Takayuki Tohge

List of Publications by Year
in descending order

189 papers	22,987 citations	10986 71 h-index	9103 144 g-index
202 all docs	202 docs citations	202 times ranked	23021 citing authors

#	ARTICLE	IF	CITATIONS
1	A Chimeric TGA Repressor Slows Down Fruit Maturation and Ripening in Tomato. Plant and Cell Physiology, 2022, 63, 120-134.	3.1	9
2	Diversification of Chemical Structures of Methoxylated Flavonoids and Genes Encoding Flavonoid-O-Methyltransferases. Plants, 2022, 11, 564.	3.5	11
3	<scp>AtGH3</scp>.10 is another jasmonic acidâ€amido synthetase in <i>Arabidopsis thaliana</i>. Plant Journal, 2022, 110, 1082-1096.	5.7	17
4	A comparative transcriptomics and eQTL approach identifies<i>SlWD40</i>as a tomato fruit ripening regulator. Plant Physiology, 2022, 190, 250-266.	4.8	9
5	High-energy-level metabolism and transport occur at the transition from closed to open flowers. Plant Physiology, 2022, 190, 319-339.	4.8	2
6	Natural Variation among Arabidopsis Accessions in the Regulation of Flavonoid Metabolism and Stress Gene Expression by Combined UV Radiation and Cold. Plant and Cell Physiology, 2021, 62, 502-514.	3.1	14
7	Cross-Species Metabolic Profiling of Floral Specialized Metabolism Facilitates Understanding of Evolutional Aspects of Metabolism Among Brassicaceae Species. Frontiers in Plant Science, 2021, 12, 640141.	3.6	1
8	An Oryza-specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. Science Bulletin, 2021, 66, 2369-2380.	9.0	35
9	Diversity of Chemical Structures and Biosynthesis of Polyphenols in Nut-Bearing Species. Frontiers in Plant Science, 2021, 12, 642581.	3.6	16
10	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.	3.6	16
11	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	19.0	403
12	Sulfur deficiency-induced genes affect seed protein accumulation and composition under sulfate deprivation. Plant Physiology, 2021, 187, 2419-2434.	4.8	20
13	Kingdom-wide analysis of the evolution of the plant type III polyketide synthase superfamily. Plant Physiology, 2021, 185, 857-875.	4.8	20
14	The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in Arabidopsis. Plant Physiology, 2020, 182, 857-869.	4.8	35
15	From Fruit Omics to Fruiting Omics: Systematic Studies of Tomato Fruiting by Metabolic Networks. Molecular Plant, 2020, 13, 1114-1116.	8.3	2
16	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. Nature Plants, 2020, 6, 1447-1454.	9.3	66
17	Metabolomic markers and physiological adaptations for high phosphate utilization efficiency in rice. Plant, Cell and Environment, 2020, 43, 2066-2079.	5.7	19
18	Diversity of anthocyanin and proanthocyanin biosynthesis in land plants. Current Opinion in Plant Biology, 2020, 55, 93-99.	7.1	119

#	Article	IF	Citations
19	Co-regulation of Clustered and Neo-functionalized Genes in Plant-Specialized Metabolism. Plants, 2020, 9, 622.	3.5	17
20	Quantitative trait loci analysis of seedâ€specialized metabolites reveals seedâ€specific flavonols and differential regulation of glycoalkaloid content in tomato. Plant Journal, 2020, 103, 2007-2024.	5.7	32
21	The <i>genomes uncoupled</i> -dependent signalling pathway coordinates plastid biogenesis with the synthesis of anthocyanins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190403.	4.0	24
22	Genetic Manipulation of Transcriptional Regulators Alters Nicotine Biosynthesis in Tobacco. Plant and Cell Physiology, 2020, 61, 1041-1053.	3.1	30
23	Manipulation of ZDS in tomato exposes carotenoidâ€•and ABAâ€specific effects on fruit development and ripening. Plant Biotechnology Journal, 2020, 18, 2210-2224.	8.3	44
24	Expression Atlas of <i>Selaginella moellendorffii</i> Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. Plant Cell, 2020, 32, 853-870.	6.6	39
