Elizabeth S Dennis

List of Publications by Year in descending order

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306 papers 33,976 citations

99 h-index 173 g-index

311 all docs

311 docs citations

times ranked

311

18207 citing authors

#	Article	IF	CITATIONS
1	Transcriptional Association between mRNAs and Their Paired Natural Antisense Transcripts Following Fusarium oxysporum Inoculation in Brassica rapa L Horticulturae, 2022, 8, 17.	2.8	8
2	Capturing hybrid vigor for lentil breeding. Crop Science, 2022, 62, 1787-1796.	1.8	2
3	Hybrid Vigour and Hybrid Mimics in Japonica Rice. Agronomy, 2022, 12, 1559.	3.0	1
4	The transcriptional response to salicylic acid plays a role in Fusarium yellows resistance in Brassica rapa L Plant Cell Reports, 2021, 40, 605-619.	5.6	7
5	Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in Brassica rapa. PLoS ONE, 2021, 16, e0242530.	2.5	8
6	Development of a New DNA Marker for Fusarium Yellows Resistance in Brassica rapa Vegetables. Plants, 2021, 10, 1082.	3.5	5
7	Characterization of Histone H3 Lysine 4 and 36 Tri-methylation in Brassica rapa L Frontiers in Plant Science, 2021, 12, 659634.	3.6	9
8	Rice hybrid mimics have stable yields equivalent to those of the F1 hybrid and suggest a basis for hybrid vigour. Planta, 2021, 254, 51.	3.2	3
9	Arabidopsis Col/Ler and Ws/Ler hybrids and Hybrid Mimics produce seed yield heterosis through increased height, inflorescence branch and silique number. Planta, 2020, 252, 40.	3.2	5
10	Early Establishment of Photosynthesis and Auxin Biosynthesis Plays a Key Role in Early Biomass Heterosis in Brassica napus (Canola) Hybrids. Plant and Cell Physiology, 2020, 61, 1134-1143.	3.1	19
11	Trichomes at the Base of the Petal Are Regulated by the Same Transcription Factors as Cotton Seed Fibers. Plant and Cell Physiology, 2020, 61, 1590-1599.	3.1	3
12	Leaf growth in early development is key to biomass heterosis in Arabidopsis. Journal of Experimental Botany, 2020, 71, 2439-2450.	4.8	27
13	In Arabidopsis thaliana Heterosis Level Varies among Individuals in an F1 Hybrid Population. Plants, 2020, 9, 414.	3.5	2
14	Genome Triplication Leads to Transcriptional Divergence of FLOWERING LOCUS C Genes During Vernalization in the Genus Brassica. Frontiers in Plant Science, 2020, 11, 619417.	3.6	20
15	Long noncoding RNAs in Brassica rapa L. following vernalization. Scientific Reports, 2019, 9, 9302.	3.3	42
16	The histone modification H3 lysine 27 tri-methylation has conserved gene regulatory roles in the triplicated genome of Brassica rapa L DNA Research, 2019, 26, 433-443.	3.4	25
17	In Arabidopsis hybrids and Hybrid Mimics, upâ€regulation of cell wall biogenesis is associated with the increased plant size. Plant Direct, 2019, 3, e00174.	1.9	6
18	The role of FRIGIDA and FLOWERING LOCUS C genes in flowering time of Brassica rapa leafy vegetables. Scientific Reports, 2019, 9, 13843.	3.3	27

