Kazuki Saito

List of Publications by Year
in descending order

555	48,192	1163 111	2883 190
papers	citations	h-index	g-index

600	600	600	34984
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MassBank: a public repository for sharing mass spectral data for life sciences. Journal of Mass Spectrometry, 2010, 45, 703-714.	0.7	1,831
2	Enhancement of oxidative and drought tolerance in Arabidopsis by overaccumulation of antioxidant flavonoids. Plant Journal, 2014, 77, 367-379.	2.8	911
3	Functional genomics by integrated analysis of metabolome and transcriptome of Arabidopsis plants over-expressing an MYB transcription factor. Plant Journal, 2005, 42, 218-235.	2.8	891
4	From The Cover: Integration of transcriptomics and metabolomics for understanding of global responses to nutritional stresses in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10205-10210.	3.3	726
5	Sulfur Assimilation in Photosynthetic Organisms: Molecular Functions and Regulations of Transporters and Assimilatory Enzymes. Annual Review of Plant Biology, 2011, 62, 157-184.	8.6	720
6	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	4.3	685
7	Omics-based identification of Arabidopsis Myb transcription factors regulating aliphatic glucosinolate biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6478-6483.	3.3	666
8	Metabolomics for Functional Genomics, Systems Biology, and Biotechnology. Annual Review of Plant Biology, 2010, 61, 463-489.	8.6	647
9	The flavonoid biosynthetic pathway in Arabidopsis: Structural and genetic diversity. Plant Physiology and Biochemistry, 2013, 72, 21-34.	2.8	637
10	Can sub-Saharan Africa feed itself?. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14964-14969.	3.3	564
11	KNApSAcK Family Databases: Integrated Metaboliteâ€“Plant Species Databases for Multifaceted Plant Research. Plant and Cell Physiology, 2012, 53, e1-e1.	1.5	529
12	The roles of three functional sulphate transporters involved in uptake and translocation of sulphate inArabidopsis thaliana. Plant Journal, 2000, 23, 171-182.	2.8	523
13	Characterization of the ABAâ€regulated global responses to dehydration in Arabidopsis by metabolomics. Plant Journal, 2009, 57, 1065-1078.	2.8	519
14	Members of theLBDFamily of Transcription Factors Repress Anthocyanin Synthesis and Affect Additional Nitrogen Responses inArabidopsisÂ Â. Plant Cell, 2009, 21, 3567-3584.	3.1	507
15	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Plant Journal, 2008, 55, 526-542.	2.8	467
16	Sulfate Transport and Assimilation in Plants1. Plant Physiology, 1999, 120, 637-644.	2.3	456
17	Elucidation of Gene-to-Gene and Metabolite-to-Gene Networks inArabidopsis by Integration of Metabolomics andTranscriptomics*. Journal of Biological Chemistry, 2005, 280, 25590-25595.	1.6	453
18	Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. Analytical Chemistry, 2016, 88, 7946-7958.	3.2	441

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19	A lipidome atlas in MS-DIAL 4. Nature Biotechnology, 2020, 38, 1159-1163.	9.4	424
20	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	9.0	403
21	Sulphur starvation induces the expression of microRNAâ€395 and one of its target genes but in different cell types. Plant Journal, 2009, 57, 313-321.	2.8	377
22	Sulfur Assimilatory Metabolism. The Long and Smelling Road. Plant Physiology, 2004, 136, 2443-2450.	2.3	362
23	Comprehensive Flavonol Profiling and Transcriptome Coexpression Analysis Leading to Decoding Geneâ€“Metabolite Correlations inArabidopsisÂ Â. Plant Cell, 2008, 20, 2160-2176.	3.1	347
24	ATTED-II: a database of co-expressed genes and cis elements for identifying co-regulated gene groups in Arabidopsis. Nucleic Acids Research, 2007, 35, D863-D869.	6.5	343
25	Arabidopsis SLIM1 Is a Central Transcriptional Regulator of Plant Sulfur Response and Metabolism. Plant Cell, 2006, 18, 3235-3251.	3.1	337
26	Recent advances in the biosynthesis and accumulation of anthocyanins. Natural Product Reports, 2003, 20, 288.	5.2	331
27	Licorice Î²-amyrin 11-oxidase, a cytochrome P450 with a key role in the biosynthesis of the triterpene sweetener glycyrrhizin. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14204-14209.	3.3	331
28	Recommendations for Reporting Metabolite Data. Plant Cell, 2011, 23, 2477-2482.	3.1	326
29	Coordinated activation of metabolic pathways for antioxidants and defence compounds by jasmonates and their roles in stress tolerance in Arabidopsis. Plant Journal, 2005, 44, 653-668.	2.8	325
30	Two distinct high-affinity sulfate transporters with different inducibilities mediate uptake of sulfate in Arabidopsis roots. Plant Journal, 2002, 29, 465-473.	2.8	320
31	Integrated metabolomics for abiotic stress responses in plants. Current Opinion in Plant Biology, 2015, 24, 10-16.	3.5	319
32	Metabolic Pathways Involved in Cold Acclimation Identified by Integrated Analysis of Metabolites and Transcripts Regulated by DREB1A and DREB2A Â Â. Plant Physiology, 2009, 150, 1972-1980.	2.3	315
33	UGT73C6 and UGT78D1, Glycosyltransferases Involved in Flavonol Glycoside Biosynthesis in Arabidopsis thaliana. Journal of Biological Chemistry, 2003, 278, 43910-43918.	1.6	311
34	Global expression profiling of sulfur-starved Arabidopsis by DNA macroarray reveals the role of O -acetyl-l -serine as a general regulator of gene expression in response to sulfur nutrition. Plant Journal, 2003, 33, 651-663.	2.8	310
35	The AtGenExpress hormone- and chemical-treatment data set: Experimental design, data evaluation, model data analysis, and data access. Plant Journal, 2008, 55, 080414150319983.	2.8	307
36	Decoding genes with coexpression networks and metabolomics â€“ â€˜majority report by precogsâ€™. Trends in Plant Science, 2008, 13, 36-43.	4.3	303

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37	RIKEN tandem mass spectral database (ReSpect) for phytochemicals: A plant-specific MS/MS-based data resource and database. Phytochemistry, 2012, 82, 38-45.	1.4	284
38	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	9.4	283
39	Pause-and-Stop: The Effects of Osmotic Stress on Cell Proliferation during Early Leaf Development in Arabidopsis and a Role for Ethylene Signaling in Cell Cycle Arrest. Plant Cell, 2011, 23, 1876-1888.	3.1	268
40	Triterpene Functional Genomics in Licorice for Identification of CYP72A154 Involved in the Biosynthesis of Glycyrrhizin Â Â. Plant Cell, 2011, 23, 4112-4123.	3.1	266
41	Widely Targeted Metabolomics Based on Large-Scale MS/MS Data for Elucidating Metabolite Accumulation Patterns in Plants. Plant and Cell Physiology, 2009, 50, 37-47.	1.5	264
42	Roles of lipids as signaling molecules and mitigators during stress response in plants. Plant Journal, 2014, 79, 584-596.	2.8	252
43	Transcript Profiling of an Arabidopsis PSEUDO RESPONSE REGULATOR Arrhythmic Triple Mutant Reveals a Role for the Circadian Clock in Cold Stress Response. Plant and Cell Physiology, 2009, 50, 447-462.	1.5	249
44	Metabolomics reveals comprehensive reprogramming involving two independent metabolic responses of Arabidopsis to UVâ€B light. Plant Journal, 2011, 67, 354-369.	2.8	249
45	CYP716A Subfamily Members are Multifunctional Oxidases in Triterpenoid Biosynthesis. Plant and Cell Physiology, 2011, 52, 2050-2061.	1.5	244
46	Identification of a Flavonol 7-O-Rhamnosyltransferase Gene Determining Flavonoid Pattern in Arabidopsis by Transcriptome Coexpression Analysis and Reverse Genetics. Journal of Biological Chemistry, 2007, 282, 14932-14941.	1.6	236
47	Acetate-mediated novel survival strategy against drought in plants. Nature Plants, 2017, 3, 17097.	4.7	232
48	Impact of clock-associated Arabidopsis pseudo-response regulators in metabolic coordination. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7251-7256.	3.3	228
49	Integrated Analysis of the Effects of Cold and Dehydration on Rice Metabolites, Phytohormones, and Gene Transcripts. Plant Physiology, 2014, 164, 1759-1771.	2.3	228
50	Metabolomic correlation-network modules in Arabidopsis based on a graph-clustering approach. BMC Systems Biology, 2011, 5, 1.	3.0	215
51	Direct evidence for anthocyanidin synthase as a 2-oxoglutarate-dependent oxygenase: molecular cloning and functional expression of cDNA from a red forma ofPerilla frutescens. Plant Journal, 1999, 17, 181-189.	2.8	209
52	MS/MS spectral tagâ€based annotation of nonâ€targeted profile of plant secondary metabolites. Plant Journal, 2009, 57, 555-577.	2.8	208
53	Sterol Side Chain Reductase 2 Is a Key Enzyme in the Biosynthesis of Cholesterol, the Common Precursor of Toxic Steroidal Glycoalkaloids in Potato Â. Plant Cell, 2014, 26, 3763-3774.	3.1	206
54	Integrated omics approaches in plant systems biology. Current Opinion in Chemical Biology, 2009, 13, 532-538.	2.8	201

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55	A Chloroplastic UDP-Glucose Pyrophosphorylase from Arabidopsis Is the Committed Enzyme for the First Step of Sulfolipid Biosynthesis Â. Plant Cell, 2009, 21, 892-909.	3.1	199
56	Metabolomic approaches toward understanding nitrogen metabolism in plants. Journal of Experimental Botany, 2011, 62, 1439-1453.	2.4	198
57	Role of camalexin, indole glucosinolates, and side chain modification of glucosinolateâ€derived isothiocyanates in defense of Arabidopsis against Sclerotinia sclerotiorum. Plant Journal, 2011, 67, 81-93.	2.8	198
58	Isoform-dependent Differences in Feedback Regulation and Subcellular Localization of Serine Acetyltransferase Involved in Cysteine Biosynthesis from Arabidopsis thaliana. Journal of Biological Chemistry, 1998, 273, 32739-32745.	1.6	195
59	Phloem-Localizing Sulfate Transporter, Sultr1;3, Mediates Re-Distribution of Sulfur from Source to Sink Organs in Arabidopsis. Plant Physiology, 2003, 131, 1511-1517.	2.3	195
60	Triterpenoid Biosynthesis and Engineering in Plants. Frontiers in Plant Science, 2011, 2, 25.	1.7	195
61	A new class of plant lipid is essential for protection against phosphorus depletion. Nature Communications, 2013, 4, 1510.	5.8	195
62	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. Nature Methods, 2019, 16, 295-298.	9.0	194
63	Integrating genomics and metabolomics for engineering plant metabolic pathways. Current Opinion in Biotechnology, 2005, 16, 174-179.	3.3	193
64	Convergent evolution in the BAHD family of acyl transferases: identification and characterization of anthocyanin acyl transferases from Arabidopsis thaliana. Plant Journal, 2007, 50, 678-695.	2.8	192
65	Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. Natural Product Reports, 2015, 32, 212-229.	5.2	190
66	Interplay of SLIM1 and miR395 in the regulation of sulfate assimilation in Arabidopsis. Plant Journal, 2011, 66, 863-876.	2.8	189
67	Integrated omics analysis of specialized metabolism in medicinal plants. Plant Journal, 2017, 90, 764-787.	2.8	185
68	Î²-Cyanoalanine Synthase Is a Mitochondrial Cysteine Synthase-Like Protein in Spinach and Arabidopsis1. Plant Physiology, 2000, 123, 1163-1172.	2.3	183
69	LC/PDA/ESI-MS Profiling and Radical Scavenging Activity of Anthocyanins in Various Berries. Journal of Biomedicine and Biotechnology, 2004, 2004, 241-247.	3.0	183
70	Mechanistic Studies on Three 2-Oxoglutarate-dependent Oxygenases of Flavonoid Biosynthesis. Journal of Biological Chemistry, 2004, 279, 1206-1216.	1.6	183
71	Disruption of Adenosine-5â€²-Phosphosulfate Kinase inArabidopsisReduces Levels of Sulfated Secondary Metabolites. Plant Cell, 2009, 21, 910-927.	3.1	180
72	OsATG7 is required for autophagy-dependent lipid metabolism in rice postmeiotic anther development. Autophagy, 2014, 10, 878-888.	4.3	176