25	Dissection of flag leaf metabolic shifts and their relationship with those occurring simultaneously in developing seed by application of non-targeted metabolomics. PLoS ONE, 2020, 15, e0227577.	2.5	6
26	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the Lycopersicum Complex. Molecular Plant, 2020, 13, 1027-1046.	8.3	56
27	Cross-Species Comparison of Fruit-Metabolomics to Elucidate Metabolic Regulation of Fruit Polyphenolics Among Solanaceous Crops. Metabolites, 2020, 10, 209.	2.9	19
28	Title is missing!. , 2020, 15, e0227577.		0
29	Title is missing!. , 2020, 15, e0227577.		0
30	Title is missing!. , 2020, 15, e0227577.		0
31	Title is missing!. , 2020, 15, e0227577.		0
32	Salt-stress secondary metabolite signatures involved in the ability of Casuarina glauca to mitigate oxidative stress. Environmental and Experimental Botany, 2019, 166, 103808.	4.2	20
33	Non-aqueous fractionation revealed changing subcellular metabolite distribution during apple fruit development. Horticulture Research, 2019, 6, 98.	6.3	15
34	Enhancement of vitamin B₆ levels in rice expressing Arabidopsis vitamin B₆ biosynthesis <i>de novo</i> genes. Plant Journal, 2019, 99, 1047-1065.	5.7	36
35	A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. Plant Physiology, 2019, 180, 87-108.	4.8	59
36	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. Nature Communications, 2019, 10, 737.	12.8	52

#	Article	IF	Citations
37	The Hot and the Colorful: Understanding the Metabolism, Genetics and Evolution of Consumer Preferred Metabolic Traits in Pepper and Related Species. Critical Reviews in Plant Sciences, 2019, 38, 339-381.	5.7	19
38	Multiâ€tissue integration of transcriptomic and specialized metabolite profiling provides tools for assessing the common bean (<i>Phaseolus vulgaris</i>) metabolome. Plant Journal, 2019, 97, 1132-1153.	5.7	33
39	Plasmodium Para-Aminobenzoate Synthesis and Salvage Resolve Avoidance of Folate Competition and Adaptation to Host Diet. Cell Reports, 2019, 26, 356-363.e4.	6.4	21
40	The Mitochondrial Thioredoxin System Contributes to the Metabolic Responses Under Drought Episodes in Arabidopsis. Plant and Cell Physiology, 2019, 60, 213-229.	3.1	26
41	Understanding the function and regulation of plant secondary metabolism through metabolomics approaches. Theoretical and Experimental Plant Physiology, 2019, 31, 127-138.	2.4	11
42	Insect egg deposition renders plant defence against hatching larvae more effective in a salicylic acidâ€dependent manner. Plant, Cell and Environment, 2019, 42, 1019-1032.	5.7	44
43	Transcription factor <scp>RD</scp>26 is a key regulator of metabolic reprogramming during darkâ€induced senescence. New Phytologist, 2018, 218, 1543-1557.	7.3	65
44	The natural variance of the Arabidopsis floral secondary metabolites. Scientific Data, 2018, 5, 180051.	5.3	14
45	Comprehensive Metabolomics Studies of Plant Developmental Senescence. Methods in Molecular Biology, 2018, 1744, 339-358.	0.9	19
46	On the natural diversity of phenylacylated-flavonoid and their in planta function under conditions of stress. Phytochemistry Reviews, 2018, 17, 279-290.	6.5	48
47	Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. Molecular Plant, 2018, 11, 118-134.	8.3	116
48	Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. Nature Communications, 2018, 9, 4680.	12.8	189
49	The Role of Persulfide Metabolism During Arabidopsis Seed Development Under Light and Dark Conditions. Frontiers in Plant Science, 2018, 9, 1381.	3.6	8
50	Metabolome and Lipidome Profiles of Populus Ã— canescens Twig Tissues During Annual Growth Show Phospholipid-Linked Storage and Mobilization of C, N, and S. Frontiers in Plant Science, 2018, 9, 1292.	3.6	18
