

# Andrew C Allan

## List of Publications by Year in descending order

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153  
papers

18,489  
citations

17440

63  
h-index

12946

131  
g-index

159  
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159  
docs citations

159  
times ranked

12490  
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosome-scale assembly of the bilberry genome identifies a complex locus controlling berry anthocyanin composition. <i>Molecular Ecology Resources</i> , 2022, 22, 345-360.	4.8	28
2	Hierarchical regulation of <i>MYBPA1</i> by anthocyanin- and proanthocyanidin-related MYB proteins is conserved in <i>Vaccinium</i> species. <i>Journal of Experimental Botany</i> , 2022, 73, 1344-1356.	4.8	20
3	A MADS-box gene with similarity to <i>FLC</i> is induced by cold and correlated with epigenetic changes to control budbreak in kiwifruit. <i>New Phytologist</i> , 2022, 233, 2111-2126.	7.3	25
4	microRNA172 targets <i>APETALA2</i> to regulate flavonoid biosynthesis in apple ( <i>Malus</i> ). <i>Tree Physiology</i> , 2022, 42, 1075-1085.	6.3	22
5	The red flesh of kiwifruit is differentially controlled by specific activation-repression systems. <i>New Phytologist</i> , 2022, 235, 630-645.	7.3	37
6	<i>Shy Girl</i> , a kiwifruit suppressor of feminization, restricts gynoecium development via regulation of cytokinin metabolism and signalling. <i>New Phytologist</i> , 2021, 230, 1461-1475.	7.3	29
7	A gene expression atlas for kiwifruit ( <i>Actinidia chinensis</i> ) and network analysis of transcription factors. <i>BMC Plant Biology</i> , 2021, 21, 121.	3.6	18
8	RNAi-mediated repression of dormancy-related genes results in evergrowing apple trees. <i>Tree Physiology</i> , 2021, 41, 1510-1523.	3.1	24
9	Genomic analysis uncovers functional variation in the C-terminus of anthocyanin-activating MYB transcription factors. <i>Horticulture Research</i> , 2021, 8, 77.	6.3	28
10	Nt <b>HHLH1</b> , a JAF13-like bHLH, interacts with Nt <b>MYB6</b> to enhance proanthocyanidin accumulation in Chinese Narcissus. <i>BMC Plant Biology</i> , 2021, 21, 275.	3.6	9
11	Time to retire? A life-changing decision made by NAC transcription factors. <i>New Phytologist</i> , 2021, 231, 505-507.	7.3	3
12	The interaction of MYB, bHLH and WD40 transcription factors in red pear ( <i>Pyrus pyrifolia</i> ) peel. <i>Plant Molecular Biology</i> , 2021, 106, 407-417.	3.9	32
13	An ethylene hypersensitive methionine sulfoxide reductase regulated by NAC transcription factors increases methionine pool size and ethylene production during kiwifruit ripening. <i>New Phytologist</i> , 2021, 232, 237-251.	7.3	37
14	MYBA and MYBPA transcription factors co-regulate anthocyanin biosynthesis in blue-coloured berries. <i>New Phytologist</i> , 2021, 232, 1350-1367.	7.3	56
15	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	8.3	47
16	Plant biology: Environmental extremes induce a jump in peach fitness. <i>Current Biology</i> , 2021, 31, R1046-R1048.	3.9	0
17	Regulation of wound ethylene biosynthesis by NAC transcription factors in kiwifruit. <i>BMC Plant Biology</i> , 2021, 21, 411.	3.6	14
18	Rate of banana fruit ripening depends on genome composition and gene expression of ethylene signaling and ethylene biosynthesis. <i>Scientia Horticulturae</i> , 2021, 290, 110552.	3.6	5

