

Asaph Aharoni

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5304236/publications.pdf>

Version: 2024-02-01

136
papers

15,381
citations

16451

64
h-index

19190

118
g-index

143
all docs

143
docs citations

143
times ranked

14774
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Uncovering Pathways Highly Correlated to NUE through a Combined Metabolomics and Transcriptomics Approach in Eggplant. <i>Plants</i> , 2022, 11, 700.	3.5	6
4	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
5	Image to insight: exploring natural products through mass spectrometry imaging. <i>Natural Product Reports</i> , 2022, 39, 1510-1530.	10.3	20
6	Plant-microbe interactions in the rhizosphere via a circular metabolic economy. <i>Plant Cell</i> , 2022, 34, 3168-3182.	6.6	37
7	AtMYB31 is a wax regulator associated with reproductive development in Arabidopsis. <i>Planta</i> , 2022, 256, .	3.2	2
8	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
9	The GORKY glycoalkaloid transporter is indispensable for preventing tomato bitterness. <i>Nature Plants</i> , 2021, 7, 468-480.	9.3	50
10	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
11	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
12	ABCG transporters export cutin precursors for the formation of the plant cuticle. <i>Current Biology</i> , 2021, 31, 2111-2123.e9.	3.9	28
13	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
14	The Plant Cuticle: An Ancient Guardian Barrier Set Against Long-Standing Rivals. <i>Frontiers in Plant Science</i> , 2021, 12, 663165.	3.6	65
15	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	19.0	403
16	Catch-22 in specialized metabolism: balancing defense and growth. <i>Journal of Experimental Botany</i> , 2021, 72, 6027-6041.	4.8	19
17	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
18	ABA homeostasis and long-distance translocation are redundantly regulated by ABCG ABA importers. <i>Science Advances</i> , 2021, 7, eabf6069.	10.3	34

#	ARTICLE	IF	CITATIONS
19	Metabolomics should be deployed in the identification and characterization of gene-edited crops. <i>Plant Journal</i> , 2020, 102, 897-902.	5.7	30
20	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
21	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
22	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
23	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
24	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
25	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
26	SUBERMAN regulates developmental suberization of the <i>Arabidopsis</i> root endodermis. <i>Plant Journal</i> , 2020, 102, 431-447.	5.7	69
27	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
28	Comparative Metabolomics and Molecular Phylogenetics of Melon (<i>Cucumis melo</i> , Cucurbitaceae) Biodiversity. <i>Metabolites</i> , 2020, 10, 121.	2.9	35
29	"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
30	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
31	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019, 9, 11769.	3.3	179
32	Editorial: Introducing TPJ Fellowships for early stage Principal Investigators. <i>Plant Journal</i> , 2019, 100, 435-435.	5.7	0
33	Pan-Genomic Illumination of Tomato Identifies Novel Gene-Trait Interactions. <i>Trends in Plant Science</i> , 2019, 24, 882-884.	8.8	10
34	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
35	Advances and future directions in betalain metabolic engineering. <i>New Phytologist</i> , 2019, 224, 1472-1478.	7.3	36
36	Appropriate Thiamin Pyrophosphate Levels Are Required for Acclimation to Changes in Photoperiod. <i>Plant Physiology</i> , 2019, 180, 185-197.	4.8	24

#	ARTICLE	IF	CITATIONS
37	Phytobiome metabolism: beneficial soil microbes steer crop plants' secondary metabolism. <i>Pest Management Science</i> , 2019, 75, 2378-2384.	3.4	34
38	Miso: an R package for multiple isotope labeling assisted metabolomics data analysis. <i>Bioinformatics</i> , 2019, 35, 3524-3526.	4.1	9
39	A MYB Triad Controls Primary and Phenylpropanoid Metabolites for Pollen Coat Patterning. <i>Plant Physiology</i> , 2019, 180, 87-108.	4.8	59
40	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
41	<i>Arabidopsis</i> HSP70 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
42	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
43	Tracking Root Interactions System (TRIS) Experiment and Quality Control. <i>Bio-protocol</i> , 2019, 9, e3211.	0.4	2
44	Efficient <i>in planta</i> gene targeting in tomato using geminiviral replicons and the CRISPR/Cas9 system. <i>Plant Journal</i> , 2018, 95, 5-16.	5.7	191
45	La Vie en Rose: Biosynthesis, Sources, and Applications of Betalain Pigments. <i>Molecular Plant</i> , 2018, 11, 7-22.	8.3	156
46	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
47	Bacterial virulence against an oceanic bloom-forming phytoplankter is mediated by algal DMSP. <i>Science Advances</i> , 2018, 4, eaau5716.	10.3	78
48	Integration of Plant Metabolomics Data with Metabolic Networks: Progresses and Challenges. <i>Methods in Molecular Biology</i> , 2018, 1778, 297-310.	0.9	10
49	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
50	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
51	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
52	The TranSeq™ second sequencing method for high-throughput transcriptomics and gene space refinement in plant genomes. <i>Plant Journal</i> , 2018, 96, 223-232.	5.7	23
53	Label-free deep shotgun proteomics reveals protein dynamics during tomato fruit tissues development. <i>Plant Journal</i> , 2017, 90, 396-417.	5.7	76
54	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

