

Takayuki Tohge

List of Publications by Year in descending order

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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	MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010, 45, 703-714.	1.6	1,831
2	Enhancement of oxidative and drought tolerance in <i>Arabidopsis</i> by overaccumulation of antioxidant flavonoids. <i>Plant Journal</i> , 2014, 77, 367-379.	5.7	911
3	Functional genomics by integrated analysis of metabolome and transcriptome of <i>Arabidopsis</i> plants over-expressing an MYB transcription factor. <i>Plant Journal</i> , 2005, 42, 218-235.	5.7	891
4	Omics-based identification of <i>Arabidopsis</i> Myb transcription factors regulating aliphatic glucosinolate biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6478-6483.	7.1	666
5	The flavonoid biosynthetic pathway in <i>Arabidopsis</i> : Structural and genetic diversity. <i>Plant Physiology and Biochemistry</i> , 2013, 72, 21-34.	5.8	637
6	<sc>M</sc>ercator: 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.	5.7	575
7	<i>JUNGBRUNNEN1</i>, a Reactive Oxygen Species-Responsive NAC Transcription Factor, Regulates Longevity in <i>Arabidopsis</i>. <i>Plant Cell</i> , 2012, 24, 482-506.	6.6	512
8	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	27.8	509
9	Members of the <i>LBD</i> Family of Transcription Factors Repress Anthocyanin Synthesis and Affect Additional Nitrogen Responses in <i>Arabidopsis</i>. <i>Plant Cell</i> , 2009, 21, 3567-3584.	6.6	507
10	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	19.0	403
11	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	21.4	391
12	Protein degradation - an alternative respiratory substrate for stressed plants. <i>Trends in Plant Science</i> , 2011, 16, 489-498.	8.8	367
13	Comprehensive Flavonol Profiling and Transcriptome Coexpression Analysis Leading to Decoding Gene-Metabolite Correlations in <i>Arabidopsis</i>. <i>Plant Cell</i> , 2008, 20, 2160-2176.	6.6	347
14	<i>Arabidopsis</i> SLIM1 Is a Central Transcriptional Regulator of Plant Sulfur Response and Metabolism. <i>Plant Cell</i> , 2006, 18, 3235-3251.	6.6	337
15	Current understanding of the pathways of flavonoid biosynthesis in model and crop plants. <i>Journal of Experimental Botany</i> , 2017, 68, 4013-4028.	4.8	328
16	Recommendations for Reporting Metabolite Data. <i>Plant Cell</i> , 2011, 23, 2477-2482.	6.6	326
17	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.	7.1	325
18	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor (<i>rin</i>) and Ethylene Receptor (<i>Nr</i>) Mutants Reveals Novel Regulatory Interactions. <i>Plant Physiology</i> , 2011, 157, 405-425.	4.8	303

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19	Metabolic Fluxes in an Illuminated <i>Arabidopsis</i> Rosette. <i>Plant Cell</i> , 2013, 25, 694-714.	6.6	303
20	Multi-level engineering facilitates the production of phenylpropanoid compounds in tomato. <i>Nature Communications</i> , 2015, 6, 8635.	12.8	303
21	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.	4.7	299
22	Rice endosperm iron biofortification by targeted and synergistic action of nicotianamine synthase and ferritin. <i>Plant Biotechnology Journal</i> , 2009, 7, 631-644.	8.3	298
23	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species. <i>Plant Cell</i> , 2011, 23, 895-910.	6.6	297
24	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. <i>Plant Cell</i> , 2010, 22, 1549-1563.	6.6	296
25	Shikimate and Phenylalanine Biosynthesis in the Green Lineage. <i>Frontiers in Plant Science</i> , 2013, 4, 62.	3.6	288
26	Analysis of PRODUCTION OF FLAVONOL GLYCOSIDES-dependent flavonol glycoside accumulation in <i>Arabidopsis thaliana</i> plants reveals MYB11, MYB12 and MYB111-independent flavonol glycoside accumulation. <i>New Phytologist</i> , 2010, 188, 985-1000.	7.3	285
27	Comprehensive Dissection of Spatiotemporal Metabolic Shifts in Primary, Secondary, and Lipid Metabolism during Developmental Senescence in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 162, 1290-1310.	4.8	278
28	AtABCG29 Is a Monoglucosyltransferase Involved in Lignin Biosynthesis. <i>Current Biology</i> , 2012, 22, 1207-1212.	3.9	265
29	Metabolomics reveals comprehensive reprogramming involving two independent metabolic responses of <i>Arabidopsis</i> to UV light. <i>Plant Journal</i> , 2011, 67, 354-369.	5.7	249
30	Identification of a Flavonol 7-O-Rhamnosyltransferase Gene Determining Flavonoid Pattern in <i>Arabidopsis</i> by Transcriptome Coexpression Analysis and Reverse Genetics. <i>Journal of Biological Chemistry</i> , 2007, 282, 14932-14941.	3.4	236
31	Differentially evolved glucosyltransferases determine natural variation of rice flavone accumulation and UV-tolerance. <i>Nature Communications</i> , 2017, 8, 1975.	12.8	233
32	The evolution of phenylpropanoid metabolism in the green lineage. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2013, 48, 123-152.	5.2	228
33	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014, 32, 1158-1165.	17.5	228
34	Antisense Inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase Enhances Photosynthesis and Growth in Tomato via an Organic Acid-Mediated Effect on Stomatal Aperture. <i>Plant Cell</i> , 2011, 23, 600-627.	6.6	221
35	Flavonoids are determinants of freezing tolerance and cold acclimation in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2016, 6, 34027.	3.3	209
36	Combining genetic diversity, informatics and metabolomics to facilitate annotation of plant gene function. <i>Nature Protocols</i> , 2010, 5, 1210-1227.	12.0	202

