Lloyd W Sumner

List of Publications by Year
in descending order

154 papers	18,212 citations	15466 65 h-index	12910 131 g-index
162 all docs	162 docs citations	162 times ranked	21448 citing authors

#	Article	IF	Citations
1	Proposed minimum reporting standards for chemical analysis. Metabolomics, 2007, 3, 211-221.	1.4	3,589
2	Plant metabolomics: large-scale phytochemistry in the functional genomics era. Phytochemistry, 2003, 62, 817-836.	1.4	1,010
3	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	4.3	685
4	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	9.0	403
5	The metabolomics standards initiative (MSI). Metabolomics, 2007, 3, 175-178.	1.4	396
6	Mass Spectrometry Strategies in Metabolomics. Journal of Biological Chemistry, 2011, 286, 25435-25442.	1.6	396
7	Overexpression of WXP1, a putative Medicago truncatula AP2 domain-containing transcription factor gene, increases cuticular wax accumulation and enhances drought tolerance in transgenic alfalfa (Medicago sativa). Plant Journal, 2005, 42, 689-707.	2.8	388
8	GCâ€“MS SPME profiling of rhizobacterial volatiles reveals prospective inducers of growth promotion and induced systemic resistance in plants. Phytochemistry, 2006, 67, 2262-2268.	1.4	349
9	Virus infection improves drought tolerance. New Phytologist, 2008, 180, 911-921.	3.5	348
10	Metabolic profiling of Medicago truncatula cell cultures reveals the effects of biotic and abiotic elicitors on metabolism. Journal of Experimental Botany, 2005, 56, 323-336.	2.4	347
11	The Metabolomics Standards Initiative. Nature Biotechnology, 2007, 25, 846-848.	9.4	328
12	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	9.4	283
13	Legume Natural Products: Understanding and Manipulating Complex Pathways for Human and Animal Health. Plant Physiology, 2003, 131, 878-885.	2.3	269
14	Genomics-based selection and functional characterization of triterpene glycosyltransferases from the model legume Medicago truncatula. Plant Journal, 2005, 41, 875-887.	2.8	262
15	MET-IDEA:Â Data Extraction Tool for Mass Spectrometry-Based Metabolomics. Analytical Chemistry, 2006, 78, 4334-4341.	3.2	249
16	MATE2 Mediates Vacuolar Sequestration of Flavonoid Glycosides and Glycoside Malonates in<i>Medicago truncatula</i>Â Â Â. Plant Cell, 2011, 23, 1536-1555.	3.1	227
17	Mapping the Proteome of Barrel Medic (Medicago truncatula),. Plant Physiology, 2003, 131, 1104-1123.	2.3	217
18	Metabolic profiling of saponins in Medicago sativa and Medicago truncatula using HPLC coupled to an electrospray ion-trap mass spectrometer. Phytochemistry, 2002, 59, 347-360.	1.4	211

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19	Metabolite identification: are you sure? And how do your peers gauge your confidence?. Metabolomics, 2014, 10, 350-353.	1.4	205
20	Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. Natural Product Reports, 2015, 32, 212-229.	5.2	190
21	Metabolomics spectral formatting, alignment and conversion tools (MSFACTs). Bioinformatics, 2003, 19, 2283-2293.	1.8	187
22	<i>LAP5</i> and <i>LAP6</i> Encode Anther-Specific Proteins with Similarity to Chalcone Synthase Essential for Pollen Exine Development in Arabidopsis. Plant Physiology, 2010, 153, 937-955.	2.3	187
23	Transcript and proteomic analysis of developing white lupin (Lupinus albus L.) roots. BMC Plant Biology, 2009, 9, 1.	1.6	182
24	Different mechanisms for phytoalexin induction by pathogen and wound signals in <i>Medicago truncatula</i>. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17909-17915.	3.3	180