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73	Dual biosynthetic pathways to phytosterol via cycloartenol and lanosterol in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 725-730.	3.3	174
74	Compensation for Systematic Cross-Contribution Improves Normalization of Mass Spectrometry Based Metabolomics Data. Analytical Chemistry, 2009, 81, 7974-7980.	3.2	173
75	Dissection of genotypeâ€“phenotype associations in rice grains using metabolome quantitative trait loci analysis. Plant Journal, 2012, 70, 624-636.	2.8	173
76	Landscape of the lipidome and transcriptome under heat stress in Arabidopsis thaliana. Scientific Reports, 2015, 5, 10533.	1.6	171
77	Application of a metabolomic method combining one-dimensional and two-dimensional gas chromatography-time-of-flight/mass spectrometry to metabolic phenotyping of natural variants in rice. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 855, 71-79.	1.2	169
78	Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in Arabidopsis thaliana. Plant Journal, 2012, 69, 154-167.	2.8	164
79	Camptothecin Biosynthetic Genes in Hairy Roots of Ophiorrhiza pumila: Cloning, Characterization and Differential Expression in Tissues and by Stress Compounds. Plant and Cell Physiology, 2003, 44, 395-403.	1.5	162
80	Physiological Roles of the Î²-Substituted Alanine Synthase Gene Family in Arabidopsis. Plant Physiology, 2008, 146, 310-320.	2.3	161
81	AtMetExpress Development: A Phytochemical Atlas of Arabidopsis Development Â. Plant Physiology, 2010, 152, 566-578.	2.3	161
82	AÎ³-Glutamyl Transpeptidase-Independent Pathway of Glutathione Catabolism to Glutamate via 5-Oxoproline in Arabidopsis Â. Plant Physiology, 2008, 148, 1603-1613.	2.3	160
83	KaPPA-View. A Web-Based Analysis Tool for Integration of Transcript and Metabolite Data on Plant Metabolic Pathway Maps. Plant Physiology, 2005, 138, 1289-1300.	2.3	155
84	Metabolomeâ€genomeâ€wide association study dissects genetic architecture for generating natural variation in rice secondary metabolism. Plant Journal, 2015, 81, 13-23.	2.8	152
85	Generation of Î±-solanine-free hairy roots of potato by CRISPR/Cas9 mediated genome editing of the St16DOX gene. Plant Physiology and Biochemistry, 2018, 131, 70-77.	2.8	150
86	Overexpression of an Arabidopsis thaliana galactinol synthase gene improves drought tolerance in transgenic rice and increased grain yield in the field. Plant Biotechnology Journal, 2017, 15, 1465-1477.	4.1	149
87	PRIMe: a Web site that assembles tools for metabolomics and transcriptomics. In Silico Biology, 2008, 8, 339-45.	0.4	149
88	Draft genome assembly and annotation of Glycyrrhiza uralensis, a medicinal legume. Plant Journal, 2017, 89, 181-194.	2.8	148
89	Phosphoenolpyruvate carboxylase intrinsically located in the chloroplast of rice plays a crucial role in ammonium assimilation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5226-5231.	3.3	147
90	From field to atlas: Upscaling of location-specific yield gap estimates. Field Crops Research, 2015, 177, 98-108.	2.3	145

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91	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. Nature Communications, 2016, 7, 12399.	5.8	145
92	Metabolic activation of mutagenic N-hydroxyarylamines by O-acetyltransferase in Salmonella typhimurium TA98. Archives of Biochemistry and Biophysics, 1985, 239, 286-295.	1.4	139
93	Reaction Mechanism from Leucoanthocyanidin to Anthocyanidin 3-Glucoside, a Key Reaction for Coloring in Anthocyanin Biosynthesis. Journal of Biological Chemistry, 2001, 276, 25797-25803.	1.6	138
94	Posttranscriptional Regulation of High-Affinity Sulfate Transporters in Arabidopsis by Sulfur Nutrition. Plant Physiology, 2007, 145, 378-388.	2.3	134
95	Metabolomics data reveal a crucial role of cytosolic glutamine synthetase 1;1 in coordinating metabolic balance in rice. Plant Journal, 2011, 66, 456-466.	2.8	133
96	Deficiency of Starch Synthase IIIa and IVb Alters Starch Granule Morphology from Polyhedral to Spherical in Rice Endosperm. Plant Physiology, 2016, 170, 1255-1270.	2.3	131
97	Alternation of flavonoid accumulation under drought stress inArabidopsis thaliana. Plant Signaling and Behavior, 2014, 9, e29518.	1.2	129
98	Molecular Cloning and Biochemical Characterization of a Novel Anthocyanin 5-O-Glucosyltransferase by mRNA Differential Display for Plant Forms Regarding Anthocyanin. Journal of Biological Chemistry, 1999, 274, 7405-7411.	1.6	128
99	Heavy metal tolerance of transgenic tobacco plants over-expressing cysteine synthase. Biotechnology Letters, 2004, 26, 153-157.	1.1	127
100	Characterization and Expression Analysis of a Serine Acetyltransferase Gene Family Involved in a Key Step of the Sulfur Assimilation Pathway in Arabidopsis. Plant Physiology, 2005, 137, 220-230.	2.3	127
101	Sulfur deficiencyâ€“induced repressor proteins optimize glucosinolate biosynthesis in plants. Science Advances, 2016, 2, e1601087.	4.7	127
102	Recent advances of metabolomics in plant biotechnology. Plant Biotechnology Reports, 2012, 6, 1-15.	0.9	125
103	Functional genomics for plant natural product biosynthesis. Natural Product Reports, 2009, 26, 1466.	5.2	124
104	Combinatorial Biosynthesis of Legume Natural and Rare Triterpenoids in Engineered Yeast. Plant and Cell Physiology, 2013, 54, 740-749.	1.5	124
105	Cloning and molecular analysis of structural genes involved in anthocyanin biosynthesis and expressed in a forma-specific manner in Perilla frutescens. Plant Molecular Biology, 1997, 35, 915-927.	2.0	123
106	Cysteine Synthase Overexpression in Tobacco Confers Tolerance to Sulfur-Containing Environmental Pollutants. Plant Physiology, 2001, 126, 973-980.	2.3	123
107	Comparative Genomics and Reverse Genetics Analysis Reveal Indispensable Functions of the Serine Acetyltransferase Gene Family in Arabidopsis Â Â. Plant Cell, 2008, 20, 2484-2496.	3.1	121
108	Statistical Indices for Simultaneous Large-Scale Metabolite Detections for a Single NMR Spectrum. Analytical Chemistry, 2010, 82, 1653-1658.	3.2	121

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109	Metabolite profiling of alkaloids and strictosidine synthase activity in camptothecin producing plants. Phytochemistry, 2003, 62, 461-470.	1.4	119
110	Using Metabolomic Approaches to Explore Chemical Diversity in Rice. Molecular Plant, 2015, 8, 58-67.	3.9	119
111	Molecular Cloning and Characterization of a Plant Serine Acetyltransferase Playing a Regulatory Role in Cysteine Biosynthesis from Watermelon. Journal of Biological Chemistry, 1995, 270, 16321-16326.	1.6	116
112	Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in Arabidopsis thaliana. BMC Systems Biology, 2007, 1, 53.	3.0	116
113	Genetic Engineering of Group 2 Ïƒ Factor SigE Widely Activates Expressions of Sugar Catabolic Genes in Synechocystis Species PCC 6803. Journal of Biological Chemistry, 2011, 286, 30962-30971.	1.6	116
114	Lysine Decarboxylase Catalyzes the First Step of Quinolizidine Alkaloid Biosynthesis and Coevolved with Alkaloid Production in Leguminosae. Plant Cell, 2012, 24, 1202-1216.	3.1	115
115	Increased Bioplastic Production with an RNA Polymerase Sigma Factor SigE during Nitrogen Starvation in Synechocystis sp. PCC 6803. DNA Research, 2013, 20, 525-535.	1.5	113
116	Phytochemical genomics â€" a new trend. Current Opinion in Plant Biology, 2013, 16, 373-380.	3.5	112
117	Jasmonate-Responsive ERF Transcription Factors Regulate Steroidal Glycoalkaloid Biosynthesis in Tomato. Plant and Cell Physiology, 2016, 57, 961-975.	1.5	112
118	Mechanisms of resistance to self-produced toxic secondary metabolites in plants. Phytochemistry Reviews, 2008, 7, 467-477.	3.1	111
119	Metabolomics-oriented isolation and structure elucidation of 37 compounds including two anthocyanins from Arabidopsis thaliana. Phytochemistry, 2009, 70, 1017-1029.	1.4	111
120	Evaluation of sixteen reference evapotranspiration methods under sahelian conditions in the Senegal River Valley. Journal of Hydrology: Regional Studies, 2015, 3, 139-159.	1.0	110
121	Covering Chemical Diversity of Genetically-Modified Tomatoes Using Metabolomics for Objective Substantial Equivalence Assessment. PLoS ONE, 2011, 6, e16989.	1.1	110
122	Structure and expression analyses of the S-adenosylmethionine synthetase gene family in Arabidopsis thaliana. Gene, 1989, 84, 359-369.	1.0	106
123	Plant lipidomics based on hydrophilic interaction chromatography coupled to ion trap time-of-flight mass spectrometry. Metabolomics, 2013, 9, 121-131.	1.4	105
124	Biosynthesis of Camptothecin. In Silico and in Vivo Tracer Study from [1-13C]Glucose. Plant Physiology, 2004, 134, 161-170.	2.3	103
125	Transgenic Medicinal Plants: Agrobacterium-Mediated Foreign Gene Transfer and Production of Secondary Metabolites. Journal of Natural Products, 1992, 55, 149-162.	1.5	102
126	Lanosterol Synthase in Dicotyledonous Plants. Plant and Cell Physiology, 2006, 47, 565-571.	1.5	102

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127	RiceAtlas, a spatial database of global rice calendars and production. Scientific Data, 2017, 4, 170074.	2.4	101
128	Yield-limiting macronutrients for rice in sub-Saharan Africa. Geoderma, 2019, 338, 546-554.	2.3	101
129	Mechanism of activation of proximate mutagens in Ames' tester strains: The acetyl-CoA dependent enzyme in Salmonella typhimurium TA98 deficient in TA981,8-DNP6 catalyzes DNA-binding as the cause of mutagenicity. Biochemical and Biophysical Research Communications, 1983, 116, 141-147.	1.0	98
130	Two flavonoid glucosyltransferases from Petunia hybrida: molecular cloning, biochemical properties and developmentally regulated expression. Plant Molecular Biology, 2002, 48, 401-411.	2.0	98
131	Leaf Oil Body Functions as a Subcellular Factory for the Production of a Phytoalexin in Arabidopsis. Plant Physiology, 2014, 164, 105-118.	2.3	98
132	Mutations in topoisomerase I as a self-resistance mechanism coevolved with the production of the anticancer alkaloid camptothecin in plants. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6782-6786.	3.3	94
133	Variability and determinants of yields in rice production systems of West Africa. Field Crops Research, 2017, 207, 1-12.	2.3	94
134	Molecular cloning and characterization of the genes encoding two isoforms of cysteine synthase in the enteric protozoan parasite Entamoeba histolytica1Note: The nucleotide sequences data reported in this paper are available in the DDBJ/EMBL/GenBankâ„¢ data bases under the accession numbers AB000266 and AB006900.1. Molecular and Biochemical Parasitology, 1998, 97, 33-44.	0.5	93
135	Metabolomics for unknown plant metabolites. Analytical and Bioanalytical Chemistry, 2013, 405, 5005-5011.	1.9	93
136	Arabidopsis Bile Acid:Sodium Symporter Family Protein 5 is Involved in Methionine-Derived Glucosinolate Biosynthesis. Plant and Cell Physiology, 2009, 50, 1579-1586.	1.5	92
137	Omics-Based Approaches to Methionine Side Chain Elongation in Arabidopsis: Characterization of the Genes Encoding Methylthioalkylmalate Isomerase and Methylthioalkylmalate Dehydrogenase. Plant and Cell Physiology, 2009, 50, 1181-1190.	1.5	92
138	Challenges and opportunities for improving N use efficiency for rice production in sub-Saharan Africa. Plant Production Science, 2019, 22, 413-427.	0.9	92
139	A WD-repeat-containing putative regulatory protein in anthocyanin biosynthesis in Perilla frutescens. Plant Molecular Biology, 2002, 50, 485-495.	2.0	91
140	Proposed quantitative and alphanumeric metabolite identification metrics. Metabolomics, 2014, 10, 1047-1049.	1.4	91
141	Phytochemical genomics in Arabidopsis thaliana: A case study for functional identification of flavonoid biosynthesis genes. Pure and Applied Chemistry, 2007, 79, 811-823.	0.9	88
142	Coupling Deep Transcriptome Analysis with Untargeted Metabolic Profiling in Ophiorrhiza pumila to Further the Understanding of the Biosynthesis of the Anti-Cancer Alkaloid Camptothecin and Anthraquinones. Plant and Cell Physiology, 2013, 54, 686-696.	1.5	88
143	Metabolomics and differential gene expression in anthocyanin chemo-varietal forms of Perilla frutescens. Phytochemistry, 2003, 62, 987-995.	1.4	87
144	Metabolomic Screening Applied to Rice FOX Arabidopsis Lines Leads to the Identification of a Gene-Changing Nitrogen Metabolism. Molecular Plant, 2010, 3, 125-142.	3.9	87