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19	Senescence and Defense Pathways Contribute to Heterosis. Plant Physiology, 2019, 180, 240-252.	4.8	21
20	<i>DEMETER</i> plays a role in DNA demethylation and disease response in somatic tissues of Arabidopsis. Epigenetics, 2019, 14, 1074-1087.	2.7	32
21	Genes Directing Flower Development in Arabidopsis. Plant Cell, 2019, 31, 1192-1193.	6.6	18
22	Cotyledons contribute to plant growth and hybrid vigor in Arabidopsis. Planta, 2019, 249, 1107-1118.	3.2	22
23	Genome-wide characterization of DNA methylation, small RNA expression, and histone H3 lysine nine di-methylation in <i>Brassica rapa</i> L DNA Research, 2018, 25, 511-520.	3.4	25
24	Recent research on the mechanism of heterosis is important for crop and vegetable breeding systems. Breeding Science, 2018, 68, 145-158.	1.9	110
25	Genome-wide analyses of four major histone modifications in Arabidopsis hybrids at the germinating seed stage. BMC Genomics, 2017, 18, 137.	2.8	23
26	PIF4-controlled auxin pathway contributes to hybrid vigor in <i>Arabidopsis thaliana </i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3555-E3562.	7.1	35
27	Patterns of gene expression in developing embryos of Arabidopsis hybrids. Plant Journal, 2017, 89, 927-939.	5.7	14
28	Comparison of transcriptome profiles by Fusarium oxysporum inoculation between Fusarium yellows resistant and susceptible lines in Brassica rapa L Plant Cell Reports, 2017, 36, 1841-1854.	5.6	20
29	Tissue and cell-specific transcriptomes in cotton reveal the subtleties of gene regulation underlying the diversity of plant secondary cell walls. BMC Genomics, 2017, 18, 539.	2.8	38
30	Analysis of Argonaute 4-Associated Long Non-Coding RNA in Arabidopsis thaliana Sheds Novel Insights into Gene Regulation through RNA-Directed DNA Methylation. Genes, 2017, 8, 198.	2.4	19
31	Genetic distance of inbred lines of Chinese cabbage and its relationship to heterosis. Plant Gene, 2016, 5, 1-7.	2.3	48
32	Early changes of gene activity in developing seedlings of Arabidopsis hybrids relative to parents may contribute to hybrid vigour. Plant Journal, 2016, 88, 597-607.	5.7	37
33	Development of primer sets that can verify the enrichment of histone modifications, and their application to examining vernalization-mediated chromatin changes in <i>Brassica rapa</i> L Genes and Genetic Systems, 2016, 91, 1-10.	0.7	29
34	Role of DNA methylation in hybrid vigor in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6704-E6711.	7.1	71
35	Trichomes control flower bud shape by linking together young petals. Nature Plants, 2016, 2, 16093.	9.3	28
36	Twenty-four–nucleotide siRNAs produce heritable trans-chromosomal methylation in F1 <i>Arabidopsis</i> hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6895-E6902.	7.1	36

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37	Molecular and cellular characteristics of hybrid vigour in a commercial hybrid of Chinese cabbage. BMC Plant Biology, 2016, 16, 45.	3.6	45
38	Genetic characterization of inbred lines of Chinese cabbage by DNA markers; towards the application of DNA markers to breeding of F1 hybrid cultivars. Data in Brief, 2016, 6, 229-237.	1.0	14
39	Nicotiana Small RNA Sequences Support a Host Genome Origin of Cucumber Mosaic Virus Satellite RNA. PLoS Genetics, 2015, 11, e1004906.	3.5	28
40	Satellite RNAs interfere with the function of viral RNA silencing suppressors. Frontiers in Plant Science, 2015, 6, 281.	3.6	33
41	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
42	Hybrid mimics and hybrid vigor in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4959-67.	7.1	51
43	Epigenetic Changes in Hybrids. Plant Physiology, 2015, 168, 1197-1205.	4.8	102
44	Hormone-regulated defense and stress response networks contribute to heterosis in <i>Arabidopsis</i> F1 hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6397-406.	7.1	110
45	Inheritance of Trans Chromosomal Methylation patterns from <i>Arabidopsis</i> F1 hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2017-2022.	7.1	69
46	DNA demethylases target promoter transposable elements to positively regulate stress responsive genes in Arabidopsis. Genome Biology, 2014, 15, 458.	8.8	243
47	Members of the MYBMIXTA-like transcription factors may orchestrate the initiation of fiber development in cotton seeds. Frontiers in Plant Science, 2014, 5, 179.	3.6	33
48	In Nicotiana species, an artificial microRNA corresponding to the virulence modulating region of Potato spindle tuber viroid directs RNA silencing of a soluble inorganic pyrophosphatase gene and the development of abnormal phenotypes. Virology, 2014, 450-451, 266-277.	2.4	61
49	Identification of candidate genes for fusarium yellows resistance in Chinese cabbage by differential expression analysis. Plant Molecular Biology, 2014, 85, 247-257.	3.9	57
50	Intraspecific Arabidopsis Hybrids Show Different Patterns of Heterosis Despite the Close Relatedness of the Parental Genomes \hat{A} \hat{A} . Plant Physiology, 2014, 166, 265-280.	4.8	77
51	The role of epigenetics in hybrid vigour. Trends in Genetics, 2013, 29, 684-690.	6.7	137
52	Arabidopsis Polycomb Repressive Complex 2 binding sites contain putative GAGA factor binding motifs within coding regions of genes. BMC Genomics, 2013, 14, 593.	2.8	94
53	Genetic and physical mapping of flowering time loci in canola (Brassica napus L.). Theoretical and Applied Genetics, 2013, 126, 119-132.	3.6	105
54	Characterization of the defense transcriptome responsive to Fusarium oxysporum-infection in Arabidopsis using RNA-seq. Gene, 2013, 512, 259-266.	2.2	120

