

# Iain W Wilson

## List of Publications by Year in Descending Order

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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	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. <i>Genes</i> , <b>2022</b> , 13, 1018	4.2	1
72	Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11, 1-14	3.2	2
71	The Research Progress of Taxol in Taxus. <i>Current Pharmaceutical Biotechnology</i> , <b>2021</b> , 22, 360-366	2.6	5
70	Co-regulation of catechins biosynthesis responses to temperature changes by shoot growth and catechin related gene expression in tea plants ( <i>Camellia sinensis</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , <b>2021</b> , 96, 228-238	1.9	3
69	Characterization and Genetic Mapping of Black Root Rot Resistance in L. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	3
68	A comparative analysis of differential N6-methyladenosine (m6A) modification between non-transgenic and LBD15 overexpressing Poplar 84 K plants. <i>Tree Genetics and Genomes</i> , <b>2021</b> , 17, 1	2.1	1
67	Genetic Identification and Transcriptome Analysis of Lintless and Fuzzless Traits in L. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	9
66	Expansion of MIR482/2118 by a class-II transposable element in cotton. <i>Plant Journal</i> , <b>2020</b> , 103, 2084-2099	6.9	4
65	The R2R3-MYB transcription factor family in : identification, characterization, expression profiling and posttranscriptional regulation analysis. <i>PeerJ</i> , <b>2020</b> , 8, e8473	3.1	4
64	A comparative metabolomics analysis of the components of heartwood and sapwood in <i>Taxus chinensis</i> (Pilger) Rehd. <i>Scientific Reports</i> , <b>2019</b> , 9, 17647	4.9	7
63	Identification of the Genes Involved in Anthocyanin Biosynthesis and Accumulation in. <i>Genes</i> , <b>2019</b> , 10,	4.2	8
62	Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 1721-1732	3.2	15
61	Genetic dissection of the fuzzless seed trait in <i>Gossypium barbadense</i> . <i>Journal of Experimental Botany</i> , <b>2018</b> , 69, 997-1009	7	22
60	Genomewide analysis of the lateral organ boundaries domain gene family in <i>Eucalyptus grandis</i> reveals members that differentially impact secondary growth. <i>Plant Biotechnology Journal</i> , <b>2018</b> , 16, 124-136	11.6	27
59	Transcriptomic Analysis of in Response to Salt Stress. <i>International Journal of Molecular Sciences</i> , <b>2018</b> , 19,	6.3	13
58	Whole transcriptome analysis of three leaf stages in two cultivars and one of their F1 hybrid of <i>Camellia sinensis</i> L. with differing EGCG content. <i>Tree Genetics and Genomes</i> , <b>2017</b> , 13, 1	2.1	7
57	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. <i>Euphytica</i> , <b>2017</b> , 213, 1	2.1	18