51	Carbon Atomic Survey for Identification of Selected Metabolic Fluxes. Methods in Molecular Biology, 2018, 1778, 59-67.	0.9	2
52	Targeted LC-MS Analysis for Plant Secondary Metabolites. Methods in Molecular Biology, 2018, 1778, 171-181.	0.9	33
53	The Effect of Single and Multiple SERAT Mutants on Serine and Sulfur Metabolism. Frontiers in Plant Science, 2018, 9, 702.	3.6	9
54	Extended darkness induces internal turnover of glucosinolates in Arabidopsis thaliana leaves. PLoS ONE, 2018, 13, e0202153.	2.5	24

#	Article	IF	Citations
55	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. BMC Plant Biology, 2017, 17, 17.	3.6	34
56	Leveraging Natural Variance towards Enhanced Understanding of Phytochemical Sunscreens. Trends in Plant Science, 2017, 22, 308-315.	8.8	46
57	From chromatogram to analyte to metabolite. How to pick horses for courses from the massive web resources for mass spectral plant metabolomics. GigaScience, 2017, 6, 1-20.	6.4	59
58	Current understanding of the pathways of flavonoid biosynthesis in model and crop plants. Journal of Experimental Botany, 2017, 68, 4013-4028.	4.8	328
59	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (Helianthus annuus L.). Plant Molecular Biology, 2017, 94, 549-564.	3.9	51
60	Performance of Arabidopsis thaliana under different light qualities: comparison of light-emitting diodes to fluorescent lamp. Functional Plant Biology, 2017, 44, 727.	2.1	6
61	Integrated transcriptomic and metabolomic analysis shows that disturbances in metabolism of tumor cells contribute to poor survival of RCC patients. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 744-752.	3.8	16
62	Canalization of Tomato Fruit Metabolism. Plant Cell, 2017, 29, 2753-2765.	6.6	47
63	13CO2 Labeling and Mass Spectral Analysis of Photorespiration. Methods in Molecular Biology, 2017, 1653, 157-166.	0.9	3
64	The Genetics of Plant Metabolism. Annual Review of Genetics, 2017, 51, 287-310.	7.6	118
65	The polyketide synthase OsPKS2 is essential for pollen exine and Ubisch body patterning in rice. Journal of Integrative Plant Biology, 2017, 59, 612-628.	8.5	47
66	Differentially evolved glucosyltransferases determine natural variation of rice flavone accumulation and UV-tolerance. Nature Communications, 2017, 8, 1975.	12.8	233
67	The SAL-PAP Chloroplast Retrograde Pathway Contributes to Plant Immunity by Regulating Glucosinolate Pathway and Phytohormone Signaling. Molecular Plant-Microbe Interactions, 2017, 30, 829-841.	2.6	50
68	Photorespiration Is Crucial for Dynamic Response of Photosynthetic Metabolism and Stomatal Movement to Altered CO 2 Availability. Molecular Plant, 2017, 10, 47-61.	8.3	91
69	Phytochrome A and B Regulate Primary Metabolism in Arabidopsis Leaves in Response to Light. Frontiers in Plant Science, 2017, 8, 1394.	3.6	30
70	Integrative field scale phenotyping for investigating metabolic components of water stress within a vineyard. Plant Methods, 2017, 13, 90.	4.3	37
71	An Overview of Compounds Derived from the Shikimate and Phenylpropanoid Pathways and Their Medicinal Importance. Mini-Reviews in Medicinal Chemistry, 2017, 17, 1013-1027.	2.4	58
72	Dealing with the sulfur part of cysteine: four enzymatic steps degrade <scp>l</scp>â€cysteine to pyruvate and thiosulfate in Arabidopsis mitochondria. Physiologia Plantarum, 2016, 157, 352-366.	5.2	20

#	Article	IF	Citations
73	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. Nature Communications, 2016, 7, 12399.	12.8	145
74	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. Plant Biotechnology Journal, 2016, 14, 719-734.	8.3	53