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55	Multiple Mechanisms and Challenges for the Application of Allopolyploidy in Plants. International Journal of Molecular Sciences, 2012, 13, 8696-8721.	4.1	24
56	Identification of High-Temperature-Responsive Genes in Cereals Â. Plant Physiology, 2012, 158, 1439-1450.	4.8	59
57	Trans-chromosomal methylation. Epigenetics, 2012, 7, 800-805.	2.7	24
58	Trans Chromosomal Methylation in <i>Arabidopsis</i> hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3570-3575.	7.1	202
59	Heterosis of <i>Arabidopsis</i> hybrids between C24 and Col is associated with increased photosynthesis capacity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7109-7114.	7.1	161
60	A comparison of transcriptome and epigenetic status between closely related species in the genus Arabidopsis. Gene, 2012, 506, 301-309.	2.2	11
61	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
62	Molecular Mechanisms of Epigenetic Variation in Plants. International Journal of Molecular Sciences, 2012, 13, 9900-9922.	4.1	54
63	Epidermal cell differentiation in cotton mediated by the homeodomain leucine zipper gene, <i>ChHD‶</i> . Plant Journal, 2012, 71, 464-478.	5.7	125
64	FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6680-6685.	7.1	325
65	Epigenetics in plantsâ€"vernalisation and hybrid vigour. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 427-437.	1.9	61
66	Vernalization-Repression of Arabidopsis FLC Requires Promoter Sequences but Not Antisense Transcripts. PLoS ONE, 2011, 6, e21513.	2.5	121
67	The low temperature response pathways for cold acclimation and vernalization are independent. Plant, Cell and Environment, 2011, 34, 1737-1748.	5.7	43
68	Polycomb proteins regulate the quantitative induction of <i>VERNALIZATION INSENSITIVE 3</i> ii> in response to low temperatures. Plant Journal, 2011, 65, 382-391.	5.7	38
69	GhMYB25â€like: a key factor in early cotton fibre development. Plant Journal, 2011, 65, 785-797.	5 . 7	229
70	Epigenetic variation in the <i>FWA</i> gene within the genus Arabidopsis. Plant Journal, 2011, 66, 831-843.	5.7	34
71	Genome wide gene expression in artificially synthesized amphidiploids of Arabidopsis. Plant Molecular Biology, 2011, 77, 419-431.	3.9	24
72	Changes in 24-nt siRNA levels in Arabidopsis hybrids suggest an epigenetic contribution to hybrid vigor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2617-2622.	7.1	310