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145	Lipidomic studies of membrane glycerolipids in plant leaves under heat stress. Progress in Lipid Research, 2019, 75, 100990.	5.3	87
146	Post-genomics approaches for the elucidation of plant adaptive mechanisms to sulphur deficiency. Journal of Experimental Botany, 2004, 55, 1871-1879.	2.4	86
147	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of Arabidopsis thaliana flavonoid accumulation mutants. Plant Journal, 2010, 62, 549-559.	2.8	85
148	Biochemistry and molecular biology of the lateâ€stage of biosynthesis of anthocyanin: lessons from Perilla frutescens as a model plant. New Phytologist, 2002, 155, 9-23.	3.5	84
149	Camptothecin: Therapeutic Potential and Biotechnology. Current Pharmaceutical Biotechnology, 2007, 8, 196-202.	0.9	83
150	Capillary electrophoresisâ€“mass spectrometry reveals the distribution of carbon metabolites during nitrogen starvation in <scp>S</scp>ynechocystis sp. <scp>PCC</scp> 6803. Environmental Microbiology, 2014, 16, 512-524.	1.8	83
151	Sustainable intensification for a larger global rice bowl. Nature Communications, 2021, 12, 7163.	5.8	82
152	Occurrence of .OMEGA.-cyclohexyl fatty acids in Curtobacterium pusillum strains.. Journal of General and Applied Microbiology, 1981, 27, 261-266.	0.4	81
153	Functional characterization of a gene encoding a fourth ATP sulfurylase isoform from Arabidopsis thaliana. Gene, 2000, 248, 51-58.	1.0	80
154	Metabolic profiling of flavonoids in Lotus japonicus using liquid chromatography Fourier transform ion cyclotron resonance mass spectrometry. Phytochemistry, 2008, 69, 99-111.	1.4	80
155	A stressâ€inducible sulphotransferase sulphonates salicylic acid and confers pathogen resistance in Arabidopsis. Plant, Cell and Environment, 2010, 33, 1383-1392.	2.8	80
156	Glycyrrhiza uralensis Transcriptome Landscape and Study of Phytochemicals. Plant and Cell Physiology, 2013, 54, 697-710.	1.5	80
157	Bioreactor production of camptothecin by hairy root cultures of Ophiorrhiza pumila. Biotechnology Letters, 2002, 24, 359-363.	1.1	79
158	A flavonoid 3â€Oâ€glucoside:2â€³â€Oâ€glucosyltransferase responsible for terminal modification of pollenâ€specific flavonols in <scp>A</scp>rabidopsis thaliana. Plant Journal, 2014, 79, 769-782.	2.8	79
159	Differential Expression of Two Cytochrome P450s Involved in the Biosynthesis of Flavones and Anthocyanins in Chemo-Varietal Forms of Perilla frutescens. Plant and Cell Physiology, 2001, 42, 1338-1344.	1.5	78
160	Integration of P acquisition efficiency, P utilization efficiency and low grain P concentrations into P-efficient rice genotypes for specific target environments. Nutrient Cycling in Agroecosystems, 2016, 104, 413-427.	1.1	78
161	Combination of Liquid Chromatographyâ€“Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry with ¹³C-Labeling for Chemical Assignment of Sulfur-Containing Metabolites in Onion Bulbs. Analytical Chemistry, 2013, 85, 1310-1315.	3.2	77
162	Metabolic Reprogramming in Leaf Lettuce Grown Under Different Light Quality and Intensity Conditions Using Narrow-Band LEDs. Scientific Reports, 2018, 8, 7914.	1.6	77

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163	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405.	5.8	77
164	Functional Compensation of Primary and Secondary Metabolites by Duplicate Genes in Arabidopsis thaliana. Molecular Biology and Evolution, 2011, 28, 377-382.	3.5	76
165	Quinolizidine alkaloid biosynthesis: recent advances and future prospects. Frontiers in Plant Science, 2012, 3, 239.	1.7	76
166	PRIMe Update: Innovative Content for Plant Metabolomics and Integration of Gene Expression and Metabolite Accumulation. Plant and Cell Physiology, 2013, 54, e5-e5.	1.5	76
167	Toward better annotation in plant metabolomics: isolation and structure elucidation of 36 specialized metabolites from Oryza sativa (rice) by using MS/MS and NMR analyses. Metabolomics, 2014, 10, 543-555.	1.4	76
168	A constitutively expressed Myc-like gene involved in anthocyanin biosynthesis from Perilla frutescens: molecular characterization, heterologous expression in transgenic plants and transactivation in yeast cells. Plant Molecular Biology, 1999, 41, 33-44.	2.0	75
169	Insertional Inactivation of the Methionine S-Methyltransferase Gene Eliminates the S-Methylmethionine Cycle and Increases the Methylation Ratio. Plant Physiology, 2003, 131, 1808-1815.	2.3	75
170	Proteomic and transcriptomic analysis of Arabidopsis seeds: molecular evidence for successive processing of seed proteins and its implication in the stress response to sulfur nutrition. Plant Journal, 2006, 48, 557-571.	2.8	75
171	Network analysis for gene discovery in plantâ€specialized metabolism. Plant, Cell and Environment, 2013, 36, 1597-1606.	2.8	75
172	S-Alk(en)ylcysteine sulfoxides in the genus Allium: proposed biosynthesis, chemical conversion, and bioactivities. Journal of Experimental Botany, 2019, 70, 4123-4137.	2.4	73
173	RiceFOX: A Database of Arabidopsis Mutant Lines Overexpressing Rice Full-Length cDNA that Contains a Wide Range of Trait Information to Facilitate Analysis of Gene Function. Plant and Cell Physiology, 2011, 52, 265-273.	1.5	72
174	Pathway-Level Acceleration of Glycogen Catabolism by a Response Regulator in the Cyanobacterium Synechocystis Species PCC 6803 Â. Plant Physiology, 2014, 164, 1831-1841.	2.3	72
175	Regulation of Serine Biosynthesis in Arabidopsis. Journal of Biological Chemistry, 1999, 274, 397-402.	1.6	71
176	HEAT INDUCIBLE LIPASE1 Remodels Chloroplastic Monogalactosyldiacylglycerol by Liberating Î±-Linolenic Acid in Arabidopsis Leaves under Heat Stress. Plant Cell, 2018, 30, 1887-1905.	3.1	71
177	A conserved strategy of chalcone isomerase-like protein to rectify promiscuous chalcone synthase specificity. Nature Communications, 2020, 11, 870.	5.8	71
178	KaPPA-View4: a metabolic pathway database for representation and analysis of correlation networks of gene co-expression and metabolite co-accumulation and omics data. Nucleic Acids Research, 2011, 39, D677-D684.	6.5	69
179	Metabolic Profiling of Developing Pear Fruits Reveals Dynamic Variation in Primary and Secondary Metabolites, Including Plant Hormones. PLoS ONE, 2015, 10, e0131408.	1.1	69
180	On-farm rice yield and its association with biophysical factors in sub-Saharan Africa. European Journal of Agronomy, 2017, 85, 1-11.	1.9	69

#	Article	IF	Citations
181	Metabolite analyses of single cells. Plant Journal, 2012, 70, 30-38.	2.8	67
182	Two Cytochrome P450 Monooxygenases Catalyze Early Hydroxylation Steps in the Potato Steroid Glycoalkaloid Biosynthetic Pathway. Plant Physiology, 2016, 171, 2458-2467.	2.3	67
183	Functional specialization of <scp>UDP</scp>â€glycosyltransferase 73P12 in licorice to produce a sweet triterpenoid saponin, glycyrrhizin. Plant Journal, 2019, 99, 1127-1143.	2.8	67
184	Differential gene expression profiles of red and green forms of Perillaâ€ƒfrutescens leading to comprehensive identification of anthocyanin biosynthetic genes. FEBS Journal, 2008, 275, 3494-3502.	2.2	64
185	Metabolomics of a Single Vacuole Reveals Metabolic Dynamism in an Alga Chara australis Â Â Â. Plant Physiology, 2011, 157, 544-551.	2.3	64
186	Assessment of Metabolome Annotation Quality: A Method for Evaluating the False Discovery Rate of Elemental Composition Searches. PLoS ONE, 2009, 4, e7490.	1.1	63
187	Exploring Tomato Gene Functions Based on Coexpression Modules Using Graph Clustering and Differential Coexpression Approaches Â Â Â. Plant Physiology, 2012, 158, 1487-1502.	2.3	63
188	The Time Is Right to Focus on Model Organism Metabolomes. Metabolites, 2016, 6, 8.	1.3	63
189	Species-independent analytical tools for next-generation agriculture. Nature Plants, 2020, 6, 1408-1417.	4.7	63
190	Beta-cyanoalanine synthase and cysteine synthase from potato: molecular cloning, biochemical characterization, and spatial and hormonal regulation. Plant Molecular Biology, 2001, 46, 749-760.	2.0	62
191	Complete blockage of the mevalonate pathway results in male gametophyte lethality. Journal of Experimental Botany, 2009, 60, 2055-2064.	2.4	62
192	RNA-seq Transcriptome Analysis of Panax japonicus, and Its Comparison with Other Panax Species to Identify Potential Genes Involved in the Saponins Biosynthesis. Frontiers in Plant Science, 2016, 7, 481.	1.7	62
193	Farmers' knowledge of soils in relation to cropping practices: A case study of farmers in upland rice based slash-and-burn systems of northern Laos. Geoderma, 2006, 136, 64-74.	2.3	61
194	Application of Gene Targeting to Designed Mutation Breeding of High-Tryptophan Rice Â Â. Plant Physiology, 2011, 156, 1269-1277.	2.3	61
195	Isolation and characterization of a cDNA encoding a sulfate transporter fromArabidopsis thaliana. FEBS Letters, 1996, 392, 95-99.	1.3	60
196	2-Hydroxyisoflavanone Dehydratase is a Critical Determinant of Isoflavone Productivity in Hairy Root Cultures of Lotus japonicus. Plant and Cell Physiology, 2007, 48, 1652-1657.	1.5	60
197	Metabolite Profiling of Root Exudates of Common Bean under Phosphorus Deficiency. Metabolites, 2014, 4, 599-611.	1.3	60
198	Multiomics in Grape Berry Skin Revealed Specific Induction of the Stilbene Synthetic Pathway by Ultraviolet-C Irradiation. Plant Physiology, 2015, 168, 47-59.	2.3	60

#	Article	IF	Citations
199	De novo transcriptome assembly and characterization of nine tissues of Lonicera japonica to identify potential candidate genes involved in chlorogenic acid, luteolosides, and secoiridoid biosynthesis pathways. Journal of Natural Medicines, 2017, 71, 1-15.	1.1	60
200	The Structural Integrity of Lignin Is Crucial for Resistance against Striga hermonthica Parasitism in Rice. Plant Physiology, 2019, 179, 1796-1809.	2.3	60
201	Retrograde sulfur flow from glucosinolates to cysteine in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	60
202	Molecular characterization of plastidic phosphoserine aminotransferase in serine biosynthesis fromArabidopsis. Plant Journal, 1998, 16, 443-452.	2.8	59
203	Metabolite profiling of soybean root exudates under phosphorus deficiency. Soil Science and Plant Nutrition, 2014, 60, 679-694.	0.8	59
204	Sulfur-Responsive Elements in the 3â€²-Nontranscribed Intergenic Region Are Essential for the Induction of SULFATE TRANSPORTER 2;1 Gene Expression in Arabidopsis Roots under Sulfur Deficiency. Plant Cell, 2015, 27, 1279-1296.	3.1	59
205	Tissue-Specific Transcriptome Analysis Reveals Cell Wall Metabolism, Flavonol Biosynthesis and Defense Responses are Activated in the Endosperm of Germinating Arabidopsis thaliana Seeds. Plant and Cell Physiology, 2012, 53, 16-27.	1.5	58
206	Ky-2, a Histone Deacetylase Inhibitor, Enhances High-Salinity Stress Tolerance inArabidopsis thaliana. Plant and Cell Physiology, 2016, 57, 776-783.	1.5	58
207	Effects of Alternate Wetting and Drying Irrigation Regime and Nitrogen Fertilizer on Yield and Nitrogen Use Efficiency of Irrigated Rice in the Sahel. Water (Switzerland), 2018, 10, 711.	1.2	58
208	A cellulose synthase-derived enzyme catalyses 3-O-glucuronosylation in saponin biosynthesis. Nature Communications, 2020, 11, 5664.	5.8	58
209	Garlic ÃŽÂ³-glutamyl transpeptidases that catalyze deglutamylation of biosynthetic intermediate of alliin. Frontiers in Plant Science, 2014, 5, 758.	1.7	57
210	Syntheses of hydroxyamino, nitroso and nitro derivatives of Trp-P-2 and Glu-P-1, amino acid pyrolysate mutagens, and their direct mutagenicities towards Salmonella typhimurium TA98 and TA98NR. Carcinogenesis, 1983, 4, 1547-1550.	1.3	56
211	Succinic Semialdehyde Dehydrogenase is Involved in the Robust Patterning of Arabidopsis Leaves along the Adaxialâ€“Abaxial Axis. Plant and Cell Physiology, 2011, 52, 1340-1353.	1.5	56
212	Identification of a flavinâ€containing Sâ€oxygenating monooxygenase involved in alliin biosynthesis in garlic. Plant Journal, 2015, 83, 941-951.	2.8	56
213	Tashiromine; a New Alkaloid from Maackia tashiroi. Heterocycles, 1990, 30, 537.	0.4	56
214	cDNA cloning and expression of cysteine synthase B localized in chloroplasts ofSpinacia oleracea. FEBS Letters, 1993, 324, 247-252.	1.3	55
215	Review: genetically modified plants for the promotion of human health. Biotechnology Letters, 2006, 28, 1983-1991.	1.1	55
216	Rice Metabolomics. Rice, 2008, 1, 63-71.	1.7	55

