

Iain W Wilson

List of Publications by Year in descending order

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76
papers

6,364
citations

94433

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74163

75
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all docs

77
docs citations

77
times ranked

7460
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. <i>Heredity</i> , 2022, 129, 103-112.	2.6	3
2	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. <i>Genes</i> , 2022, 13, 1018.	2.4	4
3	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
4	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
5	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
6	The Research Progress of Taxol in <i>Taxus</i> . <i>Current Pharmaceutical Biotechnology</i> , 2021, 22, 360-366.	1.6	15
7	A comparative analysis of differential N6-methyladenosine (m6A) modification between non-transgenic and LBD15 overexpressing Poplar 84K plants. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	3
8	Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. G3: <i>Genes, Genomes, Genetics</i> , 2021, 11, 1-14.	1.8	7
9	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
10	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
11	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
12	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
13	Identification of the Genes Involved in Anthocyanin Biosynthesis and Accumulation in <i>Taxus chinensis</i> . <i>Genes</i> , 2019, 10, 982.	2.4	14
14	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
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	Enhancing Integrated Pest Management in GM Cotton Systems Using Host Plant Resistance. <i>Frontiers in Plant Science</i> , 2016, 7, 500.	3.6	49
23	Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , 2016, 210, 135-142.	1.2	17
24	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
25	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
26	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
27	Baseline Survey of Root-Associated Microbes of <i>Taxus chinensis</i> (Pilger) Rehd. <i>PLoS ONE</i> , 2015, 10, e0123026.	2.5	14
28	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> , 2015, 5, 1187-1209.	1.8	226
29	Jasmonic acid is associated with resistance to twospotted spider mites in diploid cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over	2.1	20
30	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
31	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , 2014, 15, 69.	2.8	125
32	De novo transcriptome sequencing and digital gene expression analysis predict biosynthetic pathway of rynchophylline and isorynchophylline from <i>Uncaria rynchophylla</i> , a non-model plant with potent anti-alzheimer's properties. <i>BMC Genomics</i> , 2014, 15, 676.	2.8	74
33	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
34	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
35	Genetic and DNA Methylation Changes in Cotton (<i>Gossypium</i>) Genotypes and Tissues. <i>PLoS ONE</i> , 2014, 9, e86049.	2.5	56
36	miR482 Regulation of NBS-LRR Defense Genes during Fungal Pathogen Infection in Cotton. <i>PLoS ONE</i> , 2013, 8, e84390.	2.5	163

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37	Deep Sequencing Reveals Transcriptome Re-Programming of Taxus ã— media Cells to the Elicitation with Methyl Jasmonate. PLoS ONE, 2013, 8, e62865.	2.5	71
38	Developing controlled environment screening for high-temperature tolerance in cotton that accurately reflects performance in the field. Functional Plant Biology, 2012, 39, 670.	2.1	14
39	Molecular mapping of a new source of Fusarium wilt resistance in tetraploid cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5	2.1	26
40	An efficient approach to finding Siraítia grosvenorii triterpene biosynthetic genes by RNA-seq and digital gene expression analysis. BMC Genomics, 2011, 12, 343.	2.8	151
41	The hunt for hypoxia responsive natural antisense short interfering RNAs. Plant Signaling and Behavior, 2010, 5, 247-251.	2.4	11
42	Global Gene Expression Responses to Waterlogging in Roots and Leaves of Cotton (Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	3.1	177
43	Comparisons of early transcriptome responses to low-oxygen environments in three dicotyledonous plant species. Plant Signaling and Behavior, 2010, 5, 1006-1009.	2.4	47
44	Arabidopsis<i>RAP2.2</i>: An Ethylene Response Transcription Factor That Is Important for Hypoxia Survival Á Á. Plant Physiology, 2010, 153, 757-772.	4.8	293
45	ATAF NAC transcription factors: Regulators of plant stress signaling. Plant Signaling and Behavior, 2010, 5, 428-432.	2.4	80
46	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. Journal of Experimental Botany, 2010, 61, 165-177.	4.8	184
47	The Low-Oxygen-Induced NAC Domain Transcription Factor <i>ANAC102</i> Affects Viability of Arabidopsis Seeds following Low-Oxygen Treatment Á Á. Plant Physiology, 2009, 149, 1724-1738.	4.8	141
48	<i>VERNALIZATION INSENSITIVE 3</i> (<i>VIN3</i>) is required for the response of <i>Arabidopsis thaliana</i> seedlings exposed to low oxygen conditions. Plant Journal, 2009, 59, 576-587.	5.7	59
49	High throughput sequencing technology reveals that the taxoid elicitor methyl jasmonate regulates microRNA expression in Chinese yew (Taxus chinensis). Gene, 2009, 436, 37-44.	2.2	112
50	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.	2.1	72
51	Gene expression in <i>Eucalyptus </i>branch wood with marked variation in cellulose microfibril orientation and lacking Câ€layers. New Phytologist, 2008, 179, 94-103.	7.3	84
52	Fusarium wilt (Fusarium oxysporum f. sp. vasinfectum) genes expressed during infection of cotton (Gossypium hirsutum)+. Molecular Plant Pathology, 2006, 7, 87-101.	4.2	39
53	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in Arabidopsis. Plant Journal, 2005, 43, 745-757.	5.7	273
54	Microarray Analysis Reveals Vegetative Molecular Phenotypes of Arabidopsis Flowering-time Mutants. Plant and Cell Physiology, 2005, 46, 1190-1201.	3.1	35