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73	Transgene Expression and Transgene-Induced Silencing in Diploid and Autotetraploid Arabidopsis. Genetics, 2011, 187, 409-423.	2.9	28
74	Long non-coding RNA-mediated mechanisms independent of the RNAi pathway in animals and plants. RNA Biology, 2011, 8, 404-414.	3.1	41
7 5	<i>ODDSOC2</i> Is a MADS Box Floral Repressor That Is Down-Regulated by Vernalization in Temperate Cereals Â. Plant Physiology, 2010, 153, 1062-1073.	4.8	88
76	The hunt for hypoxia responsive natural antisense short interfering RNAs. Plant Signaling and Behavior, 2010, 5, 247-251.	2.4	11
77	Sequencing and Utilization of the Gossypium Genomes. Tropical Plant Biology, 2010, 3, 71-74.	1.9	6
78	The VQ motif protein IKU1 regulates endosperm growth and seed size in Arabidopsis. Plant Journal, 2010, 63, 670-679.	5.7	224
79	Global Gene Expression Responses to Waterlogging in Roots and Leaves of Cotton (Gossypium) Tj ETQq1 1 0.784	4314 rgBT 3.1	/Overlock 1
80	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
81	Arabidopsis <i>RAP2.2</i> : An Ethylene Response Transcription Factor That Is Important for Hypoxia Survival Â. Plant Physiology, 2010, 153, 757-772.	4.8	293
82	ATAF NAC transcription factors: Regulators of plant stress signaling. Plant Signaling and Behavior, 2010, 5, 428-432.	2.4	80
83	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. Journal of Experimental Botany, 2010, 61, 165-177.	4.8	184
84	Rice Genomics. , 2010, , 257-279.		0
85	Vernalization-induced flowering in cereals is associated with changes in histone methylation at the <i>VERNALIZATION1</i> gene. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8386-8391.	7.1	208
86	Histone Acetylation, VERNALIZATION INSENSITIVE 3 , FLOWERING LOCUS C , and the Vernalization Response. Molecular Plant, 2009, 2, 724-737.	8.3	64
87	Hypoxia. Plant Signaling and Behavior, 2009, 4, 773-776.	2.4	9
88	The influence of vernalization and daylength on expression of flowering-time genes in the shoot apex and leaves of barley (Hordeum vulgare) Journal of Experimental Botany, 2009, 60, 2169-2178.	4.8	107
89	Expression, Imprinting, and Evolution of Rice Homologs of the Polycomb Group Genes. Molecular Plant, 2009, 2, 711-723.	8.3	193
90	The Low-Oxygen-Induced NAC Domain Transcription Factor <i>ANAC102</i> Affects Viability of Arabidopsis Seeds following Low-Oxygen Treatment Â. Plant Physiology, 2009, 149, 1724-1738.	4.8	141

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91	Review: Correlations between oxygen affinity and sequence classifications of plant hemoglobins. Biopolymers, 2009, 91, 1083-1096.	2.4	120
92	Regions associated with repression of the barley (Hordeum vulgare) VERNALIZATION1 gene are not required for cold induction. Molecular Genetics and Genomics, 2009, 282, 107-117.	2.1	103
93	Vernalization in cereals. Journal of Biology, 2009, 8, 57.	2.7	52
94	The MYB transcription factor GhMYB25 regulates early fibre and trichome development. Plant Journal, 2009, 59, 52-62.	5.7	297
95	Mechanisms of gene repression by vernalization in Arabidopsis. Plant Journal, 2009, 59, 488-498.	5.7	56
96	<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
97	SPT5â€like, a new component in plant RdDM. EMBO Reports, 2009, 10, 573-575.	4.5	5
98	The molecular biology of seasonal flowering-responses in Arabidopsis and the cereals. Annals of Botany, 2009, 103, 1165-1172.	2.9	245
99	Transcript Profiling During Fiber Development Identifies Pathways in Secondary Metabolism and Cell Wall Structure That May Contribute to Cotton Fiber Quality. Plant and Cell Physiology, 2009, 50, 1364-1381.	3.1	120
100	Polycomb repression. Plant Signaling and Behavior, 2008, 3, 412-414.	2.4	2
101	Integration of seasonal flowering time responses in temperate cereals. Plant Signaling and Behavior, 2008, 3, 601-602.	2.4	4
102	UBIQUITIN-SPECIFIC PROTEASE 26 Is Required for Seed Development and the Repression of <i>PHERES1</i> in Arabidopsis. Genetics, 2008, 180, 229-236.	2.9	66
103	Hairpin RNAs derived from RNA polymerase II and polymerase III promoter-directed transgenes are processed differently in plants. Rna, 2008, 14, 903-913.	3.5	47
104	Post-Translational Modifications of the Endogenous and Transgenic FLC Protein in Arabidopsis thaliana. Plant and Cell Physiology, 2008, 49, 1859-1866.	3.1	19
105	Resetting of <i>FLOWERING LOCUS C</i> expression after epigenetic repression by vernalization. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2214-2219.	7.1	187
106	Genetic contributions to agricultural sustainability. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 591-609.	4.0	30
107	Low-Temperature and Daylength Cues Are Integrated to Regulate <i>FLOWERING LOCUS T</i> in Barley Â Â. Plant Physiology, 2008, 147, 355-366.	4.8	212
108	Synthesis of complementary RNA by RNA-dependent RNA polymerases in plant extracts is independent of an RNA primer. Functional Plant Biology, 2008, 35, 1091.	2.1	3