#	ARTICLE	IF	CITATIONS
55	Small molecules belowground: the role of specialized metabolites in the rhizosphere. <i>Plant Journal</i> , 2017, 90, 788-807.	5.7	193
56	Live imaging of root-bacteria interactions in a microfluidics setup. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4549-4554.	7.1	233
57	Plant cholesterol biosynthetic pathway overlaps with phytosterol metabolism. <i>Nature Plants</i> , 2017, 3, 16205.	9.3	201
58	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
59	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
60	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
61	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
62	The Tomato DELLA Protein PROCERA Acts in Guard Cells to Promote Stomatal Closure. <i>Plant Cell</i> , 2017, 29, 3186-3197.	6.6	90
63	The PhytoClust tool for metabolic gene clusters discovery in plant genomes. <i>Nucleic Acids Research</i> , 2017, 45, 7049-7063.	14.5	71
64	Sample Preparation for Mass Spectrometry Imaging of Plant Tissues: A Review. <i>Frontiers in Plant Science</i> , 2016, 7, 60.	3.6	125
65	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
66	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
67	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines β^2 -Diketone Biosynthesis and Glaucousness. <i>Plant Cell</i> , 2016, 28, 1440-1460.	6.6	123
68	More than Pictures: When MS Imaging Meets Histology. <i>Trends in Plant Science</i> , 2016, 21, 686-698.	8.8	79
69	MYB107 and MYB9 Homologs Regulate Suberin Deposition in Angiosperms. <i>Plant Cell</i> , 2016, 28, 2097-2116.	6.6	151
70	The WEIZMASS spectral library for high-confidence metabolite identification. <i>Nature Communications</i> , 2016, 7, 12423.	12.8	95
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	<i>Solanum pennellii</i> backcross inbred lines (<sc>BIL</sc>s) link small genomic bins with tomato traits. <i>Plant Journal</i> , 2016, 87, 151-160.	5.7	74
74	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
75	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
76	An efficient method for medium throughput screening of cuticular wax composition in different plant species. <i>Metabolomics</i> , 2016, 12, 1.	3.0	18
77	AUXIN RESPONSE FACTOR 2 Intersects Hormonal Signals in the Regulation of Tomato Fruit Ripening. <i>PLoS Genetics</i> , 2016, 12, e1005903.	3.5	128
78	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
79	Uncovering DELLA-Independent Gibberellin Responses by Characterizing New Tomato <i>procera</i> Mutants. <i>Plant Cell</i> , 2015, 27, 1579-1594.	6.6	100
80	The bitter side of the nightshades: Genomics drives discovery in Solanaceae steroidal alkaloid metabolism. <i>Phytochemistry</i> , 2015, 113, 24-32.	2.9	114
81	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
82	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
83	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. <i>Frontiers in Plant Science</i> , 2015, 6, 1194.	3.6	93
84	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
85	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
86	SEEDSTICK is a Master Regulator of Development and Metabolism in the Arabidopsis Seed Coat. <i>PLoS Genetics</i> , 2014, 10, e1004856.	3.5	86
87	The transcription factor SISHINE3 modulates defense responses in tomato plants. <i>Plant Molecular Biology</i> , 2014, 84, 37-47.	3.9	58
88	Small molecules: from structural diversity to signalling and regulatory roles. <i>Plant Journal</i> , 2014, 79, 541-543.	5.7	5
89	Small molecules that interact with <sc>RNA</sc>: 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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Biosynthesis of Antinutritional Alkaloids in Solanaceous Crops Is Mediated by Clustered Genes. <i>Science</i> , 2013, 341, 175-179.	12.6	464
93	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
94	Scratching the surface: genetic regulation of cuticle assembly in fleshy fruit. <i>Journal of Experimental Botany</i> , 2013, 65, 4653-4664.	4.8	79
95	The tomato <i>S</i> SHINE3 transcription factor regulates fruit cuticle formation and epidermal patterning. <i>New Phytologist</i> , 2013, 197, 468-480.	7.3	156
96	The challenges of cellular compartmentalization in plant metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2013, 24, 239-246.	6.6	95
97	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
98	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
99	Overexpression of AtSHN1/WIN1 Provokes Unique Defense Responses. <i>PLoS ONE</i> , 2013, 8, e70146.	2.5	29
100	Reconstruction of <i>Arabidopsis</i> 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
101	Expression of a bacterial feedback-insensitive 3-deoxy-d-arabino-heptulosonate 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
102	Cell type-specific transcriptional profiling: implications for metabolite profiling. <i>Plant Journal</i> , 2012, 70, 5-17.	5.7	57
103	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
104	Recommendations for Reporting Metabolite Data. <i>Plant Cell</i> , 2011, 23, 2477-2482.	6.6	326
105	Metabolic engineering of the plant primary-secondary metabolism interface. <i>Current Opinion in Biotechnology</i> , 2011, 22, 239-244.	6.6	209
106	GLYCOALKALOID METABOLISM1 Is Required for Steroidal Alkaloid Glycosylation and Prevention of Phytotoxicity in Tomato. <i>Plant Cell</i> , 2011, 23, 4507-4525.	6.6	205
107	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
108	SHINE Transcription Factors Act Redundantly to Pattern the Archetypal Surface of <i>Arabidopsis</i> Flower Organs. <i>PLoS Genetics</i> , 2011, 7, e1001388.	3.5	191