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19	The PyPIF5-PymiR156a-PySPL9-PyMYB114/MYB10 module regulates light-induced anthocyanin biosynthesis in red pear. <i>Molecular Horticulture</i> , 2021, 1, .	5.8	16
20	Genome-wide analysis of coding and non-coding RNA reveals a conserved miR164-NAC regulatory pathway for fruit ripening. <i>New Phytologist</i> , 2020, 225, 1618-1634.	7.3	86
21	<i>PpGST1</i> , an anthocyanin-related glutathione S-transferase gene, is essential for fruit coloration in peach. <i>Plant Biotechnology Journal</i> , 2020, 18, 1284-1295.	8.3	93
22	DNA demethylation is involved in the regulation of temperature-dependent anthocyanin accumulation in peach. <i>Plant Journal</i> , 2020, 102, 965-976.	5.7	56
23	Kiwifruit with high anthocyanin content modulates NF- $\kappa$ B activation and reduces CCL11 secretion in human alveolar epithelial cells. <i>Journal of Functional Foods</i> , 2020, 65, 103734.	3.4	13
24	Carbon starvation reduces carbohydrate and anthocyanin accumulation in red-fleshed fruit via trehalose 6-phosphate and MYB27. <i>Plant, Cell and Environment</i> , 2020, 43, 819-835.	5.7	33
25	Genomic survey and gene expression analysis of the MYB-related transcription factor superfamily in potato ( <i>Solanum tuberosum</i> L.). <i>International Journal of Biological Macromolecules</i> , 2020, 164, 2450-2464.	7.5	15
26	An improved method for transformation of <i>Actinidia arguta</i> utilized to demonstrate a central role for MYB110 in regulating anthocyanin accumulation in kiwiberry. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 143, 291-301.	2.3	8
27	The proanthocyanin-related transcription factors MYBC1 and WRKY44 regulate branch points in the kiwifruit anthocyanin pathway. <i>Scientific Reports</i> , 2020, 10, 14161.	3.3	44
28	Small RNAs With a Big Impact on Horticultural Traits. <i>Critical Reviews in Plant Sciences</i> , 2020, 39, 30-43.	5.7	19
29	The strawberry transcription factor FaRAV1 positively regulates anthocyanin accumulation by activation of <i>FaMYB10</i> and anthocyanin pathway genes. <i>Plant Biotechnology Journal</i> , 2020, 18, 2267-2279.	8.3	82
30	Genome-wide analysis and expression profiles of the StR2R3-MYB transcription factor superfamily in potato ( <i>Solanum tuberosum</i> L.). <i>International Journal of Biological Macromolecules</i> , 2020, 148, 817-832.	7.5	51
31	The Photomorphogenic Transcription Factor PpHY5 Regulates Anthocyanin Accumulation in Response to UVA and UVB Irradiation. <i>Frontiers in Plant Science</i> , 2020, 11, 603178.	3.6	20
32	Phytohormone and Transcriptomic Analysis Reveals Endogenous Cytokinins Affect Kiwifruit Growth under Restricted Carbon Supply. <i>Metabolites</i> , 2020, 10, 23.	2.9	27
33	A kiwifruit ( <i>Actinidia deliciosa</i> ) R2R3-MYB transcription factor modulates chlorophyll and carotenoid accumulation. <i>New Phytologist</i> , 2019, 221, 309-325.	7.3	160
34	<i>PbrmiR397a</i> regulates lignification during stone cell development in pear fruit. <i>Plant Biotechnology Journal</i> , 2019, 17, 103-117.	8.3	114
35	Two Y-chromosome-encoded genes determine sex in kiwifruit. <i>Nature Plants</i> , 2019, 5, 801-809.	9.3	148
36	NtMYB3, an R2R3-MYB from <i>Narcissus</i> , Regulates Flavonoid Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5456.	4.1	56

