

Iain W Wilson

List of Publications by Year in descending order

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76
papers

6,364
citations

94433

37
h-index

74163

75
g-index

77
all docs

77
docs citations

77
times ranked

7460
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 11655-11660.	7.1	1,293
2	Expression Profile Analysis of the Low-Oxygen Response in Arabidopsis Root Cultures[W]. Plant Cell, 2002, 14, 2481-2494.	6.6	362
3	Arabidopsis <i>RAP2.2</i> : An Ethylene Response Transcription Factor That Is Important for Hypoxia Survival. Plant Physiology, 2010, 153, 757-772.	4.8	293
4	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in Arabidopsis. Plant Journal, 2005, 43, 745-757.	5.7	273
5	Global Changes in Gene Expression in Response to High Light in Arabidopsis,. Plant Physiology, 2002, 130, 1109-1120.	4.8	254
6	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. G3: Genes, Genomes, Genetics, 2015, 5, 1187-1209.	1.8	226
7	Gene Expression Profile Changes in Cotton Root and Hypocotyl Tissues in Response to Infection with <i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i> . Molecular Plant-Microbe Interactions, 2004, 17, 654-667.	2.6	184
8	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. Journal of Experimental Botany, 2010, 61, 165-177.	4.8	184
9	Global Gene Expression Responses to Waterlogging in Roots and Leaves of Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 3.1 177		
10	miR482 Regulation of NBS-LRR Defense Genes during Fungal Pathogen Infection in Cotton. PLoS ONE, 2013, 8, e84390.	2.5	163
11	Systemic Gene Expression in Arabidopsis during an Incompatible Interaction with <i>Alternaria brassicicola</i> . Plant Physiology, 2003, 132, 999-1010.	4.8	160
12	An efficient approach to finding <i>Siraitia grosvenorii</i> triterpene biosynthetic genes by RNA-seq and digital gene expression analysis. BMC Genomics, 2011, 12, 343.	2.8	151
13	The Arabidopsis <i>AMP1</i> Gene Encodes a Putative Glutamate Carboxypeptidase. Plant Cell, 2001, 13, 2115-2125.	6.6	146
14	The Low-Oxygen-Induced NAC Domain Transcription Factor <i>ANAC102</i> Affects Viability of Arabidopsis Seeds following Low-Oxygen Treatment. Plant Physiology, 2009, 149, 1724-1738.	4.8	141
15	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. BMC Genomics, 2014, 15, 69.	2.8	125
16	Spatial and temporal analysis of the local response to wounding. Plant Molecular Biology, 2004, 55, 165-181.	3.9	120
17	High throughput sequencing technology reveals that the taxoid elicitor methyl jasmonate regulates microRNA expression in Chinese yew (<i>Taxus chinensis</i>). Gene, 2009, 436, 37-44.	2.2	112
18	Morphine-pathway block in top1 poppies. Nature, 2004, 431, 413-414.	27.8	108

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19	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , 2001, 13, 2115-2125.	6.6	98
20	Comparison of <i>Erysiphe cichoracearum</i> and <i>E. cruciferarum</i> and a Survey of 360 <i>Arabidopsis thaliana</i> Accessions for Resistance to These Two Powdery Mildew Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 1031-1043.	2.6	87
21	Gene expression in <i>Eucalyptus</i> branch wood with marked variation in cellulose microfibril orientation and lacking G-layers. <i>New Phytologist</i> , 2008, 179, 94-103.	7.3	84
22	New normalization methods for cDNA microarray data. <i>Bioinformatics</i> , 2003, 19, 1325-1332.	4.1	80
23	ATAF NAC transcription factors: Regulators of plant stress signaling. <i>Plant Signaling and Behavior</i> , 2010, 5, 428-432.	2.4	80
24	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> , 2014, 15, 676.	2.8	74
25	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> , 2009, 36, 960.	2.1	72
26	Deep Sequencing Reveals Transcriptome Re-Programming of <i>Taxus</i> Media Cells to the Elicitation with Methyl Jasmonate. <i>PLoS ONE</i> , 2013, 8, e62865.	2.5	71
27	Mutations affecting translational coupling between the rep genes of an IncB miniplasmid. <i>Journal of Bacteriology</i> , 1992, 174, 2376-2383.	2.2	70
28	<i>VERNALIZATION INSENSITIVE 3</i> (<i>VIN3</i>) is required for the response of <i>Arabidopsis thaliana</i> seedlings exposed to low oxygen conditions. <i>Plant Journal</i> , 2009, 59, 576-587.	5.7	59
29	Diversity analysis of cotton (<i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. <i>BMC Plant Biology</i> , 2017, 17, 37.	3.6	56
30	Genetic and DNA Methylation Changes in Cotton (<i>Gossypium</i>) Genotypes and Tissues. <i>PLoS ONE</i> , 2014, 9, e86049.	2.5	56
31	Signalling pathways: A common theme in plants and animals?. <i>Current Biology</i> , 1997, 7, R175-R178.	3.9	49
32	Enhancing Integrated Pest Management in GM Cotton Systems Using Host Plant Resistance. <i>Frontiers in Plant Science</i> , 2016, 7, 500.	3.6	49
33	Comparisons of early transcriptome responses to low-oxygen environments in three dicotyledonous plant species. <i>Plant Signaling and Behavior</i> , 2010, 5, 1006-1009.	2.4	47
34	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> , 2018, 16, 124-136.	8.3	44
35	Integrated mapping and characterization of the gene underlying the okra leaf trait in <i>Gossypium hirsutum</i> L. <i>Journal of Experimental Botany</i> , 2016, 67, 763-774.	4.8	43
36	Genome-wide identification and characterization of the SPL gene family in <i>Ziziphus jujuba</i> . <i>Gene</i> , 2017, 627, 315-321.	2.2	43

