Roger P Hellens

List of Publications by Year
in descending order

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78 papers	16,323 citations	44042 48 h-index	69214 77 g-index
78 all docs	78 docs citations	78 times ranked	15118 citing authors

#	Article	IF	Citations
1	The genome of the domesticated apple (Malus Ã— domestica Borkh.). Nature Genetics, 2010, 42, 833-839.	9.4	1,891
2	pGreen: a versatile and flexible binary Ti vector for Agrobacterium-mediated plant transformation. Plant Molecular Biology, 2000, 42, 819-832.	2.0	1,426
3	Transient expression vectors for functional genomics, quantification of promoter activity and RNA silencing in plants. Plant Methods, 2005, 1, 13.	1.9	1,290
4	Red colouration in apple fruit is due to the activity of the MYB transcription factor, MdMYB10. Plant Journal, 2007, 49, 414-427.	2.8	1,113
5	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	9.4	1,091
6	Protocol: a highly sensitive RT-PCR method for detection and quantification of microRNAs. Plant Methods, 2007, 3, 12.	1.9	1,048
7	MYB transcription factors that colour our fruit. Trends in Plant Science, 2008, 13, 99-102.	4.3	594
8	An R2R3 MYB transcription factor associated with regulation of the anthocyanin biosynthetic pathway in Rosaceae. BMC Plant Biology, 2010, 10, 50.	1.6	576
9	Multiple Repeats of a Promoter Segment Causes Transcription Factor Autoregulation in Red Apples. Plant Cell, 2009, 21, 168-183.	3.1	453
10	Technical Focus:A guide to Agrobacterium binary Ti vectors. Trends in Plant Science, 2000, 5, 446-451.	4.3	427
11	UNIFOLIATA regulates leaf and flower morphogenesis in pea. Current Biology, 1997, 7, 581-587.	1.8	375
12	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. Plant, Cell and Environment, 2011, 34, 1176-1190.	2.8	330
13	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes Â Â. Plant Physiology, 2012, 161, 225-239.	2.3	272
14	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. PLoS ONE, 2012, 7, e31745.	1.1	249
15	Transcriptional regulation of flavonoid biosynthesis in nectarine (Prunus persica) by a set of R2R3 MYB transcription factors. BMC Plant Biology, 2013, 13, 68.	1.6	247
16	The Draft Genome Sequence of European Pear (Pyrus communis L. â€˜Bartlettâ€™). PLoS ONE, 2014, 9, e92644.	1.1	241
17	Apple skin patterning is associated with differential expression of MYB10. BMC Plant Biology, 2011, 11, 93.	1.6	227
18	Environmental regulation of leaf colour in red 35S:PAP1 Arabidopsis thaliana. New Phytologist, 2009, 182, 102-115.	3.5	215

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19	The Rise and Rise of Nicotiana benthamiana: A Plant for All Reasons. Annual Review of Phytopathology, 2018, 56, 405-426.	3.5	201
20	Mapping a candidate gene (MdMYB10) for red flesh and foliage colour in apple. BMC Genomics, 2007, 8, 212.	1.2	195
21	An Upstream Open Reading Frame Is Essential for Feedback Regulation of Ascorbate Biosynthesis in Arabidopsis. Plant Cell, 2015, 27, 772-786.	3.1	192
22	Effect of 5'UTR introns on gene expression in Arabidopsis thaliana. BMC Genomics, 2006, 7, 120.	1.2	184
23	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.	1.2	178
24	A manually annotated Actinidia chinensis var. chinensis (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. BMC Genomics, 2018, 19, 257.	1.2	167
25	Identification and characterisation of F3GT1 and F3GGT1, two glycosyltransferases responsible for anthocyanin biosynthesis in redâ€fleshed kiwifruit (Actinidia chinensis). Plant Journal, 2011, 65, 106-118.	2.8	164
26	Dietary Flavonoids from Modified Apple Reduce Inflammation Markers and Modulate Gut Microbiota in Mice. Journal of Nutrition, 2014, 144, 146-154.	1.3	153
27	De Novo Transcriptome Sequence Assembly and Analysis of RNA Silencing Genes of Nicotiana benthamiana. PLoS ONE, 2013, 8, e59534.	1.1	152
28	Conservation and divergence of four kiwifruit SVP-like MADS-box genes suggest distinct roles in kiwifruit bud dormancy and flowering. Journal of Experimental Botany, 2012, 63, 797-807.	2.4	148
29	The Role of Ethylene and Cold Temperature in the Regulation of the Apple POLYGALACTURONASE1 Gene and Fruit Softening Â Â. Plant Physiology, 2010, 153, 294-305.	2.3	137
30	Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230.	1.1	135
31	The kiwifruit lycopene beta-cyclase plays a significant role in carotenoid accumulation in fruit. Journal of Experimental Botany, 2009, 60, 3765-3779.	2.4	132
32	Quantitative Stem-Loop RT-PCR for Detection of MicroRNAs. Methods in Molecular Biology, 2011, 744, 145-157.	0.4	126
33	SVP-like MADS Box Genes Control Dormancy and Budbreak in Apple. Frontiers in Plant Science, 2017, 08, 477.	1.7	121
34	In the Solanaceae, a hierarchy of bHLHs confer distinct target specificity to the anthocyanin regulatory complex. Journal of Experimental Botany, 2015, 66, 1427-1436.	2.4	117
35	The extremophile Nicotiana benthamiana has traded viral defence for early vigour. Nature Plants, 2015, 1, 15165.	4.7	114
36	The Emerging World of Small ORFs. Trends in Plant Science, 2016, 21, 317-328.	4.3	99