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37	Tissue- and Cell-Type Specific Transcriptome Profiling of Expanding Tomato Fruit Provides Insights into Metabolic and Regulatory Specialization and Cuticle Formation. <i>Plant Cell</i> , 2011, 23, 3893-3910.	6.6	193
38	Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. <i>Nature Communications</i> , 2018, 9, 4680.	12.8	189
39	Identification and Mode of Inheritance of Quantitative Trait Loci for Secondary Metabolite Abundance in Tomato. <i>Plant Cell</i> , 2015, 27, 485-512.	6.6	188
40	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.	7.1	179
41	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.	5.4	168
42	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.	6.6	166
43	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.	4.8	164
44	The Metabolic Response of <i>Arabidopsis</i> 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. <i>Molecular Plant</i> , 2009, 2, 390-406.	8.3	155
45	Tomato Fruit Photosynthesis Is Seemingly Unimportant in Primary Metabolism and Ripening But Plays a Considerable Role in Seed Development. <i>Plant Physiology</i> , 2011, 157, 1650-1663.	4.8	150
46	PRIME: a Web site that assembles tools for metabolomics and transcriptomics. <i>In Silico Biology</i> , 2008, 8, 339-45.	0.9	149
47	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. <i>Nature Communications</i> , 2016, 7, 12399.	12.8	145
48	Web-based resources for mass-spectrometry-based metabolomics: A user's guide. <i>Phytochemistry</i> , 2009, 70, 450-456.	2.9	140
49	Metabolic variation between japonica and indica rice cultivars as revealed by non-targeted metabolomics. <i>Scientific Reports</i> , 2014, 4, 5067.	3.3	129
50	Sulfur deficiency-induced repressor proteins optimize glucosinolate biosynthesis in plants. <i>Science Advances</i> , 2016, 2, e1601087.	10.3	127
51	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.	5.7	126
52	Diversity of anthocyanin and proanthocyanin biosynthesis in land plants. <i>Current Opinion in Plant Biology</i> , 2020, 55, 93-99.	7.1	119
53	Combined transcription factor profiling, microarray analysis and metabolite profiling reveals the transcriptional control of metabolic shifts occurring during tomato fruit development. <i>Plant Journal</i> , 2011, 68, 999-1013.	5.7	118
54	The Genetics of Plant Metabolism. <i>Annual Review of Genetics</i> , 2017, 51, 287-310.	7.6	118