#	Article	IF	Citations
217	Determining novel functions of Arabidopsis14-3-3 proteins in central metabolic processes. BMC Systems Biology, 2011, 5, 192.	3.0	55
218	Effects of molybdenum deficiency and defects in molybdate transporter MOT1 on transcript accumulation and nitrogen/sulphur metabolism in Arabidopsis thaliana. Journal of Experimental Botany, 2011, 62, 1483-1497.	2.4	55
219	Ectopic expression of myo-inositol 3-phosphate synthase induces a wide range of metabolic changes and confers salt tolerance in rice. Plant Science, 2015, 232, 49-56.	1.7	55
220	Rice yield growth analysis for 24 African countries over 1960â€“2012. Global Food Security, 2015, 5, 62-69.	4.0	55
221	Adaptation of the symbiotic Mesorhizobium â€“chickpea relationship to phosphate deficiency relies on reprogramming of whole-plant metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4610-9.	3.3	55
222	Activation and detoxication of N-hydroxy-Trp-P-2 by glutathione and glutathione transferases. Carcinogenesis, 1983, 4, 1551-1557.	1.3	54
223	Inhibitory Substances from Myriophyllum brasiliense on Growth of Blue-Green Algae. Journal of Natural Products, 1989, 52, 1221-1226.	1.5	54
224	Transcriptional and metabolic programs following exposure of plants to UV-B irradiation. Plant Signaling and Behavior, 2011, 6, 1987-1992.	1.2	54
225	Function of AP2/ERF Transcription Factors Involved in the Regulation of Specialized Metabolism in Ophiorrhiza pumila Revealed by Transcriptomics and Metabolomics. Frontiers in Plant Science, 2016, 7, 1861.	1.7	54
226	Two flavonol glycosides from seeds of Camellia sinensis. Phytochemistry, 1991, 30, 991-995.	1.4	53
227	Tissue-specific and stress-enhancing expression of the TR promoter for mannopine synthase in transgenic medicinal plants. Planta, 1991, 184, 40-46.	1.6	53
228	Camptothecin-related alkaloids from hairy roots of Ophiorrhiza pumila. Tetrahedron, 2002, 58, 9169-9178.	1.0	53
229	Direct isolation of flavonoids from plants using ultraâ€small anatase <scp>TiO</scp>₂ nanoparticles. Plant Journal, 2014, 77, 443-453.	2.8	53
230	Impact of the plastidial stringent response in plant growth and stress responses. Nature Plants, 2015, 1, 15167.	4.7	53
231	Molecular cloning and functional characterization of cDNAs encoding cysteine synthase and serine acetyltransferase that may be responsible for high cellular cysteine content in Allium tuberosum. Gene, 2000, 257, 269-277.	1.0	52
232	LipidBlast Templates As Flexible Tools for Creating New in-Silico Tandem Mass Spectral Libraries. Analytical Chemistry, 2014, 86, 11024-11027.	3.2	52
233	Top-down Targeted Metabolomics Reveals a Sulfur-Containing Metabolite with Inhibitory Activity against Angiotensin-Converting Enzyme in Asparagus officinalis. Journal of Natural Products, 2015, 78, 1179-1183.	1.5	52
234	A Dioxygenase Catalyzes Steroid 16Î±-Hydroxylation in Steroidal Glycoalkaloid Biosynthesis. Plant Physiology, 2017, 175, 120-133.	2.3	52

#	Article	IF	Citations
235	Regulatory mechanisms for anthocyanin biosynthesis in chemotypes of Perilla frutescens var. crispa. Biochemical Engineering Journal, 2003, 14, 191-197.	1.8	51
236	Regeneration of transformed Ophiorrhiza pumila plants producing camptothecin. Plant Biotechnology, 2004, 21, 337-342.	0.5	51
237	Suppression of camptothecin biosynthetic genes results in metabolic modification of secondary products in hairy roots of Ophiorrhiza pumila. Phytochemistry, 2013, 91, 128-139.	1.4	51
238	Integrated metabolomics and phytochemical genomics approaches for studies on rice. GigaScience, 2016, 5, 11.	3.3	51
239	Metabolic switching of astringent and beneficial triterpenoid saponins in soybean is achieved by a lossâ€ofâ€function mutation in cytochrome P450 72A69. Plant Journal, 2017, 89, 527-539.	2.8	51
240	Third DWF1 paralog in Solanaceae, sterol Î” ²⁴ -isomerase, branches withanolide biosynthesis from the general phytosterol pathway. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8096-E8103.	3.3	51
241	Camptothecins and Two New Monoterpene Glucosides from Ophiorrhiza liukiuensis. Chemical and Pharmaceutical Bulletin, 2005, 53, 1355-1358.	0.6	50
242	GCâ€“TOF-MS- and CEâ€“TOF-MS-Based Metabolic Profiling of Cheonggukjang (Fast-Fermented Bean Paste) during Fermentation and Its Correlation with Metabolic Pathways. Journal of Agricultural and Food Chemistry, 2012, 60, 9746-9753.	2.4	50
243	Transcriptome data modeling for targeted plant metabolic engineering. Current Opinion in Biotechnology, 2013, 24, 285-290.	3.3	50
244	Studies on Vacuolar Membrane Microdomains Isolated from Arabidopsis Suspension-Cultured Cells: Local Distribution of Vacuolar Membrane Proteins. Plant and Cell Physiology, 2013, 54, 1571-1584.	1.5	50
245	Molecular Evolution and Functional Characterization of a Bifunctional Decarboxylase Involved in Lycopodium Alkaloid Biosynthesis. Plant Physiology, 2016, 171, 2432-2444.	2.3	50
246	Biosynthesis of riccionidins and marchantins is regulated by R2R3-MYB transcription factors in Marchantia polymorpha. Journal of Plant Research, 2018, 131, 849-864.	1.2	50
247	General Regulatory Patterns of Plant Mineral Nutrient Depletion as Revealed by serat Quadruple Mutants Disturbed in Cysteine Synthesis. Molecular Plant, 2010, 3, 438-466.	3.9	49
248	Metabolomic Characterization of Knockout Mutants in Arabidopsis: Development of a Metabolite Profiling Database for Knockout Mutants in Arabidopsis Â Â. Plant Physiology, 2014, 165, 948-961.	2.3	49
249	On-farm testing of a nutrient management decision-support tool for rice in the Senegal River valley. Computers and Electronics in Agriculture, 2015, 116, 36-44.	3.7	49
250	Integrating transcriptome and target metabolome variability in doubled haploids of Allium cepa for abiotic stress protection. Molecular Breeding, 2015, 35, 1.	1.0	49
251	Progress in varietal improvement for increasing upland rice productivity in the tropics. Plant Production Science, 2018, 21, 145-158.	0.9	49
252	Integrated analysis of transcriptome and metabolome of Arabidopsis albino or pale green mutants with disrupted nuclear-encoded chloroplast proteins. Plant Molecular Biology, 2014, 85, 411-428.	2.0	48

#	Article	IF	Citations
253	Assessing metabolomic and chemical diversity of a soybean lineage representing 35Âyears of breeding. Metabolomics, 2015, 11, 261-270.	1.4	48
254	The Basic Helixâ€“Loopâ€“Helix Transcription Factor GubHLH3 Positively Regulates Soyasaponin Biosynthetic Genes in Glycyrrhiza uralensis. Plant and Cell Physiology, 2018, 59, 783-796.	1.5	48
255	Phosphorus micro-dosing as an entry point to sustainable intensification of rice systems in sub-Saharan Africa. Field Crops Research, 2018, 222, 39-49.	2.3	48
256	Status quo of chemical weed control in rice in sub-Saharan Africa. Food Security, 2019, 11, 69-92.	2.4	47
257	Pyrophosphate inhibits gluconeogenesis by restricting UDP-glucose formation in vivo. Scientific Reports, 2018, 8, 14696.	1.6	46
258	Metabolomics and complementary techniques to investigate the plant phytochemical cosmos. Natural Product Reports, 2021, 38, 1729-1759.	5.2	46
259	DNA binding of N-hydroxy-Trp-P-2 and N-hydroxy-Glu-P-1 by acetyl-CoA dependent enzyme in mammalian liver cytosol. Carcinogenesis, 1985, 6, 305-307.	1.3	45
260	Determination of the sites required for the allosteric inhibition of serine acetyltransferase by L-cysteine in plants. FEBS Journal, 1999, 266, 220-227.	0.2	45
261	12-Oxo-Phytodienoic Acidâ€“Glutathione Conjugate is Transported into the Vacuole in Arabidopsis. Plant and Cell Physiology, 2011, 52, 205-209.	1.5	45
262	Plastidic Pathway of Serine Biosynthesis. Journal of Biological Chemistry, 1999, 274, 11007-11012.	1.6	44
263	Evidence for the existence of rhodanese (thiosulfate:cyanide sulfurtransferase) in plants: preliminary characterization of two rhodanese cDNAs fromArabidopsis thaliana. FEBS Letters, 2000, 470, 147-150.	1.3	44
264	METABOLITE PROFILING OF SHOOT EXTRACTS, ROOT EXTRACTS, AND ROOT EXUDATES OF RICE PLANT UNDER PHOSPHORUS DEFICIENCY. Journal of Plant Nutrition, 2013, 36, 1138-1159.	0.9	44
265	Limited Si-nutrient status of rice plants in relation to plant-available Si of soils, nitrogen fertilizer application, and rice-growing environments across Sub-Saharan Africa. Field Crops Research, 2014, 155, 1-9.	2.3	44
266	Efficient and High-Throughput Vector Construction and Agrobacterium-Mediated Transformation of Arabidopsis thaliana Suspension-Cultured Cells for Functional Genomics. Plant and Cell Physiology, 2008, 49, 242-250.	1.5	43
267	Effects of freezeâ€drying of samples on metabolite levels in metabolome analyses. Journal of Separation Science, 2011, 34, 3561-3567.	1.3	43
268	CYP716A179 functions as a triterpene C-28 oxidase in tissue-cultured stolons of Glycyrrhiza uralensis. Plant Cell Reports, 2017, 36, 437-445.	2.8	43
269	Biogenetic implication of lupin alkaloid biosynthesis in bitter and sweet forms of Lupinus luteus and L. albus. Phytochemistry, 1993, 34, 1041-1044.	1.4	42
270	High-Throughput Cryopreservation of Plant Cell Cultures for Functional Genomics. Plant and Cell Physiology, 2012, 53, 943-952.	1.5	42

#	Article	IF	Citations
271	Linkage mapping, molecular cloning and functional analysis of soybean gene Fg2 encoding flavonol 3-O-glucoside (1Ââ†'Â6) rhamnosyltransferase. Plant Molecular Biology, 2014, 84, 287-300.	2.0	42
272	Omics data input for metabolic modeling. Current Opinion in Biotechnology, 2016, 37, 127-134.	3.3	42
273	Near-infrared, mid-infrared or combined diffuse reflectance spectroscopy for assessing soil fertility in rice fields in sub-Saharan Africa. Geoderma, 2019, 354, 113840.	2.3	42
274	Genetic transformation of foxglove (Digitalis purpurea) by chimeric foreign genes and production of cardioactive glycosides. Plant Cell Reports, 1990, 9, 121-4.	2.8	41
275	Alliinase [S-alk(en)yl- L-cysteine sulfoxide lyase] from Allium tuberosum (Chinese chive) . Purification, localization, cDNA cloning and heterologous functional expression. FEBS Journal, 1998, 257, 21-30.	0.2	41
276	Enhanced radical scavenging activity of genetically modified Arabidopsis seeds. Biotechnology Letters, 2005, 27, 297-303.	1.1	41
277	Transport of camptothecin in hairy roots of Ophiorrhiza pumila. Phytochemistry, 2007, 68, 2881-2886.	1.4	41
278	The function of SULTR2;1 sulfate transporter during seed development in Arabidopsis thaliana. Physiologia Plantarum, 2005, 125, 95-105.	2.6	40
279	Novel bioresources for studies of <scp>B</scp>rassica oleracea: identification of a kale <scp>MYB</scp> transcription factor responsible for glucosinolate production. Plant Biotechnology Journal, 2013, 11, 1017-1027.	4.1	40
280	Tomato Glutamate Decarboxylase GenesSlGAD2andSlGAD3Play Key Roles in Regulating Î³-Aminobutyric Acid Levels in Tomato (Solanum lycopersicum). Plant and Cell Physiology, 2015, 56, 1533-1545.	1.5	40
281	Strategic phosphorus (P) application to the nursery bed increases seedling growth and yield of transplanted rice at low P supply. Field Crops Research, 2016, 186, 10-17.	2.3	40
282	Metabolic variation in the pulps of two durian cultivars: Unraveling the metabolites that contribute to the flavor. Food Chemistry, 2018, 268, 118-125.	4.2	40
283	N-Hydroxyarylamine O-Acetyltransferase in Hamster Liver: Identity with Arylhydroxamic Acid N,O-Acetyltransferase and Arylamine N-Acetyltransferase1. Journal of Biochemistry, 1986, 99, 1689-1697.	0.9	40
284	High-Throughput Sequencing and De Novo Assembly of Red and Green Forms of the Perilla frutescens var. crispa Transcriptome. PLoS ONE, 2015, 10, e0129154.	1.1	40
285	Camptothecin Production by in Vitro Cultures of Ophiorrhiza liukiuensis and O. kuroiwai. Plant Biotechnology, 2004, 21, 275-281.	0.5	39
286	Expression of bacterial tyrosine ammonia-lyase creates a novel p-coumaric acid pathway in the biosynthesis of phenylpropanoids in Arabidopsis. Planta, 2010, 232, 209-218.	1.6	39
287	Medicago glucosyltransferase UGT72L1: potential roles in proanthocyanidin biosynthesis. Planta, 2013, 238, 139-154.	1.6	39
288	Genetic Improvement of Iron Toxicity Tolerance in Rice-Progress, Challenges and Prospects in West Africa. Plant Production Science, 2015, 18, 423-434.	0.9	39