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37	Analysis of genetically modified redâ€fleshed apples reveals effects on growth and consumer attributes. Plant Biotechnology Journal, 2013, 11, 408-419.	4.1	92
38	Advanced Engineering of Lipid Metabolism in Nicotiana benthamiana Using a Draft Genome and the V2 Viral Silencing-Suppressor Protein. PLoS ONE, 2012, 7, e52717.	1.1	85
39	Phenotypic changes associated with <scp>RNA</scp> interference silencing of chalcone synthase in apple (Malus Ã— domestica). Plant Journal, 2013, 74, 398-410.	2.8	78
40	A copia-like element in Pisum demonstrates the uses of dispersed repeated sequences in genetic analysis. Plant Molecular Biology, 1990, 15, 707-722.	2.0	74
41	Transcriptional analysis of apple fruit proanthocyanidin biosynthesis. Journal of Experimental Botany, 2012, 63, 5437-5450.	2.4	74
42	Identification of a cis-regulatory element by transient analysis of co-ordinately regulated genes. Plant Methods, 2008, 4, 17.	1.9	73
43	An R2R3 MYB transcription factor determines red petal colour in an Actinidia (kiwifruit) hybrid population. BMC Genomics, 2013, 14, 28.	1.2	73
44	Homologs of <scp>FT</scp>,<scp>CEN</scp> and <scp>FD</scp> respond to developmental and environmental signals affecting growth and flowering in the perennial vine kiwifruit. New Phytologist, 2013, 198, 732-746.	3.5	72
45	Increasing ascorbate levels in crops to enhance human nutrition and plant abiotic stress tolerance. Current Opinion in Biotechnology, 2017, 44, 153-160.	3.3	72
46	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. Journal of Experimental Botany, 2014, 65, 4985-4995.	2.4	59
47	Mendel, 150 years on. Trends in Plant Science, 2011, 16, 590-596.	4.3	58
48	A rapid transcriptional activation is induced by the dormancy-breaking chemical hydrogen cyanamide in kiwifruit (Actinidia deliciosa) buds. Journal of Experimental Botany, 2009, 60, 3835-3848.	2.4	56
49	Kiwifruit floral gene APETALA2 is alternatively spliced and accumulates in aberrant indeterminate flowers in the absence of miR172. Plant Molecular Biology, 2012, 78, 417-429.	2.0	51
50	The organisation and expression of the genes encoding the mitochondrial glycine decarboxylase complex and serine hydroxymethyltransferase in pea (Pisum sativum). Molecular Genetics and Genomics, 1993, 236-236, 402-408.	2.4	45
51	Manipulation of Ascorbate Biosynthetic, Recycling, and Regulatory Pathways for Improved Abiotic Stress Tolerance in Plants. International Journal of Molecular Sciences, 2020, 21, 1790.	1.8	44
52	Identification and characterization of flowering genes in kiwifruit: sequence conservation and role in kiwifruit flower development. BMC Plant Biology, 2011, 11, 72.	1.6	43
53	Multiple Copies of a Simple MYB-Binding Site Confers Trans-regulation by Specific Flavonoid-Related R2R3 MYBs in Diverse Species. Frontiers in Plant Science, 2017, 8, 1864.	1.7	38
54	Coding in non-coding RNAs. Nature, 2015, 520, 41-42.	13.7	36

