Iain W Wilson

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

73 papers	5,193 citations	33 h-index	72 g-index
77 ext. papers	5,853 ext. citations	5.3 avg, IF	5.2 L-index

#	Paper	IF	Citations
73	Coordinated plant defense responses in Arabidopsis revealed by microarray analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 11655-60	11.5	1159
72	Expression profile analysis of the low-oxygen response in Arabidopsis root cultures. *Plant Cell*, **2002** , 14, 2481-94	11.6	314
71	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in Arabidopsis. *Plant Journal*, **2005**, 43, 745-57	6.9	234
70	Global changes in gene expression in response to high light in Arabidopsis. *Plant Physiology*, **2002**, 130, 1109-20	6.6	234
69	Arabidopsis RAP2.2: an ethylene response transcription factor that is important for hypoxia survival. *Plant Physiology*, **2010**, 153, 757-72	6.6	230
68	Gene expression profile changes in cotton root and hypocotyl tissues in response to infection with Fusarium oxysporum f. sp. vasinfectum. *Molecular Plant-Microbe Interactions*, **2004**, 17, 654-67	3.6	159
67	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. *Journal of Experimental Botany*, **2010**, 61, 165-77	7	151
66	Systemic gene expression in Arabidopsis during an incompatible interaction with Alternaria brassicicola. *Plant Physiology*, **2003**, 132, 999-1010	6.6	149
65	Global gene expression responses to waterlogging in roots and leaves of cotton (Gossypium hirsutum L.). *Plant and Cell Physiology*, **2010**, 51, 21-37	4.9	146
64	The Arabidopsis AMP1 gene encodes a putative glutamate carboxypeptidase. *Plant Cell*, **2001**, 13, 2115-25	11.6	136
63	An efficient approach to finding Siraitia grosvenorii triterpene biosynthetic genes by RNA-seq and digital gene expression analysis. *BMC Genomics*, **2011**, 12, 343	4.5	130
62	miR482 regulation of NBS-LRR defense genes during fungal pathogen infection in cotton. *PLoS ONE*, **2013**, 8, e84390	3.7	123
61	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of Gossypium spp. *G3: Genes, Genomes, Genetics*, **2015**, 5, 1187-209	3.2	117
60	The low-oxygen-induced NAC domain transcription factor ANAC102 affects viability of Arabidopsis seeds following low-oxygen treatment. *Plant Physiology*, **2009**, 149, 1724-38	6.6	114
59	Spatial and temporal analysis of the local response to wounding in Arabidopsis leaves. *Plant Molecular Biology*, **2004**, 55, 165-81	4.6	106
58	High throughput sequencing technology reveals that the taxoid elicitor methyl jasmonate regulates microRNA expression in Chinese yew (Taxus chinensis). *Gene*, **2009**, 436, 37-44	3.8	105
57	Analgesia: morphine-pathway block in top1 poppies. *Nature*, **2004**, 431, 413-4	50.4	91