25	Metabolomics Reveals Novel Pathways and Differential Mechanistic and Elicitor-Specific Responses in Phenylpropanoid and Isoflavonoid Biosynthesis in <i>Medicago truncatula</i> Cell Cultures. Plant Physiology, 2008, 146, 323-324.	2.3	179
26	Methyl jasmonate and yeast elicitor induce differential transcriptional and metabolic re-programming in cell suspension cultures of the model legume Medicago truncatula. Planta, 2005, 220, 696-707.	1.6	175
27	Antifungal Activity of Citrus Essential Oils. Journal of Agricultural and Food Chemistry, 2014, 62, 3011-3033.	2.4	174
28	Current and emerging mass-spectrometry technologies for metabolomics. TrAC - Trends in Analytical Chemistry, 2008, 27, 238-250.	5.8	171
29	Genomic and Coexpression Analyses Predict Multiple Genes Involved in Triterpene Saponin Biosynthesis in <i>Medicago truncatula</i> Â Â. Plant Cell, 2010, 22, 850-866.	3.1	168
30	Heterologous expression of two Medicago truncatula putative ERF transcription factor genes, WXP1 and WXP2, in Arabidopsis led to increased leaf wax accumulation and improved drought tolerance, but differential response in freezing tolerance. Plant Molecular Biology, 2007, 64, 265-278.	2.0	162
31	Altered Profile of Secondary Metabolites in the Root Exudates of Arabidopsis ATP-Binding Cassette Transporter Mutants. Plant Physiology, 2008, 146, 323-324.	2.3	158
32	Citrus fruit bitter flavors: isolation and functional characterization of the gene Cm1,2RhaT encoding a 1,2 rhamnosyltransferase, a key enzyme in the biosynthesis of the bitter flavonoids of citrus. Plant Journal, 2004, 40, 88-100.	2.8	152
33	Metabolic profiling and systematic identification of flavonoids and isoflavonoids in roots and cell suspension cultures of Medicago truncatula using HPLCâ€"UVâ€"ESIâ€"MS and GCâ€"MS. Phytochemistry, 2007, 68, 342-354.	1.4	144
34	Root-Microbe Communication through Protein Secretion. Journal of Biological Chemistry, 2008, 283, 25247-25255.	1.6	144
35	Global reprogramming of transcription and metabolism in <scp><i>M</i></scp><i>edicago truncatula</i> during progressive drought and after rewatering. Plant, Cell and Environment, 2014, 37, 2553-2576.	2.8	138
36	A WD40 Repeat Protein from<i>Medicago truncatula</i>Is Necessary for Tissue-Specific Anthocyanin and Proanthocyanidin Biosynthesis But Not for Trichome Development Â Â. Plant Physiology, 2009, 151, 1114-1129.	2.3	137

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37	<i>STENOFOLIA</i>Regulates Blade Outgrowth and Leaf Vascular Patterning in<i>Medicago truncatula</i>and<i>Nicotiana sylvestris</i>Â Â Â. Plant Cell, 2011, 23, 2125-2142.	3.1	133
38	Regiospecific hydroxylation of isoflavones by cytochrome P450 81E enzymes fromMedicago truncatula. Plant Journal, 2003, 36, 471-484.	2.8	132
39	Soybean Metabolites Regulated in Root Hairs in Response to the Symbiotic Bacterium<i>Bradyrhizobium japonicum</i>Â Â Â. Plant Physiology, 2010, 153, 1808-1822.	2.3	132
40	Functional Characterization of Proanthocyanidin Pathway Enzymes from Tea and Their Application for Metabolic Engineering Â Â. Plant Physiology, 2013, 161, 1103-1116.	2.3	130
41	A Large-Scale Genetic Screen in Arabidopsis to Identify Genes Involved in Pollen Exine Production Â Â Â. Plant Physiology, 2011, 157, 947-970.	2.3	120
42	Minimum reporting standards for plant biology context information in metabolomic studies. Metabolomics, 2007, 3, 195-201.	1.4	116
43	Proteomics of Medicago sativa cell walls. Phytochemistry, 2004, 65, 1709-1720.	1.4	113
44	A Two-dimensional Electrophoresis Proteomic Reference Map and Systematic Identification of 1367 Proteins from a Cell Suspension Culture of the Model Legume Medicago truncatula. Molecular and Cellular Proteomics, 2005, 4, 1812-1825.	2.5	108
