

# 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	Effect of Rice GDP-L-Galactose Phosphorylase Constitutive Overexpression on Ascorbate Concentration, Stress Tolerance, and Iron Bioavailability in Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 595439.	1.7	18
2	Manipulation of Ascorbate Biosynthetic, Recycling, and Regulatory Pathways for Improved Abiotic Stress Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1790.	1.8	44
3	The Rapid Methylation of T-DNAs Upon <i>Agrobacterium</i> Inoculation in Plant Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 312.	1.7	17
4	Genome-wide identification and characterization of the GDP-L-galactose phosphorylase gene family in bread wheat. <i>BMC Plant Biology</i> , 2019, 19, 515.	1.6	10
5	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.	1.2	167
6	Ac<sc>FT</sc> promotes kiwifruit in vitro flowering when overexpressed and <i>Arabidopsis</i> flowering when expressed in the vasculature under its own promoter. <i>Plant Direct</i> , 2018, 2, e00068.	0.8	11
7	The Rise and Rise of <i>Nicotiana benthamiana</i> : A Plant for All Reasons. <i>Annual Review of Phytopathology</i> , 2018, 56, 405-426.	3.5	201
8	Increasing ascorbate levels in crops to enhance human nutrition and plant abiotic stress tolerance. <i>Current Opinion in Biotechnology</i> , 2017, 44, 153-160.	3.3	72
9	Molecular architectures of benzoic acid-specific type III polyketide synthases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 1007-1019.	1.1	11
10	SVP-like MADS Box Genes Control Dormancy and Budbreak in Apple. <i>Frontiers in Plant Science</i> , 2017, 08, 477.	1.7	121
11	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.	1.7	38
12	The widely used <i>Nicotiana benthamiana</i> 16c line has an unusual T-DNA integration pattern including a transposon sequence. <i>PLoS ONE</i> , 2017, 12, e0171311.	1.1	32
13	Infiltration-RNAseq: transcriptome profiling of <i>Agrobacterium</i> -mediated infiltration of transcription factors to discover gene function and expression networks in plants. <i>Plant Methods</i> , 2016, 12, 41.	1.9	26
14	The Emerging World of Small ORFs. <i>Trends in Plant Science</i> , 2016, 21, 317-328.	4.3	99
15	The extremophile <i>Nicotiana benthamiana</i> has traded viral defence for early vigour. <i>Nature Plants</i> , 2015, 1, 15165.	4.7	114
16	éžã, 3ãf¼ãf%oRNAã«ã€ãfšãf—ãfãf%ãCEã, 3ãf¼ãf%ã•ã, CEã¼ã,ãŸ¼ã. <i>Nature Digest</i> , 2015, 12, 31-32.	0.0	0
17	An Upstream Open Reading Frame Is Essential for Feedback Regulation of Ascorbate Biosynthesis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 772-786.	3.1	192
18	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.	2.4	117

