

Asaph Aharoni

List of Publications by Year in descending order

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Version: 2024-02-01

136
papers

15,381
citations

16451

64
h-index

19190

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143
all docs

143
docs citations

143
times ranked

14774
citing authors

#	ARTICLE	IF	CITATIONS
1	The SHINE Clade of AP2 Domain Transcription Factors Activates Wax Biosynthesis, Alters Cuticle Properties, and Confers Drought Tolerance when Overexpressed in Arabidopsis[W]. <i>Plant Cell</i> , 2004, 16, 2463-2480.	6.6	743
2	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. <i>Plant Cell</i> , 2000, 12, 647-661.	6.6	496
3	Genetic Engineering of Terpenoid Metabolism Attracts Bodyguards to Arabidopsis. <i>Science</i> , 2005, 309, 2070-2072.	12.6	482
4	Biosynthesis of Antinutritional Alkaloids in Solanaceous Crops Is Mediated by Clustered Genes. <i>Science</i> , 2013, 341, 175-179.	12.6	464
5	Terpenoid Metabolism in Wild-Type and Transgenic Arabidopsis Plants[W]. <i>Plant Cell</i> , 2003, 15, 2866-2884.	6.6	461
6	Gain and Loss of Fruit Flavor Compounds Produced by Wild and Cultivated Strawberry Species. <i>Plant Cell</i> , 2004, 16, 3110-3131.	6.6	427
7	Nontargeted Metabolome Analysis by Use of Fourier Transform Ion Cyclotron Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 217-234.	2.0	415
8	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	19.0	403
9	Volatile science? Metabolic engineering of terpenoids in plants. <i>Trends in Plant Science</i> , 2005, 10, 594-602.	8.8	361
10	Recommendations for Reporting Metabolite Data. <i>Plant Cell</i> , 2011, 23, 2477-2482.	6.6	326
11	Rhizosphere microbiome mediates systemic root metabolite exudation by root-to-root signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3874-3883.	7.1	326
12	Functional Characterization of Enzymes Forming Volatile Esters from Strawberry and Banana. <i>Plant Physiology</i> , 2004, 135, 1865-1878.	4.8	315
13	Gene Expression and Metabolism in Tomato Fruit Surface Tissues. <i>Plant Physiology</i> , 2008, 147, 823-851.	4.8	313
14	TOMATO AGAMOUS-LIKE1 is a component of the fruit ripening regulatory network. <i>Plant Journal</i> , 2009, 60, 1081-1095.	5.7	298
15	The Arabidopsis <i>DESPERADO</i> / <i>AtWBC11</i> Transporter Is Required for Cutin and Wax Secretion. <i>Plant Physiology</i> , 2007, 145, 1345-1360.	4.8	283
16	Reconfiguration of the Achene and Receptacle Metabolic Networks during Strawberry Fruit Development. <i>Plant Physiology</i> , 2008, 148, 730-750.	4.8	276
17	GAME9 regulates the biosynthesis of steroidal alkaloids and upstream isoprenoids in the plant mevalonate pathway. <i>Nature Communications</i> , 2016, 7, 10654.	12.8	239
18	Reconstruction of Arabidopsis metabolic network models accounting for subcellular compartmentalization and tissue-specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 339-344.	7.1	237