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37	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. <i>Euphytica</i> , 2017, 213, 1.	1.2	42
38	Mutations affecting pseudoknot control of the replication of B group plasmids. <i>Journal of Bacteriology</i> , 1993, 175, 6476-6483.	2.2	39
39	Fusarium wilt (<i>Fusarium oxysporum</i> f. sp. <i>vasinfectum</i>) genes expressed during infection of cotton (<i>Gossypium hirsutum</i>)+. <i>Molecular Plant Pathology</i> , 2006, 7, 87-101.	4.2	39
40	Identification of novel and conserved microRNAs in <i>Panax notoginseng</i> roots by high-throughput sequencing. <i>BMC Genomics</i> , 2015, 16, 835.	2.8	38
41	DNA microarrays: new tools in the analysis of plant defence responses. <i>Molecular Plant Pathology</i> , 2001, 2, 177-185.	4.2	35
42	Microarray Analysis Reveals Vegetative Molecular Phenotypes of Arabidopsis Flowering-time Mutants. <i>Plant and Cell Physiology</i> , 2005, 46, 1190-1201.	3.1	35
43	Genetic dissection of the fuzzless seed trait in <i>Gossypium barbadense</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 997-1009.	4.8	34
44	Molecular analysis of RNAi control of repB translation in IncB plasmids. <i>Journal of Bacteriology</i> , 1994, 176, 6497-6508.	2.2	30
45	Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1721-1732.	1.8	30
46	Polygenic powdery mildew disease resistance in <i>Arabidopsis thaliana</i> : quantitative trait analysis of the accession Warschau-1. <i>Plant Pathology</i> , 2001, 50, 690-701.	2.4	26
47	Molecular mapping of a new source of Fusarium wilt resistance in tetraploid cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	2.1	26
48	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> , 2014, 41, 56.	2.1	24
49	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> , 2014, 4, 1893-1905.	1.8	22
50	Molecular cloning and characterization of a cytochrome P450 taxoid 9Å ₁ -hydroxylase in <i>Ginkgo biloba</i> cells. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 938-943.	2.1	22
51	Importance of structural differences between complementary RNA molecules to control of replication of an IncB plasmid. <i>Journal of Bacteriology</i> , 1997, 179, 742-753.	2.2	20
52	Jasmonic acid is associated with resistance to twospotted spider mites in diploid cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.1	20
53	Genetic Identification and Transcriptome Analysis of Lintless and Fuzzless Traits in <i>Gossypium arboreum</i> L.. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1675.	4.1	19
54	Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , 2016, 210, 135-142.	1.2	17

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55	Transcriptomic Analysis of <i>Betula halophila</i> in Response to Salt Stress. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3412.	4.1	17
56	A comparative metabolomics analysis of the components of heartwood and sapwood in <i>Taxus chinensis</i> (Pilger) Rehd.. <i>Scientific Reports</i> , 2019, 9, 17647.	3.3	15
57	Expansion of <i>MIR482/2118</i> by a class II transposable element in cotton. <i>Plant Journal</i> , 2020, 103, 2084-2099.	5.7	15
58	The Research Progress of Taxol in <i>Taxus</i> . <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, 360-366.	1.6	15
59	Developing controlled environment screening for high-temperature tolerance in cotton that accurately reflects performance in the field. <i>Functional Plant Biology</i> , 2012, 39, 670.	2.1	14
60	Baseline Survey of Root-Associated Microbes of <i>Taxus chinensis</i> (Pilger) Rehd. <i>PLoS ONE</i> , 2015, 10, e0123026.	2.5	14
61	Identification of the Genes Involved in Anthocyanin Biosynthesis and Accumulation in <i>Taxus chinensis</i> . <i>Genes</i> , 2019, 10, 982.	2.4	14
62	CRISPR/Cas9-mediated saturated mutagenesis of the cotton <i>MIR482</i> family for dissecting the functionality of individual members in disease response. <i>Plant Direct</i> , 2022, 6, .	1.9	14
63	The hunt for hypoxia responsive natural antisense short interfering RNAs. <i>Plant Signaling and Behavior</i> , 2010, 5, 247-251.	2.4	11
64	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> , 2021, 96, 228-238.	1.9	11
65	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> , 2017, 13, 1.	1.6	10
66	Plant functional genomics: opportunities in microarray databases and data mining. <i>Functional Plant Biology</i> , 2004, 31, 295.	2.1	9
67	Characterization and Genetic Mapping of Black Root Rot Resistance in <i>Gossypium arboreum</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2642.	4.1	9
68	The R2R3-MYB transcription factor family in <i>Taxus chinensis</i> : identification, characterization, expression profiling and posttranscriptional regulation analysis. <i>PeerJ</i> , 2020, 8, e8473.	2.0	8
69	Australian Cotton Germplasm Resources. , 0, , .		7
70	Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-14.	1.8	7
71	Mapping-by-sequencing enabled fast forward genetics in crops with complex genomes.. <i>CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources</i> , 0, , 1-12.	1.0	5
72	Genome-wide identification and characterization of the homeodomain-leucine zipper I family of genes in cotton (<i>Gossypium</i> spp.). <i>Plant Gene</i> , 2016, 7, 50-61.	2.3	4

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73	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. <i>Genes</i> , 2022, 13, 1018.	2.4	4
74	A comparative analysis of differential N6-methyladenosine (m6A) modification between non-transgenic and LBD15 overexpressing Poplar 84ÅK plants. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	3
75	Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. <i>Heredity</i> , 2022, 129, 103-112.	2.6	3
76	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , 2001, 13, 2115.	6.6	2