#	ARTICLE	IF	CITATIONS
109	The Arabidopsis DSO/ABCG11 Transporter Affects Cutin Metabolism in Reproductive Organs and Suberin in Roots. <i>Molecular Plant</i> , 2010, 3, 563-575.	8.3	156
110	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
111	An <i>Orange Ripening</i> 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
112	The Arabidopsis <i>DCR</i> Encoding a Soluble BAHD Acyltransferase Is Required for Cutin Polyester Formation and Seed Hydration Properties. <i>Plant Physiology</i> , 2009, 151, 1773-1789.	4.8	154
113	Fruit-Surface Flavonoid Accumulation in Tomato Is Controlled by a SIMYB12-Regulated Transcriptional Network. <i>PLoS Genetics</i> , 2009, 5, e1000777.	3.5	219
114	Bioengineering. , 2009, , 435-473.		3
115	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
116	TOMATO AGAMOUS-LIKE1 is a component of the fruit ripening regulatory network. <i>Plant Journal</i> , 2009, 60, 1081-1095.	5.7	298
117	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
118	Switching the light on plant riboswitches. <i>Trends in Plant Science</i> , 2008, 13, 526-533.	8.8	45
119	Gene Expression and Metabolism in Tomato Fruit Surface Tissues. <i>Plant Physiology</i> , 2008, 147, 823-851.	4.8	313
120	The Transcript and Metabolite Networks Affected by the Two Clades of Arabidopsis Glucosinolate Biosynthesis Regulators. <i>Plant Physiology</i> , 2008, 148, 2021-2049.	4.8	188
121	Reconfiguration of the Achene and Receptacle Metabolic Networks during Strawberry Fruit Development. <i>Plant Physiology</i> , 2008, 148, 730-750.	4.8	276
122	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
123	Riboswitch-dependent gene regulation and its evolution in the plant kingdom. <i>Genes and Development</i> , 2007, 21, 2874-2879.	5.9	156
124	Metabolic Engineering of Terpenoid Biosynthesis in Plants. , 2007, , 219-236.		6
125	Metabolic Engineering of Terpenoid Biosynthesis in Plants. <i>Phytochemistry Reviews</i> , 2006, 5, 49-58.	6.5	147
126	Genetic engineering of strawberry flavour. <i>Developments in Food Science</i> , 2006, , 39-44.	0.0	2

#	ARTICLE	IF	CITATIONS
127	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
128	Genetic Engineering of Terpenoid Metabolism Attracts Bodyguards to Arabidopsis. <i>Science</i> , 2005, 309, 2070-2072.	12.6	482
129	Volatile science? Metabolic engineering of terpenoids in plants. <i>Trends in Plant Science</i> , 2005, 10, 594-602.	8.8	361
130	Functional Characterization of Enzymes Forming Volatile Esters from Strawberry and Banana. <i>Plant Physiology</i> , 2004, 135, 1865-1878.	4.8	315
131	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
132	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
133	Terpenoid Metabolism in Wild-Type and Transgenic Arabidopsis Plants[W]. <i>Plant Cell</i> , 2003, 15, 2866-2884.	6.6	461
134	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
135	Gene expression analysis of strawberry achene and receptacle maturation using DNA microarrays. <i>Journal of Experimental Botany</i> , 2002, 53, 2073-2087.	4.8	166
136	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