75	Characterization of ubiquitin ligase SlATL31 and proteomic analysis of 14-3-3 targets in tomato fruit tissue (Solanum lycopersicum L.). Journal of Proteomics, 2016, 143, 254-264.	2.4	20
76	Vacuolar Chloride Fluxes Impact Ion content and Distribution during Early Salinity Stress. Plant Physiology, 2016, 172, pp.00183.2016.	4.8	45
77	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. Plant Physiology, 2016, 172, pp.00261.2016.	4.8	35
78	Specialized Metabolites of the Flavonol Class Mediate Root Phototropism and Growth. Molecular Plant, 2016, 9, 1554-1555.	8.3	18
79	Identification of Conserved and Diverse Metabolic Shifts during Rice Grain Development. Scientific Reports, 2016, 6, 20942.	3.3	64
80	Evolutionary interplay between sister cytochrome P450 genes shapes plasticity in plant metabolism. Nature Communications, 2016, 7, 13026.	12.8	44
81	Flavonoids are determinants of freezing tolerance and cold acclimation in Arabidopsis thaliana. Scientific Reports, 2016, 6, 34027.	3.3	209
82	Sulfur deficiencyâ€“induced repressor proteins optimize glucosinolate biosynthesis in plants. Science Advances, 2016, 2, e1601087.	10.3	127
83	Alterations in primary and secondary metabolism in <i>Vitis vinifera</i> â€˜MalvasÃa de Banyalbufarâ€™ upon infection withÂGrapevine leafrollâ€associated virus 3. Physiologia Plantarum, 2016, 157, 442-452.	5.2	49
84	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. Plant Science, 2016, 242, 47-64.	3.6	60
85	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. Plant Physiology, 2016, 170, 1878-1894.	4.8	63
86	Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. Plant Physiology, 2016, 170, 136-146.	4.8	62
87	Balancing of B₆ Vitamers Is Essential for Plant Development and Metabolism in Arabidopsis. Plant Cell, 2016, 28, 439-453.	6.6	60
88	The Role of SWI/SNF Chromatin Remodeling Complexes in Hormone Crosstalk. Trends in Plant Science, 2016, 21, 594-608.	8.8	95
89	Natural variation in flavonol accumulation in Arabidopsis is determined by the flavonol glucosyltransferase BGLU6. Journal of Experimental Botany, 2016, 67, 1505-1517.	4.8	67
90	A proteinâ€“protein interaction network linking the energy-sensor kinase SnRK1 to multiple signaling pathways in Arabidopsis thaliana. Current Plant Biology, 2016, 5, 36-44.	4.7	61

#	Article	IF	Citations
91	Ectopic expression of snapdragon transcription factors facilitates the identification of genes encoding enzymes of anthocyanin decoration in tomato. Plant Journal, 2015, 83, 686-704.	5.7	62
92	Global Analysis of the Role of Autophagy in Cellular Metabolism and Energy Homeostasis in Arabidopsis Seedlings under Carbon Starvation. Plant Cell, 2015, 27, 306-322.	6.6	166
93	Thioredoxin, a master regulator of the tricarboxylic acid cycle in plant mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1392-400.	7.1	179
94	Liquid chromatography highâ€resolution mass spectrometry for fatty acid profiling. Plant Journal, 2015, 81, 529-536.	5.7	54
95	Natural variation in flavonol and anthocyanin metabolism during cold acclimation in <scp><i>A</i></scp><i>rabidopsis thaliana</i> accessions. Plant, Cell and Environment, 2015, 38, 1658-1672.	5.7	126
96	Salt-Related MYB1 Coordinates Abscisic Acid Biosynthesis and Signaling during Salt Stress in Arabidopsis. Plant Physiology, 2015, 169, 1027-1041.	4.8	66
97	Profiling of primary metabolites and flavonols in leaves of two table grape varieties collected from semiarid and temperate regions. Phytochemistry, 2015, 117, 444-455.	2.9	30
98	Differential metabolic and coexpression networks of plant metabolism. Trends in Plant Science, 2015, 20, 266-268.	8.8	35
99	Identification and Mode of Inheritance of Quantitative Trait Loci for Secondary Metabolite Abundance in Tomato. Plant Cell, 2015, 27, 485-512.	6.6	188