45	Quantification of Saponins in Aerial and Subterranean Tissues ofMedicago truncatula. Journal of Agricultural and Food Chemistry, 2005, 53, 1914-1920.	2.4	108
46	Plant neighbor identity influences plant biochemistry and physiology related to defense. BMC Plant Biology, 2010, 10, 115.	1.6	107
47	Root Secretion of Defense-related Proteins Is Development-dependent and Correlated with Flowering Time. Journal of Biological Chemistry, 2010, 285, 30654-30665.	1.6	103
48	Establishing Reporting Standards for Metabolomic and Metabonomic Studies: A Call for Participation. OMICS A Journal of Integrative Biology, 2006, 10, 158-163.	1.0	100
49	TrichOME: A Comparative Omics Database for Plant Trichomes Â Â Â. Plant Physiology, 2009, 152, 44-54.	2.3	98
50	Expression of a bacterial feedbackâ€insensitive 3â€deoxyâ€<scp>d</scp>â€arabinoâ€heptulosonate 7â€phosphate synthase of the shikimate pathway in Arabidopsis elucidates potential metabolic bottlenecks between primary and secondary metabolism. New Phytologist, 2012, 194, 430-439.	3.5	98
51	PlantMetabolomics.org: A Web Portal for Plant Metabolomics Experiments. Plant Physiology, 2010, 152, 1807-1816.	2.3	93
52	The molecular and enzymatic basis of bitter/nonâ€bitter flavor of citrus fruit: evolution of branchâ€forming rhamnosyltransferases under domestication. Plant Journal, 2013, 73, 166-178.	2.8	92
53	Bisphenol A and bisphenol S disruptions of the mouse placenta and potential effects on the placentaâ€"brain axis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4642-4652.	3.3	92
54	Proposed quantitative and alphanumeric metabolite identification metrics. Metabolomics, 2014, 10, 1047-1049.	1.4	91

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55	Biomarker metabolites capturing the metabolite variance present in a rice plant developmental period. BMC Plant Biology, 2005, 5, 8.	1.6	90
56	MedicCyc: a biochemical pathway database for Medicago truncatula. Bioinformatics, 2007, 23, 1418-1423.	1.8	89
57	Jasmonateâ€mediated stomatal closure under elevated <scp>CO</scp>₂ revealed by timeâ€resolved metabolomics. Plant Journal, 2016, 88, 947-962.	2.8	87
58	Integrated Metabolomics and Transcriptomics Reveal Enhanced Specialized Metabolism in <i>Medicago truncatula</i> Root Border Cells Â. Plant Physiology, 2015, 167, 1699-1716.	2.3	84
59	Influence of Host Chloroplast Proteins on <i>Tobacco mosaic virus</i> Accumulation and Intercellular Movement Â Â Â. Plant Physiology, 2012, 161, 134-147.	2.3	83
60	Metabolomics as a Hypothesis-Generating Functional Genomics Tool for the Annotation of Arabidopsis thaliana Genes of â€œUnknown Functionâ€. Frontiers in Plant Science, 2012, 3, 15.	1.7	82
61	Analytical and biological variances associated with proteomic studies of Medicago truncatula by two-dimensional polyacrylamide gel electrophoresis. Proteomics, 2002, 2, 960.	1.3	81
62	Characterization of an Isoflavonoid-Specific Prenyltransferase from <i>Lupinus albus</i> Â Â Â. Plant Physiology, 2012, 159, 70-80.	2.3	73
63	Profiling phenolic metabolites in transgenic alfalfa modified in lignin biosynthesis. Phytochemistry, 2003, 64, 1013-1021.	1.4	68
64	Amino acid profiling in plant cell cultures: An inter-laboratory comparison of CE-MS and GC-MS. Electrophoresis, 2007, 28, 1371-1379.	1.3	66
65	Characterization of the Formation of Branched Short-Chain Fatty Acid:CoAs for Bitter Acid Biosynthesis in Hop Glandular Trichomes. Molecular Plant, 2013, 6, 1301-1317.	3.9	64
66	The Time Is Right to Focus on Model Organism Metabolomes. Metabolites, 2016, 6, 8.	1.3	63