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109	HKT1;5-Like Cation Transporters Linked to Na+ Exclusion Loci in Wheat, Nax2 and Kna1. Plant Physiology, 2007, 143, 1918-1928.	4.8	378
110	Short Vegetative Phase-Like MADS-Box Genes Inhibit Floral Meristem Identity in Barley. Plant Physiology, 2007, 143, 225-235.	4.8	174
111	ABA Regulates Apoplastic Sugar Transport and is a Potential Signal for Cold-Induced Pollen Sterility in Rice. Plant and Cell Physiology, 2007, 48, 1319-1330.	3.1	271
112	The FLX Gene of Arabidopsis is Required for FRI-Dependent Activation of FLC Expression. Plant and Cell Physiology, 2007, 49, 191-200.	3.1	31
113	The molecular basis of vernalization-induced flowering in cereals. Trends in Plant Science, 2007, 12, 352-357.	8.8	340
114	Cloning and characterization of microRNAs from <i>Brassica napus</i> . FEBS Letters, 2007, 581, 3848-3856.	2.8	52
115	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1 Plant Physiology, 2007, 145, 1303-1310.	4.8	390
116	Vernalization-Induced Trimethylation of Histone H3 Lysine 27 at FLC Is Not Maintained in Mitotically Quiescent Cells. Current Biology, 2007, 17, 1978-1983.	3.9	221
117	Epigenetic regulation of flowering. Current Opinion in Plant Biology, 2007, 10, 520-527.	7.1	172
118	compact shoot and leafy head 1, a mutation affects leaf initiation and developmental transition in rice (Oryza sativa L.). Plant Cell Reports, 2007, 26, 421-427.	5.6	12
119	Laser capture microdissection and cDNA microarrays used to generate gene expression profiles of the rapidly expanding fibre initial cells on the surface of cotton ovules. Planta, 2007, 226, 1475-1490.	3.2	70
120	The Molecular Basis of Cold-Induced Pollen Sterility in Rice. , 2007, , 205-207.		7
121	Phenotyping cotton ovule fibre initiation with spatial statistics. Australian Journal of Botany, 2007, 55, 608.	0.6	7
122	Vernalization: Spring into Flowering. Developmental Cell, 2006, 11, 1-2.	7.0	25
123	Transgene structures suggest that multiple mechanisms are involved in T-DNA integration in plants. Plant Science, 2006, 171, 308-322.	3.6	34
124	Nomenclature for HKT transporters, key determinants of plant salinity tolerance. Trends in Plant Science, 2006, 11, 372-374.	8.8	329
125	Hemoglobin is essential for normal growth of Arabidopsis organs. Physiologia Plantarum, 2006, 127, 157-166.	5.2	75
126	Quantitative effects of vernalization on FLC and SOC1 expression. Plant Journal, 2006, 45, 871-883.	5.7	98