100	The Arabidopsis transcription factor MYB112 promotes anthocyanin formation during salinity and under high light stress. Plant Physiology, 2015, 169, pp.00605.2015.	4.8	164
101	Multi-level engineering facilitates the production of phenylpropanoid compounds in tomato. Nature Communications, 2015, 6, 8635.	12.8	303
102	Integrative Approaches to Enhance Understanding of Plant Metabolic Pathway Structure and Regulation. Plant Physiology, 2015, 169, 1499-1511.	4.8	40
103	Location, location, location â€“ no more! The unravelling of chromatin remodeling regulatory aspects of plant metabolic gene clusters. New Phytologist, 2015, 205, 458-460.	7.3	8
104	Metabolomics-Inspired Insight into Developmental, Environmental and Genetic Aspects of Tomato Fruit Chemical Composition and Quality: Fig. 1. Plant and Cell Physiology, 2015, 56, 1681-1696.	3.1	66
105	Analysis of knockout mutants reveals non-redundant functions of poly(ADP-ribose)polymerase isoforms in Arabidopsis. Plant Molecular Biology, 2015, 89, 319-338.	3.9	21
106	Overexpression of the<i>Arabidopsis thaliana</i>signalling peptide TAXIMIN1 affects lateral organ development. Journal of Experimental Botany, 2015, 66, 5337-5349.	4.8	13
107	Comparative metabolomics and transcriptomics of plant response to Tomato yellow leaf curl virus infection in resistant and susceptible tomato cultivars. Metabolomics, 2015, 11, 81-97.	3.0	77
108	A cross-kingdom history. ELife, 2015, 4, .	6.0	3

#	Article	IF	Citations
109	In High-Light-Acclimated Coffee Plants the Metabolic Machinery Is Adjusted to Avoid Oxidative Stress Rather than to Benefit from Extra Light Enhancement in Photosynthetic Yield. PLoS ONE, 2014, 9, e94862.	2.5	39
110	Lignin, mitochondrial family, and photorespiratory transporter classification as case studies in using co-expression, co-response, and protein locations to aid in identifying transport functions. Frontiers in Plant Science, 2014, 5, 75.	3.6	4
111	Analysis of metabolic alterations in <i>Arabidopsis</i> following changes in the carbon dioxide and oxygen partial pressures. Journal of Integrative Plant Biology, 2014, 56, 941-959.	8.5	20
112	Enhancement of oxidative and drought tolerance in Arabidopsis by overaccumulation of antioxidant flavonoids. Plant Journal, 2014, 77, 367-379.	5.7	911
113	Metabolomicsâ€assisted refinement of the pathways of steroidal glycoalkaloid biosynthesis in the tomato clade. Journal of Integrative Plant Biology, 2014, 56, 864-875.	8.5	60
114	Transcript and Metabolite Profiling for the Evaluation of Tobacco Tree and Poplar as Feedstock for the Bio-based Industry. Journal of Visualized Experiments, 2014, , .	0.3	3
115	2-Oxoglutarate: linking TCA cycle function with amino acid, glucosinolate, flavonoid, alkaloid, and gibberellin biosynthesis. Frontiers in Plant Science, 2014, 5, 552.	3.6	91
116	Genome-enabled plant metabolomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 966, 7-20.	2.3	47
117	Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species Â Â Â. Plant Physiology, 2014, 164, 55-68.	4.8	50
118	<scp>M</scp>ercator: a fast and simple web server for genome scale functional annotation of plant sequence data. Plant, Cell and Environment, 2014, 37, 1250-1258.	5.7	575
119	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. Nature Biotechnology, 2014, 32, 1158-1165.	17.5	228
120	A flavonoid 3â€<i>O</i>â€glucoside:2â€³â€<i>O</i>â€glucosyltransferase responsible for terminal modification of pollenâ€specific flavonols in <i><scp>A</scp>rabidopsis thaliana</i>. Plant Journal, 2014, 79, 769-782.	5.7	79
121	Analysis of Short-Term Metabolic Alterations in Arabidopsis Following Changes in the Prevailing Environmental Conditions. Molecular Plant, 2014, 7, 893-911.	8.3	17