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19	Coding in non-coding RNAs. <i>Nature</i> , 2015, 520, 41-42.	13.7	36
20	Failure to launch: the self-regulating Md-MYB10 R6 gene from apple is active in flowers but not leaves of <i>Petunia</i> . <i>Plant Cell Reports</i> , 2015, 34, 1817-1823.	2.8	11
21	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.	2.4	59
22	Dietary Flavonoids from Modified Apple Reduce Inflammation Markers and Modulate Gut Microbiota in Mice. <i>Journal of Nutrition</i> , 2014, 144, 146-154.	1.3	153
23	The Draft Genome Sequence of European Pear ( <i>Pyrus communis</i> L. "Bartlett"™). <i>PLoS ONE</i> , 2014, 9, e92644.	1.1	241
24	An R2R3 MYB transcription factor determines red petal colour in an <i>Actinidia</i> (kiwifruit) hybrid population. <i>BMC Genomics</i> , 2013, 14, 28.	1.2	73
25	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.	1.6	247
26	Transient Gene Expression in <i>Medicago truncatula</i> Leaves via Agroinfiltration. <i>Methods in Molecular Biology</i> , 2013, 1069, 215-226.	0.4	16
27	Phenotypic changes associated with RNA interference silencing of chalcone synthase in apple ( <i>Malus domestica</i> ). <i>Plant Journal</i> , 2013, 74, 398-410.	2.8	78
28	The role of enoyl reductase genes in phloridzin biosynthesis in apple. <i>Plant Physiology and Biochemistry</i> , 2013, 72, 54-61.	2.8	19
29	Analysis of genetically modified red-fleshed apples reveals effects on growth and consumer attributes. <i>Plant Biotechnology Journal</i> , 2013, 11, 408-419.	4.1	92
30	Homologs of FT, CEN and FD respond to developmental and environmental signals affecting growth and flowering in the perennial vine kiwifruit. <i>New Phytologist</i> , 2013, 198, 732-746.	3.5	72
31	RNA interference silencing of CHS greatly alters the growth pattern of apple ( <i>Malus domestica</i> ). <i>Plant Signaling and Behavior</i> , 2013, 8, e25033.	1.2	14
32	De Novo Transcriptome Sequence Assembly and Analysis of RNA Silencing Genes of <i>Nicotiana benthamiana</i> . <i>PLoS ONE</i> , 2013, 8, e59534.	1.1	152
33	<i>Actinidia</i> DRM1 - An Intrinsically Disordered Protein Whose mRNA Expression Is Inversely Correlated with Spring Budbreak in Kiwifruit. <i>PLoS ONE</i> , 2013, 8, e57354.	1.1	25
34	Conservation and divergence of four kiwifruit SVP-like MADS-box genes suggest distinct roles in kiwifruit bud dormancy and flowering. <i>Journal of Experimental Botany</i> , 2012, 63, 797-807.	2.4	148
35	Transcriptional analysis of apple fruit proanthocyanidin biosynthesis. <i>Journal of Experimental Botany</i> , 2012, 63, 5437-5450.	2.4	74
36	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes. <i>Plant Physiology</i> , 2012, 161, 225-239.	2.3	272

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37	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. <i>PLoS ONE</i> , 2012, 7, e31745.	1.1	249
38	Advanced Engineering of Lipid Metabolism in <i>Nicotiana benthamiana</i> Using a Draft Genome and the V2 Viral Silencing-Suppressor Protein. <i>PLoS ONE</i> , 2012, 7, e52717.	1.1	85
39	Coincident sequence-specific RNA degradation of linked transgenes in the plant genome. <i>Plant Molecular Biology</i> , 2012, 78, 259-273.	2.0	17
40	Kiwifruit floral gene APETALA2 is alternatively spliced and accumulates in aberrant indeterminate flowers in the absence of miR172. <i>Plant Molecular Biology</i> , 2012, 78, 417-429.	2.0	51
41	Quantitative Stem-Loop RT-PCR for Detection of MicroRNAs. <i>Methods in Molecular Biology</i> , 2011, 744, 145-157.	0.4	126
42	Mendel, 150 years on. <i>Trends in Plant Science</i> , 2011, 16, 590-596.	4.3	58
43	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. <i>Plant, Cell and Environment</i> , 2011, 34, 1176-1190.	2.8	330
44	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.	2.8	164
45	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
46	Identification and characterization of flowering genes in kiwifruit: sequence conservation and role in kiwifruit flower development. <i>BMC Plant Biology</i> , 2011, 11, 72.	1.6	43
47	Apple skin patterning is associated with differential expression of MYB10. <i>BMC Plant Biology</i> , 2011, 11, 93.	1.6	227
48	A transient assay for recombination demonstrates that <i>Arabidopsis</i> SNM1 and XRCC3 enhance non-homologous recombination. <i>Genetics and Molecular Research</i> , 2011, 10, 2104-32.	0.3	4
49	An R2R3 MYB transcription factor associated with regulation of the anthocyanin biosynthetic pathway in Rosaceae. <i>BMC Plant Biology</i> , 2010, 10, 50.	1.6	576
50	The genome of the domesticated apple ( <i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	9.4	1,891
51	Identification of Mendel's White Flower Character. <i>PLoS ONE</i> , 2010, 5, e13230.	1.1	135
52	qRT-PCR of Small RNAs. <i>Methods in Molecular Biology</i> , 2010, 631, 109-122.	0.4	34
53	The Role of Ethylene and Cold Temperature in the Regulation of the Apple POLYGALACTURONASE1 Gene and Fruit Softening. <i>Plant Physiology</i> , 2010, 153, 294-305.	2.3	137
54	Environmental regulation of leaf colour in red PAP1 <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2009, 182, 102-115.	3.5	215

