

Richard D Thompson

List of Publications by Year in descending order

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76
papers

4,116
citations

94433

37
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114465

63
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all docs

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docs citations

78
times ranked

4021
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Chitinase-1</i> Controls the Accumulation of the Major Saponins Present in Pea (<i>Pisum sativum</i> L.)	10.78431	16
2	PeaMUST (Pea MultiStress Tolerance), a multidisciplinary French project uniting researchers, plant breeders, and the food industry. , 2021, 3, e108.		4
3	A Cytokinin Signaling Type-B Response Regulator Transcription Factor Acting in Early Nodulation. <i>Plant Physiology</i> , 2020, 183, 1319-1330.	4.8	19
4	Structural Variations in LysM Domains of LysM-RLK PsK1 May Result in a Different Effect on Pea-Rhizobial Symbiosis Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1624.	4.1	12
5	Functional Genomics and Seed Development in <i>Medicago truncatula</i> : An Overview. <i>Methods in Molecular Biology</i> , 2018, 1822, 175-195.	0.9	2
6	Targeting Induced Local Lesions IN Genomes (TILLING) in <i>Medicago truncatula</i> . <i>Methods in Molecular Biology</i> , 2018, 1822, 71-82.	0.9	2
7	Role of a receptor-like kinase K1 in pea <i>Rhizobium</i> symbiosis development. <i>Planta</i> , 2018, 248, 1101-1120.	3.2	25
8	Genome-wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. <i>New Phytologist</i> , 2017, 214, 1597-1613.	7.3	38
9	Evidence that auxin is required for normal seed size and starch synthesis in pea. <i>New Phytologist</i> , 2017, 216, 193-204.	7.3	54
10	PUB1 Interacts with the Receptor Kinase DMI2 and Negatively Regulates Rhizobial and Arbuscular Mycorrhizal Symbioses through Its Ubiquitination Activity in <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2016, 170, 2312-2324.	4.8	49
11	DASH transcription factor impacts <i>Medicago truncatula</i> seed size by its action on embryo morphogenesis and auxin homeostasis. <i>Plant Journal</i> , 2015, 81, 453-466.	5.7	31
12	The role of the testa during development and in establishment of dormancy of the legume seed. <i>Frontiers in Plant Science</i> , 2014, 5, 351.	3.6	154
13	Anatomical bases of sex- and size-related acoustic variation in herring gull alarm calls. <i>Journal of Avian Biology</i> , 2014, 45, 157-166.	1.2	17
14	In vitro auxin treatment promotes cell division and delays endoreduplication in developing seeds of the model legume species <i>Medicago truncatula</i> . <i>Physiologia Plantarum</i> , 2013, 148, 549-559.	5.2	16
15	The role of the DNA-binding One Zinc Finger (DOF) transcription factor family in plants. <i>Plant Science</i> , 2013, 209, 32-45.	3.6	241
16	The seed nuclear proteome. <i>Frontiers in Plant Science</i> , 2012, 3, 289.	3.6	9
17	Biosynthesis of the Halogenated Auxin, 4-Chloroindole-3-Acetic Acid. <i>Plant Physiology</i> , 2012, 159, 1055-1063.	4.8	69
18	A role for an endosperm-localized subtilase in the control of seed size in legumes. <i>New Phytologist</i> , 2012, 196, 738-751.	7.3	44