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37	Red to Brown: An Elevated Anthocyanic Response in Apple Drives Ethylene to Advance Maturity and Fruit Flesh Browning. <i>Frontiers in Plant Science</i> , 2019, 10, 1248.	3.6	41
38	Domestication: Colour and Flavour Joined by a Shared Transcription Factor. <i>Current Biology</i> , 2019, 29, R57-R59.	3.9	7
39	PbrMYB169 positively regulates lignification of stone cells in pear fruit. <i>Journal of Experimental Botany</i> , 2019, 70, 1801-1814.	4.8	73
40	StMYB44 negatively regulates anthocyanin biosynthesis at high temperatures in tuber flesh of potato. <i>Journal of Experimental Botany</i> , 2019, 70, 3809-3824.	4.8	95
41	Apple B-box factors regulate light-responsive anthocyanin biosynthesis genes. <i>Scientific Reports</i> , 2019, 9, 17762.	3.3	38
42	The involvement of PybZIPa in light-induced anthocyanin accumulation via the activation of PyUFGT through binding to tandem G-boxes in its promoter. <i>Horticulture Research</i> , 2019, 6, 134.	6.3	61
43	Activator-type R2R3-MYB genes induce a repressor-type R2R3-MYB gene to balance anthocyanin and proanthocyanidin accumulation. <i>New Phytologist</i> , 2019, 221, 1919-1934.	7.3	190
44	Histone modification and activation by SOC1-like and drought stress-related transcription factors may regulate AcSVP2 expression during kiwifruit winter dormancy. <i>Plant Science</i> , 2019, 281, 242-250.	3.6	28
45	Differential regulation of the anthocyanin profile in purple kiwifruit ( <i>Actinidia</i> species). <i>Horticulture Research</i> , 2019, 6, 3.	6.3	94
46	Mutagenesis of kiwifruit <i>CENTRORADIALIS</i> -like genes transforms a climbing woody perennial with long juvenility and axillary flowering into a compact plant with rapid terminal flowering. <i>Plant Biotechnology Journal</i> , 2019, 17, 869-880.	8.3	106
47	The effect of 1-methylcyclopropene (1-MCP) on expression of ethylene receptor genes in durian pulp during ripening. <i>Plant Physiology and Biochemistry</i> , 2018, 125, 232-238.	5.8	31
48	Solar UV light regulates flavonoid metabolism in apple ( <i>Malus domestica</i> ). <i>Plant, Cell and Environment</i> , 2018, 41, 675-688.	5.7	146
49	A manually annotated <i>Actinidia chinensis</i> var. <i>chinensis</i> (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. <i>BMC Genomics</i> , 2018, 19, 257.	2.8	167
50	Kiwifruit SVP2 controls developmental and drought-stress pathways. <i>Plant Molecular Biology</i> , 2018, 96, 233-244.	3.9	17
51	Identification of Genes Involved in Flavonoid Biosynthesis of Chinese Narcissus ( <i>Narcissus tazetta</i> L.)	1.8	13
52	Orange is not just a colour. <i>Nature Plants</i> , 2018, 4, 865-866.	9.3	1
53	MYBA From Blueberry ( <i>Vaccinium</i> Section <i>Cyanococcus</i> ) Is a Subgroup 6 Type R2R3MYB Transcription Factor That Activates Anthocyanin Production. <i>Frontiers in Plant Science</i> , 2018, 9, 1300.	3.6	55
54	Characterization and differential expression of ethylene receptor genes during fruit development and dehiscence of durian ( <i>Durio zibethinus</i> ). <i>Scientia Horticulturae</i> , 2018, 240, 623-630.	3.6	13