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127	The Arabidopsis FLC protein interacts directlyin vivowith SOC1 and FT chromatin and is part of a high-molecular-weight protein complex. Plant Journal, 2006, 46, 183-192.	5.7	502
128	Dissociation (Ds) constructs, mapped Ds launch pads and a transiently-expressed transposase system suitable for localized insertional mutagenesis in rice. Theoretical and Applied Genetics, 2006, 112, 1326-1341.	3.6	51
129	HvVRN2 Responds to Daylength, whereas HvVRN1 Is Regulated by Vernalization and Developmental Status. Plant Physiology, 2006, 140, 1397-1405.	4.8	209
130	A global assembly of cotton ESTs. Genome Research, 2006, 16, 441-450.	5 . 5	138
131	The Arabidopsis thaliana vernalization response requires a polycomb-like protein complex that also includes VERNALIZATION INSENSITIVE 3. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14631-14636.	7.1	335
132	Expression Profiling Identifies Genes Expressed Early During Lint Fibre Initiation in Cotton. Plant and Cell Physiology, 2006, 47, 107-127.	3.1	165
133	A Sodium Transporter (HKT7) Is a Candidate for Nax1, a Gene for Salt Tolerance in Durum Wheat. Plant Physiology, 2006, 142, 1718-1727.	4.8	266
134	Genomic approaches to the discovery of promoters for sustained expression in cotton (Gossypium) Tj ETQq0 0 0 Rubisco small subunit promoter identified using EST sequence analysis and cDNA microarrays. Plant Biotechnology, 2006, 23, 437-450.	rgBT /Ove 1.0	rlock 10 Tf 50
135	A novel T-DNA vector design for selection of transgenic lines with simple transgene integration and stable transgene expression. Functional Plant Biology, 2005, 32, 671.	2.1	18
136	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in Arabidopsis. Plant Journal, 2005, 43, 745-757.	5.7	273
137	The downregulation of FLOWERING LOCUS C (FLC) expression in plants with low levels of DNA methylation and by vernalization occurs by distinct mechanisms. Plant Journal, 2005, 44, 420-432.	5.7	125
138	Cold-induced repression of the rice anther-specific cell wall invertase gene OSINV4 is correlated with sucrose accumulation and pollen sterility. Plant, Cell and Environment, 2005, 28, 1534-1551.	5.7	309
139	Isolation and characterization of a Ds-tagged rice (Oryza sativa L.) GA-responsive dwarf mutant defective in an early step of the gibberellin biosynthesis pathway. Plant Cell Reports, 2005, 23, 819-833.	5.6	61
140	Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. Molecular Genetics and Genomics, 2005, 274, 477-493.	2.1	21
141	Microarray Analysis Reveals Vegetative Molecular Phenotypes of Arabidopsis Flowering-time Mutants. Plant and Cell Physiology, 2005, 46, 1190-1201.	3.1	35
142	MINISEED3 (MINI3), a WRKY family gene, and HAIKU2 (IKU2), a leucine-rich repeat (LRR) KINASE gene, are regulators of seed size in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17531-17536.	7.1	476
143	Response of larval Chironomus tepperi (Diptera: Chironomidae) to individual Bacillus thuringiensis var. israelensis toxins and toxin mixtures. Journal of Invertebrate Pathology, 2005, 88, 34-39.	3.2	37

Simple sequence repeat (SSR) markers reveal low levels of polymorphism between cotton (Gossypium) Tj ETQq $0.0\,\Omega_{1.5}$ gBT /Overlock 10^{-1}