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19	Networks of Seed Storage Protein Regulation in Cereals and Legumes at the Dawn of the Omics Era. , 2012, , 187-210.		1
20	Metabolic Specialization of Maternal and Filial Tissues. , 2012, , 407-432.		0
21	Sultr4;1 mutant seeds of Arabidopsis have an enhanced sulphate content and modified proteome suggesting metabolic adaptations to altered sulphate compartmentalization. BMC Plant Biology, 2010, 10, 78.	3.6	37
22	The Seed Composition of Arabidopsis Mutants for the Group 3 Sulfate Transporters Indicates a Role in Sulfate Translocation within Developing Seeds. Plant Physiology, 2010, 154, 913-926.	4.8	61
23	Model legumes contribute to faba bean breeding. Field Crops Research, 2010, 115, 253-269.	5.1	64
24	Post-Genomics Studies of Developmental Processes in Legume Seeds. Plant Physiology, 2009, 151, 1023-1029.	4.8	36
25	Optimizing TILLING populations for reverse genetics in <i>Medicago truncatula</i> . Plant Biotechnology Journal, 2009, 7, 430-441.	8.3	106
26	Gene expression profiling of <i>M. truncatula</i> transcription factors identifies putative regulators of grain legume seed filling. Plant Molecular Biology, 2008, 67, 567-580.	3.9	85
27	Exploring the nuclear proteome of <i>Medicago truncatula</i> at the switch towards seed filling. Plant Journal, 2008, 56, 398-410.	5.7	60
28	UTILLdb, a <i>Pisum sativum</i> in silico forward and reverse genetics tool. Genome Biology, 2008, 9, R43.	9.6	157
29	Reserve accumulation in legume seeds. Comptes Rendus - Biologies, 2008, 331, 755-762.	0.2	72
30	Transcriptional Regulation of Storage Protein Synthesis During Dicotyledon Seed Filling. Plant and Cell Physiology, 2008, 49, 1263-1271.	3.1	131
31	A Combined Proteome and Transcriptome Analysis of Developing <i>Medicago truncatula</i> Seeds. Molecular and Cellular Proteomics, 2007, 6, 2165-2179.	3.8	237
32	In vitro culture of immature <i>M. truncatula</i> grains under conditions permitting embryo development comparable to that observed in vivo. Plant Science, 2006, 170, 1052-1058.	3.6	32
33	Changes in gene expression in maize kernel in response to water and salt stress. Plant Cell Reports, 2006, 25, 71-79.	5.6	69
34	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	7.1	35
35	In situ expression of two storage protein genes in relation to histo-differentiation at mid-embryogenesis in <i>Medicago truncatula</i> and <i>Pisum sativum</i> seeds. Journal of Experimental Botany, 2005, 56, 2019-2028.	4.8	16
36	Interaction of maize Opaque-2 and the transcriptional co-activators GCN5 and ADA2, in the modulation of transcriptional activity. Plant Molecular Biology, 2004, 55, 239-252.	3.9	42

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37	The Tobacco BY-2 Cell Line as a Model System to Understand in Planta Nuclear Coactivator Interactions. <i>Biotechnology in Agriculture and Forestry</i> , 2004, , 316-331.	0.2	2
38	Alteration of GCN5 levels in maize reveals dynamic responses to manipulating histone acetylation. <i>Plant Journal</i> , 2003, 33, 455-469.	5.7	42
39	Proteomics of <i>Medicago truncatula</i> Seed Development Establishes the Time Frame of Diverse Metabolic Processes Related to Reserve Accumulation. <i>Plant Physiology</i> , 2003, 133, 664-682.	4.8	241
40	Establishment of Cereal Endosperm Expression Domains. <i>Plant Cell</i> , 2002, 14, 599-610.	6.6	116
41	Subcellular localisation of BETL-1, -2 and -4 in <i>Zea mays</i> L. endosperm. <i>Sexual Plant Reproduction</i> , 2002, 15, 85-98.	2.2	19
42	Post-phloem protein trafficking in the maize caryopsis: zmTRXh1, a thioredoxin specifically expressed in the pedicel parenchyma of <i>Zea mays</i> L., is found predominantly in the placental chalazal. <i>Plant Molecular Biology</i> , 2002, 50, 743-756.	3.9	14
43	Development and functions of seed transfer cells. <i>Plant Science</i> , 2001, 160, 775-783.	3.6	141
44	Maize endosperm secretes a novel antifungal protein into adjacent maternal tissue. <i>Plant Journal</i> , 2001, 25, 687-698.	5.7	82
45	rgf1, a mutation reducing grain filling in maize through effects on basal endosperm and pedicel development+. <i>Plant Journal</i> , 2000, 23, 29-42.	5.7	68
46	Turning fields into grains. <i>Nature</i> , 2000, 408, 39-41.	27.8	6
47	Genetic Control of Endosperm Development. , 1999, , 185-197.		4
48	Identification of a Promoter Sequence from the BETL1 Gene Cluster Able to Confer Transfer-Cell-Specific Expression in Transgenic Maize. <i>Plant Physiology</i> , 1999, 121, 1143-1152.	4.8	55
49	Evidence for factors regulating transfer cell-specific expression in maize endosperm. <i>Plant Molecular Biology</i> , 1999, 41, 403-414.	3.9	70
50	A maize FK506-sensitive immunophilin, mzFKBP-66, is a peptidylproline cis - trans -isomerase that interacts with calmodulin and a 36-kDa cytoplasmic protein. <i>Planta</i> , 1998, 205, 121-131.	3.2	37
51	The activation domain of the maize transcription factor Opaque-2 resides in a single acidic region. <i>Nucleic Acids Research</i> , 1997, 25, 756-763.	14.5	19
52	Genetic Regulation of Carbohydrate and Protein Accumulation in Seeds. <i>Advances in Cellular and Molecular Biology of Plants</i> , 1997, , 479-522.	0.2	11
53	Nitrogen and hormonal responsiveness of the 22 kDa alpha-zein and b-32 genes in maize endosperm is displayed in the absence of the transcriptional regulator Opaque-2. <i>Plant Journal</i> , 1997, 12, 281-291.	5.7	29
54	Genetic manipulations of protein quality in maize grain. <i>Field Crops Research</i> , 1996, 45, 37-48.	5.1	7

