

Takayuki Tohge

List of Publications by Year in descending order

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189
papers

22,987
citations

12597

71
h-index

10399

144
g-index

202
all docs

202
docs citations

202
times ranked

25317
citing authors

#	ARTICLE	IF	CITATIONS
1	A Chimeric TGA Repressor Slows Down Fruit Maturation and Ripening in Tomato. <i>Plant and Cell Physiology</i> , 2022, 63, 120-134.	1.5	9
2	Diversification of Chemical Structures of Methoxylated Flavonoids and Genes Encoding Flavonoid-O-Methyltransferases. <i>Plants</i> , 2022, 11, 564.	1.6	11
3	<scp>AtGH3</scp>.10 is another jasmonic acidâ€œamido synthetase in <i>Arabidopsis thaliana</i>. <i>Plant Journal</i> , 2022, 110, 1082-1096.	2.8	17
4	A comparative transcriptomics and eQTL approach identifies<i>SIWD40</i> as a tomato fruit ripening regulator. <i>Plant Physiology</i> , 2022, 190, 250-266.	2.3	9
5	High-energy-level metabolism and transport occur at the transition from closed to open flowers. <i>Plant Physiology</i> , 2022, 190, 319-339.	2.3	2
6	Natural Variation among Arabidopsis Accessions in the Regulation of Flavonoid Metabolism and Stress Gene Expression by Combined UV Radiation and Cold. <i>Plant and Cell Physiology</i> , 2021, 62, 502-514.	1.5	14
7	Cross-Species Metabolic Profiling of Floral Specialized Metabolism Facilitates Understanding of Evolutional Aspects of Metabolism Among Brassicaceae Species. <i>Frontiers in Plant Science</i> , 2021, 12, 640141.	1.7	1
8	An Oryza-specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. <i>Science Bulletin</i> , 2021, 66, 2369-2380.	4.3	35
9	Diversity of Chemical Structures and Biosynthesis of Polyphenols in Nut-Bearing Species. <i>Frontiers in Plant Science</i> , 2021, 12, 642581.	1.7	16
10	Assessing Dynamic Changes of Taste-Related Primary Metabolism During Ripening of Durian Pulp Using Metabolomic and Transcriptomic Analyses. <i>Frontiers in Plant Science</i> , 2021, 12, 687799.	1.7	16
11	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	9.0	403
12	Sulfur deficiency-induced genes affect seed protein accumulation and composition under sulfate deprivation. <i>Plant Physiology</i> , 2021, 187, 2419-2434.	2.3	20
13	Kingdom-wide analysis of the evolution of the plant type III polyketide synthase superfamily. <i>Plant Physiology</i> , 2021, 185, 857-875.	2.3	20
14	The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in Arabidopsis. <i>Plant Physiology</i> , 2020, 182, 857-869.	2.3	35
15	From Fruit Omics to Fruiting Omics: Systematic Studies of Tomato Fruiting by Metabolic Networks. <i>Molecular Plant</i> , 2020, 13, 1114-1116.	3.9	2
16	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. <i>Nature Plants</i> , 2020, 6, 1447-1454.	4.7	66
17	Metabolomic markers and physiological adaptations for high phosphate utilization efficiency in rice. <i>Plant, Cell and Environment</i> , 2020, 43, 2066-2079.	2.8	19
18	Diversity of anthocyanin and proanthocyanin biosynthesis in land plants. <i>Current Opinion in Plant Biology</i> , 2020, 55, 93-99.	3.5	119