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55	Ectopic Overexpression of a Novel R2R3-MYB, NtMYB2 from Chinese Narcissus Represses Anthocyanin Biosynthesis in Tobacco. <i>Molecules</i> , 2018, 23, 781.	3.8	50
56	MYBs Drive Novel Consumer Traits in Fruits and Vegetables. <i>Trends in Plant Science</i> , 2018, 23, 693-705.	8.8	116
57	AcFT promotes kiwifruit in vitro flowering when overexpressed and Arabidopsis flowering when expressed in the vasculature under its own promoter. <i>Plant Direct</i> , 2018, 2, e00068.	1.9	11
58	Overexpression of both AcSVP1 and AcSVP4 delays budbreak in kiwifruit <i>A. chinensis</i> var. <i>deliciosa</i> , but only AcSVP1 delays flowering in model plants. <i>Environmental and Experimental Botany</i> , 2018, 153, 262-270.	4.2	14
59	Carotenoid accumulation and gene expression during durian ( <i>Durio zibethinus</i> ) fruit growth and ripening. <i>Scientia Horticulturae</i> , 2017, 220, 233-242.	3.6	28
60	Carotenoid accumulation in durian ( <i>Durio zibethinus</i> ) fruit is affected by ethylene via modulation of carotenoid pathway gene expression. <i>Plant Physiology and Biochemistry</i> , 2017, 115, 308-319.	5.8	28
61	Three FT and multiple CEN and BFT genes regulate maturity, flowering, and vegetative phenology in kiwifruit. <i>Journal of Experimental Botany</i> , 2017, 68, 1539-1553.	4.8	39
62	Kiwifruit SVP2 gene prevents premature budbreak during dormancy. <i>Journal of Experimental Botany</i> , 2017, 68, 1071-1082.	4.8	62
63	Map-based cloning of the pear gene <i>MYB114</i> identifies an interaction with other transcription factors to coordinately regulate fruit anthocyanin biosynthesis. <i>Plant Journal</i> , 2017, 92, 437-451.	5.7	279
64	Molecular architectures of benzoic acid-specific type III polyketide synthases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 1007-1019.	2.3	11
65	SVP-like MADS Box Genes Control Dormancy and Budbreak in Apple. <i>Frontiers in Plant Science</i> , 2017, 08, 477.	3.6	121
66	Differential Sensitivity of Fruit Pigmentation to Ultraviolet Light between Two Peach Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 1552.	3.6	57
67	Multiple Copies of a Simple MYB-Binding Site Confers Trans-regulation by Specific Flavonoid-Related R2R3 MYBs in Diverse Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1864.	3.6	38
68	Genetics of Pigment Biosynthesis and Degradation. <i>Compendium of Plant Genomes</i> , 2016, , 149-161.	0.5	6
69	The Citrus transcription factor, CitERF13, regulates citric acid accumulation via a protein-protein interaction with the vacuolar proton pump, CitVHA-c4. <i>Scientific Reports</i> , 2016, 6, 20151.	3.3	49
70	The Genetics of Kiwifruit Flavor and Fragrance. <i>Compendium of Plant Genomes</i> , 2016, , 135-147.	0.5	7
71	Functional diversification of the potato R2R3 MYB anthocyanin activators AN1, MYBA1, and MYB113 and their interaction with basic helix-loop-helix cofactors. <i>Journal of Experimental Botany</i> , 2016, 67, 2159-2176.	4.8	163
72	Peach MYB7 activates transcription of the proanthocyanidin pathway gene encoding leucoanthocyanidin reductase, but not anthocyanidin reductase. <i>Frontiers in Plant Science</i> , 2015, 6, 908.	3.6	45