#	Article	IF	Citations
289	Does reducing seed-P concentrations affect seedling vigor and grain yield of rice?. Plant and Soil, 2015, 392, 253-266.	1.8	39
290	Species differences in the N-acetylation by liver cytosol of mutagenic heterocyclic aromatic amines in protein pyrolysates. Carcinogenesis, 1984, 5, 683-686.	1.3	38
291	Constituents of regenerated plants of Ophiorrhiza pumila; formation of a new glycocamptothecin and predominant formation of (3R)-deoxypumiloside over (3S)-congener. Tetrahedron Letters, 1997, 38, 8997-9000.	0.7	38
292	Consolidating metabolite identifiers to enable contextual and multi-platform metabolomics data analysis. BMC Bioinformatics, 2010, 11, 214.	1.2	38
293	Solidâ€phase extraction for metabolomic analysis of highâ€salinity samples by capillary electrophoresisâ€“mass spectrometry. Journal of Separation Science, 2011, 34, 1063-1068.	1.3	38
294	Responses of Populus trichocarpa galactinol synthase genes to abiotic stresses. Journal of Plant Research, 2014, 127, 347-358.	1.2	38
295	Alternative translational initiation of ATP sulfurylase underlying dual localization of sulfate assimilation pathways in plastids and cytosol in Arabidopsis thaliana. Frontiers in Plant Science, 2014, 5, 750.	1.7	38
296	High-throughput sequencing and de novo transcriptome assembly of Swertia japonica to identify genes involved in the biosynthesis of therapeutic metabolites. Plant Cell Reports, 2016, 35, 2091-2111.	2.8	38
297	Mutations in jasmonoyl-L-isoleucine-12-hydroxylases suppress multiple JA-dependent wound responses in Arabidopsis thaliana. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 1396-1408.	1.2	38
298	De Novo RNA Sequencing and Expression Analysis of Aconitum carmichaelii to Analyze Key Genes Involved in the Biosynthesis of Diterpene Alkaloids. Molecules, 2017, 22, 2155.	1.7	38
299	Biotransformation of nicotine alkaloids by tobacco shooty teratomas induced by a Ti plasmid mutant. Plant Cell Reports, 1989, 7, 607-610.	2.8	37
300	Exploring molecular backgrounds of quality traits in rice by predictive models based on high-coverage metabolomics. BMC Systems Biology, 2011, 5, 176.	3.0	37
301	Pleiotropic effect of sigE overâ€expression on cell morphology, photosynthesis and hydrogen production in Synechocystis sp. <scp>PCC</scp> 6803. Plant Journal, 2013, 76, 456-465.	2.8	37
302	Genotypic Variation in Grain P Loading across Diverse Rice Growing Environments and Implications for Field P Balances. Frontiers in Plant Science, 2016, 7, 1435.	1.7	37
303	Unbiased profiling of volatile organic compounds in the headspace of Allium plants using an in-tube extraction device. BMC Research Notes, 2016, 9, 133.	0.6	37
304	Cytochrome P450 Monooxygenase CYP716A141 is a Unique Î²-Amyrin C-16Î² Oxidase Involved in Triterpenoid Saponin Biosynthesis in Platycodon grandiflorus. Plant and Cell Physiology, 2017, 58, 874-884.	1.5	37
305	Stable transfer and expression of chimeric genes in licorice (Glycyrrhiza uralensis) using an Ri plasmid binary vector. Plant Cell Reports, 1990, 8, 718-721.	2.8	36
306	Subcellular localization of acyltransferases for quinolizidine alkaloid biosynthesis in Lupinus. Phytochemistry, 1996, 42, 1557-1562.	1.4	36

#	Article	IF	Citations
307	Serine Acetyltransferase Involved in Cysteine Biosynthesis from Spinach: Molecular Cloning, Characterization and Expression Analysis of cDNA Encoding a Plastidic Isoform. Plant and Cell Physiology, 2001, 42, 627-634.	1.5	36
308	A New Member of Plant CS-lyases. Journal of Biological Chemistry, 2003, 278, 10291-10296.	1.6	36
309	Metabolomic Evaluation of the Quality of Leaf Lettuce Grown in Practical Plant Factory to Capture Metabolite Signature. Frontiers in Plant Science, 2018, 9, 665.	1.7	36
310	Molecular Characterization of a Novel Quinolizidine Alkaloid O-Tigloyltransferase: cDNA Cloning, Catalytic Activity of Recombinant Protein and Expression Analysis in Lupinus Plants. Plant and Cell Physiology, 2005, 46, 233-244.	1.5	35
311	An MYB transcription factor regulating specialized metabolisms in <i>Ophiorrhiza pumila</i>. Plant Biotechnology, 2016, 33, 1-9.	0.5	35
312	Metabolism of solanaceous alkaloids in transgenic plant teratomas integrated with genetically engineered genes. Tetrahedron, 1991, 47, 5955-5968.	1.0	34
313	Geranylgeranyl Diphosphate Synthase from Scoparia dulcis and Croton sublyratus. Plastid Localization and Conversion to a Farnesyl Diphosphate Synthase by Mutagenesis.. Chemical and Pharmaceutical Bulletin, 2001, 49, 197-202.	0.6	34
314	Induced accumulation of glucuronosyldiacylglycerol in tomato and soybean under phosphorus deprivation. Physiologia Plantarum, 2015, 155, 33-42.	2.6	34
315	Fruit setting rewires central metabolism via gibberellin cascades. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23970-23981.	3.3	34
316	Defective cytokinin signaling reprograms lipid and flavonoid gene-to-metabolite networks to mitigate high salinity in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
317	Transgenic herbicide-resistant Atropa belladonna using an Ri binary vector and inheritance of the transgenic trait. Plant Cell Reports, 1992, 11-11, 219-24.	2.8	33
318	Soil-based screening for iron toxicity tolerance in rice using pots. Plant Production Science, 2016, 19, 489-496.	0.9	33
319	Identification of a 3Î²-Hydroxysteroid Dehydrogenase/ 3-Ketosteroid Reductase Involved in Î±-Tomatine Biosynthesis in Tomato. Plant and Cell Physiology, 2019, 60, 1304-1315.	1.5	33
320	Determination of a functional lysine residue of a plant cysteine synthase by site-directed mutagenesis, and the molecular evolutionary implications. FEBS Letters, 1993, 328, 111-114.	1.3	32
321	Significance of accumulation of the alarmone (p)ppGpp in chloroplasts for controlling photosynthesis and metabolite balance during nitrogen starvation in Arabidopsis. Photosynthesis Research, 2018, 135, 299-308.	1.6	32
322	Metabolite profiling of shoot extract, root extract, and root exudate of rice under nitrogen and phosphorus deficiency. Soil Science and Plant Nutrition, 2018, 64, 312-322.	0.8	32
323	Efficient genome engineering using Platinum TALEN in potato. Plant Biotechnology, 2019, 36, 167-173.	0.5	32
324	Steric Course of Reaction Catalyzed by the Enoyl Acyl-Carrier-Protein Reductase of Escherichia coli. FEBS Journal, 1981, 116, 581-586.	0.2	31

#	Article	IF	Citations
325	(-)-5Î±-Hydroxysophocarpine, a New Lupin Alkaloid from the Seeds ofSophora flavescensvar.angustifolia1. Planta Medica, 1990, 56, 487-488.	0.7	31
326	Widely targeted metabolomics and coexpression analysis as tools to identify genes involved in the side-chain elongation steps of aliphatic glucosinolate biosynthesis. Amino Acids, 2010, 39, 1067-1075.	1.2	31
327	De Novo Deep Transcriptome Analysis of Medicinal Plants for Gene Discovery in Biosynthesis of Plant Natural Products. Methods in Enzymology, 2016, 576, 19-45.	0.4	31
328	Ultrahigh resolution metabolomics for S-containing metabolites. Current Opinion in Biotechnology, 2017, 43, 8-16.	3.3	31
329	Ancient rice cultivar extensively replaces phospholipids with nonâ€phosphorus glycolipid under phosphorus deficiency. Physiologia Plantarum, 2018, 163, 297-305.	2.6	31
330	Analysis of lupine alkaloids in plants by high-performance liquid chromatography. Journal of Chromatography A, 1989, 462, 333-340.	1.8	30
331	Mass Spectra-Based Framework for Automated Structural Elucidation of Metabolome Data to Explore Phytochemical Diversity. Frontiers in Plant Science, 2011, 2, 40.	1.7	30
332	Linkage mapping, molecular cloning and functional analysis of soybean gene Fg3 encoding flavonol 3-O-glucoside/galactoside (1â€‰â†'â€‰2) glucosyltransferase. BMC Plant Biology, 2015, 15, 126.	1.6	30
333	A survival strategy: The coevolution of the camptothecin biosynthetic pathway and self-resistance mechanism. Phytochemistry, 2009, 70, 1894-1898.	1.4	29
334	Deciphering Starch Quality of Rice Kernels Using Metabolite Profiling and Pedigree Network Analysis. Molecular Plant, 2012, 5, 442-451.	3.9	29
335	Identification of Î±-Tomatine 23-Hydroxylase Involved in the Detoxification of a Bitter Glycoalkaloid. Plant and Cell Physiology, 2020, 61, 21-28.	1.5	29
336	Transgenic fertile Scoparia dulcis L., a folk medicinal plant, conferred with a herbicide-resistant trait using an Ri binary vector. Plant Cell Reports, 1996, 15, 317-321.	2.8	28
337	Chemical Assignment of Structural Isomers of Sulfur-Containing Metabolites in Garlic by Liquid Chromatographyâ^'Fourier Transform Ion Cyclotron Resonanceâ^'Mass Spectrometry. Journal of Nutrition, 2016, 146, 397S-402S.	1.3	28
338	Biochar use in a legumeâ€"rice rotation system: effects on soil fertility and crop performance. Archives of Agronomy and Soil Science, 2016, 62, 199-215.	1.3	28
339	Plant Lipidomics Using UPLC-QTOF-MS. Methods in Molecular Biology, 2018, 1778, 157-169.	0.4	28
340	Metabolic Control of Gametophore Shoot Formation through Arginine in the Moss Physcomitrium patens. Cell Reports, 2020, 32, 108127.	2.9	28
341	Glutathione conjugation of arylnitroso compound: Detection and monitoring labile intermediates in situ inside a fast atom bombardment mass spectrometer. Biochemical and Biophysical Research Communications, 1984, 124, 1-5.	1.0	27
342	Acyltransferases for lupin alkaloids in Lupinus hirsutus. Phytochemistry, 1992, 32, 87-91.	1.4	27