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55	Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2007, 1, 53.	3.0	116
56	Mapping the <i>Arabidopsis</i> Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. <i>Molecular Plant</i> , 2018, 11, 118-134.	8.3	116
57	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.	3.5	115
58	Metabolomics-oriented isolation and structure elucidation of 37 compounds including two anthocyanins from <i>Arabidopsis thaliana</i> . <i>Phytochemistry</i> , 2009, 70, 1017-1029.	2.9	111
59	DELLA-Interacting SWI3C Core Subunit of Switch/Sucrose Nonfermenting Chromatin Remodeling Complex Modulates Gibberellin Responses and Hormonal Cross Talk in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 163, 305-317.	4.8	98
60	Identification of Genes in the Phenylalanine Metabolic Pathway by Ectopic Expression of a MYB Transcription Factor in Tomato Fruit. <i>Plant Cell</i> , 2011, 23, 2738-2753.	6.6	97
61	The Role of SWI/SNF Chromatin Remodeling Complexes in Hormone Crosstalk. <i>Trends in Plant Science</i> , 2016, 21, 594-608.	8.8	95
62	Toward the Storage Metabolome: Profiling the Barley Vacuole. <i>Plant Physiology</i> , 2011, 157, 1469-1482.	4.8	92
63	On the regulation and function of secondary metabolism during fruit development and ripening. <i>Journal of Experimental Botany</i> , 2013, 65, 4599-4611.	4.8	92
64	2-Oxoglutarate: linking TCA cycle function with amino acid, glucosinolate, flavonoid, alkaloid, and gibberellin biosynthesis. <i>Frontiers in Plant Science</i> , 2014, 5, 552.	3.6	91
65	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.	8.3	91
66	Phytochemical genomics in <i>Arabidopsis thaliana</i> : A case study for functional identification of flavonoid biosynthesis genes. <i>Pure and Applied Chemistry</i> , 2007, 79, 811-823.	1.9	88
67	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.	6.6	88
68	<i>Arabidopsis</i> 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.	6.6	86
69	Metabolic profiling and cytological analysis of proanthocyanidins in immature seeds of <i>Arabidopsis thaliana</i> flavonoid accumulation mutants. <i>Plant Journal</i> , 2010, 62, 549-559.	5.7	85
70	Characterization of the Branched-Chain Amino Acid Aminotransferase Enzyme Family in Tomato. <i>Plant Physiology</i> , 2010, 153, 925-936.	4.8	80
71	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.	5.7	79
72	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.	3.0	77

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73	Pleiotropic physiological consequences of feedback-insensitive phenylalanine biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2010, 63, 823-835.	5.7	69
74	BRAHMA ATPase of the SWI/SNF Chromatin Remodeling Complex Acts as a Positive Regulator of Gibberellin-Mediated Responses in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2013, 8, e58588.	2.5	69
75	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.	4.8	67
76	Salt-Related MYB1 Coordinates Abscisic Acid Biosynthesis and Signaling during Salt Stress in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 169, 1027-1041.	4.8	66
77	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.	3.1	66
78	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. <i>Nature Plants</i> , 2020, 6, 1447-1454.	9.3	66
79	Transcription factor <i>RD26</i> is a key regulator of metabolic reprogramming during dark-induced senescence. <i>New Phytologist</i> , 2018, 218, 1543-1557.	7.3	65
80	Identification of Conserved and Diverse Metabolic Shifts during Rice Grain Development. <i>Scientific Reports</i> , 2016, 6, 20942.	3.3	64
81	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. <i>Plant Physiology</i> , 2016, 170, 1878-1894.	4.8	63
82	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.	5.7	62
83	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.	4.8	62
84	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.	4.7	61
85	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.	8.5	60
86	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <i>Plant Science</i> , 2016, 242, 47-64.	3.6	60
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.	6.6	60
88	Metabolic and miRNA Profiling of TMV Infected Plants Reveals Biphasic Temporal Changes. <i>PLoS ONE</i> , 2011, 6, e28466.	2.5	59
89	Flux profiling of photosynthetic carbon metabolism in intact plants. <i>Nature Protocols</i> , 2014, 9, 1803-1824.	12.0	59
90	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.	6.4	59

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91	A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. <i>Plant Physiology</i> , 2019, 180, 87-108.	4.8	59
92	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.	2.4	58
93	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.	8.3	56
94	Transcriptional and metabolic programs following exposure of plants to UV-B irradiation. <i>Plant Signaling and Behavior</i> , 2011, 6, 1987-1992.	2.4	54
95	Liquid chromatography high-resolution mass spectrometry for fatty acid profiling. <i>Plant Journal</i> , 2015, 81, 529-536.	5.7	54
96	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. <i>Plant Biotechnology Journal</i> , 2016, 14, 719-734.	8.3	53
97	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. <i>Nature Communications</i> , 2019, 10, 737.	12.8	52
98	Co-expression and co-responses: within and beyond transcription. <i>Frontiers in Plant Science</i> , 2012, 3, 248.	3.6	51
99	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.	3.9	51
100	Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species. <i>Plant Physiology</i> , 2014, 164, 55-68.	4.8	50
101	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.	2.6	50
102	Metabolomic Characterization of Knockout Mutants in Arabidopsis: Development of a Metabolite Profiling Database for Knockout Mutants in Arabidopsis. <i>Plant Physiology</i> , 2014, 165, 948-961.	4.8	49
103	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.	5.2	49
104	On the natural diversity of phenylacylated-flavonoid and their in planta function under conditions of stress. <i>Phytochemistry Reviews</i> , 2018, 17, 279-290.	6.5	48
105	Genome-enabled plant metabolomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2014, 966, 7-20.	2.3	47
106	Canalization of Tomato Fruit Metabolism. <i>Plant Cell</i> , 2017, 29, 2753-2765.	6.6	47
107	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.	8.5	47
108	Leveraging Natural Variance towards Enhanced Understanding of Phytochemical Sunscreens. <i>Trends in Plant Science</i> , 2017, 22, 308-315.	8.8	46