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73	De Novo Assembly and Characterization of the Transcriptome of the Chinese Medicinal Herb, <i>Gentiana rigescens</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 11550-11573.	4.1	47
74	Natural Variation in Monoterpene Synthesis in Kiwifruit: Transcriptional Regulation of Terpene Synthases by NAC and ETHYLENE-INSENSITIVE3-Like Transcription Factors. <i>Plant Physiology</i> , 2015, 167, 1243-1258.	4.8	178
75	Molecular genetics of blood-fleshed peach reveals activation of anthocyanin biosynthesis by <scp>NAC</scp> transcription factors. <i>Plant Journal</i> , 2015, 82, 105-121.	5.7	404
76	In the Solanaceae, a hierarchy of bHLHs confer distinct target specificity to the anthocyanin regulatory complex. <i>Journal of Experimental Botany</i> , 2015, 66, 1427-1436.	4.8	117
77	The Phytoene synthase gene family of apple ( <i>Malus x domestica</i> ) and its role in controlling fruit carotenoid content. <i>BMC Plant Biology</i> , 2015, 15, 185.	3.6	65
78	Comparative Transcriptome Analysis of White and Purple Potato to Identify Genes Involved in Anthocyanin Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0129148.	2.5	75
79	Transcriptome analysis and transient transformation suggest an ancient duplicated MYB transcription factor as a candidate gene for leaf red coloration in peach. <i>BMC Plant Biology</i> , 2014, 14, 388.	3.6	89
80	Engineering the anthocyanin regulatory complex of strawberry ( <i>Fragaria vesca</i> ). <i>Frontiers in Plant Science</i> , 2014, 5, 651.	3.6	124
81	The red sport of 'Zaosu' pear and its red-striped pigmentation pattern are associated with demethylation of the PyMYB10 promoter. <i>Phytochemistry</i> , 2014, 107, 16-23.	2.9	60
82	Overexpression of the kiwifruit SVP3 gene affects reproductive development and suppresses anthocyanin biosynthesis in petals, but has no effect on vegetative growth, dormancy, or flowering time. <i>Journal of Experimental Botany</i> , 2014, 65, 4985-4995.	4.8	59
83	Regulation of lignin biosynthesis in fruit pericarp hardening of mangosteen ( <i>Garcinia mangostana</i> L.) after impact. <i>Postharvest Biology and Technology</i> , 2014, 97, 68-76.	6.0	54
84	Dietary Flavonoids from Modified Apple Reduce Inflammation Markers and Modulate Gut Microbiota in Mice. <i>Journal of Nutrition</i> , 2014, 144, 146-154.	2.9	153
85	Isolation of a Novel Peroxisomal Catalase Gene from Sugarcane, Which Is Responsive to Biotic and Abiotic Stresses. <i>PLoS ONE</i> , 2014, 9, e84426.	2.5	81
86	The Draft Genome Sequence of European Pear ( <i>Pyrus communis</i> L. 'Bartlett'). <i>PLoS ONE</i> , 2014, 9, e92644.	2.5	241
87	Identification of Regulatory Genes Implicated in Continuous Flowering of Longan ( <i>Dimocarpus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.5	26
88	Feasibility of Genome-wide Association Analysis Using a Small Single Nucleotide Polymorphism Panel in an Apple Breeding Population Segregating for Fruit Skin Color. <i>Journal of the American Society for Horticultural Science</i> , 2014, 139, 619-626.	1.0	7
89	An R2R3 MYB transcription factor determines red petal colour in an Actinidia (kiwifruit) hybrid population. <i>BMC Genomics</i> , 2013, 14, 28.	2.8	73
90	Transcriptional regulation of flavonoid biosynthesis in nectarine ( <i>Prunus persica</i> ) by a set of R2R3 MYB transcription factors. <i>BMC Plant Biology</i> , 2013, 13, 68.	3.6	247