#	Article	IF	Citations
343	Overproduction of L-cysteine and L-cystine by expression of genes for feedback inhibition-insensitive serine acetyltransferase fromArabidopsis thalianainEscherichia coli. FEMS Microbiology Letters, 1999, 179, 453-459.	0.7	27
344	Biochemical and Partial Molecular Characterization of Bitter and Sweet Forms of Lupinus angustifolius, an Experimental Model for Study of Molecular Regulation of Quinolizidine Alkaloid Biosynthesis.. Chemical and Pharmaceutical Bulletin, 2000, 48, 1458-1461.	0.6	27
345	Inhibition of CUTIN DEFICIENT 2 Causes Defects in Cuticle Function and Structure and Metabolite Changes in Tomato Fruit. Plant and Cell Physiology, 2013, 54, 1535-1548.	1.5	27
346	Comparative Characterization of the Leaf Tissue of Physalis alkekengi and Physalis peruviana Using RNA-seq and Metabolite Profiling. Frontiers in Plant Science, 2016, 7, 1883.	1.7	27
347	Cloning and characterization of soybean gene Fg1 encoding flavonol 3-O-glucoside/galactoside (1â†'6) glucosyltransferase. Plant Molecular Biology, 2016, 92, 445-456.	2.0	27
348	Transcriptomic and Metabolomic Reprogramming from Roots to Haustoria in the Parasitic Plant, Thesium chinense. Plant and Cell Physiology, 2018, 59, 729-738.	1.5	27
349	Lupin alkaloids from the seeds of Thermopsis lupinoides. Phytochemistry, 1988, 27, 3715-3716.	1.4	26
350	Absolute configuration of (+)-5,6-dehydrolupanine, a key intermediate in biosynthesis of lupin alkaloids. Phytochemistry, 1989, 28, 958-959.	1.4	26
351	Greening induced production of (+)-lupanine in tissue culture of Thermopsis lupinoides. Phytochemistry, 1989, 28, 2341-2344.	1.4	26
352	Lupin alkaloids in tissue culture of Sophora flavescens var. angustifolia: Greening induced production of matrine.. Chemical and Pharmaceutical Bulletin, 1989, 37, 3001-3004.	0.6	26
353	Analysis of systemic sulfur metabolism in plants using integrated â€˜-omicsâ€™ strategies. Molecular BioSystems, 2008, 4, 967.	2.9	26
354	HIGH STEROL ESTER 1 is a key factor in plant sterol homeostasis. Nature Plants, 2019, 5, 1154-1166.	4.7	26
355	A new era in plant functional genomics. Current Opinion in Systems Biology, 2019, 15, 58-67.	1.3	26
356	Keeping the shape of plant tissue for visualizing metabolite features in segmentation and correlation analysis of imaging mass spectrometry in Asparagus officinalis. Metabolomics, 2019, 15, 24.	1.4	26
357	Integrative omics approaches revealed a crosstalk among phytohormones during tuberous root development in cassava. Plant Molecular Biology, 2022, 109, 249-269.	2.0	26
358	Metabolite profiling of the hyphal exudates of Rhizophagus clarus and Rhizophagus irregularis under phosphorus deficiency. Mycorrhiza, 2021, 31, 403-412.	1.3	26
359	Characterization of PAP1-upregulated Glutathione S-transferase genes in Arabidopsis thaliana. Plant Biotechnology, 2008, 25, 191-196.	0.5	25
360	Rice-Arabidopsis FOX line screening with FT-NIR-based fingerprinting for GC-TOF/MS-based metabolite profiling. Metabolomics, 2010, 6, 137-145.	1.4	25

#	Article	IF	Citations
361	Phytochemical Genomics on the Way. Plant and Cell Physiology, 2013, 54, 645-646.	1.5	25
362	Top-down Metabolomic Approaches for Nitrogen-Containing Metabolites. Analytical Chemistry, 2017, 89, 2698-2703.	3.2	25
363	De Novo Transcriptome Assembly and Characterization of Lithospermum officinale to Discover Putative Genes Involved in Specialized Metabolites Biosynthesis. Planta Medica, 2018, 84, 920-934.	0.7	25
364	Cytosolic GLUTAMINE SYNTHETASE1;1 Modulates Metabolism and Chloroplast Development in Roots. Plant Physiology, 2020, 182, 1894-1909.	2.3	25
365	The biosynthetic pathway of potato solanidanes diverged from that of spirosolanes due to evolution of a dioxygenase. Nature Communications, 2021, 12, 1300.	5.8	25
366	Agronomic gain: Definition, approach, and application. Field Crops Research, 2021, 270, 108193.	2.3	25
367	An acyltransferase-like gene obtained by differential gene expression profiles of quinolizidine alkaloid-producing and nonproducing cultivars of Lupinus angustifolius. Plant Biotechnology, 2011, 28, 89-94.	0.5	25
368	Molecular cloning, characterization and expression of cDNA encoding phosphoserine aminotransferase involved in phosphorylated pathway of serine biosynthesis from spinach. Plant Molecular Biology, 1997, 33, 359-366.	2.0	24
369	Network Analyses Reveal Shifts in Transcript Profiles and Metabolites That Accompany the Expression of SUN and an Elongated Tomato Fruit. Plant Physiology, 2015, 168, 1164-1178.	2.3	24
370	Transgenic rice seed expressing flavonoid biosynthetic genes accumulate glycosylated and/or acylated flavonoids in protein bodies. Journal of Experimental Botany, 2016, 67, 95-106.	2.4	24
371	Lysine-derived Alkaloids: Overview and Update on Biosynthesis and Medicinal Applications with Emphasis on Quinolizidine Alkaloids. Mini-Reviews in Medicinal Chemistry, 2017, 17, 1002-1012.	1.1	24
372	Steric Course of Deuterium Incorporation from [2-2H2]Manlonyl-CoA into Fatty Acids by Fatty Acid Synthetases1. Journal of Biochemistry, 1981, 90, 1697-1704.	0.9	23
373	Simultaneous quantitative measurement of fourteen adrenal steroids by capillary column gas chromatographyî—¸mass spectrometry, and its clinical application. Biomedical Applications, 1986, 374, 5-16.	1.7	23
374	Expressed sequence tags from rhizomes of Glycyrrhiza uralensis. Plant Biotechnology, 2009, 26, 105-107.	0.5	23
375	Plasma Membrane Aquaporin AqpZ Protein Is Essential for Glucose Metabolism during Photomixotrophic Growth of Synechocystis sp. PCC 6803. Journal of Biological Chemistry, 2011, 286, 25224-25235.	1.6	23
376	ACR11 is an Activator of Plastid-Type Glutamine Synthetase GS2 in Arabidopsis thaliana. Plant and Cell Physiology, 2017, 58, 650-657.	1.5	23
377	UGT79B31 is responsible for the final modification step of pollen-specific flavonoid biosynthesis in Petunia hybrida. Planta, 2018, 247, 779-790.	1.6	23
378	Lupin alkaloids fromSophora exigua. Phytochemistry, 1991, 30, 3793-3795.	1.4	22

#	Article	IF	Citations
379	Transcriptome Analysis of Nine Tissues to Discover Genes Involved in the Biosynthesis of Active Ingredients in <i>Sophora flavescens</i>. Biological and Pharmaceutical Bulletin, 2015, 38, 876-883.	0.6	22
380	Labor-Saving Weed Technologies for Lowland Rice Farmers in sub-Saharan Africa. Weed Technology, 2015, 29, 751-757.	0.4	22
381	Characterization of steroid 5Î±-reductase involved in Î±-tomatine biosynthesis in tomatoes. Plant Biotechnology, 2019, 36, 253-263.	0.5	22
382	Differential expression of SlKLUH controlling fruit and seed weight is associated with changes in lipid metabolism and photosynthesis-related genes. Journal of Experimental Botany, 2021, 72, 1225-1244.	2.4	22
383	History and progress in genetic improvement for enhancing rice yield in sub-Saharan Africa. Field Crops Research, 2021, 267, 108159.	2.3	22
384	(+)-13.BETA.-Hydroxymamanine, a new lupin alkaloid from Maackia amurensis var. buergeri.. Chemical and Pharmaceutical Bulletin, 1986, 34, 3982-3985.	0.6	21
385	Isolation of (+)-maackiamine (norammodendrine) from the flowers of Maackia amurensis. Phytochemistry, 1989, 28, 2533-2534.	1.4	21
386	Modification and Stabilization of Anthocyanins. , 2008, , 169-190.		21
387	Role of Metabolomics in Crop Improvement. Journal of Plant Biochemistry and Biotechnology, 2012, 21, 24-31.	0.9	21
388	A Screening Protocol for Vegetativeâ€stage Tolerance to Phosphorus Deficiency in Upland Rice. Crop Science, 2015, 55, 1223-1229.	0.8	21
389	Transcriptomic landscape of Pueraria lobata demonstrates potential for phytochemical study. Frontiers in Plant Science, 2015, 6, 426.	1.7	21
390	Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. Plant Physiology, 2017, 173, 2010-2028.	2.3	21
391	Targeted genome editing in tetraploid potato through transient TALEN expression by <i>Agrobacterium</i> infection. Plant Biotechnology, 2020, 37, 205-211.	0.5	21
392	Origin of Hydrogen Atoms in the Fatty Acids Synthesized with Yeast Fatty Acid Synthetase1. Journal of Biochemistry, 1977, 82, 1325-1329.	0.9	20
393	Spatial and temporal variation in yield of rainfed lowland rice in inland valley as affected by fertilizer application and bunding in North-West Benin. Agricultural Water Management, 2013, 126, 119-124.	2.4	20
394	An improved tolerance to cadmium by overexpression of two genes for cysteine synthesis in tobacco. Plant Biotechnology, 2014, 31, 141-147.	0.5	20
395	The significance of cysteine synthesis for acclimation to high light conditions. Frontiers in Plant Science, 2014, 5, 776.	1.7	20
396	Lipidomic analysis of soybean leaves revealed tissue-dependent difference in lipid remodeling under phosphorus-limited growth conditions. Plant Biotechnology, 2017, 34, 57-63.	0.5	20

#	Article	IF	Citations
397	Seasonal Alterations in Organic Phosphorus Metabolism Drive the Phosphorus Economy of Annual Growth in F. sylvatica Trees on P-Impoverished Soil. Frontiers in Plant Science, 2018, 9, 723.	1.7	20
398	Dual-Localized Enzymatic Components Constitute the Fatty Acid Synthase Systems in Mitochondria and Plastids. Plant Physiology, 2020, 183, 517-529.	2.3	20
399	Thirty years of agronomy research for development in irrigated rice-based cropping systems in the West African Sahel: Achievements and perspectives. Field Crops Research, 2021, 266, 108149.	2.3	20
400	Comparative metabolomics charts the impact of genotype-dependent methionine accumulation in Arabidopsis thaliana. Amino Acids, 2010, 39, 1013-1021.	1.2	19
401	Exploring Matrix Effects and Quantification Performance in Metabolomics Experiments Using Artificial Biological Gradients. Analytical Chemistry, 2011, 83, 5645-5651.	3.2	19
402	Metabolome Analysis of <i>Oryza sativa</i> (Rice) Using Liquid Chromatography-Mass Spectrometry for Characterizing Organ Specificity of Flavonoids with Anti-inflammatory and Anti-oxidant Activity. Chemical and Pharmaceutical Bulletin, 2016, 64, 952-956.	0.6	19
403	Metabolomics with ¹⁵N Labeling for Characterizing Missing Monoterpene Indole Alkaloids in Plants. Analytical Chemistry, 2020, 92, 5670-5675.	3.2	19
404	Absolute configuration of (-)-lusitanine, a new lupin alkaloid in Maackia species.. Chemical and Pharmaceutical Bulletin, 1987, 35, 1308-1310.	0.6	18
405	Isolation of a New Alkaloid (-)-0- Acetylbaptifoline and the Absolute Stereochemical Relationships of Lupine Alkaloids in Thermopsis chinensis. Journal of Natural Products, 1989, 52, 1032-1035.	1.5	18
406	Lupin alkaloids from the seeds of Lupinus termis. Phytochemistry, 1991, 30, 3111-3115.	1.4	18
407	Chemistry, biochemistry and chemotaxonomy of lupine alkaloids in the leguminosae. Studies in Natural Products Chemistry, 1995, , 519-549.	0.8	18
408	Chapter 1 Lupine Alkaloids. Alkaloids: Chemistry and Pharmacology, 1995, , 1-114.	0.2	18
409	Genomic structure and expression analyses of serine acetyltransferase gene in Citrullus vulgaris (watermelon). Gene, 1997, 189, 57-63.	1.0	18
410	Mechanistic Study on the Oxidation of Anthocyanidin Synthase by Quantum Mechanical Calculation. Journal of Biological Chemistry, 2006, 281, 21387-21398.	1.6	18
411	Correlation of Camptothecin-producing Ability and Phylogenetic Relationship in the GenusOphiorrhiza. Planta Medica, 2011, 77, 759-764.	0.7	18
412	Development of a Direct Headspace Collection Method from Arabidopsis Seedlings Using HS-SPME-GC-TOF-MS Analysis. Metabolites, 2013, 3, 223-242.	1.3	18
413	Revisiting anabasine biosynthesis in tobacco hairy roots expressing plant lysine decarboxylase gene by using ¹⁵N-labeled lysine. Plant Biotechnology, 2014, 31, 511-518.	0.5	18
414	Metabolomic analysis reveals rewiring of <scp>S</scp>ynechocystisâ€¦<scp>sp</scp>. <scp>PCC</scp> 6803 primary metabolism by ntcA overexpression. Environmental Microbiology, 2014, 16, 3304-3317.	1.8	18