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19	Live imaging of root-bacteria interactions in a microfluidics setup. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4549-4554.	7.1	233
20	Fruit-Surface Flavonoid Accumulation in Tomato Is Controlled by a SIMYB12-Regulated Transcriptional Network. PLoS Genetics, 2009, 5, e1000777.	3.5	219
21	Metabolic engineering of the plant primary-secondary metabolism interface. Current Opinion in Biotechnology, 2011, 22, 239-244.	6.6	209
22	GLYCOALKALOID METABOLISM1 Is Required for Steroidal Alkaloid Glycosylation and Prevention of Phytotoxicity in Tomato. Plant Cell, 2011, 23, 4507-4525.	6.6	205
23	Plant cholesterol biosynthetic pathway overlaps with phytosterol metabolism. Nature Plants, 2017, 3, 16205.	9.3	201
24	Tissue- and Cell-Type Specific Transcriptome Profiling of Expanding Tomato Fruit Provides Insights into Metabolic and Regulatory Specialization and Cuticle Formation. Plant Cell, 2011, 23, 3893-3910.	6.6	193
25	Small molecules belowground: the role of specialized metabolites in the rhizosphere. Plant Journal, 2017, 90, 788-807.	5.7	193
26	SHINE Transcription Factors Act Redundantly to Pattern the Archetypal Surface of Arabidopsis Flower Organs. PLoS Genetics, 2011, 7, e1001388.	3.5	191
27	Efficient <i>in planta</i> gene targeting in tomato using geminiviral replicons and the CRISPR/Cas9 system. Plant Journal, 2018, 95, 5-16.	5.7	191
28	The Transcript and Metabolite Networks Affected by the Two Clades of Arabidopsis Glucosinolate Biosynthesis Regulators. Plant Physiology, 2008, 148, 2021-2049.	4.8	188
29	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. Scientific Reports, 2019, 9, 11769.	3.3	179
30	Gene expression analysis of strawberry achene and receptacle maturation using DNA microarrays. Journal of Experimental Botany, 2002, 53, 2073-2087.	4.8	166
31	Riboswitch-dependent gene regulation and its evolution in the plant kingdom. Genes and Development, 2007, 21, 2874-2879.	5.9	156
32	The Arabidopsis DSO/ABCG11 Transporter Affects Cutin Metabolism in Reproductive Organs and Suberin in Roots. Molecular Plant, 2010, 3, 563-575.	8.3	156
33	The tomato <i>S</i> SHINE3 transcription factor regulates fruit cuticle formation and epidermal patterning. New Phytologist, 2013, 197, 468-480.	7.3	156
34	La Vie en Rose: Biosynthesis, Sources, and Applications of Betalain Pigments. Molecular Plant, 2018, 11, 7-22.	8.3	156
35	The Arabidopsis <i>DCR</i> Encoding a Soluble BAHD Acyltransferase Is Required for Cutin Polyester Formation and Seed Hydration Properties. Plant Physiology, 2009, 151, 1773-1789.	4.8	154
36	MYB107 and MYB9 Homologs Regulate Suberin Deposition in Angiosperms. Plant Cell, 2016, 28, 2097-2116.	6.6	151

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37	Metabolic Engineering of Terpenoid Biosynthesis in Plants. <i>Phytochemistry Reviews</i> , 2006, 5, 49-58.	6.5	147
38	Elucidation of the first committed step in betalain biosynthesis enables the heterologous engineering of betalain pigments in plants. <i>New Phytologist</i> , 2016, 210, 269-283.	7.3	147
39	Rewiring Host Lipid Metabolism by Large Viruses Determines the Fate of <i>Emiliania huxleyi</i> , a Bloom-Forming Alga in the Ocean. <i>Plant Cell</i> , 2014, 26, 2689-2707.	6.6	132
40	High-resolution metabolic mapping of cell types in plant roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1232-41.	7.1	131
41	Auxin Response Factor SlARF2 Is an Essential Component of the Regulatory Mechanism Controlling Fruit Ripening in Tomato. <i>PLoS Genetics</i> , 2015, 11, e1005649.	3.5	128
42	AUXIN RESPONSE FACTOR 2 Intersects Hormonal Signals in the Regulation of Tomato Fruit Ripening. <i>PLoS Genetics</i> , 2016, 12, e1005903.	3.5	128
43	Sample Preparation for Mass Spectrometry Imaging of Plant Tissues: A Review. <i>Frontiers in Plant Science</i> , 2016, 7, 60.	3.6	125
44	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. <i>Plant Cell</i> , 2016, 28, 1440-1460.	6.6	123
45	The bitter side of the nightshades: Genomics drives discovery in Solanaceae steroidal alkaloid metabolism. <i>Phytochemistry</i> , 2015, 113, 24-32.	2.9	114
46	Engineered gray mold resistance, antioxidant capacity, and pigmentation in betalain-producing crops and ornamentals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9062-9067.	7.1	111
47	Cinnamate Metabolism in Ripening Fruit. Characterization of a UDP-Glucose:Cinnamate Glucosyltransferase from Strawberry. <i>Plant Physiology</i> , 2006, 140, 1047-1058.	4.8	104
48	Analysis of wild tomato introgression lines elucidates the genetic basis of transcriptome and metabolome variation underlying fruit traits and pathogen response. <i>Nature Genetics</i> , 2020, 52, 1111-1121.	21.4	103
49	Uncovering DELLA-Independent Gibberellin Responses by Characterizing New Tomato <i>procera</i> Mutants. <i>Plant Cell</i> , 2015, 27, 1579-1594.	6.6	100
50	Expression of a bacterial feedback-insensitive 3-deoxy- α -D-arabinoheptulosonate 7-phosphate synthase of the shikimate pathway in <i>Arabidopsis</i> elucidates potential metabolic bottlenecks between primary and secondary metabolism. <i>New Phytologist</i> , 2012, 194, 430-439.	7.3	98
51	Orchestration of Thiamin Biosynthesis and Central Metabolism by Combined Action of the Thiamin Pyrophosphate Riboswitch and the Circadian Clock in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 288-307.	6.6	98
52	Viral infection of the marine alga <i>Emiliania huxleyi</i> triggers lipidome remodeling and induces the production of highly saturated triacylglycerol. <i>New Phytologist</i> , 2016, 210, 88-96.	7.3	98
53	The challenges of cellular compartmentalization in plant metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2013, 24, 239-246.	6.6	95
54	The WEIZMASS spectral library for high-confidence metabolite identification. <i>Nature Communications</i> , 2016, 7, 12423.	12.8	95