67	Functional analysis of members of the isoflavone and isoflavanone O-methyltransferase enzyme families from the model legume Medicago truncatula. Plant Molecular Biology, 2006, 62, 715-733.	2.0	61
68	LAP3, a novel plant protein required for pollen development, is essential for proper exine formation. Sexual Plant Reproduction, 2009, 22, 167-177.	2.2	60
69	Template Effect for O2Addition acrosscis-Sulfur Sites in Nickel Dithiolates. Journal of the American Chemical Society, 1996, 118, 1791-1792.	6.6	57
70	Integrated Metabolite and Transcript Profiling Identify a Biosynthetic Mechanism for Hispidol in <i>Medicago truncatula</i> Cell Cultures Â Â Â. Plant Physiology, 2009, 151, 1096-1113.	2.3	56
71	Patterns of Metabolite Changes Identified from Large-Scale Gene Perturbations in Arabidopsis Using a Genome-Scale Metabolic Network Â. Plant Physiology, 2015, 167, 1685-1698.	2.3	55
72	PlantMAT: A Metabolomics Tool for Predicting the Specialized Metabolic Potential of a System and for Large-Scale Metabolite Identifications. Analytical Chemistry, 2016, 88, 11373-11383.	3.2	55

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73	The Folylpolyglutamate Synthetase Plastidial Isoform Is Required for Postembryonic Root Development in Arabidopsis Â Â. Plant Physiology, 2011, 155, 1237-1251.	2.3	54
74	MET-COFEA: A Liquid Chromatography/Mass Spectrometry Data Processing Platform for Metabolite Compound Feature Extraction and Annotation. Analytical Chemistry, 2014, 86, 6245-6253.	3.2	54
75	Root Secreted Metabolites and Proteins Are Involved in the Early Events of Plant-Plant Recognition Prior to Competition. PLoS ONE, 2012, 7, e46640.	1.1	54
76	High-performance Liquid Chromatography/Continuous-flow Liquid Secondary Ion Mass Spectrometry of Flavonoid Glycosides in Leguminous Plant Extracts. , 1996, 31, 472-485.		53
77	Generation of a Collision Cross Section Library for Multi-Dimensional Plant Metabolomics Using UHPLC-Trapped Ion Mobility-MS/MS. Metabolites, 2020, 10, 13.	1.3	52
78	Retention projection enables accurate calculation of liquid chromatographic retention times across labs and methods. Journal of Chromatography A, 2015, 1412, 43-51.	1.8	47
79	Suppression of Phospholipase DÎ³s Confers Increased Aluminum Resistance in Arabidopsis thaliana. PLoS ONE, 2011, 6, e28086.	1.1	45
80	Subâ€lethal Levels of Electric Current Elicit the Biosynthesis of Plant Secondary Metabolites. Biotechnology Progress, 2008, 24, 377-384.	1.3	42
81	Metabolite profiles of essential oils in citrus peels and their taxonomic implications. Metabolomics, 2015, 11, 952-963.	1.4	41
82	Construction of an Ultrahigh Pressure Liquid Chromatography-Tandem Mass Spectral Library of Plant Natural Products and Comparative Spectral Analyses. Analytical Chemistry, 2015, 87, 7373-7381.	3.2	41
83	Metabolic Engineering of Plant Cells for Biotransformation of Hesperedin into Neohesperidin, a Substrate for Production of the Low-Calorie Sweetener and Flavor Enhancer NHDC. Journal of Agricultural and Food Chemistry, 2005, 53, 9708-9712.	2.4	39
84	Medicago glucosyltransferase UGT72L1: potential roles in proanthocyanidin biosynthesis. Planta, 2013, 238, 139-154.	1.6	39
85	Abatement of 2,4-D by H2O2 solar photolysis and solar photo-Fenton-like process with minute Fe(III) concentrations. Water Research, 2018, 144, 572-580.	5.3	39
86	NP-MRD: the Natural Products Magnetic Resonance Database. Nucleic Acids Research, 2022, 50, D665-D677.	6.5	39
87	Pentacoordinate (Î¼-Oxo)diiron(III) Thiolate Complexes and Dimeric Iron(II) Precursors. Inorganic Chemistry, 1998, 37, 4086-4093.	1.9	37