56	Genome-wide identification and characterization of the SPL gene family in <i>Ziziphus jujuba</i> . <i>Gene</i> , <b>2017</b> , 627, 315-321	3.8	15
55	Diversity analysis of cotton ( <i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. <i>BMC Plant Biology</i> , <b>2017</b> , 17, 37	5.3	32
54	Genome-wide identification and characterization of the homeodomain-leucine zipper I family of genes in cotton ( <i>Gossypium</i> spp.). <i>Plant Gene</i> , <b>2016</b> , 7, 50-61	3.1	3
53	Integrated mapping and characterization of the gene underlying the okra leaf trait in <i>Gossypium hirsutum</i> L. <i>Journal of Experimental Botany</i> , <b>2016</b> , 67, 763-74	7	33
52	Enhancing Integrated Pest Management in GM Cotton Systems Using Host Plant Resistance. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 500	6.2	33
51	Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , <b>2016</b> , 210, 135-142	2.1	11
50	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 1187-209	3.2	117
49	Identification of novel and conserved microRNAs in <i>Panax notoginseng</i> roots by high-throughput sequencing. <i>BMC Genomics</i> , <b>2015</b> , 16, 835	4.5	29
48	Baseline survey of root-associated microbes of <i>Taxus chinensis</i> (Pilger) Rehd. <i>PLoS ONE</i> , <b>2015</b> , 10, e0123026	3.7	10
47	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , <b>2014</b> , 15, 69	4.5	85
46	De novo transcriptome sequencing and digital gene expression analysis predict biosynthetic pathway of rhynchophylline and isorhynchophylline from <i>Uncaria rhynchophylla</i> , a non-model plant with potent anti-alzheimer's properties. <i>BMC Genomics</i> , <b>2014</b> , 15, 676	4.5	50
45	Molecular cloning and characterization of a cytochrome P450 taxoid 9 $\beta$ hydroxylase in <i>Ginkgo biloba</i> cells. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 443, 938-43	3.4	18
44	Jasmonic acid is associated with resistance to twospotted spider mites in diploid cotton ( <i>Gossypium arboreum</i> ). <i>Functional Plant Biology</i> , <b>2014</b> , 41, 748-757	2.7	16
43	Transcriptome and complexity-reduced, DNA-based identification of intraspecies single-nucleotide polymorphisms in the polyploid <i>Gossypium hirsutum</i> L. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 1893-905	3.2	16
42	Genetic and DNA methylation changes in cotton ( <i>Gossypium</i> ) genotypes and tissues. <i>PLoS ONE</i> , <b>2014</b> , 9, e86049	3.7	43
41	Understanding the molecular events underpinning cultivar differences in the physiological performance and heat tolerance of cotton ( <i>Gossypium hirsutum</i> ). <i>Functional Plant Biology</i> , <b>2013</b> , 41, 56-67	2.7	20
40	miR482 regulation of NBS-LRR defense genes during fungal pathogen infection in cotton. <i>PLoS ONE</i> , <b>2013</b> , 8, e84390	3.7	123
39	Deep sequencing reveals transcriptome re-programming of <i>Taxus</i> media cells to the elicitation with methyl jasmonate. <i>PLoS ONE</i> , <b>2013</b> , 8, e62865	3.7	65

38	Molecular mapping of a new source of Fusarium wilt resistance in tetraploid cotton ( <i>Gossypium hirsutum</i> L.). <i>Molecular Breeding</i> , <b>2012</b> , 30, 1181-1191	3.4	20
37	Developing controlled environment screening for high-temperature tolerance in cotton that accurately reflects performance in the field. <i>Functional Plant Biology</i> , <b>2012</b> , 39, 670-678	2.7	9
36	An efficient approach to finding <i>Siraitia grosvenorii</i> triterpene biosynthetic genes by RNA-seq and digital gene expression analysis. <i>BMC Genomics</i> , <b>2011</b> , 12, 343	4.5	130
35	Global gene expression responses to waterlogging in roots and leaves of cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant and Cell Physiology</i> , <b>2010</b> , 51, 21-37	4.9	146
34	Comparisons of early transcriptome responses to low-oxygen environments in three dicotyledonous plant species. <i>Plant Signaling and Behavior</i> , <b>2010</b> , 5, 1006-9	2.5	37
33	<i>Arabidopsis</i> RAP2.2: an ethylene response transcription factor that is important for hypoxia survival. <i>Plant Physiology</i> , <b>2010</b> , 153, 757-72	6.6	230
32	ATAF NAC transcription factors: regulators of plant stress signaling. <i>Plant Signaling and Behavior</i> , <b>2010</b> , 5, 428-32	2.5	65
31	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , <b>2010</b> , 61, 165-77	7	151
30	The hunt for hypoxia responsive natural antisense short interfering RNAs. <i>Plant Signaling and Behavior</i> , <b>2010</b> , 5, 247-51	2.5	9
29	The low-oxygen-induced NAC domain transcription factor ANAC102 affects viability of <i>Arabidopsis</i> seeds following low-oxygen treatment. <i>Plant Physiology</i> , <b>2009</b> , 149, 1724-38	6.6	114
28	VERNALIZATION INSENSITIVE 3 (VIN3) is required for the response of <i>Arabidopsis thaliana</i> seedlings exposed to low oxygen conditions. <i>Plant Journal</i> , <b>2009</b> , 59, 576-87	6.9	48
27	High throughput sequencing technology reveals that the taxoid elicitor methyl jasmonate regulates microRNA expression in Chinese yew ( <i>Taxus chinensis</i> ). <i>Gene</i> , <b>2009</b> , 436, 37-44	3.8	105
26	The shoot and root growth of <i>Brachypodium</i> and its potential as a model for wheat and other cereal crops. <i>Functional Plant Biology</i> , <b>2009</b> , 36, 960-969	2.7	60
25	Gene expression in <i>Eucalyptus</i> branch wood with marked variation in cellulose microfibril orientation and lacking G-layers. <i>New Phytologist</i> , <b>2008</b> , 179, 94-103	9.8	76
24	Fusarium wilt ( <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> ) genes expressed during infection of cotton ( <i>Gossypium hirsutum</i> )dagger. <i>Molecular Plant Pathology</i> , <b>2006</b> , 7, 87-101	5.7	27
23	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in <i>Arabidopsis</i> . <i>Plant Journal</i> , <b>2005</b> , 43, 745-57	6.9	234
22	Microarray analysis reveals vegetative molecular phenotypes of <i>Arabidopsis</i> flowering-time mutants. <i>Plant and Cell Physiology</i> , <b>2005</b> , 46, 1190-201	4.9	32
21	Analgesia: morphine-pathway block in top1 poppies. <i>Nature</i> , <b>2004</b> , 431, 413-4	50.4	91