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55	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015, 6, 1194.	3.6	93
56	The Tomato DELLA Protein PROCERA Acts in Guard Cells to Promote Stomatal Closure. <i>Plant Cell</i> , 2017, 29, 3186-3197.	6.6	90
57	SEEDSTICK is a Master Regulator of Development and Metabolism in the Arabidopsis Seed Coat. <i>PLoS Genetics</i> , 2014, 10, e1004856.	3.5	86
58	Expression of a bacterial bifunctional chorismate mutase/prephenate dehydratase modulates primary and secondary metabolism associated with aromatic amino acids in Arabidopsis. <i>Plant Journal</i> , 2009, 60, 156-167.	5.7	80
59	Scratching the surface: genetic regulation of cuticle assembly in fleshy fruit. <i>Journal of Experimental Botany</i> , 2013, 65, 4653-4664.	4.8	79
60	More than Pictures: When MS Imaging Meets Histology. <i>Trends in Plant Science</i> , 2016, 21, 686-698.	8.8	79
61	Bacterial virulence against an oceanic bloom-forming phytoplankton is mediated by algal DMSP. <i>Science Advances</i> , 2018, 4, eaau5716.	10.3	78
62	Genome investigation suggests <i>MdSHN3</i> , an APETALA2-domain transcription factor gene, to be a positive regulator of apple fruit cuticle formation and an inhibitor of russet development. <i>Journal of Experimental Botany</i> , 2015, 66, 6579-6589.	4.8	76
63	Label-free deep shotgun proteomics reveals protein dynamics during tomato fruit tissues development. <i>Plant Journal</i> , 2017, 90, 396-417.	5.7	76
64	Transcriptome and Metabolic Profiling Provides Insights into Betalain Biosynthesis and Evolution in <i>Mirabilis jalapa</i> . <i>Molecular Plant</i> , 2018, 11, 189-204.	8.3	76
65	<i>Solanum pennellii</i> backcross inbred lines (BILs) link small genomic bins with tomato traits. <i>Plant Journal</i> , 2016, 87, 151-160.	5.7	74
66	The PhytoClust tool for metabolic gene clusters discovery in plant genomes. <i>Nucleic Acids Research</i> , 2017, 45, 7049-7063.	14.5	71
67	SUBERMAN regulates developmental suberization of the Arabidopsis root endodermis. <i>Plant Journal</i> , 2020, 102, 431-447.	5.7	69
68	The Tomato MIXTA-like Transcription Factor Coordinates Fruit Epidermis Conical Cell Development and Cuticular Lipid Biosynthesis and Assembly. <i>Plant Physiology</i> , 2015, 169, pp.01145.2015.	4.8	67
69	Plant terpenoid metabolism co-opts a component of the cell wall biosynthesis machinery. <i>Nature Chemical Biology</i> , 2020, 16, 740-748.	8.0	67
70	Short-chain dehydrogenase/reductase governs steroidal specialized metabolites structural diversity and toxicity in the genus <i>Solanum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5419-E5428.	7.1	66
71	The Plant Cuticle: An Ancient Guardian Barrier Set Against Long-Standing Rivals. <i>Frontiers in Plant Science</i> , 2021, 12, 663165.	3.6	65
72	An Orange Ripening Mutant Links Plastid NAD(P)H Dehydrogenase Complex Activity to Central and Specialized Metabolism during Tomato Fruit Maturation. <i>Plant Cell</i> , 2010, 22, 1977-1997.	6.6	61