#	Article	IF	Citations
415	Onocerin Biosynthesis Requires Two Highly Dedicated Triterpene Cyclases in a Fern Lycopodium clavatum. ChemBioChem, 2016, 17, 288-290.	1.3	18
416	Conferring highâ€temperature tolerance to nontransgenic tomato scions using graft transmission of <scp>RNA</scp> silencing of the fatty acid desaturase gene. Plant Biotechnology Journal, 2016, 14, 783-790.	4.1	18
417	Metabolomics analysis of 'Housui' Japanese pear flower buds during endodormancy reveals metabolic suppression by thermal fluctuation. Plant Physiology and Biochemistry, 2018, 126, 134-141.	2.8	18
418	WIND1 induces dynamic metabolomic reprogramming during regeneration in Brassica napus. Developmental Biology, 2018, 442, 40-52.	0.9	18
419	Divergent metabolic adjustments in nodules are indispensable for efficient N2 fixation of soybean under phosphate stress. Plant Science, 2019, 289, 110249.	1.7	18
420	Higher dimensional metabolomics using stable isotope labeling for identifying the missing specialized metabolism in plants. Current Opinion in Plant Biology, 2020, 55, 84-92.	3.5	18
421	Food Lipidomics for 155 Agricultural Plant Products. Journal of Agricultural and Food Chemistry, 2021, 69, 8981-8990.	2.4	18
422	Camptothecin Production by In Vitro Cultures and Plant Regeneration in Ophiorrhiza Species. Methods in Molecular Biology, 2009, 547, 337-345.	0.4	18
423	Glycosidic alkaloids from Lupinus hirsutus. Phytochemistry, 1990, 29, 3923-3926.	1.4	17
424	New Lupine Alkaloids from the Seedlings of Lupinus hirsutus and Change of Alkaloid Pattern with Germination. Journal of Natural Products, 1991, 54, 477-482.	1.5	17
425	Biosynthetic system of camptothecin: An anticancer plant product. Pure and Applied Chemistry, 2010, 82, 213-218.	0.9	17
426	Perspective: functional genomics towards new biotechnology in medicinal plants. Plant Biotechnology Reports, 2018, 12, 69-75.	0.9	17
427	Metabolite and Phytohormone Profiling Illustrates Metabolic Reprogramming as an Escape Strategy of Deepwater Rice during Partially Submerged Stress. Metabolites, 2020, 10, 68.	1.3	17
428	A new assay for N-hydroxyarylamine O-acetyltransferase: Reduction of N-hydroxyarylamines through N-acetoxyarylamines. Analytical Biochemistry, 1986, 152, 226-231.	1.1	16
429	A New Lupine Alkaloid, (-)-Î”5S-Dehydromultiflorine, from the Seeds of Lupinus termis. Journal of Natural Products, 1990, 53, 1578-1580.	1.5	16
430	Isolation and enzymatic synthesis of an ester alkaloid, (âˆ’)-3Î²-hydroxy-13Î±-tigloyloxylupanine, from Cytisus scoparius. Phytochemistry, 1994, 36, 309-311.	1.4	16
431	Expression and functional analyses of a putative phenylcoumaran benzylic ether reductase in Arabidopsis thaliana. Plant Cell Reports, 2016, 35, 513-526.	2.8	16
432	Effects of Combined Low Glutathione with Mild Oxidative and Low Phosphorus Stress on the Metabolism of Arabidopsis thaliana. Frontiers in Plant Science, 2017, 8, 1464.	1.7	16

#	Article	IF	Citations
433	Acceleration of Mechanistic Investigation of Plant Secondary Metabolism Based on Computational Chemistry. Frontiers in Plant Science, 2019, 10, 802.	1.7	16
434	Assessing Dynamic Changes of Taste-Related Primary Metabolism During Ripening of Durian Pulp Using Metabolomic and Transcriptomic Analyses. Frontiers in Plant Science, 2021, 12, 687799.	1.7	16
435	Camptothecin. Advances in Botanical Research, 2013, 68, 139-161.	0.5	15
436	Structural insight of DNA topoisomerases I from camptothecin-producing plants revealed by molecular dynamics simulations. Phytochemistry, 2015, 113, 50-56.	1.4	15
437	A novel role for methyl cysteinate, a cysteine derivative, in cesium accumulation in Arabidopsis thaliana. Scientific Reports, 2017, 7, 43170.	1.6	15
438	How Can West African Rice Compete in Urban Markets? A Demand Perspective for Policymakers. EuroChoices, 2018, 17, 51-57.	0.6	15
439	Comparative transcriptome analyses of three medicinal Forsythia species and prediction of candidate genes involved in secondary metabolisms. Journal of Natural Medicines, 2018, 72, 867-881.	1.1	15
440	Transcriptome analysis of Pueraria candollei var. mirifica for gene discovery in the biosyntheses of isoflavones and miroestrol. BMC Plant Biology, 2019, 19, 581.	1.6	15
441	Metabolomics continues to expand: highlights from the 2015 metabolomics conference. Metabolomics, 2015, 11, 1036-1040.	1.4	14
442	Enhancement of abiotic stress tolerance in poplar by overexpression of key Arabidopsis stress response genes, AtSRK2C and AtGolS2. Molecular Breeding, 2017, 37, 1.	1.0	14
443	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in Arabidopsis thaliana Accessions. Molecular Biology and Evolution, 2017, 34, 3111-3122.	3.5	14
444	Feeding the world while reducing farmer poverty? Analysis of rice relative yield and labour productivity gaps in two Beninese villages. European Journal of Agronomy, 2018, 93, 95-112.	1.9	14
445	Maize Glossy2 and Glossy2-like Genes Have Overlapping and Distinct Functions in Cuticular Lipid Deposition. Plant Physiology, 2020, 183, 840-853.	2.3	14
446	Tomato E8 Encodes a C-27 Hydroxylase in Metabolic Detoxification of Î±-Tomatine during Fruit Ripening. Plant and Cell Physiology, 2021, 62, 775-783.	1.5	14
447	Intercellular Localization of Cysteine Synthase and Alliinase in Bundle Sheaths of Allium Plants. Plant Biotechnology, 2002, 19, 7-10.	0.5	14
448	The prediction of local modular structures in a co-expression network based on gene expression datasets. Genome Informatics, 2009, 23, 117-27.	0.4	14
449	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. Journal of Plant Research, 2010, 123, 291-298.	1.2	13
450	A polyhedral approach for understanding flavonoid biosynthesis in Arabidopsis. New Biotechnology, 2010, 27, 829-836.	2.4	13

#	Article	IF	Citations
451	Multidisciplinary assessment of agricultural innovation and its impact: a case study of lowland rice variety WITA 9 in CÃ´te dâ€™Ivoire. Plant Production Science, 2019, 22, 428-442.	0.9	13
452	Transcriptome Analysis of the Hierarchical Response of Histone Deacetylase Proteins That Respond in an Antagonistic Manner to Salinity Stress. Frontiers in Plant Science, 2019, 10, 1323.	1.7	13
453	Identification of potential genes involved in triterpenoid saponins biosynthesis in Gleditsia sinensis by transcriptome and metabolome analyses. Journal of Natural Medicines, 2019, 73, 369-380.	1.1	13
454	Creating the data basis to adapt agricultural decision support tools to new environments, land management and climate changeâ€”A case study of the RiceAdvice App. Journal of Agronomy and Crop Science, 2020, 206, 423-432.	1.7	13
455	Seed-coat protective neolignans are produced by the dirigent protein AtDP1 and the laccase AtLAC5 in Arabidopsis. Plant Cell, 2021, 33, 129-152.	3.1	13
456	(+)-Acacialactam, a new seven-membered lactam from the seeds of Acacia concinna.. Chemical and Pharmaceutical Bulletin, 1989, 37, 3164-3165.	0.6	12
457	Predicting state transitions in the transcriptome and metabolome using a linear dynamical system model. BMC Bioinformatics, 2007, 8, 343.	1.2	12
458	Automation of chemical assignment for identifying molecular formula of S-containing metabolites by combining metabolomics and chemoinformatics with 34S labeling. Metabolomics, 2016, 12, 1.	1.4	12
459	Effect of exogenous GA4â€¯+â€¯7 and BAâ€¯+â€¯CPPU treatments on fruit lignin and primary metabolites in Japanese pear â€œGold Nijisseikiâ€• Scientia Horticulturae, 2020, 272, 109593.	1.7	12
460	CRISPR/Cas9-mediated disruption of the PYRROLIDINE KETIDE SYNTHASE gene reduces the accumulation of tropane alkaloids in Atropa belladonna hairy roots. Bioscience, Biotechnology and Biochemistry, 2021, 85, 2404-2409.	0.6	12
461	Taxonomic significance of the position of double bonds of unsaturated fatty acids in Corynebacteria.. Journal of General and Applied Microbiology, 1982, 28, 409-416.	0.4	12
462	[Special Issue: Fact Databases and Freewares] Integrated Data Mining of Transcriptome and Metabolome Based on BL-SOM. Journal of Computer Aided Chemistry, 2006, 7, 125-136.	0.3	12
463	DNA single-strand breaks by nitropyrenes and related compounds in Chinese hamster V79 cells. Cancer Letters, 1984, 24, 121-127.	3.2	11
464	Inhibition of acetyl-coenzyme A dependent activation of N-hydroxyarylamines by phenolic compounds, pentachlorophenol and 1-nitro-2-naphthol. Chemico-Biological Interactions, 1986, 60, 275-285.	1.7	11
465	Genetic Engineering in Tissue Culture of Medicinal Plants.. Plant Tissue Culture Letters, 1993, 10, 1-8.	0.1	11
466	KAGIANA: An Excel-Based Tool for Retrieving Summary Information on Arabidopsis Genes. Plant and Cell Physiology, 2009, 50, 173-177.	1.5	11
467	Linkage between circadian clock and tricarboxylic acid cycle in Arabidopsis. Plant Signaling and Behavior, 2009, 4, 660-662.	1.2	11
468	Transcriptome Coexpression Analysis Using ATTED-II for Integrated Transcriptomic/Metabolomic Analysis. Methods in Molecular Biology, 2013, 1011, 317-326.	0.4	11

#	Article	IF	Citations
469	Identification of Serratane Synthase Gene from the Fern Lycopodium clavatum. Organic Letters, 2017, 19, 496-499.	2.4	11
470	Molecular components of Arabidopsis intact vacuoles clarified with metabolomic and proteomic analyses. Plant and Cell Physiology, 2018, 59, 1353-1362.	1.5	11
471	The Energetic Viability of Î”1-Piperideine Dimerization in Lysine-derived Alkaloid Biosynthesis. Metabolites, 2018, 8, 48.	1.3	11
472	Metabolic diversification of nitrogenâ€containing metabolites by the expression of a heterologous lysine decarboxylase gene in Arabidopsis. Plant Journal, 2019, 100, 505-521.	2.8	11
473	Molecular Basis of C-30 Product Regioselectivity of Legume Oxidases Involved in High-Value Triterpenoid Biosynthesis. Frontiers in Plant Science, 2019, 10, 1520.	1.7	11
474	FARMERSâ€™ PERCEPTIONS ON MECHANICAL WEEDERS FOR RICE PRODUCTION IN SUB-SAHARAN AFRICA. Experimental Agriculture, 2019, 55, 117-131.	0.4	11
475	cDNA Cloning and Gene Expression of Anthocyanidin Synthase from Torenia fournieri.. Plant Biotechnology, 2000, 17, 331-335.	0.5	11
476	Interactions between the active metabolite of tryptophan pyrolysate mutagen, N-hydroxy-Trp-P-2, and lipids: The role of lipid peroxides in the conversion of N-hydroxy-Trp-P-2 to non-reactive forms. Chemico-Biological Interactions, 1983, 45, 295-304.	1.7	10
477	A glycosidic lupin alkaloid from Lupinus hirsutus. Phytochemistry, 1994, 37, 591-592.	1.4	10
478	Production of Pharmaceuticals by Plant Tissue Cultures. , 2010, , 615-628.		10
479	Successful expression of a novel bacterial gene for pinoresinol reductase and its effect on lignan biosynthesis in transgenic Arabidopsis thaliana. Applied Microbiology and Biotechnology, 2014, 98, 8165-8177.	1.7	10
480	Factors affecting farmersâ€™ adoption of NERICA upland rice varieties: the case of a seed producing village in central Benin. Food Security, 2016, 8, 197-209.	2.4	10
481	Variations in agronomic and grain quality traits of rice grown under irrigated lowland conditions in West Africa. Food Science and Nutrition, 2018, 6, 970-982.	1.5	10
482	New otonecine-type pyrrolizidine alkaloid from Petasites japonicus. Journal of Natural Medicines, 2019, 73, 602-607.	1.1	10
483	Metabolomic analysis of night-released soybean root exudates under high- and low-K conditions. Plant and Soil, 2020, 456, 259-276.	1.8	10
484	Metabolite/phytohormoneâ€“gene regulatory networks in soybean organs under dehydration conditions revealed by integration analysis. Plant Journal, 2020, 103, 197-211.	2.8	10
485	Differential hydrogen exchange during the fatty acid synthetase reaction: Deuterium distribution of fatty acids synthesized from [2-2H2]malonyl-CoA. Biochemical and Biophysical Research Communications, 1982, 108, 995-1001.	1.0	9
486	Boosting Sensitivity in Liquid Chromatographyâ€“Fourier Transform Ion Cyclotron Resonanceâ€“Tandem Mass Spectrometry for Product Ion Analysis of Monoterpene Indole Alkaloids. Frontiers in Plant Science, 2015, 6, 1127.	1.7	9