122	Biosynthesis of the Essential Respiratory Cofactor Ubiquinone from Phenylalanine in Plants. Molecular Plant, 2014, 7, 1403-1405.	8.3	8
123	Flux profiling of photosynthetic carbon metabolism in intact plants. Nature Protocols, 2014, 9, 1803-1824.	12.0	59
124	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	21.4	391
125	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.	4.8	49
126	Metabolic variation between japonica and indica rice cultivars as revealed by non-targeted metabolomics. Scientific Reports, 2014, 4, 5067.	3.3	129

#	Article	IF	Citations
127	Analysis of Kinetic Labeling of Amino Acids and Organic Acids by GC-MS. Methods in Molecular Biology, 2014, 1090, 107-119.	0.9	9
128	Molecular mechanisms of desiccation tolerance in the resurrection glacial relic Haberlea rhodopensis. Cellular and Molecular Life Sciences, 2013, 70, 689-709.	5.4	168
129	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2655-62.	7.1	325
130	Arabidopsis BPM Proteins Function as Substrate Adaptors to a CULLIN3-Based E3 Ligase to Affect Fatty Acid Metabolism in Plants. Plant Cell, 2013, 25, 2253-2264.	6.6	86
131	Analysis of the Interface between Primary and Secondary Metabolism in Catharanthus roseus Cell Cultures Using 13C-Stable Isotope Feeding and Coupled Mass Spectrometry. Molecular Plant, 2013, 6, 581-584.	8.3	16
132	DELLA-Interacting SWI3C Core Subunit of Switch/Sucrose Nonfermenting Chromatin Remodeling Complex Modulates Gibberellin Responses and Hormonal Cross Talk in Arabidopsis. Plant Physiology, 2013, 163, 305-317.	4.8	98
133	Plastic, fantastic! Phenotypic variance in the transcriptional landscape of the grape berry. Genome Biology, 2013, 14, 119.	8.8	22
134	On the regulation and function of secondary metabolism during fruit development and ripening. Journal of Experimental Botany, 2013, 65, 4599-4611.	4.8	92
135	The flavonoid biosynthetic pathway in Arabidopsis: Structural and genetic diversity. Plant Physiology and Biochemistry, 2013, 72, 21-34.	5.8	637
136	Activation of <i><scp>R</scp></i>â€mediated innate immunity and disease susceptibility is affected by mutations in a cytosolic <i><scp>O</scp></i>â€acetylserine (thiol) lyase in <scp>A</scp>rabidopsis. Plant Journal, 2013, 73, 118-130.	5.7	36
137	The evolution of phenylpropanoid metabolism in the green lineage. Critical Reviews in Biochemistry and Molecular Biology, 2013, 48, 123-152.	5.2	228
138	Comprehensive Dissection of Spatiotemporal Metabolic Shifts in Primary, Secondary, and Lipid Metabolism during Developmental Senescence in Arabidopsis Â. Plant Physiology, 2013, 162, 1290-1310.	4.8	278
139	Shikimate and Phenylalanine Biosynthesis in the Green Lineage. Frontiers in Plant Science, 2013, 4, 62.	3.6	288
140	Trichoderma-Plant Root Colonization: Escaping Early Plant Defense Responses and Activation of the Antioxidant Machinery for Saline Stress Tolerance. PLoS Pathogens, 2013, 9, e1003221.	4.7	299
141	Metabolic Fluxes in an Illuminated <i>Arabidopsis</i> Rosette Â. Plant Cell, 2013, 25, 694-714.	6.6	303
142	BRAHMA ATPase of the SWI/SNF Chromatin Remodeling Complex Acts as a Positive Regulator of Gibberellin-Mediated Responses in Arabidopsis. PLoS ONE, 2013, 8, e58588.	2.5	69
143	Co-expression and co-responses: within and beyond transcription. Frontiers in Plant Science, 2012, 3, 248.	3.6	51
144	Metabolic Profiling of a Mapping Population Exposes New Insights in the Regulation of Seed Metabolism and Seed, Fruit, and Plant Relations. PLoS Genetics, 2012, 8, e1002612.	3.5	115

#	Article	IF	Citations
145	Phosphonate Analogs of 2-Oxoglutarate Perturb Metabolism and Gene Expression in Illuminated Arabidopsis Leaves. Frontiers in Plant Science, 2012, 3, 114.	3.6	30