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73	Genetics of Flavonoid, Carotenoid, and Chlorophyll Pigments in Melon Fruit Rinds. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 10722-10728.	5.2	60
74	Tomato fruits expressing a bacterial feedback-insensitive 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase of the shikimate pathway possess enhanced levels of multiple specialized metabolites and upgraded aroma. <i>Journal of Experimental Botany</i> , 2013, 64, 4441-4452.	4.8	60
75	Pathways to defense metabolites and evading fruit bitterness in genus <i>Solanum</i> evolved through 2-oxoglutarate-dependent dioxygenases. <i>Nature Communications</i> , 2019, 10, 5169.	12.8	60
76	A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. <i>Plant Physiology</i> , 2019, 180, 87-108.	4.8	59
77	The transcription factor SISHINE3 modulates defense responses in tomato plants. <i>Plant Molecular Biology</i> , 2014, 84, 37-47.	3.9	58
78	Viral serine palmitoyltransferase induces metabolic switch in sphingolipid biosynthesis and is required for infection of a marine alga. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1907-16.	7.1	58
79	Cell type-specific transcriptional profiling: implications for metabolite profiling. <i>Plant Journal</i> , 2012, 70, 5-17.	5.7	57
80	A Multilevel Study of Melon Fruit Reticulation Provides Insight into Skin Ligno-Suberization Hallmarks. <i>Plant Physiology</i> , 2019, 179, 1486-1501.	4.8	52
81	In plaque-mass spectrometry imaging of a bloom-forming alga during viral infection reveals a metabolic shift towards odd-chain fatty acid lipids. <i>Nature Microbiology</i> , 2019, 4, 527-538.	13.3	52
82	Composition of cuticular waxes coating flag leaf blades and peduncles of <i>Triticum aestivum</i> cv. Bethlehem. <i>Phytochemistry</i> , 2016, 130, 182-192.	2.9	51
83	The GORKY glycoalkaloid transporter is indispensable for preventing tomato bitterness. <i>Nature Plants</i> , 2021, 7, 468-480.	9.3	50
84	Small molecules that interact with <i>scp>RNA</scp></i> : riboswitch-based gene control and its involvement in metabolic regulation in plants and algae. <i>Plant Journal</i> , 2014, 79, 693-703.	5.7	49
85	Switching the light on plant riboswitches. <i>Trends in Plant Science</i> , 2008, 13, 526-533.	8.8	45
86	pc8.1, a major QTL for pigment content in pepper fruit, is associated with variation in plastid compartment size. <i>Planta</i> , 2012, 235, 579-588.	3.2	45
87	Glycosylation of N-hydroxy-pipecolic acid equilibrates between systemic acquired resistance response and plant growth. <i>Molecular Plant</i> , 2021, 14, 440-455.	8.3	44
88	Assimilation of omics™ strategies to study the cuticle layer and suberin lamellae in plants. <i>Journal of Experimental Botany</i> , 2017, 68, 5389-5400.	4.8	42
89	Inhibition of gibberellin accumulation by water deficiency promotes fast and long-term drought avoidance™ responses in tomato. <i>New Phytologist</i> , 2021, 232, 1985-1998.	7.3	42
90	Dual Labeling of Metabolites for Metabolome Analysis (DLEMMA): A New Approach for the Identification and Relative Quantification of Metabolites by Means of Dual Isotope Labeling and Liquid Chromatography-Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 9257-9266.	6.5	41