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55	Morphine-pathway block in top1 poppies. <i>Nature</i> , 2004, 431, 413-414.	27.8	108
56	Spatial and temporal analysis of the local response to wounding. <i>Plant Molecular Biology</i> , 2004, 55, 165-181.	3.9	120
57	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> , 2004, 17, 654-667.	2.6	184
58	Plant functional genomics: opportunities in microarray databases and data mining. <i>Functional Plant Biology</i> , 2004, 31, 295.	2.1	9
59	New normalization methods for cDNA microarray data. <i>Bioinformatics</i> , 2003, 19, 1325-1332.	4.1	80
60	Systemic Gene Expression in Arabidopsis during an Incompatible Interaction with <i>Alternaria brassicicola</i> . <i>Plant Physiology</i> , 2003, 132, 999-1010.	4.8	160
61	Expression Profile Analysis of the Low-Oxygen Response in Arabidopsis Root Cultures[W]. <i>Plant Cell</i> , 2002, 14, 2481-2494.	6.6	362
62	Global Changes in Gene Expression in Response to High Light in Arabidopsis,. <i>Plant Physiology</i> , 2002, 130, 1109-1120.	4.8	254
63	DNA microarrays: new tools in the analysis of plant defence responses. <i>Molecular Plant Pathology</i> , 2001, 2, 177-185.	4.2	35
64	Polygenic powdery mildew disease resistance in Arabidopsis thaliana: quantitative trait analysis of the accession Warschau-1. <i>Plant Pathology</i> , 2001, 50, 690-701.	2.4	26
65	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , 2001, 13, 2115.	6.6	2
66	The Arabidopsis <i>AMP1</i> Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , 2001, 13, 2115-2125.	6.6	146
67	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. <i>Plant Cell</i> , 2001, 13, 2115-2125.	6.6	98
68	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> , 2000, 97, 11655-11660.	7.1	1,293
69	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> , 1999, 12, 1031-1043.	2.6	87
70	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
71	Signalling pathways: A common theme in plants and animals?. <i>Current Biology</i> , 1997, 7, R175-R178.	3.9	49
72	Molecular analysis of RNAi control of repB translation in IncB plasmids. <i>Journal of Bacteriology</i> , 1994, 176, 6497-6508.	2.2	30

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73	Mutations affecting pseudoknot control of the replication of B group plasmids. Journal of Bacteriology, 1993, 175, 6476-6483.	2.2	39
74	Mutations affecting translational coupling between the rep genes of an IncB miniplasmid. Journal of Bacteriology, 1992, 174, 2376-2383.	2.2	70
75	Mapping-by-sequencing enabled fast forward genetics in crops with complex genomes.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , 1-12.	1.0	5
76	Australian Cotton Germplasm Resources. , 0, , .		7