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19	Co-regulation of Clustered and Neo-functionalized Genes in Plant-Specialized Metabolism. <i>Plants</i> , 2020, 9, 622.	1.6	17
20	Quantitative trait loci analysis of seed-specific metabolites reveals seed-specific flavonols and differential regulation of glycoalkaloid content in tomato. <i>Plant Journal</i> , 2020, 103, 2007-2024.	2.8	32
21	The <i>genome uncoupled</i> -dependent signalling pathway coordinates plastid biogenesis with the synthesis of anthocyanins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190403.	1.8	24
22	Genetic Manipulation of Transcriptional Regulators Alters Nicotine Biosynthesis in Tobacco. <i>Plant and Cell Physiology</i> , 2020, 61, 1041-1053.	1.5	30
23	Manipulation of ZDS in tomato exposes carotenoid and ABA-specific effects on fruit development and ripening. <i>Plant Biotechnology Journal</i> , 2020, 18, 2210-2224.	4.1	44
24	Expression Atlas of <i>Selaginella moellendorffii</i> Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. <i>Plant Cell</i> , 2020, 32, 853-870.	3.1	39
25	Dissection of flag leaf metabolic shifts and their relationship with those occurring simultaneously in developing seed by application of non-targeted metabolomics. <i>PLoS ONE</i> , 2020, 15, e0227577.	1.1	6
26	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the <i>Lycopersicon</i> Complex. <i>Molecular Plant</i> , 2020, 13, 1027-1046.	3.9	56
27	Cross-Species Comparison of Fruit-Metabolomics to Elucidate Metabolic Regulation of Fruit Polyphenolics Among Solanaceous Crops. <i>Metabolites</i> , 2020, 10, 209.	1.3	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 <i>Casuarina glauca</i> to mitigate oxidative stress. <i>Environmental and Experimental Botany</i> , 2019, 166, 103808.	2.0	20
33	Non-aqueous fractionation revealed changing subcellular metabolite distribution during apple fruit development. <i>Horticulture Research</i> , 2019, 6, 98.	2.9	15
34	Enhancement of vitamin B ₆ levels in rice expressing <i>Arabidopsis</i> vitamin B ₆ biosynthesis <i>de novo</i> genes. <i>Plant Journal</i> , 2019, 99, 1047-1065.	2.8	36
35	A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. <i>Plant Physiology</i> , 2019, 180, 87-108.	2.3	59
36	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. <i>Nature Communications</i> , 2019, 10, 737.	5.8	52

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37	The Hot and the Colorful: Understanding the Metabolism, Genetics and Evolution of Consumer Preferred Metabolic Traits in Pepper and Related Species. <i>Critical Reviews in Plant Sciences</i> , 2019, 38, 339-381.	2.7	19
38	Multi-tissue integration of transcriptomic and specialized metabolite profiling provides tools for assessing the common bean (<i>Phaseolus vulgaris</i>) metabolome. <i>Plant Journal</i> , 2019, 97, 1132-1153.	2.8	33
39	Plasmodium Para-Aminobenzoate Synthesis and Salvage Resolve Avoidance of Folate Competition and Adaptation to Host Diet. <i>Cell Reports</i> , 2019, 26, 356-363.e4.	2.9	21
40	The Mitochondrial Thioredoxin System Contributes to the Metabolic Responses Under Drought Episodes in Arabidopsis. <i>Plant and Cell Physiology</i> , 2019, 60, 213-229.	1.5	26
41	Understanding the function and regulation of plant secondary metabolism through metabolomics approaches. <i>Theoretical and Experimental Plant Physiology</i> , 2019, 31, 127-138.	1.1	11
42	Insect egg deposition renders plant defence against hatching larvae more effective in a salicylic acid-dependent manner. <i>Plant, Cell and Environment</i> , 2019, 42, 1019-1032.	2.8	44
43	Transcription factor RD26 is a key regulator of metabolic reprogramming during dark-induced senescence. <i>New Phytologist</i> , 2018, 218, 1543-1557.	3.5	65
44	The natural variance of the Arabidopsis floral secondary metabolites. <i>Scientific Data</i> , 2018, 5, 180051.	2.4	14
45	Comprehensive Metabolomics Studies of Plant Developmental Senescence. <i>Methods in Molecular Biology</i> , 2018, 1744, 339-358.	0.4	19
46	On the natural diversity of phenylacylated-flavonoid and their in planta function under conditions of stress. <i>Phytochemistry Reviews</i> , 2018, 17, 279-290.	3.1	48
47	Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. <i>Molecular Plant</i> , 2018, 11, 118-134.	3.9	116
48	Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. <i>Nature Communications</i> , 2018, 9, 4680.	5.8	189
49	The Role of Persulfide Metabolism During Arabidopsis Seed Development Under Light and Dark Conditions. <i>Frontiers in Plant Science</i> , 2018, 9, 1381.	1.7	8
50	Metabolome and Lipidome Profiles of <i>Populus alba</i> Twig Tissues During Annual Growth Show Phospholipid-Linked Storage and Mobilization of C, N, and S. <i>Frontiers in Plant Science</i> , 2018, 9, 1292.	1.7	18
51	Carbon Atomic Survey for Identification of Selected Metabolic Fluxes. <i>Methods in Molecular Biology</i> , 2018, 1778, 59-67.	0.4	2
52	Targeted LC-MS Analysis for Plant Secondary Metabolites. <i>Methods in Molecular Biology</i> , 2018, 1778, 171-181.	0.4	33
53	The Effect of Single and Multiple SERAT Mutants on Serine and Sulfur Metabolism. <i>Frontiers in Plant Science</i> , 2018, 9, 702.	1.7	9
54	Extended darkness induces internal turnover of glucosinolates in Arabidopsis thaliana leaves. <i>PLoS ONE</i> , 2018, 13, e0202153.	1.1	24