146	Antisense Inhibition of the 2-Oxoglutarate Dehydrogenase Complex in Tomato Demonstrates Its Importance for Plant Respiration and during Leaf Senescence and Fruit Maturation. Plant Cell, 2012, 24, 2328-2351.	6.6	88
147	Annotation of Plant Gene Function via Combined Genomics, Metabolomics and Informatics. Journal of Visualized Experiments, 2012, , e3487.	0.3	12
148	AtABCG29 Is a Monolignol Transporter Involved in Lignin Biosynthesis. Current Biology, 2012, 22, 1207-1212.	3.9	265
149	Tissue specificity and differential expression of transcription factors in tomato provide hints of unique regulatory networks during fruit ripening. Plant Signaling and Behavior, 2012, 7, 1639-1647.	2.4	16
150	<i>JUNGBRUNNEN1</i>, a Reactive Oxygen Speciesâ€"Responsive NAC Transcription Factor, Regulates Longevity in <i>Arabidopsis</i>. Plant Cell, 2012, 24, 482-506.	6.6	512
151	Metabolic priming by a secreted fungal effector. Nature, 2011, 478, 395-398.	27.8	509
152	Recommendations for Reporting Metabolite Data. Plant Cell, 2011, 23, 2477-2482.	6.6	326
153	Antisense Inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase Enhances Photosynthesis and Growth in Tomato via an Organic Acidâ€"Mediated Effect on Stomatal Aperture Â. Plant Cell, 2011, 23, 600-627.	6.6	221
154	Protein degradation â€" an alternative respiratory substrate for stressed plants. Trends in Plant Science, 2011, 16, 489-498.	8.8	367
155	From models to crop species: caveats and solutions for translational metabolomics. Frontiers in Plant Science, 2011, 2, 61.	3.6	33
156	Metabolic and miRNA Profiling of TMV Infected Plants Reveals Biphasic Temporal Changes. PLoS ONE, 2011, 6, e28466.	2.5	59
157	Metabolomics reveals comprehensive reprogramming involving two independent metabolic responses of Arabidopsis to UVâ€B light. Plant Journal, 2011, 67, 354-369.	5.7	249
158	Combined transcription factor profiling, microarray analysis and metabolite profiling reveals the transcriptional control of metabolic shifts occurring during tomato fruit development. Plant Journal, 2011, 68, 999-1013.	5.7	118
159	Transcriptional and metabolic programs following exposure of plants to UV-B irradiation. Plant Signaling and Behavior, 2011, 6, 1987-1992.	2.4	54
160	Analysis of a Range of Catabolic Mutants Provides Evidence That Phytanoyl-Coenzyme A Does Not Act as a Substrate of the Electron-Transfer Flavoprotein/Electron-Transfer Flavoprotein:Ubiquinone Oxidoreductase Complex in Arabidopsis during Dark-Induced Senescence Â Â. Plant Physiology, 2011, 157, 55-69.	4.8	39
161	Tomato Fruit Photosynthesis Is Seemingly Unimportant in Primary Metabolism and Ripening But Plays a Considerable Role in Seed Development Â Â. Plant Physiology, 2011, 157, 1650-1663.	4.8	150
162	Identification of Genes in the Phenylalanine Metabolic Pathway by Ectopic Expression of a MYB Transcription Factor in Tomato Fruit. Plant Cell, 2011, 23, 2738-2753.	6.6	97

#	Article	IF	Citations
163	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor (<i>nor, rin</i>) and Ethylene Receptor (<i>Nr</i>) Mutants Reveals Novel Regulatory Interactions Â Â. Plant Physiology, 2011, 157, 405-425.	4.8	303
164	Tissue- and Cell-Type Specific Transcriptome Profiling of Expanding Tomato Fruit Provides Insights into Metabolic and Regulatory Specialization and Cuticle Formation Â. Plant Cell, 2011, 23, 3893-3910.	6.6	193
165	Toward the Storage Metabolome: Profiling the Barley Vacuole Â Â. Plant Physiology, 2011, 157, 1469-1482.	4.8	92
166	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species Â. Plant Cell, 2011, 23, 895-910.	6.6	297
167	MassBank: a public repository for sharing mass spectral data for life sciences. Journal of Mass Spectrometry, 2010, 45, 703-714.	1.6	1,831