88	Nonflowering Plants Possess a Unique Folate-Dependent Phenylalanine Hydroxylase That Is Localized in Chloroplasts. Plant Cell, 2010, 22, 3410-3422.	3.1	37
89	12-Hydroxy-Jasmonoyl-l-Isoleucine Is an Active Jasmonate That Signals through CORONATINE INSENSITIVE 1 and Contributes to the Wound Response in Arabidopsis. Plant and Cell Physiology, 2019, 60, 2152-2166.	1.5	35
90	Apoplastic Extracts from a Transgenic Wheat Line Exhibiting Lesion-Mimic Phenotype Have Multiple Pathogenesis-Related Proteins That Are Antifungal. Molecular Plant-Microbe Interactions, 2004, 17, 1306-1317.	1.4	33

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91	Metabolomics Data Analysis, Visualization, and Integration. , 2005, 406, 409-436.		33
92	Citrate is a major component of snake venoms. Toxicon, 1992, 30, 461-464.	0.8	32
93	Methyl Jasmonate Induces ATP Biosynthesis Deficiency and Accumulation of Proteins Related to Secondary Metabolism in Catharanthus roseus (L.) G. Hairy Roots. Plant and Cell Physiology, 2011, 52, 1401-1421.	1.5	32
94	MET-XAlign: A Metabolite Cross-Alignment Tool for LC/MS-Based Comparative Metabolomics. Analytical Chemistry, 2015, 87, 9114-9119.	3.2	32
95	Silver stain removal using H2O2 for enhanced peptide mass mapping by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 2002, 16, 160-168.	0.7	31
96	Identification and quantification of phytosterols in black walnut kernels. Journal of Food Composition and Analysis, 2019, 75, 61-69.	1.9	31
97	MetExpert: An expert system to enhance gas chromatographyâ€'mass spectrometry-based metabolite identifications. Analytica Chimica Acta, 2018, 1037, 316-326.	2.6	30
98	A legume specific protein database (LegProt) improves the number of identified peptides, confidence scores and overall protein identification success rates for legume proteomics. Phytochemistry, 2011, 72, 1020-1027.	1.4	29
99	Sub-cellular proteomics of Medicago truncatula. Frontiers in Plant Science, 2013, 4, 112.	1.7	29
100	Identifying Antibacterial Compounds in Black Walnuts (Juglans nigra) Using a Metabolomics Approach. Metabolites, 2018, 8, 58.	1.3	29
101	Over-expression of cinnamate 4-hydroxylase leads to increased accumulation of acetosyringone in elicited tobacco cell-suspension cultures. Planta, 2002, 214, 902-910.	1.6	28
102	MET-IDEA version 2.06; improved efficiency and additional functions for mass spectrometry-based metabolomics data processing. Metabolomics, 2012, 8, 105-110.	1.4	28
103	Suppression of plant defense responses by extracellular metabolites from Pseudomonas syringae pv. tabaci in Nicotiana benthamiana. BMC Plant Biology, 2013, 13, 65.	1.6	28
104	Loss of function of folylpolyglutamate synthetase 1 reduces lignin content and improves cell wall digestibility in Arabidopsis. Biotechnology for Biofuels, 2015, 8, 224.	6.2	27
105	Ectopic Defense Gene Expression Is Associated with Growth Defects in <i>Medicago truncatula</i> Lignin Pathway Mutants. Plant Physiology, 2019, 181, 63-84.	2.3	27
106	Integrated metabolomics identifies CYP72A67 and CYP72A68 oxidases in the biosynthesis of Medicago truncatula oleanate sapogenins. Metabolomics, 2019, 15, 85.	1.4	26
107	UHPLC-QTOF-MS/MS-SPE-NMR: A Solution to the Metabolomics Grand Challenge of Higher-Throughput, Confident Metabolite Identifications. Methods in Molecular Biology, 2019, 2037, 113-133.	0.4	24
108	Developmental exposure of California mice to endocrine disrupting chemicals and potential effects on the microbiome-gut-brain axis at adulthood. Scientific Reports, 2020, 10, 10902.	1.6	23