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55	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. <i>BMC Plant Biology</i> , 2017, 17, 17.	1.6	34
56	Leveraging Natural Variance towards Enhanced Understanding of Phytochemical Sunscreens. <i>Trends in Plant Science</i> , 2017, 22, 308-315.	4.3	46
57	From chromatogram to analyte to metabolite. How to pick horses for courses from the massive web resources for mass spectral plant metabolomics. <i>GigaScience</i> , 2017, 6, 1-20.	3.3	59
58	Current understanding of the pathways of flavonoid biosynthesis in model and crop plants. <i>Journal of Experimental Botany</i> , 2017, 68, 4013-4028.	2.4	328
59	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (<i>Helianthus annuus</i> L.). <i>Plant Molecular Biology</i> , 2017, 94, 549-564.	2.0	51
60	Performance of <i>Arabidopsis thaliana</i> under different light qualities: comparison of light-emitting diodes to fluorescent lamp. <i>Functional Plant Biology</i> , 2017, 44, 727.	1.1	6
61	Integrated transcriptomic and metabolomic analysis shows that disturbances in metabolism of tumor cells contribute to poor survival of RCC patients. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017, 1863, 744-752.	1.8	16
62	Canalization of Tomato Fruit Metabolism. <i>Plant Cell</i> , 2017, 29, 2753-2765.	3.1	47
63	¹³ CO ₂ Labeling and Mass Spectral Analysis of Photorespiration. <i>Methods in Molecular Biology</i> , 2017, 1653, 157-166.	0.4	3
64	The Genetics of Plant Metabolism. <i>Annual Review of Genetics</i> , 2017, 51, 287-310.	3.2	118
65	The polyketide synthase OsPKS2 is essential for pollen exine and Ubisch body patterning in rice. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 612-628.	4.1	47
66	Differentially evolved glucosyltransferases determine natural variation of rice flavone accumulation and UV-tolerance. <i>Nature Communications</i> , 2017, 8, 1975.	5.8	233
67	The SAL-PAP Chloroplast Retrograde Pathway Contributes to Plant Immunity by Regulating Glucosinolate Pathway and Phytohormone Signaling. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 829-841.	1.4	50
68	Photorespiration Is Crucial for Dynamic Response of Photosynthetic Metabolism and Stomatal Movement to Altered CO ₂ Availability. <i>Molecular Plant</i> , 2017, 10, 47-61.	3.9	91
69	Phytochrome A and B Regulate Primary Metabolism in <i>Arabidopsis</i> Leaves in Response to Light. <i>Frontiers in Plant Science</i> , 2017, 8, 1394.	1.7	30
70	Integrative field scale phenotyping for investigating metabolic components of water stress within a vineyard. <i>Plant Methods</i> , 2017, 13, 90.	1.9	37
71	An Overview of Compounds Derived from the Shikimate and Phenylpropanoid Pathways and Their Medicinal Importance. <i>Mini-Reviews in Medicinal Chemistry</i> , 2017, 17, 1013-1027.	1.1	58
72	Dealing with the sulfur part of cysteine: four enzymatic steps degrade cysteine to pyruvate and thiosulfate in <i>Arabidopsis</i> mitochondria. <i>Physiologia Plantarum</i> , 2016, 157, 352-366.	2.6	20