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55	qRT-PCR of Small RNAs. Methods in Molecular Biology, 2010, 631, 109-122.	0.4	34
56	Epigenetic Inactivation of Chalcone Synthase-A Transgene Transcription in Petunia Leads to a Reversion of the Post-Transcriptional Gene Silencing Phenotype. Plant and Cell Physiology, 2007, 48, 638-647.	1.5	33
57	The widely used Nicotiana benthamiana 16c line has an unusual T-DNA integration pattern including a transposon sequence. PLoS ONE, 2017, 12, e0171311.	1.1	32
58	Infiltration-RNAseq: transcriptome profiling of Agrobacterium-mediated infiltration of transcription factors to discover gene function and expression networks in plants. Plant Methods, 2016, 12, 41.	1.9	26
59	Developmentally and transgene regulated nuclear processing of primary transcripts of chalcone synthase A in petunia. Plant Journal, 2000, 23, 63-72.	2.8	25
60	Actinidia DRM1 - An Intrinsically Disordered Protein Whose mRNA Expression Is Inversely Correlated with Spring Budbreak in Kiwifruit. PLoS ONE, 2013, 8, e57354.	1.1	25
61	Mini-scale method for nuclear run-on transcription assay in plants. Plant Molecular Biology Reporter, 2000, 18, 377-383.	1.0	22
62	Inheritance of qualitative and quantitative trypsin inhibitor variants in Pisum. Theoretical and Applied Genetics, 1994, 89, 387-391.	1.8	20
63	The role of enoyl reductase genes in phloridzin biosynthesis in apple. Plant Physiology and Biochemistry, 2013, 72, 54-61.	2.8	19
64	Effect of Rice GDP-L-Galactose Phosphorylase Constitutive Overexpression on Ascorbate Concentration, Stress Tolerance, and Iron Bioavailability in Rice. Frontiers in Plant Science, 2020, 11, 595439.	1.7	18
65	The Binding of Nuclear Factors to the as-1 Element in the CaMV 35S Promoter is Affected by Cytosine Methylation in Vitro. Plant Biology, 2007, 9, 435-441.	1.8	17
66	Coincident sequence-specific RNA degradation of linked transgenes in the plant genome. Plant Molecular Biology, 2012, 78, 259-273.	2.0	17
67	The Rapid Methylation of T-DNAs Upon Agrobacterium Inoculation in Plant Leaves. Frontiers in Plant Science, 2019, 10, 312.	1.7	17
68	Transient Gene Expression in Medicago truncatula Leaves via Agroinfiltration. Methods in Molecular Biology, 2013, 1069, 215-226.	0.4	16
69	Genetic aspects of the organization of legumin genes in pea. Plant Molecular Biology, 1993, 22, 101-112.	2.0	14
70	Characterisation of a glutathione reductase gene and its genetic locus from pea (Pisum sativum L.). Planta, 1996, 200, 186-94.	1.6	14
71	RNA interference silencing ofCHSgreatly alters the growth pattern of apple (Malusxdomestica). Plant Signaling and Behavior, 2013, 8, e25033.	1.2	14
72	Failure to launch: the self-regulating Md-MYB10 R6 gene from apple is active in flowers but not leaves of Petunia. Plant Cell Reports, 2015, 34, 1817-1823.	2.8	11

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73	Molecular architectures of benzoic acid-specific type III polyketide synthases. Acta Crystallographica Section D: Structural Biology, 2017, 73, 1007-1019.	1.1	11
74	Ac<scp>FT</scp> promotes kiwifruit inÂvitro flowering when overexpressed and Arabidopsis flowering when expressed in the vasculature under its own promoter. Plant Direct, 2018, 2, e00068.	0.8	11
75	Repeated sequences as genetic markers in pooled tissue samples. Plant Molecular Biology, 1993, 22, 153-157.	2.0	10
76	Genome-wide identification and characterization of the GDP-L-galactose phosphorylase gene family in bread wheat. BMC Plant Biology, 2019, 19, 515.	1.6	10
77	A transient assay for recombination demonstrates that Arabidopsis SNM1 and XRCC3 enhance non-homologous recombination. Genetics and Molecular Research, 2011, 10, 2104-32.	0.3	4
78	éžã‚³ãƒ¼ãƒ‰RNAã«ã€ãƒšãƒ—ãƒãƒ‰ã‚‚ã•ã‚ã¦ã„ã¾ã™ï¼ Nature Digest, 2015, 12, 31-32.	0.0	0