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91	QTL involved in the modification of cyanidin compounds in black and red raspberry fruit. <i>Theoretical and Applied Genetics</i> , 2013, 126, 847-865.	3.6	17
92	The role of MrbHLH1 and MrMYB1 in regulating anthocyanin biosynthetic genes in tobacco and Chinese bayberry ( <i>Myrica rubra</i> ) during anthocyanin biosynthesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 285-298.	2.3	60
93	Differential activation of anthocyanin biosynthesis in <i>Arabidopsis</i> and tobacco over-expressing an R2R3 MYB from Chinese bayberry. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 113, 491-499.	2.3	34
94	Red-leafed apples affect the establishment, growth, and development of the light brown apple moth, <i>Pipha postvittana</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2013, 146, 261-275.	1.4	11
95	Analysis of genetically modified red-fleshed apples reveals effects on growth and consumer attributes. <i>Plant Biotechnology Journal</i> , 2013, 11, 408-419.	8.3	92
96	A Genome-Wide Expression Profile of Salt-Responsive Genes in the Apple Rootstock <i>Malus zumi</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 21053-21070.	4.1	25
97	Endogenous cytokinin in developing kiwifruit is implicated in maintaining fruit flesh chlorophyll levels. <i>Annals of Botany</i> , 2013, 112, 57-68.	2.9	29
98	Transcriptional analysis of apple fruit proanthocyanidin biosynthesis. <i>Journal of Experimental Botany</i> , 2012, 63, 5437-5450.	4.8	74
99	Metabolic and gene expression analysis of apple ( <i>Malus domestica</i> ) carotenogenesis. <i>Journal of Experimental Botany</i> , 2012, 63, 4497-4511.	4.8	75
100	The control of chlorophyll levels in maturing kiwifruit. <i>Planta</i> , 2012, 236, 1615-1628.	3.2	55
101	Transcriptomic analysis of Chinese bayberry ( <i>Myrica rubra</i> ) fruit development and ripening using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 19.	2.8	199
102	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes. <i>Plant Physiology</i> , 2012, 161, 225-239.	4.8	272
103	Effect of hot air treatment on organic acid- and sugar-metabolism in Ponkan ( <i>Citrus reticulata</i> ) fruit. <i>Scientia Horticulturae</i> , 2012, 147, 118-125.	3.6	124
104	The mQTL hotspot on linkage group 16 for phenolic compounds in apple fruits is probably the result of a leucoanthocyanidin reductase gene at that locus. <i>BMC Research Notes</i> , 2012, 5, 618.	1.4	14
105	Postharvest temperature influences volatile lactone production via regulation of acyl-CoA oxidases in peach fruit. <i>Plant, Cell and Environment</i> , 2012, 35, 534-545.	5.7	58
106	Differential expression of kiwifruit ERF genes in response to postharvest abiotic stress. <i>Postharvest Biology and Technology</i> , 2012, 66, 1-7.	6.0	40
107	Enhancing ascorbate in fruits and tubers through over-expression of the galactose pathway gene GDP-l-galactose phosphorylase. <i>Plant Biotechnology Journal</i> , 2012, 10, 390-397.	8.3	199
108	QTL and candidate gene mapping for polyphenolic composition in apple fruit. <i>BMC Plant Biology</i> , 2012, 12, 12.	3.6	117

