Brendan Davies

List of Publications by Year
in descending order

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45 papers	5,417 citations	156536 32 h-index	286692 43 g-index
47 all docs	47 docs citations	47 times ranked	6268 citing authors

#	Article	IF	Citations
1	Plants utilise ancient conserved peptide upstream open reading frames in stressâ€responsive translational regulation. Plant, Cell and Environment, 2022, 45, 1229-1241.	2.8	10
2	The loss of SMG1 causes defects in quality control pathways in Physcomitrella patens. Nucleic Acids Research, 2018, 46, 5822-5836.	6.5	24
3	An Immune-Responsive Cytoskeletal-Plasma Membrane Feedback Loop in Plants. Current Biology, 2018, 28, 2136-2144.e7.	1.8	32
4	Conservation of Nonsense-Mediated mRNA Decay Complex Components Throughout Eukaryotic Evolution. Scientific Reports, 2017, 7, 16692.	1.6	34
5	Stem Cell Regulation by Arabidopsis WOX Genes. Molecular Plant, 2016, 9, 1028-1039.	3.9	137
6	MAF2 Is Regulated by Temperature-Dependent Splicing and Represses Flowering at Low Temperatures in Parallel with FLM. PLoS ONE, 2015, 10, e0126516.	1.1	89
7	The (r)evolution of gene regulatory networks controlling Arabidopsis plant reproduction: a two-decade history. Journal of Experimental Botany, 2014, 65, 4731-4745.	2.4	106
8	Flower Development in the Asterid Lineage. Methods in Molecular Biology, 2014, 1110, 35-55.	0.4	7
9	Flower Development: Open Questions and Future Directions. Methods in Molecular Biology, 2014, 1110, 103-124.	0.4	26
10	SMG1 is an ancient nonsenseâ€mediated <scp>mRNA</scp> decay effector. Plant Journal, 2013, 76, 800-810.	2.8	58
11	TOPLESS co-repressor interactions and their evolutionary conservation in plants. Plant Signaling and Behavior, 2012, 7, 325-328.	1.2	59
12	The salicylic acid dependent and independent effects of NMD in plants. Plant Signaling and Behavior, 2012, 7, 1434-1437.	1.2	12
13	The TOPLESS Interactome: A Framework for Gene Repression in Arabidopsis Â Â. Plant Physiology, 2012, 158, 423-438.	2.3	481
14	Gene Duplication and the Evolution of Plant MADS-box Transcription Factors. Journal of Genetics and Genomics, 2012, 39, 157-165.	1.7	120
15	A Role for Nonsense-Mediated mRNA Decay in Plants: Pathogen Responses Are Induced in Arabidopsis thaliana NMD Mutants. PLoS ONE, 2012, 7, e31917.	1.1	114
16	TCP14 and TCP15 affect internode length and leaf shape in Arabidopsis. Plant Journal, 2011, 68, 147-158.	2.8	261
17	Tracing the Evolution of the Floral Homeotic B- and C-Function Genes through Genome Synteny. Molecular Biology and Evolution, 2010, 27, 2651-2664.	3.5	36
18	Single amino acid change alters the ability to specify male or female organ identity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18898-18902.	3.3	50

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19	An Atlas of Type I MADS Box Gene Expression during Female Gametophyte and Seed Development in Arabidopsis. Plant Physiology, 2010, 154, 287-300.	2.3	117
20	Floral organ identity: 20 years of ABCs. Seminars in Cell and Developmental Biology, 2010, 21, 73-79.	2.3	306
21	Forward. Seminars in Cell and Developmental Biology, 2010, 21, 72.	2.3	0
22	Conserved intragenic elements were critical for the evolution of the floral Câ€function. Plant Journal, 2009, 58, 41-52.	2.8	33
23	The <i>S</i> locusâ€linked <i>Primula</i> homeotic mutant <i>sepaloid</i> shows characteristics of a Bâ€function mutant but does not result from mutation in a Bâ€function gene. Plant Journal, 2008, 56, 1-12.	2.8	16
24	Analysis of the Transcription Factor WUSCHEL and Its Functional Homologue in Antirrhinum Reveals a Potential Mechanism for Their Roles in Meristem Maintenance. Plant Cell, 2006, 18, 560-573.	3.1	203
25	Flower Development: The Antirrhinum Perspective. Advances in Botanical Research, 2006, 44, 279-321.	0.5	28
26	UPF1 is required for nonsense-mediated mRNA decay (NMD) and RNAi in Arabidopsis. Plant Journal, 2006, 47, 480-489.	2.8	183
27	Arabidopsis group Ie formins localize to specific cell membrane domains, interact with actinâ€binding proteins and cause defects in cell expansion upon aberrant expression. New Phytologist, 2005, 168, 529-540.	3.5	122
28	Evolution in Action: Following Function in Duplicated Floral Homeotic Genes. Current Biology, 2005, 15, 1508-1512.	1.8	165
29	Comprehensive Interaction Map of the Arabidopsis MADS Box Transcription Factors. Plant Cell, 2005, 17, 1424-1433.	3.1	528
30	CUPULIFORMIS establishes lateral organ boundaries in Antirrhinum. Development (Cambridge), 2004, 131, 915-922.	1.2	155
31	Arabidopsis NAP1 Is Essential for Arp2/3-Dependent Trichome Morphogenesis. Current Biology, 2004, 14, 1410-1414.	1.8	95
32	An antirrhinum ternary complex factor specifically interacts with C-function and SEPALLATA-like MADS-box factors. Plant Molecular Biology, 2003, 52, 1051-1062.	2.0	34
33	An everlasting pioneer: the story of Antirrhinum research. Nature Reviews Genetics, 2003, 4, 655-664.	7.7	102
34	Molecular and Phylogenetic Analyses of the Complete MADS-Box Transcription Factor Family in Arabidopsis. Plant Cell, 2003, 15, 1538-1551.	3.1	758
35	PLANT BIOLOGY: MADS-Box Genes Reach Maturity. Science, 2002, 296, 275-276.	6.0	62
36	Formins: intermediates in signal-transduction cascades that affect cytoskeletal reorganization. Trends in Plant Science, 2002, 7, 492-498.	4.3	149

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37	Analysing protein-protein interactions with the yeast two-hybrid system. Plant Molecular Biology, 2002, 50, 855-870.	2.0	103
38	Developmental programmes in floral organ formation. Seminars in Cell and Developmental Biology, 2001, 12, 373-380.	2.3	22
39	Beyond the ABCs: ternary complex formation in the control of floral organ identity. Trends in Plant Science, 2000, 5, 471-476.	4.3	96
40	PLENA and FARINELLI: redundancy and regulatory interactions between two Antirrhinum MADS-box factors controlling flower development. EMBO Journal, 1999, 18, 4023-4034.	3.5	237
41	Flower Development: Genetic Views and Molecular News. , 1999, , 167-183.		6
42	DNA binding and dimerisation determinants of Antirrhinum majus MADS-box transcription factors. Nucleic Acids Research, 1998, 26, 5277-5287.	6.5	77
43	Two is company: The complex travel arrangements of floral homeotic factors. BioEssays, 1996, 18, 863-866.	1.2	2
44	Alteration of tobacco floral organ identity by expression of combinations of Antirrhinum MADS-box genes. Plant Journal, 1996, 10, 663-677.	2.8	80
45	Control of Floral Organ Identity by Homeotic MADS-Box Transcription Factors. Results and Problems in Cell Differentiation, 1994, 20, 235-258.	0.2	81