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109	Vacuolar Chloride Fluxes Impact Ion content and Distribution during Early Salinity Stress. <i>Plant Physiology</i> , 2016, 172, pp.00183.2016.	4.8	45
110	Evolutionary interplay between sister cytochrome P450 genes shapes plasticity in plant metabolism. <i>Nature Communications</i> , 2016, 7, 13026.	12.8	44
111	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.	5.7	44
112	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.	8.3	44
113	Enhanced radical scavenging activity of genetically modified <i>Arabidopsis</i> seeds. <i>Biotechnology Letters</i> , 2005, 27, 297-303.	2.2	41
114	Integrative Approaches to Enhance Understanding of Plant Metabolic Pathway Structure and Regulation. <i>Plant Physiology</i> , 2015, 169, 1499-1511.	4.8	40
115	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 <i>Arabidopsis</i> during Dark-Induced Senescence. <i>Plant Physiology</i> , 2011, 157, 55-69.	4.8	39
116	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.	2.5	39
117	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.	6.6	39
118	Integrative field scale phenotyping for investigating metabolic components of water stress within a vineyard. <i>Plant Methods</i> , 2017, 13, 90.	4.3	37
119	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 <i>Arabidopsis</i> . <i>Plant Journal</i> , 2013, 73, 118-130.	5.7	36
120	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.	5.7	36
121	Differential metabolic and coexpression networks of plant metabolism. <i>Trends in Plant Science</i> , 2015, 20, 266-268.	8.8	35
122	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. <i>Plant Physiology</i> , 2016, 172, pp.00261.2016.	4.8	35
123	The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2020, 182, 857-869.	4.8	35
124	An <i>Oryza</i> -specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. <i>Science Bulletin</i> , 2021, 66, 2369-2380.	9.0	35
125	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. <i>BMC Plant Biology</i> , 2017, 17, 17.	3.6	34
126	From models to crop species: caveats and solutions for translational metabolomics. <i>Frontiers in Plant Science</i> , 2011, 2, 61.	3.6	33

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127	Targeted LC-MS Analysis for Plant Secondary Metabolites. <i>Methods in Molecular Biology</i> , 2018, 1778, 171-181.	0.9	33
128	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.	5.7	33
129	Quantitative trait loci analysis of seed-specialized metabolites reveals seed-specific flavonols and differential regulation of glycoalkaloid content in tomato. <i>Plant Journal</i> , 2020, 103, 2007-2024.	5.7	32
130	Phosphonate Analogs of 2-Oxoglutarate Perturb Metabolism and Gene Expression in Illuminated Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2012, 3, 114.	3.6	30
131	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.	2.9	30
132	Phytochrome A and B Regulate Primary Metabolism in Arabidopsis Leaves in Response to Light. <i>Frontiers in Plant Science</i> , 2017, 8, 1394.	3.6	30
133	Genetic Manipulation of Transcriptional Regulators Alters Nicotine Biosynthesis in Tobacco. <i>Plant and Cell Physiology</i> , 2020, 61, 1041-1053.	3.1	30
134	The Mitochondrial Thioredoxin System Contributes to the Metabolic Responses Under Drought Episodes in Arabidopsis. <i>Plant and Cell Physiology</i> , 2019, 60, 213-229.	3.1	26
135	Extended darkness induces internal turnover of glucosinolates in Arabidopsis thaliana leaves. <i>PLoS ONE</i> , 2018, 13, e0202153.	2.5	24
136	The <i>genomes 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.	4.0	24
137	Plastic, fantastic! Phenotypic variance in the transcriptional landscape of the grape berry. <i>Genome Biology</i> , 2013, 14, 119.	8.8	22
138	Analysis of knockout mutants reveals non-redundant functions of poly(ADP-ribose)polymerase isoforms in Arabidopsis. <i>Plant Molecular Biology</i> , 2015, 89, 319-338.	3.9	21
139	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.	6.4	21
140	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.	8.5	20
141	Dealing with the sulfur part of cysteine: four enzymatic steps degrade α -cysteine to pyruvate and thiosulfate in Arabidopsis mitochondria. <i>Physiologia Plantarum</i> , 2016, 157, 352-366.	5.2	20
142	Characterization of ubiquitin ligase SIATL31 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.	2.4	20
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