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55	A rapid transcriptional activation is induced by the dormancy-breaking chemical hydrogen cyanamide in kiwifruit ( <i>Actinidia deliciosa</i> ) buds. <i>Journal of Experimental Botany</i> , 2009, 60, 3835-3848.	2.4	56
56	Multiple Repeats of a Promoter Segment Causes Transcription Factor Autoregulation in Red Apples. <i>Plant Cell</i> , 2009, 21, 168-183.	3.1	453
57	The kiwifruit lycopene beta-cyclase plays a significant role in carotenoid accumulation in fruit. <i>Journal of Experimental Botany</i> , 2009, 60, 3765-3779.	2.4	132
58	Analysis of expressed sequence tags from <i>Actinidia</i> : applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. <i>BMC Genomics</i> , 2008, 9, 351.	1.2	178
59	Identification of a cis-regulatory element by transient analysis of co-ordinately regulated genes. <i>Plant Methods</i> , 2008, 4, 17.	1.9	73
60	MYB transcription factors that colour our fruit. <i>Trends in Plant Science</i> , 2008, 13, 99-102.	4.3	594
61	Epigenetic Inactivation of Chalcone Synthase-A Transgene Transcription in <i>Petunia</i> Leads to a Reversion of the Post-Transcriptional Gene Silencing Phenotype. <i>Plant and Cell Physiology</i> , 2007, 48, 638-647.	1.5	33
62	Protocol: a highly sensitive RT-PCR method for detection and quantification of microRNAs. <i>Plant Methods</i> , 2007, 3, 12.	1.9	1,048
63	Red colouration in apple fruit is due to the activity of the MYB transcription factor, MdMYB10. <i>Plant Journal</i> , 2007, 49, 414-427.	2.8	1,113
64	Mapping a candidate gene (MdMYB10) for red flesh and foliage colour in apple. <i>BMC Genomics</i> , 2007, 8, 212.	1.2	195
65	The Binding of Nuclear Factors to the as-1 Element in the CaMV 35S Promoter is Affected by Cytosine Methylation in Vitro. <i>Plant Biology</i> , 2007, 9, 435-441.	1.8	17
66	Effect of 5'UTR introns on gene expression in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2006, 7, 120.	1.2	184
67	Transient expression vectors for functional genomics, quantification of promoter activity and RNA silencing in plants. <i>Plant Methods</i> , 2005, 1, 13.	1.9	1,290
68	Developmentally and transgene regulated nuclear processing of primary transcripts of chalcone synthase A in <i>petunia</i> . <i>Plant Journal</i> , 2000, 23, 63-72.	2.8	25
69	pGreen: a versatile and flexible binary Ti vector for <i>Agrobacterium</i> -mediated plant transformation. <i>Plant Molecular Biology</i> , 2000, 42, 819-832.	2.0	1,426
70	Mini-scale method for nuclear run-on transcription assay in plants. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 377-383.	1.0	22
71	Technical Focus:A guide to <i>Agrobacterium</i> binary Ti vectors. <i>Trends in Plant Science</i> , 2000, 5, 446-451.	4.3	427
72	UNIFOLIATA regulates leaf and flower morphogenesis in pea. <i>Current Biology</i> , 1997, 7, 581-587.	1.8	375

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73	Characterisation of a glutathione reductase gene and its genetic locus from pea ( <i>Pisum sativum</i> L.). <i>Planta</i> , 1996, 200, 186-94.	1.6	14
74	Inheritance of qualitative and quantitative trypsin inhibitor variants in <i>Pisum</i> . <i>Theoretical and Applied Genetics</i> , 1994, 89, 387-391.	1.8	20
75	The organisation and expression of the genes encoding the mitochondrial glycine decarboxylase complex and serine hydroxymethyltransferase in pea ( <i>Pisum sativum</i> ). <i>Molecular Genetics and Genomics</i> , 1993, 236-236, 402-408.	2.4	45
76	Genetic aspects of the organization of legumin genes in pea. <i>Plant Molecular Biology</i> , 1993, 22, 101-112.	2.0	14
77	Repeated sequences as genetic markers in pooled tissue samples. <i>Plant Molecular Biology</i> , 1993, 22, 153-157.	2.0	10
78	A copia-like element in <i>Pisum</i> demonstrates the uses of dispersed repeated sequences in genetic analysis. <i>Plant Molecular Biology</i> , 1990, 15, 707-722.	2.0	74