168	Analysis of PRODUCTION OF FLAVONOL GLYCOSIDESâ€dependent flavonol glycoside accumulation in <i>Arabidopsis thaliana</i> plants reveals MYB11â€; MYB12â€•and MYB111â€independent flavonol glycoside accumulation. New Phytologist, 2010, 188, 985-1000.	7.3	285
169	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of Arabidopsis thaliana flavonoid accumulation mutants. Plant Journal, 2010, 62, 549-559.	5.7	85
170	Pleiotropic physiological consequences of feedback-insensitive phenylalanine biosynthesis in Arabidopsis thaliana. Plant Journal, 2010, 63, 823-835.	5.7	69
171	Characterization of the Branched-Chain Amino Acid Aminotransferase Enzyme Family in Tomato Â Â. Plant Physiology, 2010, 153, 925-936.	4.8	80
172	Combining genetic diversity, informatics and metabolomics to facilitate annotation of plant gene function. Nature Protocols, 2010, 5, 1210-1227.	12.0	202
173	Identification of the 2-Hydroxyglutarate and Isovaleryl-CoA Dehydrogenases as Alternative Electron Donors Linking Lysine Catabolism to the Electron Transport Chain of <i>Arabidopsis</i> Mitochondria Â. Plant Cell, 2010, 22, 1549-1563.	6.6	296
174	The Metabolic Response of Arabidopsis Roots to Oxidative Stress is Distinct from that of Heterotrophic Cells in Culture and Highlights a Complex Relationship between the Levels of Transcripts, Metabolites, and Flux. Molecular Plant, 2009, 2, 390-406.	8.3	155
175	Members of the<i>LBD</i>Family of Transcription Factors Repress Anthocyanin Synthesis and Affect Additional Nitrogen Responses in<i>Arabidopsis</i>Â Â. Plant Cell, 2009, 21, 3567-3584.	6.6	507
176	Rice endosperm iron biofortification by targeted and synergistic action of nicotianamine synthase and ferritin. Plant Biotechnology Journal, 2009, 7, 631-644.	8.3	298
177	Web-based resources for mass-spectrometry-based metabolomics: A userâ€™s guide. Phytochemistry, 2009, 70, 450-456.	2.9	140
178	Metabolomics-oriented isolation and structure elucidation of 37 compounds including two anthocyanins from Arabidopsis thaliana. Phytochemistry, 2009, 70, 1017-1029.	2.9	111
179	Comprehensive Flavonol Profiling and Transcriptome Coexpression Analysis Leading to Decoding Geneâ€“Metabolite Correlations in<i>Arabidopsis</i>Â Â. Plant Cell, 2008, 20, 2160-2176.	6.6	347
180	PRIMe: a Web site that assembles tools for metabolomics and transcriptomics. In Silico Biology, 2008, 8, 339-45.	0.9	149

#	Article	IF	Citations
181	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.	3.4	236
182	Phytochemical genomics in Arabidopsis thaliana: A case study for functional identification of flavonoid biosynthesis genes. Pure and Applied Chemistry, 2007, 79, 811-823.	1.9	88
183	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.	7.1	666
184	Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in Arabidopsis thaliana. BMC Systems Biology, 2007, 1, 53.	3.0	116
185	Identification of Genes Involved in Anthocyanin Accumulation by Integrated Analysis of Metabolome and Transcriptome in Pap1-Overexpressing Arabidopsis Plants. , 2007, , 159-168.		2
186	Arabidopsis SLIM1 Is a Central Transcriptional Regulator of Plant Sulfur Response and Metabolism. Plant Cell, 2006, 18, 3235-3251.	6.6	337
187	Functional genomics by integrated analysis of metabolome and transcriptome of Arabidopsis plants over-expressing an MYB transcription factor. Plant Journal, 2005, 42, 218-235.	5.7	891
188	Enhanced radical scavenging activity of genetically modified Arabidopsis seeds. Biotechnology Letters, 2005, 27, 297-303.	2.2	41
189	Sugarcane cell suspension reveals major metabolic changes under different nitrogen starvation regimes. Bragantia, 0, 80, .	1.3	2