

Jennifer M Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

9,111
citations

50276

46
h-index

71685

76
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84
all docs

84
docs citations

84
times ranked

15707
citing authors

#	ARTICLE	IF	CITATIONS
1	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. <i>BMC Biology</i> , 2021, 19, 203.	3.8	15
2	A Near-Complete Haplotype-Phased Genome of the Dikaryotic Wheat Stripe Rust Fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Reveals High Interhaplotype Diversity. <i>MBio</i> , 2018, 9, .	4.1	112
3	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , 2018, 19, 2094-2110.	4.2	350
4	<i>De Novo</i> Assembly and Phasing of Dikaryotic Genomes from Two Isolates of <i>Puccinia coronata</i> f. sp. <i>avenae</i> , the Causal Agent of Oat Crown Rust. <i>MBio</i> , 2018, 9, .	4.1	57
5	<i>ApoplastP</i> : prediction of effectors and plant proteins in the apoplast using machine learning. <i>New Phytologist</i> , 2018, 217, 1764-1778.	7.3	180
6	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. <i>Genome Biology</i> , 2018, 19, 112.	8.8	41
7	Asexual Female Gametogenesis Involves Contact with a Sexually-Fated Megaspore in Apomictic <i>Hieracium</i> . <i>Plant Physiology</i> , 2018, 177, 1027-1049.	4.8	28
8	Assembled genomic and tissue-specific transcriptomic data resources for two genetically distinct lines of Cowpea (<i>Vigna unguiculata</i> (L.) Walp). <i>Gates Open Research</i> , 2018, 2, 7.	1.1	25
9	Patterns of gene expression in developing embryos of <i>Arabidopsis</i> hybrids. <i>Plant Journal</i> , 2017, 89, 927-939.	5.7	14
10	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. <i>Scientific Reports</i> , 2017, 7, 44598.	3.3	340
11	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
12	Loss of <i>AvrSr50</i> by somatic exchange in stem rust leads to virulence for <i>Sr50</i> resistance in wheat. <i>Science</i> , 2017, 358, 1607-1610.	12.6	206
13	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , 2017, 1659, 73-83.	0.9	19
14	Generation of an integrated <i>Hieracium</i> genomic and transcriptomic resource enables exploration of small RNA pathways during apomixis initiation. <i>BMC Biology</i> , 2016, 14, 86.	3.8	19
15	Cellular and molecular characterization of a stem rust resistance locus on wheat chromosome 7AL. <i>BMC Research Notes</i> , 2016, 9, 502.	1.4	8
16	Molecular and cellular characteristics of hybrid vigour in a commercial hybrid of Chinese cabbage. <i>BMC Plant Biology</i> , 2016, 16, 45.	3.6	45
17	<i>EffectorP</i> : predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016, 210, 743-761.	7.3	438
18	Deep Sequencing of the Fruit Transcriptome and Lipid Accumulation in a Non-Seed Tissue of Chinese Tallow, a Potential Biofuel Crop. <i>Plant and Cell Physiology</i> , 2016, 57, 125-137.	3.1	17