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73	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. <i>Nature Communications</i> , 2016, 7, 12399.	5.8	145
74	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. <i>Plant Biotechnology Journal</i> , 2016, 14, 719-734.	4.1	53
75	Characterization of ubiquitin ligase SLTL31 and proteomic analysis of 14-3-3 targets in tomato fruit tissue (<i>Solanum lycopersicum</i> L.). <i>Journal of Proteomics</i> , 2016, 143, 254-264.	1.2	20
76	Vacuolar Chloride Fluxes Impact Ion content and Distribution during Early Salinity Stress. <i>Plant Physiology</i> , 2016, 172, pp.00183.2016.	2.3	45
77	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. <i>Plant Physiology</i> , 2016, 172, pp.00261.2016.	2.3	35
78	Specialized Metabolites of the Flavonol Class Mediate Root Phototropism and Growth. <i>Molecular Plant</i> , 2016, 9, 1554-1555.	3.9	18
79	Identification of Conserved and Diverse Metabolic Shifts during Rice Grain Development. <i>Scientific Reports</i> , 2016, 6, 20942.	1.6	64
80	Evolutionary interplay between sister cytochrome P450 genes shapes plasticity in plant metabolism. <i>Nature Communications</i> , 2016, 7, 13026.	5.8	44
81	Flavonoids are determinants of freezing tolerance and cold acclimation in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2016, 6, 34027.	1.6	209
82	Sulfur deficiency-induced repressor proteins optimize glucosinolate biosynthesis in plants. <i>Science Advances</i> , 2016, 2, e1601087.	4.7	127
83	Alterations in primary and secondary metabolism in <i>Vitis vinifera</i> "Malvasia de Banyalbufar" upon infection with Grapevine leafroll-associated virus 3. <i>Physiologia Plantarum</i> , 2016, 157, 442-452.	2.6	49
84	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <i>Plant Science</i> , 2016, 242, 47-64.	1.7	60
85	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. <i>Plant Physiology</i> , 2016, 170, 1878-1894.	2.3	63
86	Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. <i>Plant Physiology</i> , 2016, 170, 136-146.	2.3	62
87	Balancing of B ₆ Vitamers Is Essential for Plant Development and Metabolism in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2016, 28, 439-453.	3.1	60
88	The Role of SWI/SNF Chromatin Remodeling Complexes in Hormone Crosstalk. <i>Trends in Plant Science</i> , 2016, 21, 594-608.	4.3	95
89	Natural variation in flavonol accumulation in <i>Arabidopsis</i> is determined by the flavonol glucosyltransferase BGLU6. <i>Journal of Experimental Botany</i> , 2016, 67, 1505-1517.	2.4	67
90	A protein-protein interaction network linking the energy-sensor kinase SnRK1 to multiple signaling pathways in <i>Arabidopsis thaliana</i> . <i>Current Plant Biology</i> , 2016, 5, 36-44.	2.3	61

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91	Ectopic expression of snapdragon transcription factors facilitates the identification of genes encoding enzymes of anthocyanin decoration in tomato. <i>Plant Journal</i> , 2015, 83, 686-704.	2.8	62
92	Global Analysis of the Role of Autophagy in Cellular Metabolism and Energy Homeostasis in <i>Arabidopsis</i> Seedlings under Carbon Starvation. <i>Plant Cell</i> , 2015, 27, 306-322.	3.1	166
93	Thioredoxin, a master regulator of the tricarboxylic acid cycle in plant mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1392-400.	3.3	179
94	Liquid chromatography high-resolution mass spectrometry for fatty acid profiling. <i>Plant Journal</i> , 2015, 81, 529-536.	2.8	54
95	Natural variation in flavonol and anthocyanin metabolism during cold acclimation in <i>Arabidopsis thaliana</i> accessions. <i>Plant, Cell and Environment</i> , 2015, 38, 1658-1672.	2.8	126
96	Salt-Related MYB1 Coordinates Abscisic Acid Biosynthesis and Signaling during Salt Stress in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 169, 1027-1041.	2.3	66
97	Profiling of primary metabolites and flavonols in leaves of two table grape varieties collected from semiarid and temperate regions. <i>Phytochemistry</i> , 2015, 117, 444-455.	1.4	30
98	Differential metabolic and coexpression networks of plant metabolism. <i>Trends in Plant Science</i> , 2015, 20, 266-268.	4.3	35
99	Identification and Mode of Inheritance of Quantitative Trait Loci for Secondary Metabolite Abundance in Tomato. <i>Plant Cell</i> , 2015, 27, 485-512.	3.1	188
100	The <i>Arabidopsis</i> transcription factor MYB112 promotes anthocyanin formation during salinity and under high light stress. <i>Plant Physiology</i> , 2015, 169, pp.00605.2015.	2.3	164
101	Multi-level engineering facilitates the production of phenylpropanoid compounds in tomato. <i>Nature Communications</i> , 2015, 6, 8635.	5.8	303
102	Integrative Approaches to Enhance Understanding of Plant Metabolic Pathway Structure and Regulation. <i>Plant Physiology</i> , 2015, 169, 1499-1511.	2.3	40
103	Location, location, location – no more! The unravelling of chromatin remodeling regulatory aspects of plant metabolic gene clusters. <i>New Phytologist</i> , 2015, 205, 458-460.	3.5	8
104	Metabolomics-Inspired Insight into Developmental, Environmental and Genetic Aspects of Tomato Fruit Chemical Composition and Quality: Fig. 1. <i>Plant and Cell Physiology</i> , 2015, 56, 1681-1696.	1.5	66
105	Analysis of knockout mutants reveals non-redundant functions of poly(ADP-ribose)polymerase isoforms in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2015, 89, 319-338.	2.0	21
106	Overexpression of the <i>Arabidopsis thaliana</i> signalling peptide TAXIMIN1 affects lateral organ development. <i>Journal of Experimental Botany</i> , 2015, 66, 5337-5349.	2.4	13
107	Comparative metabolomics and transcriptomics of plant response to Tomato yellow leaf curl virus infection in resistant and susceptible tomato cultivars. <i>Metabolomics</i> , 2015, 11, 81-97.	1.4	77
108	A cross-kingdom history. <i>ELife</i> , 2015, 4, .	2.8	3