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145	The ANTHER INDEHISCENCE1 Gene Encoding a Single MYB Domain Protein Is Involved in Anther Development in Rice. Plant Physiology, 2004, 135, 1514-1525.	4.8	152
146	On the role of RNA silencing in the pathogenicity and evolution of viroids and viral satellites. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3275-3280.	7.1	273
147	A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice (Oryza sativa L.). Plant Biotechnology Journal, 2004, 2, 367-380.	8.3	40
148	A Cluster of Arabidopsis Genes with a Coordinate Response to an Environmental Stimulus. Current Biology, 2004, 14, 911-916.	3.9	74
149	Spatial and temporal analysis of the local response to wounding. Plant Molecular Biology, 2004, 55, 165-181.	3.9	120
150	Approaches for the Isolation of Arabidopsisadh 1 Regulatory Mutants Using Allyl Alcohol Selection. Russian Journal of Plant Physiology, 2003, 50, 762-773.	1.1	2
151	Opposing effects of reduced DNA methylation on flowering time in Arabidopsis thaliana. Planta, 2003, 216, 461-466.	3.2	34
152	Cell signalling and gene regulation. Current Opinion in Plant Biology, 2003, 6, 405-409.	7.1	69
153	Ds tagging of BRANCHED FLORETLESS 1 (BFL1) that mediates the transition from spikelet to floret meristem in rice (Oryza sativa L). BMC Plant Biology, 2003, 3, 6.	3.6	67
154	Reciprocal control of flowering time by OsSOC1 in transgenic Arabidopsis and by FLC in transgenic rice. Plant Biotechnology Journal, 2003, 1, 361-369.	8.3	81
155	Enhanced Low Oxygen Survival in Arabidopsis through Increased Metabolic Flux in the Fermentative Pathway. Plant Physiology, 2003, 132, 1292-1302.	4.8	243
156	Enhancing the Anaerobic Response. Annals of Botany, 2003, 91, 111-117.	2.9	63
157	MADS box genes control vernalization-induced flowering in cereals. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13099-13104.	7.1	409
158	Expression Profile Analysis of the Low-Oxygen Response in Arabidopsis Root Cultures[W]. Plant Cell, 2002, 14, 2481-2494.	6.6	362
159	Different Regulatory Regions Are Required for the Vernalization-Induced Repression of FLOWERING LOCUS C and for the Epigenetic Maintenance of Repression. Plant Cell, 2002, 14, 2527-2537.	6.6	243
160	Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. Asia Pacific Biotech News, 2002, 06, 936-942.	0.0	4
161	Increased level of hemoglobin 1 enhances survival of hypoxic stress and promotes early growth in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17197-17202.	7.1	170
162	Isolation and functional characterization of cytochrome P450s in Gibberellin biosynthesis pathway. Methods in Enzymology, 2002, 357, 381-388.	1.0	4

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163	Investigation of the chromosomal location of the bacterial blight resistance gene present in an Australian cotton (Gossypium hirsutum L.) cultivar. Australian Journal of Agricultural Research, 2002, 53, 551.	1.5	24
164	Overexpression of alcohol dehydrogenase or pyruvate decarboxylase improves growth of hairy roots at reduced oxygen concentrations. Biotechnology and Bioengineering, 2002, 77, 455-461.	3.3	54
165	A quick and easy method for isolating good-quality RNA from cotton (Gossypium hirsutum L.) tissues. Plant Molecular Biology Reporter, 2002, 20, 213-218.	1.8	56
166	FLC, a repressor of flowering, is regulated by genes in different inductive pathways. Plant Journal, 2002, 29, 183-191.	5.7	116
167	An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. Functional Plant Biology, 2002, 29, 547.	2.1	65
168	Control of Early Seed Development. Annual Review of Cell and Developmental Biology, 2001, 17, 677-699.	9.4	184
169	Expression of pathogenesis-related genes in cotton stems in response to infection by Verticillium dahliae. Physiological and Molecular Plant Pathology, 2001, 58, 119-131.	2.5	67
170	<i>GAMYB-like</i> Genes, Flowering, and Gibberellin Signaling in Arabidopsis. Plant Physiology, 2001, 127, 1682-1693.	4.8	291
171	A plastid envelope location of Arabidopsis ent-kaurene oxidase links the plastid and endoplasmic reticulum steps of the gibberellin biosynthesis pathway. Plant Journal, 2001, 28, 201-208.	5.7	143
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