</b> , 72, 3847-52	7.8	27
148	Nanoflow LC-MS for High-Performance Chemical Isotope Labeling Quantitative Metabolomics. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 11468-74	7.8	26
147	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> , <b>2013</b> , 12, 4478-89	5.6	26
146	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> , <b>2012</b> , 750, 161-72	6.6	26
145	Investigation of the quantitative capabilities of an electrospray ionization ion trap/linear time-of-flight mass spectrometer. <i>Rapid Communications in Mass Spectrometry</i> , <b>1998</b> , 12, 695-700	2.2	26
144	Parallel Metabolomic Profiling of Cerebrospinal Fluid and Serum for Identifying Biomarkers of Injury Severity after Acute Human Spinal Cord Injury. <i>Scientific Reports</i> , <b>2016</b> , 6, 38718	4.9	26
143	Development of Chemical Isotope Labeling LC-MS for Milk Metabolomics: Comprehensive and Quantitative Profiling of the Amine/Phenol Submetabolome. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 4435-4443	7.8	25
142	High glucose promotes gastric cancer chemoresistance in vivo and in vitro. <i>Molecular Medicine Reports</i> , <b>2015</b> , 12, 843-50	2.9	25
141	MALDI mass spectrometry combined with avidin-biotin chemistry for analysis of protein modifications. <i>Analytical Chemistry</i> , <b>1998</b> , 70, 1569-75	7.8	25
140	Metabolite Analysis and Histology on the Exact Same Tissue: Comprehensive Metabolomic Profiling and Metabolic Classification of Prostate Cancer. <i>Scientific Reports</i> , <b>2016</b> , 6, 32272	4.9	24
139	Dansylation isotope labeling liquid chromatography mass spectrometry for parallel profiling of human urinary and fecal submetabolomes. <i>Analytica Chimica Acta</i> , <b>2016</b> , 903, 100-9	6.6	24
138	ECatenin, a Sox2 binding partner, regulates the DNA binding and transcriptional activity of Sox2 in breast cancer cells. <i>Cellular Signalling</i> , <b>2014</b> , 26, 492-501	4.9	24

137	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> , <b>1997</b> , 8, 1085-1093	3.5	24
136	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> , <b>2021</b> , 417, 126003	12.8	24
135	Microwave-assisted protein solubilization for mass spectrometry-based shotgun proteome analysis. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 6181-91	7.8	23
134	Altered Gut Microbial Metabolites in Amnesic Mild Cognitive Impairment and Alzheimer's Disease: Signals in Host-Microbe Interplay. <i>Nutrients</i> , <b>2021</b> , 13,	6.7	23
133	Dansylhydrazine Isotope Labeling LC-MS for Comprehensive Carboxylic Acid Submetabolome Profiling. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 13514-13522	7.8	23
132	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> , <b>2018</b> , 1558, 50-58	4.5	23
131	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> , <b>2014</b> , 86, 3568-74	7.8	22
130	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> , <b>2017</b> , 89, 7847-7851	7.8	22
129	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> , <b>2002</b> , 74, 1729-36	7.8	22
128	Integrated analyses utilizing metabolomics and transcriptomics reveal perturbation of the polyamine pathway in oral cavity squamous cell carcinoma. <i>Analytica Chimica Acta</i> , <b>2019</b> , 1050, 113-122	6.6	22
127	Effect of 2MEGA labeling on membrane proteome analysis using LC-ESI QTOF MS. <i>Journal of Proteome Research</i> , <b>2006</b> , 5, 2567-76	5.6	21
126	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> , <b>2002</b> , 782, 217-22	3.2	21
125	Photoinduced dissociation of electrospray-generated ions in an ion trap/time-of-flight mass spectrometer using a pulsed CO <sub>2</sub> laser. <i>Rapid Communications in Mass Spectrometry</i> , <b>2002</b> , 16, 1805-11	2.2	21
124	Overcoming Sample Matrix Effect in Quantitative Blood Metabolomics Using Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 9424-9431	7.8	19
123	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> , <b>2015</b> , 2015, 379287	3.9	19
122	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> , <b>2000</b> , 14, 2175-81	2.2	19
121	Nanoliter sample handling combined with microspot MALDI-MS for detection of gel-separated phosphoproteins. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 515-22	5.6	18
120	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> , <b>2019</b> , 1050, 95-104	6.6	18



119	Metabolomic analysis of oxidative stress: Superoxide dismutase mutation and paraquat induced stress in <i>Drosophila melanogaster</i> . <i>Free Radical Biology and Medicine</i> , <b>2017</b> , 113, 323-334	7.8	17
118	Development of versatile isotopic labeling reagents for profiling the amine submetabolome by liquid chromatography-mass spectrometry. <i>Analytica Chimica Acta</i> , <b>2015</b> , 881, 107-16	6.6	17
117	Brain Transforming Growth Factor- $\beta$ Resists Hypertension Via Regulating Microglial Activation. <i>Stroke</i> , <b>2017</b> , 48, 2557-2564	6.7	17
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