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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. <i>PLoS ONE</i> , 2014, 9, e94862.	1.1	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. <i>Frontiers in Plant Science</i> , 2014, 5, 75.	1.7	4
111	Analysis of metabolic alterations in <i>Arabidopsis</i> following changes in the carbon dioxide and oxygen partial pressures. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 941-959.	4.1	20
112	Enhancement of oxidative and drought tolerance in <i>Arabidopsis</i> by overaccumulation of antioxidant flavonoids. <i>Plant Journal</i> , 2014, 77, 367-379.	2.8	911
113	Metabolomics-assisted refinement of the pathways of steroidal glycoalkaloid biosynthesis in the tomato clade. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 864-875.	4.1	60
114	Transcript and Metabolite Profiling for the Evaluation of Tobacco Tree and Poplar as Feedstock for the Bio-based Industry. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	3
115	2-Oxoglutarate: linking TCA cycle function with amino acid, glucosinolate, flavonoid, alkaloid, and gibberellin biosynthesis. <i>Frontiers in Plant Science</i> , 2014, 5, 552.	1.7	91
116	Genome-enabled plant metabolomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2014, 966, 7-20.	1.2	47
117	Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species <i>A</i> <i>A</i> . <i>Plant Physiology</i> , 2014, 164, 55-68.	2.3	50
118	MECAT: a fast and simple web server for genome scale functional annotation of plant sequence data. <i>Plant, Cell and Environment</i> , 2014, 37, 1250-1258.	2.8	575
119	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014, 32, 1158-1165.	9.4	228
120	A flavonoid O-glucoside:2-O-glucosyltransferase responsible for terminal modification of pollen-specific flavonols in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2014, 79, 769-782.	2.8	79
121	Analysis of Short-Term Metabolic Alterations in <i>Arabidopsis</i> Following Changes in the Prevailing Environmental Conditions. <i>Molecular Plant</i> , 2014, 7, 893-911.	3.9	17
122	Biosynthesis of the Essential Respiratory Cofactor Ubiquinone from Phenylalanine in Plants. <i>Molecular Plant</i> , 2014, 7, 1403-1405.	3.9	8
123	Flux profiling of photosynthetic carbon metabolism in intact plants. <i>Nature Protocols</i> , 2014, 9, 1803-1824.	5.5	59
124	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	9.4	391
125	Metabolomic Characterization of Knockout Mutants in <i>Arabidopsis</i> : Development of a Metabolite Profiling Database for Knockout Mutants in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2014, 165, 948-961.	2.3	49
126	Metabolic variation between japonica and indica rice cultivars as revealed by non-targeted metabolomics. <i>Scientific Reports</i> , 2014, 4, 5067.	1.6	129