56	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. *Plant Cell*, **2001**, 13, 2115-2125	11.6	90
55	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus Penicillium aurantiogriseum NRRL 62431. *BMC Genomics*, **2014**, 15, 69	4.5	85
54	Gene expression in Eucalyptus branch wood with marked variation in cellulose microfibril orientation and lacking G-layers. *New Phytologist*, **2008**, 179, 94-103	9.8	76
53	Comparison of Erysiphe cichoracearum and E. cruciferarum and a survey of 360 Arabidopsis thaliana accessions for resistance to these two powdery mildew pathogens. *Molecular Plant-Microbe Interactions*, **1999**, 12, 1031-43	3.6	74
52	New normalization methods for cDNA microarray data. *Bioinformatics*, **2003**, 19, 1325-32	7.2	72
51	ATAF NAC transcription factors: regulators of plant stress signaling. *Plant Signaling and Behavior*, **2010**, 5, 428-32	2.5	65
50	Deep sequencing reveals transcriptome re-programming of Taxus media cells to the elicitation with methyl jasmonate. *PLoS ONE*, **2013**, 8, e62865	3.7	65
49	The shoot and root growth of Brachypodium and its potential as a model for wheat and other cereal crops. *Functional Plant Biology*, **2009**, 36, 960-969	2.7	60
48	Mutations affecting translational coupling between the rep genes of an IncB miniplasmid. *Journal of Bacteriology*, **1992**, 174, 2376-83	3.5	60
47	De novo transcriptome sequencing and digital gene expression analysis predict biosynthetic pathway of rhynchophylline and isorhynchophylline from Uncaria rhynchophylla, a non-model plant with potent anti-alzheimer's properties. *BMC Genomics*, **2014**, 15, 676	4.5	50
46	VERNALIZATION INSENSITIVE 3 (VIN3) is required for the response of Arabidopsis thaliana seedlings exposed to low oxygen conditions. *Plant Journal*, **2009**, 59, 576-87	6.9	48
45	Genetic and DNA methylation changes in cotton (Gossypium) genotypes and tissues. *PLoS ONE*, **2014**, 9, e86049	3.7	43
44	Signalling pathways: a common theme in plants and animals?. *Current Biology*, **1997**, 7, R175-8	6.3	41
43	Comparisons of early transcriptome responses to low-oxygen environments in three dicotyledonous plant species. *Plant Signaling and Behavior*, **2010**, 5, 1006-9	2.5	37
42	Mutations affecting pseudoknot control of the replication of B group plasmids. *Journal of Bacteriology*, **1993**, 175, 6476-83	3.5	35
41	Integrated mapping and characterization of the gene underlying the okra leaf trait in Gossypium hirsutum L. *Journal of Experimental Botany*, **2016**, 67, 763-74	7	33
40	Enhancing Integrated Pest Management in GM Cotton Systems Using Host Plant Resistance. *Frontiers in Plant Science*, **2016**, 7, 500	6.2	33
39	Diversity analysis of cotton (Gossypium hirsutum L.) germplasm using the CottonSNP63K Array. *BMC Plant Biology*, **2017**, 17, 37	5.3	32

38	Microarray analysis reveals vegetative molecular phenotypes of Arabidopsis flowering-time mutants. *Plant and Cell Physiology*, **2005**, 46, 1190-201	4.9	32
37	DNA microarrays: new tools in the analysis of plant defence responses. *Molecular Plant Pathology*, **2001**, 2, 177-85	5.7	32
36	Identification of novel and conserved microRNAs in Panax notoginseng roots by high-throughput sequencing. *BMC Genomics*, **2015**, 16, 835	4.5	29
35	Genomewide analysis of the lateral organ boundaries domain gene family in Eucalyptus grandis reveals members that differentially impact secondary growth. *Plant Biotechnology Journal*, **2018**, 16, 124-136	11.6	27
34	Fusarium wilt (Fusarium oxysporum f. sp. vasinfectum) genes expressed during infection of cotton (Gossypium hirsutum)dagger. *Molecular Plant Pathology*, **2006**, 7, 87-101	5.7	27
33	Molecular analysis of RNAI control of repB translation in IncB plasmids. *Journal of Bacteriology*, **1994**, 176, 6497-508	3.5	26
32	Genetic dissection of the fuzzless seed trait in Gossypium barbadense. *Journal of Experimental Botany*, **2018**, 69, 997-1009	7	22
31	Understanding the molecular events underpinning cultivar differences in the physiological performance and heat tolerance of cotton (Gossypium hirsutum). *Functional Plant Biology*, **2013**, 41, 56-67	2.7	20
30	Molecular mapping of a new source of Fusarium wilt resistance in tetraploid cotton (Gossypium hirsutum L.). *Molecular Breeding*, **2012**, 30, 1181-1191	3.4	20
29	Polygenic powdery mildew disease resistance in Arabidopsis thaliana: quantitative trait analysis of the accession Warschau-1. *Plant Pathology*, **2001**, 50, 690-701	2.8	20
28	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. *Euphytica*, **2017**, 213, 1	2.1	18
27	Molecular cloning and characterization of a cytochrome P450 taxoid 9-hydroxylase in Ginkgo biloba cells. *Biochemical and Biophysical Research Communications*, **2014**, 443, 938-43	3.4	18
26	Jasmonic acid is associated with resistance to twospotted spider mites in diploid cotton (Gossypium arboreum). *Functional Plant Biology*, **2014**, 41, 748-757	2.7	16
25	Transcriptome and complexity-reduced, DNA-based identification of intraspecies single-nucleotide polymorphisms in the polyploid Gossypium hirsutum L. *G3: Genes, Genomes, Genetics*, **2014**, 4, 1893-905	3.2	16
24	Importance of structural differences between complementary RNA molecules to control of replication of an IncB plasmid. *Journal of Bacteriology*, **1997**, 179, 742-53	3.5	16
23	Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1721-1732	3.2	15
22	Genome-wide identification and characterization of the SPL gene family in Ziziphus jujuba. *Gene*, **2017**, 627, 315-321	3.8	15
21	Transcriptomic Analysis of in Response to Salt Stress. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	13