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109	Improvement of drought tolerance in white clover (Trifolium repens) by transgenic expression of a transcription factor gene WXP1. Functional Plant Biology, 2010, 37, 157.	1.1	21
110	Early genistein exposure of California mice and effects on the gut microbiotaâ€"brain axis. Journal of Endocrinology, 2019, 242, 139-157.	1.2	21
111	â€œRetention Projectionâ€•Enables Reliable Use of Shared Gas Chromatographic Retention Data Across Laboratories, Instruments, and Methods. Analytical Chemistry, 2013, 85, 11650-11657.	3.2	19
112	Soy-Induced Fecal Metabolome Changes in Ovariectomized and Intact Female Rats: Relationship with Cardiometabolic Health. Scientific Reports, 2018, 8, 16896.	1.6	19
113	Pathway-specific metabolome analysis with 18O2-labeled Medicago truncatula via a mass spectrometry-based approach. Metabolomics, 2018, 14, 71.	1.4	19
114	UHPLCâ€MS Analyses of Plant Flavonoids. Current Protocols in Plant Biology, 2019, 4, e20085.	2.8	18
115	Medicago truncatula Oleanolic-Derived Saponins Are Correlated with Caterpillar Deterrence. Journal of Chemical Ecology, 2017, 43, 712-724.	0.9	16
116	Identification and Quantification of Bioactive Molecules Inhibiting Pro-inflammatory Cytokine Production in Spent Coffee Grounds Using Metabolomics Analyses. Frontiers in Pharmacology, 2020, 11, 229.	1.6	16
117	Large-Scale Profiling of Saponins in Different Ecotypes of Medicago truncatula. Frontiers in Plant Science, 2019, 10, 850.	1.7	15
118	Proteomic and Metabolomic Analysis of <i>Azospirillum brasilense</i> <i>ntrC</i> Mutant under High and Low Nitrogen Conditions. Journal of Proteome Research, 2020, 19, 92-105.	1.8	14
119	Efficient and Sensitive Method for Quantitative Analysis of Alkaloids in Hardinggrass (Phalaris) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.4	12
120	Comparative Proteomics of Yeast-ElicitedMedicago truncatulaCell Suspensions Reveals Induction of Isoflavonoid Biosynthesis and Cell Wall Modifications. Journal of Proteome Research, 2010, 9, 6220-6231.	1.8	12
121	Malonylation of Glucosylated N-Lauroylethanolamine A NEW PATHWAY THAT DETERMINES N-ACYLETHANOLAMINE METABOLIC FATE IN PLANTS. Journal of Biological Chemistry, 2016, 291, 27112-27121.	1.6	12
122	Black Walnut (Juglans nigra) Extracts Inhibit Proinflammatory Cytokine Production From Lipopolysaccharide-Stimulated Human Promonocytic Cell Line U-937. Frontiers in Pharmacology, 2019, 10, 1059.	1.6	12
123	Recent advances in plant metabolomics and greener pastures. F1000 Biology Reports, 2010, 2, .	4.0	12
124	Chapter Three Metabolomics: A developing and integral component in functional genomic studies of medicago truncatula. Recent Advances in Phytochemistry, 2002, , 31-61.	0.5	11
125	Seminal fluid metabolome and epididymal changes after antibiotic treatment in mice. Reproduction, 2018, 156, 1-10.	1.1	11
126	Integration of genomics, metagenomics, and metabolomics to identify interplay between susceptibility alleles and microbiota in adenoma initiation. BMC Cancer, 2020, 20, 600.	1.1	11

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127	Allelopathic Potential of Rice and Identification of Published Allelochemicals by Cloud-Based Metabolomics Platform. Metabolites, 2020, 10, 244.	1.3	9
128	Recent Developments Toward Integrated Metabolomics Technologies (UHPLC-MS-SPE-NMR and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7 Biosciences, 2021, 8, 720955.	1.6	9
129	Switchgrass Metabolomics Reveals Striking Genotypic and Developmental Differences in Specialized Metabolic Phenotypes. Journal of Agricultural and Food Chemistry, 2022, 70, 8010-8023.	2.4	9