#	Article	IF	Citations
487	Intraspecific comparative analyses of metabolites between diploid and tetraploid Arabidopsis thaliana and Pyrus communis. New Negatives in Plant Science, 2015, 1-2, 53-61.	0.9	9
488	A Systems Analysis With â€œSimplified Source-Sink Modelâ€•Reveals Metabolic Reprogramming in a Pair of Source-to-Sink Organs During Early Fruit Development in Tomato by LED Light Treatments. Frontiers in Plant Science, 2018, 9, 1439.	1.7	9
489	Producing the sulfur-containing metabolite asparaptine in <i>Asparagus</i> calluses and a suspension cell line. Plant Biotechnology, 2019, 36, 265-267.	0.5	9
490	Genes in Alkaloid Metabolism. , 1998, , 147-157.		9
491	Cryopreservation and metabolic profiling analysis of Arabidopsis T87 suspension-cultured cells. Cryo-Letters, 2008, 29, 427-36.	0.1	9
492	Isotopic Combinatomer Analysis Provides in Vivo Evidence of the Direct Epimerization of Monoglucosyl Diacylglycerol in Cyanobacteria. Biochemistry, 2016, 55, 5689-5701.	1.2	8
493	Computational study on a puzzle in the biosynthetic pathway of anthocyanin: Why is an enzymatic oxidation/ reduction process required for a simple tautomerization?. PLoS ONE, 2018, 13, e0198944.	1.1	8
494	Multiomics-based characterization of specialized metabolites biosynthesis in Cornus Officinalis. DNA Research, 2020, 27, .	1.5	8
495	Expression of theEscherichia coli fabA gene encoding Î²-hydroxydecanoyl thioester dehydrase and transport to chloroplasts in transgenic tobacco. Transgenic Research, 1995, 4, 60-69.	1.3	7
496	In silico assessment of gene function involved in cysteine biosynthesis in Arabidopsis: expression analysis of multiple isoforms of serine acetyltransferase. Amino Acids, 2006, 30, 163-171.	1.2	7
497	A screening protocol for developing high-yielding upland rice varieties with superior weed-suppressive ability. Field Crops Research, 2014, 168, 119-125.	2.3	7
498	Plant Characteristics of Highâ€Yielding Upland Rice Cultivars in West Africa. Crop Science, 2016, 56, 276-286.	0.8	7
499	Temporal lag between gene expression and metabolite accumulation in flavonol biosynthesis of Arabidopsis roots. Phytochemistry Letters, 2017, 22, 44-48.	0.6	7
500	Why did farmers stop cultivating NERICA upland rice varieties in central Benin?. International Journal of Agricultural Sustainability, 2017, 15, 724-734.	1.3	7
501	Genetic divergence in transcriptional regulators of defense metabolism: insight into plant domestication and improvement. Plant Molecular Biology, 2022, 109, 401-411.	2.0	7
502	Characterization of Câ€26 aminotransferase, indispensable for steroidal glycoalkaloid biosynthesis. Plant Journal, 2021, 108, 81-92.	2.8	7
503	A multimodal metabolomics approach using imaging mass spectrometry and liquid chromatography-tandem mass spectrometry for spatially characterizing monoterpene indole alkaloids secreted from roots. Plant Biotechnology, 2021, 38, 305-310.	0.5	7
504	Plant Cell Cultures as Producers of Secondary Compounds. , 2002, , .		7

#	Article	IF	Citations
505	Overexpression of a plant cysteine synthase gene and biosynthesis of a plant specific metabolite, Î²-(pyrazol-1-yl)-L-alanine, in Escherichia coli. Canadian Journal of Chemistry, 1994, 72, 188-192.	0.6	6
506	Sulfur-responsive promoter of sulfate transporter gene is potentially useful to detect and quantify selenate and chromate. Plant Biotechnology, 2007, 24, 261-263.	0.5	6
507	Changes in Primary and Secondary Metabolite Levels in Response to Gene Targeting-Mediated Site-Directed Mutagenesis of the Anthranilate Synthase Gene in Rice. Metabolites, 2012, 2, 1123-1138.	1.3	6
508	Molecular Biology and Biotechnology of Quinolizidine Alkaloid Biosynthesis in Leguminosae Plants. , 2013, , 263-273.		6
509	Changes intrans-S-1-Propenyl-l-cysteine Sulfoxide and Related Sulfur-Containing Amino Acids during Onion Storage. Journal of Agricultural and Food Chemistry, 2016, 64, 9063-9071.	2.4	6
510	Informatics framework of traditional Sino-Japanese medicine (Kampo) unveiled by factor analysis. Journal of Natural Medicines, 2016, 70, 107-114.	1.1	6
511	Plant and soil P determine functional attributes of subalpine Australian plants. Arctic, Antarctic, and Alpine Research, 2018, 50, .	0.4	6
512	Spatial metabolomics using imaging mass spectrometry to identify the localization of asparaptine A in <i>Asparagus officinalis</i>. Plant Biotechnology, 2021, 38, 311-315.	0.5	6
513	Biosynthesis of S-Alk(en)yl-l-Cysteine Sulfoxides in Allium: Retro Perspective. Proceedings of the International Plant Sulfur Workshop, 2017, , 49-60.	0.1	6
514	Transformation of Perilla frutescens var. crispa Using an Agrobacterium-Ri Binary Vector System.. Plant Biotechnology, 1997, 14, 169-173.	0.5	6
515	Critical Role of Alanine-161 in Delila Protein Involved in Regulation of Anthocyanin Pigmentation for Transcriptional Activation in Yeast.. Plant Biotechnology, 2000, 17, 309-314.	0.5	6
516	Visualization of metabolite identifier information. Plant Biotechnology, 2009, 26, 479-483.	0.5	6
517	Development of RIKEN Plant Metabolome MetaDatabase. Plant and Cell Physiology, 2022, 63, 433-440.	1.5	6
518	Reconfirmation of the structure of (+)-retamine fromLygos raetam Var.sarcocarpa by X-ray analysis. Phytochemical Analysis, 1995, 6, 302-305.	1.2	5
519	Anionic Nutrient Transport in Plants: The Molecular Basis of the Sulfate Transporter Gene Family. , 2006, 27, 67-80.		5
520	Molecular Genetic Study on the Anthocyanin Chemotypes of Perilla frutescens var. crispa. Natural Product Communications, 2011, 6, 1934578X1100600.	0.2	5
521	Changes in the concentrations of vitamin E analogs and their metabolites in rat liver and kidney after oral administration. Journal of Clinical Biochemistry and Nutrition, 2015, 56, 143-148.	0.6	5
522	The metabolic profile of grape berry skin and a comparison of metabolomes before veraison and at harvest. Plant Biotechnology, 2015, 32, 267-272.	0.5	5

#	Article	IF	Citations
523	Epigenetic floral homeotic mutation in pD991-AP3-derived T-DNA-tagged lines for CTP:Phosphorylcholine cytidylyltransferase (CCT) Genes: The homeotic mutation of the cct1-1 allele is enhanced by the cct2 allele and alleviated by CCT1 overexpression. Journal of Plant Biology, 2015, 58, 183-192.	0.9	5
524	MassBase: A large-scaled depository of mass spectrometry datasets for metabolome analysis. Plant Biotechnology, 2021, 38, 167-171.	0.5	5
525	Tandem Gene Duplication of Dioxygenases Drives the Structural Diversity of Steroidal Glycoalkaloids in the Tomato Clade. Plant and Cell Physiology, 2022, 63, 981-990.	1.5	5
526	Synthesis of polyunsaturated fatty acid-containing glucuronosyl-diacylglycerol through direct glycosylation. Tetrahedron Letters, 2017, 58, 2915-2918.	0.7	4
527	Allylic Hydroxylation Activity Is a Source of Saponin Chemodiversity in the Genus Glycyrrhiza. Plant and Cell Physiology, 2021, 62, 262-271.	1.5	4
528	Tandem Mass Spectrum Similarity-Based Network Analysis Using ¹³C-Labeled and Non-labeled Metabolome Data to Identify the Biosynthetic Pathway of the Blood Pressure-Lowering Asparagus Metabolite Asparaptine A. Journal of Agricultural and Food Chemistry, 2021, 69, 8571-8577.	2.4	4
529	Improvement of the quantitative differential metabolome pipeline for gas chromatography-mass spectrometry data by automated reliable peak selection. Plant Biotechnology, 2009, 26, 445-449.	0.5	4
530	Stereochemistry of Î²-hydroxydodecanoyl thioester dehydration catalyzed by fatty acid synthetase from. Tetrahedron Letters, 1982, 23, 1689-1692.	0.7	3
531	Recent Advances in the Biosynthesis and Accumulation of Anthocyanins. ChemInform, 2003, 34, no.	0.1	3
532	Metabolic Engineering of Sulfur Assimilation in Plants. , 2007, , 297-309.		3
533	Oleanane-type Triterpene Glycosides from Glycyrrhiza Uralensis. Natural Product Communications, 2007, 2, 1934578X0700200.	0.2	3
534	Using metabolomic approaches to explore chemical diversity in rice. Molecular Plant, 2014, , .	3.9	3
535	Association analysis of phenotypic and metabolomic changes in Arabidopsis accessions and their F₁ hybrids affected by different photoperiod and sucrose supply. Plant Biotechnology, 2019, 36, 155-165.	0.5	3
536	Editorial: The Origin of Plant Chemodiversity â€“ Conceptual and Empirical Insights. Frontiers in Plant Science, 2020, 11, 890.	1.7	3
537	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in Mallotus japonicus. International Journal of Molecular Sciences, 2021, 22, 8835.	1.8	3
538	Molecular Biology and Functional Genomics for Identification of Regulatory Networks of Plant Sulfate Uptake and Assimilatory Metabolism. Advances in Photosynthesis and Respiration, 2008, , 149-159.	1.0	3
539	Over-expression of transcription associated factor genes co-expressed with genes of the mevalonate pathway, upstream of isoprenoid biosynthesis, in Arabidopsis cultured cells. Plant Biotechnology, 2008, 25, 583-587.	0.5	3
540	Transcriptomic, Hormonomic and Metabolomic Analyses Highlighted the Common Modules Related to Photosynthesis, Sugar Metabolism and Cell Division in Parthenocarpic Tomato Fruits during Early Fruit Set. Cells, 2022, 11, 1420.	1.8	3

#	Article	IF	Citations
541	The ability of callus tissues induced from three Allium plants to accumulate health-beneficial natural products, S-alk(en)ylcysteine sulfoxides. Journal of Natural Medicines, 2022, 76, 803-810.	1.1	3
542	Graft polymerization of methyl methacrylate onto wool initiated by ferric acetylacetonate/dichloroacetic acid system. Journal of Applied Polymer Science, 1980, 25, 1991-2000.	1.3	2
543	Purification, Properties and Function of N-Hydroxyarylamine O- Acetyltransferase. Advances in Experimental Medicine and Biology, 1986, 197, 551-561.	0.8	2
544	Identification of Genes Involved in Anthocyanin Accumulation by Integrated Analysis of Metabolome and Transcriptome in Pap1-Overexpressing Arabidopsis Plants. , 2007, , 159-168.		2
545	Camptothecin Production and Biosynthesis in Plant Cell Cultures. , 2013, , 43-54.		2
546	Coupled Transcript-Metabolite Profiling: Towards Systems Biology Approaches to Unravel Regulation of Seed Secondary Metabolism. , 2012, , 367-385.		1
547	Cysteine Biosynthesis as a Sulfur Assimilation Pathway in Plants: Molecular and Biochemical Approach. , 1995, , 4239-4244.		1
548	Molecular and Cellular Regulation of Sulfate Transport and Assimilation. , 2012, , 25-33.		1
549	Metabolic Control of Gametophore Shoot Formation Through Arginine in the Moss Physcomitrella Patens. SSRN Electronic Journal, 0, , .	0.4	1
550	Metabolomics in Arabidopsis thaliana. , 2005, , 141-153.		0
551	Will Multiple-Answer Multiple-Choice Questions Work Effectively in the Common Test from 2020? (Course name: What does a test measure?). Juntendo Medical Journal, 2021, 67, 96-102.	0.1	0
552	Suppression of carotenoid synthesis in transgenic Arabidopsis cultured cells over-expressing the AHL29/SOB3 gene. Plant Biotechnology, 2008, 25, 573-577.	0.5	0
553	Recent Progress in the Research of Fatty Acid Synthetase. Journal of Japan Oil Chemists Society, 1981, 30, 659-665.	0.1	0
554	Molecular Aspects of Sulfur Assimilation and Acclimation to Sulfur Supply in Plants. , 1998, , 215-226.		0
555	Top-Down Metabolomics Approaches: Nitrogen- and Sulfur-Omics by Ultrahigh-Resolution Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry. , 2020, , 138-155.		0