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55	The transcriptional activator Opaque-2 controls the expression of a cytosolic form of pyruvate orthophosphate dikinase-1 in maize endosperms. <i>Molecular Genetics and Genomics</i> , 1996, 250, 647-654.	2.4	54
56	Regulation of cytosolic pyruvate, orthophosphate dikinase expression in developing maize endosperm. <i>Plant Molecular Biology</i> , 1996, 31, 45-55.	3.9	32
57	The role of multiple binding sites in the activation of zein gene expression by. <i>Molecular Genetics and Genomics</i> , 1996, 252, 723.	2.4	4
58	Molecular analysis of <i>opaque</i> -2 alleles from <i>Zea mays</i> L. reveals the nature of mutational events and the presence of a hypervariable region in the 5' part of the gene. <i>Genetical Research</i> , 1995, 65, 11-19.	0.9	20
59	Molecular characterization of BET1, a gene expressed in the endosperm transfer cells of maize.. <i>Plant Cell</i> , 1995, 7, 747-757.	6.6	108
60	ZEMA, a member of a novel group of MADS box genes, is alternatively spliced in maize endosperm. <i>Nucleic Acids Research</i> , 1995, 23, 2168-2177.	14.5	47
61	Regulation of Storage Protein Synthesis in Cereal Seeds: Developmental and Nutritional Aspects. <i>Journal of Plant Physiology</i> , 1995, 145, 606-613.	3.5	32
62	Structural and functional analysis of an Opaque-2-related gene from sorghum. <i>Plant Molecular Biology</i> , 1994, 24, 515-523.	3.9	28
63	The most abundant soluble basic protein of the stilar transmitting tract in potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgt / Overlock 10	3.2	50
64	Differences in cell type-specific expression of the gene Opaque 2 in maize and transgenic tobacco. <i>Molecular Genetics and Genomics</i> , 1994, 244, 391-400.	2.4	40
65	Functional expression of the transcriptional activator Opaque-2 of <i>Zea mays</i> in transformed yeast. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 319-326.	2.4	38
66	The accumulation of zein polypeptides and zein mRNA in cultured endosperms of maize is modulated by nitrogen supply. <i>Plant Journal</i> , 1993, 3, 325-334.	5.7	17
67	Translation of the mRNA of the Maize Transcriptional Activator Opaque-2 Is Inhibited by Upstream Open Reading Frames Present in the Leader Sequence. <i>Plant Cell</i> , 1993, 5, 65.	6.6	34
68	Analysis of HMW glutenin subunits encoded by chromosome 1A of bread wheat (<i>Triticum aestivum</i> L.) indicates quantitative effects on grain quality. <i>Theoretical and Applied Genetics</i> , 1992, 83, 373-378.	3.6	225
69	The S locus of flowering plants: when self-rejection is self-interest. <i>Trends in Genetics</i> , 1992, 8, 381-387.	6.7	74
70	The S locus of flowering plants: when self-rejection is self-interest. <i>Trends in Genetics</i> , 1992, 8, 381-387.	6.7	57
71	Molecular analysis of the Bg-rbg transposable element system of <i>Zea mays</i> L.. <i>Molecular Genetics and Genomics</i> , 1991, 227, 91-96.	2.4	23
72	Investigation of a self-compatible mutation in <i>Solanum tuberosum</i> clones inhibiting S-allele activity in pollen differentially. <i>Molecular Genetics and Genomics</i> , 1991, 226-226, 283-288.	2.4	43

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73	Genetic and Molecular Studies on Endosperm Storage Proteins in Maize. , 1991, , 627-634.		0
74	The b-32 protein from maize endosperm: characterization of genomic sequences encoding two alternative central domains. <i>Plant Molecular Biology</i> , 1990, 14, 1031-1040.	3.9	34
75	The characterization of cDNA clones coding for wheat storage proteins. <i>Nucleic Acids Research</i> , 1983, 11, 2961-2977.	14.5	147
76	A Novel Recombinant of Phage Lambda and a Conserved 3000-Base-Pair Fragment of <i>Xenopus laevis</i> Ribosomal Deoxyribonucleic Acid Produced by Restriction with Endonucleases <i>Hind</i> III/ <i>Bam</i> I. <i>Biochemical Society Transactions</i> , 1978, 6, 1232-1233.	3.4	2