130	Metabolomics across the globe. Metabolomics, 2013, 9, 258-264.	1.4	8
131	Metabolomics of Two Pecan Varieties Provides Insights into Scab Resistance. Metabolites, 2018, 8, 56.	1.3	8
132	Identification of health-promoting bioactive phenolics in black walnut using cloud-based metabolomics platform. Journal of Food Measurement and Characterization, 2020, 14, 770-777.	1.6	8
133	CASMI 2014: Challenges, Solutions and Results. Current Metabolomics, 2017, 5, 5-17.	0.5	8
134	An Optimized SPME-GC-MS Method for Volatile Metabolite Profiling of Different Alfalfa (Medicago) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	8
135	Methods, applications and concepts of metabolite profiling: Secondary metabolism. , 2007, 97, 195-212.		7
136	Role of cytosolic, tyrosineâ€insensitive prephenate dehydrogenase in <i>MedicagoÂtruncatula</i>. Plant Direct, 2020, 4, e00218.	0.8	7
137	Identification and quantification of bioactive compounds suppressing SARS-CoV-2 signals in wastewater-based epidemiology surveillance. Water Research, 2022, 221, 118824.	5.3	7
138	Determination of cinnamic acid and 4-coumaric acid in alfalfa (Medicago sativa L.) cell suspension cultures by gas chromatography. Phytochemical Analysis, 1993, 4, 124-130.	1.2	6
139	Characterization of Proteins Utilized in the Desulfurization of Petroleum Products by Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry. Analytical Biochemistry, 1998, 260, 117-127.	1.1	6
140	Proteome analysis of <i>Pithecellobium dulce</i> seeds using twoâ€dimensional gel electrophoresis and tandem mass spectrometry. Journal of the Science of Food and Agriculture, 2009, 89, 1284-1291.	1.7	4
141	A Medicago truncatula Metabolite Atlas Enables the Visualization of Differential Accumulation of Metabolites in Root Tissues. Metabolites, 2021, 11, 238.	1.3	4
142	Bridging the Gap between Analytical and Microbial Sciences in Microbiome Research. MSystems, 2021, 6, e0058521.	1.7	4
143	Introducing the USA Plant, Algae and Microbial Metabolomics Research Coordination Network (PAMM-NET). Metabolomics, 2015, 11, 3-5.	1.4	3
144	Protein Precipitation to Remove Carbohydrates that Interfere in Protein-Bound Tryptophan Quantification in Soybean Seeds. Journal of Analysis and Testing, 2020, 4, 238-247.	2.5	3

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145	Nontargeted fecal metabolomics: an emerging tool to probe the role of the gut microbiome in host health. Bioanalysis, 2020, 12, 351-353.	0.6	3
146	Proteomics of Legume Plants. , 0, , 179-189.		2
147	Assessing Anti-Inflammatory Activities and Compounds in Switchgrass (Panicum virgatum). Agriculture (Switzerland), 2022, 12, 936.	1.4	2
148	Plant Metabolomics: Large-Scale Phytochemistry in the Functional Genomics Era.. ChemInform, 2003, 34, no.	0.1	1
149	852 BILOPHILA WADSWORTHIA SUPPLEMENTATION REDUCES ADENOMA BURDEN IN THE APC-MIN MOUSE MODEL OF COLORECTAL CANCER. Gastroenterology, 2020, 158, S-173.	0.6	1
150	Modern Plant Metabolomics for the Discovery and Characterization of Natural Products and Their Biosynthetic Genes. , 2020, , 156-188.		1
151	A novel mobile phase for continuous-flow liquid secondary ion mass spectrometry of high molecular mass phthalocyanines. Organic Mass Spectrometry, 1993, 28, 475-477.	1.3	0
152	2014 Honorary fellows of the Metabolomics Society. Metabolomics, 2014, 10, 537-538.	1.4	0
153	Abstract 4076: Gut microbiota and metabolite-driven phenotype modulation in a mouse model of colorectal cancer. , 2018, , .		0
154	Abstract 2400: Complex gut microbiota modulate rat colon adenoma susceptibility, metabolites, and host gene expression. , 2018, , .		0