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19	RNA-Seq Analysis of the Expression of Genes Encoding Cell Wall Degrading Enzymes during Infection of Lupin (<i>Lupinus angustifolius</i>) by <i>Phytophthora parasitica</i> . <i>PLoS ONE</i> , 2015, 10, e0136899.	2.5	48
20	Evaluation of Secretion Prediction Highlights Differing Approaches Needed for Oomycete and Fungal Effectors. <i>Frontiers in Plant Science</i> , 2015, 6, 1168.	3.6	85
21	Genome-Wide Analysis in Three <i>Fusarium</i> Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. <i>Genome Biology and Evolution</i> , 2015, 7, 1613-1627.	2.5	77
22	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
23	Advances and Challenges in Computational Prediction of Effectors from Plant Pathogenic Fungi. <i>PLoS Pathogens</i> , 2015, 11, e1004806.	4.7	197
24	A reference genetic linkage map of apomictic <i>Hieracium</i> species based on expressed markers derived from developing ovule transcripts. <i>Annals of Botany</i> , 2015, 115, 567-580.	2.9	10
25	DNA demethylases target promoter transposable elements to positively regulate stress responsive genes in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2014, 15, 458.	8.8	243
26	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 372.	3.6	45
27	Long noncoding <i>RNA</i> s responsive to <i>Fusarium oxysporum</i> infection in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2014, 201, 574-584.	7.3	188
28	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
29	Identification of candidate genes for fusarium yellows resistance in Chinese cabbage by differential expression analysis. <i>Plant Molecular Biology</i> , 2014, 85, 247-257.	3.9	57
30	A novel splicing outcome reveals more than 2000 new mammalian protein isoforms. <i>Bioinformatics</i> , 2014, 30, 151-156.	4.1	11
31	<i>Arabidopsis</i> Polycomb Repressive Complex 2 binding sites contain putative GAGA factor binding motifs within coding regions of genes. <i>BMC Genomics</i> , 2013, 14, 593.	2.8	94
32	Roles for blue light, jasmonate and nitric oxide in the regulation of dormancy and germination in wheat grain (<i>Triticum aestivum</i> L.). <i>Planta</i> , 2013, 238, 121-138.	3.2	103
33	Characterization of the defense transcriptome responsive to <i>Fusarium oxysporum</i> -infection in <i>Arabidopsis</i> using RNA-seq. <i>Gene</i> , 2013, 512, 259-266.	2.2	120
34	Enlarging Cells Initiating Apomixis in <i>Hieracium praealtum</i> Transition to an Embryo Sac Program prior to Entering Mitosis. <i>Plant Physiology</i> , 2013, 163, 216-231.	4.8	78
35	Genetic, Hormonal, and Physiological Analysis of Late Maturity α -Amylase in Wheat. <i>Plant Physiology</i> , 2013, 161, 1265-1277.	4.8	71
36	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. <i>BMC Genomics</i> , 2013, 14, 807.	2.8	26

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37	nEASE: a method for gene ontology subclassification of high-throughput gene expression data. <i>Bioinformatics</i> , 2012, 28, 726-728.	4.1	6
38	Trans Chromosomal Methylation in <i>Arabidopsis</i> hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3570-3575.	7.1	202
39	Heterosis of <i>Arabidopsis</i> hybrids between C24 and Col is associated with increased photosynthesis capacity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7109-7114.	7.1	161
40	Somatic small RNA pathways promote the mitotic events of megagametogenesis during female reproductive development in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2012, 139, 1399-1404.	2.5	145
41	miRNA regulation in the early development of barley seed. <i>BMC Plant Biology</i> , 2012, 12, 120.	3.6	68
42	A comparison of transcriptome and epigenetic status between closely related species in the genus <i>Arabidopsis</i> . <i>Gene</i> , 2012, 506, 301-309.	2.2	11
43	Efficient experimental design and analysis strategies for the detection of differential expression using RNA-Sequencing. <i>BMC Genomics</i> , 2012, 13, 484.	2.8	179
44	Advanced Engineering of Lipid Metabolism in <i>Nicotiana benthamiana</i> Using a Draft Genome and the V2 Viral Silencing-Suppressor Protein. <i>PLoS ONE</i> , 2012, 7, e52717.	2.5	85
45	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 703-708.	8.3	45
46	FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6680-6685.	7.1	325
47	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. <i>Genome Research</i> , 2011, 21, 1042-1054.	5.5	63
48	ALTERED MERISTEM PROGRAM 1 Is involved in Development of Seed Dormancy in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2011, 6, e20408.	2.5	25
49	Epigenetic variation in the <i>FWA</i> gene within the genus <i>Arabidopsis</i> . <i>Plant Journal</i> , 2011, 66, 831-843.	5.7	34
50	Genome wide gene expression in artificially synthesized amphidiploids of <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2011, 77, 419-431.	3.9	24
51	<i>Foxp2</i> Regulates Gene Networks Implicated in Neurite Outgrowth in the Developing Brain. <i>PLoS Genetics</i> , 2011, 7, e1002145.	3.5	256
52	A Genome-Wide Survey of Imprinted Genes in Rice Seeds Reveals Imprinting Primarily Occurs in the Endosperm. <i>PLoS Genetics</i> , 2011, 7, e1002125.	3.5	213
53	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. <i>PLoS ONE</i> , 2011, 6, e22070.	2.5	36
54	Global microRNA expression profiles in insulin target tissues in a spontaneous rat model of type 2 diabetes. <i>Diabetologia</i> , 2010, 53, 1099-1109.	6.3	261