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109	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. <i>Plant, Cell and Environment</i> , 2011, 34, 1176-1190.	5.7	330
110	Identification and characterisation of F3GT1 and F3GGT1, two glycosyltransferases responsible for anthocyanin biosynthesis in red-fleshed kiwifruit ( <i>Actinidia chinensis</i> ). <i>Plant Journal</i> , 2011, 65, 106-118.	5.7	164
111	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	21.4	1,091
112	Differential Gene Expression Analysis of Yunnan Red Pear, <i>Pyrus Pyrifolia</i> , During Fruit Skin Coloration. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 305-314.	1.8	78
113	Apple skin patterning is associated with differential expression of MYB10. <i>BMC Plant Biology</i> , 2011, 11, 93.	3.6	227
114	Coordinated regulation of anthocyanin biosynthesis in Chinese bayberry ( <i>Myrica rubra</i> ) fruit by a R2R3 MYB transcription factor. <i>Planta</i> , 2010, 231, 887-899.	3.2	254
115	QTL analysis and candidate gene mapping for skin and flesh color in sweet cherry fruit ( <i>Prunus avium</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	1.6	73
116	An R2R3 MYB transcription factor associated with regulation of the anthocyanin biosynthetic pathway in Rosaceae. <i>BMC Plant Biology</i> , 2010, 10, 50.	3.6	576
117	The genome of the domesticated apple ( <i>Malus Æ— domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
118	Identification of Mendel's White Flower Character. <i>PLoS ONE</i> , 2010, 5, e13230.	2.5	135
119	Kiwifruit <i>EIL</i> and <i>ERF</i> Genes Involved in Regulating Fruit Ripening. <i>Plant Physiology</i> , 2010, 153, 1280-1292.	4.8	249
120	Colour development and quality of mangosteen ( <i>Garcinia mangostana</i> L.) fruit during ripening and after harvest. <i>Postharvest Biology and Technology</i> , 2009, 51, 349-353.	6.0	94
121	Ethylene-related genes show a differential response to low temperature during "Hayward" kiwifruit ripening. <i>Postharvest Biology and Technology</i> , 2009, 52, 9-15.	6.0	53
122	Expression of ROP/RAC GTPase genes in postharvest loquat fruit in association with senescence and cold regulated lignification. <i>Postharvest Biology and Technology</i> , 2009, 54, 9-14.	6.0	17
123	A MYB transcription factor regulates anthocyanin biosynthesis in mangosteen ( <i>Garcinia mangostana</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	3.2	120
124	Effects of red-leaved transgenic tobacco expressing a MYB transcription factor on two herbivorous insects, <i>Spodoptera litura</i> and <i>Helicoverpa armigera</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2009, 133, 117-127.	1.4	36
125	Environmental regulation of leaf colour in red <i>35S:PAP1 Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2009, 182, 102-115.	7.3	215
126	Multiple Repeats of a Promoter Segment Causes Transcription Factor Autoregulation in Red Apples. <i>Plant Cell</i> , 2009, 21, 168-183.	6.6	453



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127	Apple Functional Genomics. , 2009, , 121-142.		3
128	The kiwifruit lycopene beta-cyclase plays a significant role in carotenoid accumulation in fruit. Journal of Experimental Botany, 2009, 60, 3765-3779.	4.8	132
129	Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. BMC Genomics, 2008, 9, 351.	2.8	178
130	Identification of a cis-regulatory element by transient analysis of co-ordinately regulated genes. Plant Methods, 2008, 4, 17.	4.3	73
131	MYB transcription factors that colour our fruit. Trends in Plant Science, 2008, 13, 99-102.	8.8	594
132	Ethylene-induced modulation of genes associated with the ethylene signalling pathway in ripening kiwifruit. Journal of Experimental Botany, 2008, 59, 2097-2108.	4.8	112
133	Red colouration in apple fruit is due to the activity of the MYB transcription factor, MdMYB10. Plant Journal, 2007, 49, 414-427.	5.7	1,113
134	Mapping a candidate gene (MdMYB10) for red flesh and foliage colour in apple. BMC Genomics, 2007, 8, 212.	2.8	195
135	Characterisation of the DELLA subfamily in apple (Malus x domestica Borkh.). Tree Genetics and Genomes, 2007, 3, 187-197.	1.6	43
136	Analyses of Expressed Sequence Tags from Apple. Plant Physiology, 2006, 141, 147-166.	4.8	246
137	Heat-induced oxidative activity protects suspension-cultured plant cells from low temperature damage. Functional Plant Biology, 2006, 33, 67.	2.1	10
138	Flow cytometric analysis of tracheary element differentiation in Zinnia elegans cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2005, 68A, 81-91.	1.5	20
139	Transient expression vectors for functional genomics, quantification of promoter activity and RNA silencing in plants. Plant Methods, 2005, 1, 13.	4.3	1,290
140	Efficient transient transformation of suspension culture-derived apple protoplasts. Plant Cell, Tissue and Organ Culture, 2002, 70, 77-82.	2.3	19
141	Heat-induced protection against death of suspension-cultured apple fruit cells exposed to low temperature. Plant, Cell and Environment, 2001, 24, 1199-1207.	5.7	36
142	An Early Tobacco Mosaic Virus-Induced Oxidative Burst in Tobacco Indicates Extracellular Perception of the Virus Coat Protein. Plant Physiology, 2001, 126, 97-108.	4.8	96
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