20	Molecular mapping of bunchy top disease resistance in Gossypium hirsutum L.. *Euphytica*, **2016**, 210, 135-142	2.1	11
19	Baseline survey of root-associated microbes of Taxus chinensis (Pilger) Rehd. *PLoS ONE*, **2015**, 10, e0123026	3.7	10
18	Genetic Identification and Transcriptome Analysis of Lintless and Fuzzless Traits in L. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	9
17	Developing controlled environment screening for high-temperature tolerance in cotton that accurately reflects performance in the field. *Functional Plant Biology*, **2012**, 39, 670-678	2.7	9
16	The hunt for hypoxia responsive natural antisense short interfering RNAs. *Plant Signaling and Behavior*, **2010**, 5, 247-51	2.5	9
15	Identification of the Genes Involved in Anthocyanin Biosynthesis and Accumulation in. *Genes*, **2019**, 10,	4.2	8
14	Whole transcriptome analysis of three leaf stages in two cultivars and one of their F1 hybrid of Camellia sinensis L. with differing EGCG content. *Tree Genetics and Genomes*, **2017**, 13, 1	2.1	7
13	Plant functional genomics: opportunities in microarray databases and data mining. *Functional Plant Biology*, **2004**, 31, 295-314	2.7	7
12	A comparative metabolomics analysis of the components of heartwood and sapwood in Taxus chinensis (Pilger) Rehd. *Scientific Reports*, **2019**, 9, 17647	4.9	7
11	Australian Cotton Germplasm Resources		6
10	The Research Progress of Taxol in Taxus. *Current Pharmaceutical Biotechnology*, **2021**, 22, 360-366	2.6	5
9	Expansion of MIR482/2118 by a class-II transposable element in cotton. *Plant Journal*, **2020**, 103, 2084-2099	6.9	4
8	The R2R3-MYB transcription factor family in : identification, characterization, expression profiling and posttranscriptional regulation analysis. *PeerJ*, **2020**, 8, e8473	3.1	4
7	Genome-wide identification and characterization of the homeodomain-leucine zipper I family of genes in cotton (Gossypium spp.). *Plant Gene*, **2016**, 7, 50-61	3.1	3
6	Co-regulation of catechins biosynthesis responses to temperature changes by shoot growth and catechin related gene expression in tea plants (Camellia sinensis L.). *Journal of Horticultural Science and Biotechnology*, **2021**, 96, 228-238	1.9	3
5	Characterization and Genetic Mapping of Black Root Rot Resistance in L. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
4	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. *Plant Cell*, **2001**, 13, 2115	11.6	2
3	Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. *G3: Genes, Genomes, Genetics*, **2021**, 11, 1-14	3.2	2

2	A comparative analysis of differential N6-methyladenosine (m6A) modification between non-transgenic and LBD15 overexpressing Poplar 84 K plants. *Tree Genetics and Genomes*, **2021**, 17, 1	2.1	1
1	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. *Genes*, **2022**, 13, 1018	4.2	1