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55	Variability of gene expression profiles in human blood and lymphoblastoid cell lines. <i>BMC Genomics</i> , 2010, 11, 96.	2.8	75
56	Therapeutic Implications of GIPC1 Silencing in Cancer. <i>PLoS ONE</i> , 2010, 5, e15581.	2.5	22
57	Dynamic and Physical Clustering of Gene Expression during Epidermal Barrier Formation in Differentiating Keratinocytes. <i>PLoS ONE</i> , 2009, 4, e7651.	2.5	26
58	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009, 19, 1133-1140.	5.5	69
59	Smad4-dependent pathways control basement membrane deposition and endodermal cell migration at early stages of mouse development. <i>BMC Developmental Biology</i> , 2009, 9, 54.	2.1	46
60	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. <i>BMC Medical Genomics</i> , 2009, 2, 54.	1.5	105
61	Copper chelator ATN-224 inhibits endothelial function by multiple mechanisms. <i>Microvascular Research</i> , 2009, 77, 314-326.	2.5	35
62	Regulation of multiple angiogenic pathways by Dll4 and Notch in human umbilical vein endothelial cells. <i>Microvascular Research</i> , 2008, 75, 144-154.	2.5	202
63	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. <i>Genomics</i> , 2008, 91, 508-511.	2.9	48
64	Chromatin profiling across the human tumour necrosis factor gene locus reveals a complex, cell type-specific landscape with novel regulatory elements. <i>Nucleic Acids Research</i> , 2008, 36, 4845-4862.	14.5	23
65	VACTERL/caudal regression/Currarino syndrome-like malformations in mice with mutation in the proprotein convertase <i>Pcsk5</i> . <i>Genes and Development</i> , 2008, 22, 1465-1477.	5.9	110
66	QuantisNP: an Objective Bayes Hidden-Markov Model to detect and accurately map copy number variation using SNP genotyping data. <i>Nucleic Acids Research</i> , 2007, 35, 2013-2025.	14.5	525
67	High-Throughput Analysis of Promoter Occupancy Reveals Direct Neural Targets of FOXP2, a Gene Mutated in Speech and Language Disorders. <i>American Journal of Human Genetics</i> , 2007, 81, 1232-1250.	6.2	232
68	A genome-wide association study of global gene expression. <i>Nature Genetics</i> , 2007, 39, 1202-1207.	21.4	882
69	Potential Contribution of NF- κ B in Neuronal Cell Death in the Glutathione Peroxidase-1 Knockout Mouse in Response to Ischemia-Reperfusion Injury. <i>Stroke</i> , 2006, 37, 1533-1538.	2.0	81
70	The chromosome 6p22 haplotype associated with dyslexia reduces the expression of KIAA0319, a novel gene involved in neuronal migration. <i>Human Molecular Genetics</i> , 2006, 15, 1659-1666.	2.9	240
71	Transcriptional Profiling in Coronary Artery Disease. <i>Circulation</i> , 2006, 114, 1811-1820.	1.6	51
72	Genetic expression profile of olfactory ensheathing cells is distinct from that of Schwann cells and astrocytes. <i>Glia</i> , 2005, 51, 132-147.	4.9	103

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73	A microarray study of post-mortem mRNA degradation in mouse brain tissue. <i>Molecular Brain Research</i> , 2005, 138, 164-177.	2.3	95
74	Microarray expression profiling in melanoma reveals a BRAF mutation signature. <i>Oncogene</i> , 2004, 23, 4060-4067.	5.9	169
75	Genetic Diversity of the Human Serotonin Receptor 1B (HTR1B) Gene. <i>Genomics</i> , 2001, 72, 1-14.	2.9	34
76	No support for linkage to the bipolar regions on chromosomes 4p, 18p, or 18q in 43 schizophrenia pedigrees. , 2000, 96, 224-227.		6
77	Follow-up study on a susceptibility locus for schizophrenia on chromosome 6q. , 1999, 88, 337-343.		95
78	Follow-up study on a susceptibility locus for schizophrenia on chromosome 6q. <i>American Journal of Medical Genetics Part A</i> , 1999, 88, 337-343.	2.4	2