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127	Analysis of Kinetic Labeling of Amino Acids and Organic Acids by GC-MS. <i>Methods in Molecular Biology</i> , 2014, 1090, 107-119.	0.4	9
128	Molecular mechanisms of desiccation tolerance in the resurrection glacial relic <i>Haberlea rhodopensis</i> . <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 689-709.	2.4	168
129	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2655-62.	3.3	325
130	Arabidopsis BPM Proteins Function as Substrate Adaptors to a CULLIN3-Based E3 Ligase to Affect Fatty Acid Metabolism in Plants. <i>Plant Cell</i> , 2013, 25, 2253-2264.	3.1	86
131	Analysis of the Interface between Primary and Secondary Metabolism in <i>Catharanthus roseus</i> Cell Cultures Using ¹³ C-Stable Isotope Feeding and Coupled Mass Spectrometry. <i>Molecular Plant</i> , 2013, 6, 581-584.	3.9	16
132	DELLA-Interacting SWI3C Core Subunit of Switch/Sucrose Nonfermenting Chromatin Remodeling Complex Modulates Gibberellin Responses and Hormonal Cross Talk in Arabidopsis. <i>Plant Physiology</i> , 2013, 163, 305-317.	2.3	98
133	Plastic, fantastic! Phenotypic variance in the transcriptional landscape of the grape berry. <i>Genome Biology</i> , 2013, 14, 119.	3.8	22
134	On the regulation and function of secondary metabolism during fruit development and ripening. <i>Journal of Experimental Botany</i> , 2013, 65, 4599-4611.	2.4	92
135	The flavonoid biosynthetic pathway in Arabidopsis: Structural and genetic diversity. <i>Plant Physiology and Biochemistry</i> , 2013, 72, 21-34.	2.8	637
136	Activation of <i>R</i> -mediated innate immunity and disease susceptibility is affected by mutations in a cytosolic <i>O</i> -acetylserine (thiol) lyase in Arabidopsis. <i>Plant Journal</i> , 2013, 73, 118-130.	2.8	36
137	The evolution of phenylpropanoid metabolism in the green lineage. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2013, 48, 123-152.	2.3	228
138	Comprehensive Dissection of Spatiotemporal Metabolic Shifts in Primary, Secondary, and Lipid Metabolism during Developmental Senescence in Arabidopsis. <i>Plant Physiology</i> , 2013, 162, 1290-1310.	2.3	278
139	Shikimate and Phenylalanine Biosynthesis in the Green Lineage. <i>Frontiers in Plant Science</i> , 2013, 4, 62.	1.7	288
140	Trichoderma-Plant Root Colonization: Escaping Early Plant Defense Responses and Activation of the Antioxidant Machinery for Saline Stress Tolerance. <i>PLoS Pathogens</i> , 2013, 9, e1003221.	2.1	299
141	Metabolic Fluxes in an Illuminated Arabidopsis Rosette. <i>Plant Cell</i> , 2013, 25, 694-714.	3.1	303
142	BRAHMA ATPase of the SWI/SNF Chromatin Remodeling Complex Acts as a Positive Regulator of Gibberellin-Mediated Responses in Arabidopsis. <i>PLoS ONE</i> , 2013, 8, e58588.	1.1	69
143	Co-expression and co-responses: within and beyond transcription. <i>Frontiers in Plant Science</i> , 2012, 3, 248.	1.7	51
144	Metabolic Profiling of a Mapping Population Exposes New Insights in the Regulation of Seed Metabolism and Seed, Fruit, and Plant Relations. <i>PLoS Genetics</i> , 2012, 8, e1002612.	1.5	115

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145	Phosphonate Analogs of 2-Oxoglutarate Perturb Metabolism and Gene Expression in Illuminated Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2012, 3, 114.	1.7	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. <i>Plant Cell</i> , 2012, 24, 2328-2351.	3.1	88
147	Annotation of Plant Gene Function via Combined Genomics, Metabolomics and Informatics. <i>Journal of Visualized Experiments</i> , 2012, , e3487.	0.2	12
148	AtABCG29 Is a Monoglignol Transporter Involved in Lignin Biosynthesis. <i>Current Biology</i> , 2012, 22, 1207-1212.	1.8	265
149	Tissue specificity and differential expression of transcription factors in tomato provide hints of unique regulatory networks during fruit ripening. <i>Plant Signaling and Behavior</i> , 2012, 7, 1639-1647.	1.2	16
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