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91	Uncovering tomato quantitative trait loci and candidate genes for fruit cuticular lipid composition using the <i>Solanum pennellii</i> introgression line population. <i>Journal of Experimental Botany</i> , 2017, 68, 2703-2716.	4.8	41
92	Dynamic metabolic reprogramming of steroidal glycol-alkaloid and phenylpropanoid biosynthesis may impart early blight resistance in wild tomato (<i>Solanum arcanum</i> Peralta). <i>Plant Molecular Biology</i> , 2017, 95, 411-423.	3.9	41
93	Plant-microbe interactions in the rhizosphere via a circular metabolic economy. <i>Plant Cell</i> , 2022, 34, 3168-3182.	6.6	37
94	Advances and future directions in betalain metabolic engineering. <i>New Phytologist</i> , 2019, 224, 1472-1478.	7.3	36
95	Metabolic Engineering of the Phenylpropanoid and Its Primary, Precursor Pathway to Enhance the Flavor of Fruits and the Aroma of Flowers. <i>Bioengineering</i> , 2015, 2, 204-212.	3.5	35
96	Comparative Metabolomics and Molecular Phylogenetics of Melon (<i>Cucumis melo</i> , Cucurbitaceae) Biodiversity. <i>Metabolites</i> , 2020, 10, 121.	2.9	35
97	Phytobiome metabolism: beneficial soil microbes steer crop plants' secondary metabolism. <i>Pest Management Science</i> , 2019, 75, 2378-2384.	3.4	34
98	Developmental programs interact with abscisic acid to coordinate root suberization in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 104, 241-251.	5.7	34
99	ABA homeostasis and long-distance translocation are redundantly regulated by ABCG ABA importers. <i>Science Advances</i> , 2021, 7, eabf6069.	10.3	34
100	<i>Arabidopsis</i> HSP70 ¹⁶ is required for flower opening under normal or mild heat stress temperatures. <i>Plant, Cell and Environment</i> , 2019, 42, 1190-1204.	5.7	30
101	Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , 2020, 102, 897-902.	5.7	30
102	High mass resolution, spatial metabolite mapping enhances the current plant gene and pathway discovery toolbox. <i>New Phytologist</i> , 2020, 228, 1986-2002.	7.3	30
103	Overexpression of AtSHN1/WIN1 Provokes Unique Defense Responses. <i>PLoS ONE</i> , 2013, 8, e70146.	2.5	29
104	ABCG transporters export cutin precursors for the formation of the plant cuticle. <i>Current Biology</i> , 2021, 31, 2111-2123.e9.	3.9	28
105	"Hijacking" core metabolism: a new panache for the evolution of steroidal glycoalkaloids structural diversity. <i>Current Opinion in Plant Biology</i> , 2020, 55, 118-128.	7.1	25
106	Pathogen and Pest Responses Are Altered Due to RNAi-Mediated Knockdown of <i>GLYCOALKALOID METABOLISM 4</i> in <i>Solanum tuberosum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 876-885.	2.6	24
107	Appropriate Thiamin Pyrophosphate Levels Are Required for Acclimation to Changes in Photoperiod. <i>Plant Physiology</i> , 2019, 180, 185-197.	4.8	24
108	CRISPR/Cas9 mutants of tomato <i>MICRORNA164</i> genes uncover their functional specialization in development. <i>Plant Physiology</i> , 2021, 187, 1636-1652.	4.8	24