20	Spatial and temporal analysis of the local response to wounding in Arabidopsis leaves. <i>Plant Molecular Biology</i> , <b>2004</b> , 55, 165-81	4.6	106
19	Gene expression profile changes in cotton root and hypocotyl tissues in response to infection with <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>2004</b> , 17, 654-67	3.6	159
18	Plant functional genomics: opportunities in microarray databases and data mining. <i>Functional Plant Biology</i> , <b>2004</b> , 31, 295-314	2.7	7
17	New normalization methods for cDNA microarray data. <i>Bioinformatics</i> , <b>2003</b> , 19, 1325-32	7.2	72
16	Systemic gene expression in Arabidopsis during an incompatible interaction with <i>Alternaria brassicicola</i> . <i>Plant Physiology</i> , <b>2003</b> , 132, 999-1010	6.6	149
15	Expression profile analysis of the low-oxygen response in Arabidopsis root cultures. <i>Plant Cell</i> , <b>2002</b> , 14, 2481-94	11.6	314
14	Global changes in gene expression in response to high light in Arabidopsis. <i>Plant Physiology</i> , <b>2002</b> , 130, 1109-20	6.6	234
13	DNA microarrays: new tools in the analysis of plant defence responses. <i>Molecular Plant Pathology</i> , <b>2001</b> , 2, 177-85	5.7	32
12	Polygenic powdery mildew disease resistance in Arabidopsis thaliana: quantitative trait analysis of the accession Warschau-1. <i>Plant Pathology</i> , <b>2001</b> , 50, 690-701	2.8	20
11	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , <b>2001</b> , 13, 2115-2125	11.6	2
10	The Arabidopsis AMP1 gene encodes a putative glutamate carboxypeptidase. <i>Plant Cell</i> , <b>2001</b> , 13, 2115-2125	11.6	136
9	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , <b>2001</b> , 13, 2115-2125	11.6	90
8	Coordinated plant defense responses in Arabidopsis revealed by microarray analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 11655-60	11.5	1159
7	Comparison of <i>Erysiphe cichoracearum</i> and <i>E. cruciferarum</i> and a survey of 360 Arabidopsis thaliana accessions for resistance to these two powdery mildew pathogens. <i>Molecular Plant-Microbe Interactions</i> , <b>1999</b> , 12, 1031-43	3.6	74
6	Importance of structural differences between complementary RNA molecules to control of replication of an IncB plasmid. <i>Journal of Bacteriology</i> , <b>1997</b> , 179, 742-53	3.5	16
5	Signalling pathways: a common theme in plants and animals?. <i>Current Biology</i> , <b>1997</b> , 7, R175-8	6.3	41
4	Molecular analysis of RNAi control of repB translation in IncB plasmids. <i>Journal of Bacteriology</i> , <b>1994</b> , 176, 6497-508	3.5	26
3	Mutations affecting pseudoknot control of the replication of B group plasmids. <i>Journal of Bacteriology</i> , <b>1993</b> , 175, 6476-83	3.5	35

2	Mutations affecting translational coupling between the rep genes of an IncB miniplasmid. <i>Journal of Bacteriology</i> , <b>1992</b> , 174, 2376-83	3.5	60
1	Australian Cotton Germplasm Resources		6