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109	The "TranSeq"™ 3 rd -end sequencing method for high-throughput transcriptomics and gene space refinement in plant genomes. <i>Plant Journal</i> , 2018, 96, 223-232.	5.7	23
110	Altered metabolite accumulation in tomato fruits by coexpressing a feedback-insensitive AroG and the Ph ODO 1 MYB type transcription factor. <i>Plant Biotechnology Journal</i> , 2016, 14, 2300-2309.	8.3	22
111	DLEMMA-MS-Imaging for Identification of Spatially Localized Metabolites and Metabolic Network Map Reconstruction. <i>Analytical Chemistry</i> , 2018, 90, 10231-10238.	6.5	21
112	Steroidal alkaloids defence metabolism and plant growth are modulated by the joint action of gibberellin and jasmonate signalling. <i>New Phytologist</i> , 2022, 233, 1220-1237.	7.3	21
113	Image to insight: exploring natural products through mass spectrometry imaging. <i>Natural Product Reports</i> , 2022, 39, 1510-1530.	10.3	20
114	Catch-22 in specialized metabolism: balancing defense and growth. <i>Journal of Experimental Botany</i> , 2021, 72, 6027-6041.	4.8	19
115	An efficient method for medium throughput screening of cuticular wax composition in different plant species. <i>Metabolomics</i> , 2016, 12, 1.	3.0	18
116	Altered Levels of Aroma and Volatiles by Metabolic Engineering of Shikimate Pathway Genes in Tomato Fruits. <i>AIMS Bioengineering</i> , 2015, 2, 75-92.	1.1	15
117	Analysis of Steroidal Alkaloids and Saponins in Solanaceae Plant Extracts Using UPLC-qTOF Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2014, 1153, 171-185.	0.9	13
118	The isocitrate dehydrogenase 1 gene is associated with the climacteric response in tomato fruit ripening. <i>Postharvest Biology and Technology</i> , 2020, 166, 111219.	6.0	12
119	2-oxoglutarate-dependent dioxygenases drive expansion of steroidal alkaloid structural diversity in the genus <i>Solanum</i> . <i>New Phytologist</i> , 2022, 234, 1394-1410.	7.3	12
120	A hairy-root transformation protocol for <i>Trigonella foenum-graecum</i> L. as a tool for metabolic engineering and specialised metabolite pathway elucidation. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 451-462.	5.8	11
121	Integration of Plant Metabolomics Data with Metabolic Networks: Progresses and Challenges. <i>Methods in Molecular Biology</i> , 2018, 1778, 297-310.	0.9	10
122	Pan-Genomic Illumination of Tomato Identifies Novel Gene-Trait Interactions. <i>Trends in Plant Science</i> , 2019, 24, 882-884.	8.8	10
123	The metabolic and proteomic repertoires of periderm tissue in skin of the reticulated Sikkim cucumber fruit. <i>Horticulture Research</i> , 2022, 9, .	6.3	10
124	Miso: an R package for multiple isotope labeling assisted metabolomics data analysis. <i>Bioinformatics</i> , 2019, 35, 3524-3526.	4.1	9
125	Gene Expression in 1-Methylcyclopropene (1-MCP) Treated Tomatoes during Pre-Climacteric Ripening Suggests Shared Regulation of Methionine Biosynthesis, Ethylene Production and Respiration. <i>Agronomy</i> , 2020, 10, 1669.	3.0	8
126	Metabolic Engineering of Terpenoid Biosynthesis in Plants. , 2007, , 219-236.		6

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127	Uncovering Pathways Highly Correlated to NUE through a Combined Metabolomics and Transcriptomics Approach in Eggplant. <i>Plants</i> , 2022, 11, 700.	3.5	6
128	Small molecules: from structural diversity to signalling and regulatory roles. <i>Plant Journal</i> , 2014, 79, 541-543.	5.7	5
129	Bioengineering. , 2009, , 435-473.		3
130	A Complete Pipeline for Generating a High-Resolution LC-MS-Based Reference Mass Spectra Library. <i>Methods in Molecular Biology</i> , 2018, 1778, 193-206.	0.9	3
131	Phenylpropanoid Metabolism in Astringent and Nonstringent Persimmon (<i>Diospyros kaki</i>) Cultivars Determines Sensitivity to <i>Alternaria</i> Infection. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 5628-5637.	5.2	3
132	Genetic engineering of strawberry flavour. <i>Developments in Food Science</i> , 2006, , 39-44.	0.0	2
133	Characterization of the PRODUCTION of ANTHOCYANIN PIGMENT 1 Arabidopsis dominant mutant using DLEMMA dual isotope labeling approach. <i>Phytochemistry</i> , 2021, 186, 112740.	2.9	2
134	Tracking Root Interactions System (TRIS) Experiment and Quality Control. <i>Bio-protocol</i> , 2019, 9, e3211.	0.4	2
135	AtMYB31 is a wax regulator associated with reproductive development in Arabidopsis. <i>Planta</i> , 2022, 256, .	3.2	2
136	Editorial: Introducing TPJ Fellowships for early stage Principal Investigators. <i>Plant Journal</i> , 2019, 100, 435-435.	5.7	0