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List of Publications by Year in descending order

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237 papers	28,210 citations	4960 84 h-index	6130 159 g-index
238 all docs	238 docs citations	238 times ranked	21228 citing authors

#	Article	IF	Citations
1	Ancestral polyploidy in seed plants and angiosperms. Nature, 2011, 473, 97-100.	27.8	1,862
2	The protein encoded by the Arabidopsis homeotic gene agamous resembles transcription factors. Nature, 1990, 346, 35-39.	27.8	1,643
3	The Amborella Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	12.6	743
4	Control of rice grain-filling and yield by a gene with a potential signature of domestication. Nature Genetics, 2008, 40, 1370-1374.	21.4	706
5	Patterns of gene action in plant development revealed by enhancer trap and gene trap transposable elements.. Genes and Development, 1995, 9, 1797-1810.	5.9	671
6	Widespread genome duplications throughout the history of flowering plants. Genome Research, 2006, 16, 738-749.	5.5	664
7	The Rice Tapetum Degeneration Retardation Gene Is Required for Tapetum Degradation and Anther Development. Plant Cell, 2006, 18, 2999-3014.	6.6	615
8	The SCFCOI1 Ubiquitin-Ligase Complexes Are Required for Jasmonate Response in Arabidopsis. Plant Cell, 2002, 14, 1919-1935.	6.6	600
9	AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and transcription factor genes.. Genes and Development, 1991, 5, 484-495.	5.9	577
10	MOLECULAR GENETIC ANALYSES OF MICROSPOROGENESIS AND MICROGAMETOGENESIS IN FLOWERING PLANTS. Annual Review of Plant Biology, 2005, 56, 393-434.	18.7	572
11	Plasmid construction by homologous recombination in yeast. Gene, 1987, 58, 201-216.	2.2	569
12	Genome-Wide Analysis of Basic/Helix-Loop-Helix Transcription Factor Family in Rice and Arabidopsis. Plant Physiology, 2006, 141, 1167-1184.	4.8	527
13	Ectopic expression of the floral homeotic gene AGAMOUS in transgenic Arabidopsis plants alters floral organ identity. Cell, 1992, 71, 119-131.	28.9	467
14	Identification of an SCF ubiquitin-ligase complex required for auxin response in Arabidopsis thaliana. Genes and Development, 1999, 13, 1678-1691.	5.9	454
15	The EXCESS MICROSPOROCYTES1 gene encodes a putative leucine-rich repeat receptor protein kinase that controls somatic and reproductive cell fates in the Arabidopsis anther. Genes and Development, 2002, 16, 2021-2031.	5.9	439
16	Regulation of Arabidopsis tapetum development and function by DYSFUNCTIONAL TAPETUM1 (DYT1) encoding a putative bHLH transcription factor. Development (Cambridge), 2006, 133, 3085-3095.	2.5	400
17	Patterns of gene duplication in the plant SKP1 gene family in angiosperms: evidence for multiple mechanisms of rapid gene birth. Plant Journal, 2007, 50, 873-885.	5.7	361
18	The Evolution of the SEPALLATA Subfamily of MADS-Box GenesSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY850178, AY850179, AY850180, AY850181, AY850182, AY850183, AY850184, AY850185, AY850186.. Genetics, 2005, 169, 2209-2223.	2.9	343

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19	The Arabidopsis AtRAD51 gene is dispensable for vegetative development but required for meiosis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10596-10601.	7.1	286
20	Expression Pattern Shifts Following Duplication Indicative of Subfunctionalization and Neofunctionalization in Regulatory Genes of Arabidopsis. Molecular Biology and Evolution, 2006, 23, 469-478.	8.9	273
21	Brassinosteroids control male fertility by regulating the expression of key genes involved in Arabidopsis anther and pollen development. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6100-6105.	7.1	269
22	Origins and evolution of the recA/RAD51 gene family: Evidence for ancient gene duplication and endosymbiotic gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10328-10333.	7.1	268
23	Evolution of F-box genes in plants: Different modes of sequence divergence and their relationships with functional diversification. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 835-840.	7.1	268
24	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. Molecular Biology and Evolution, 2016, 33, 394-412.	8.9	259
25	Carbon Starved AntherEncodes a MYB Domain Protein That Regulates Sugar Partitioning Required for Rice Pollen Development Â. Plant Cell, 2010, 22, 672-689.	6.6	255
26	Genome-Wide Analysis of the Cyclin Family in Arabidopsis and Comparative Phylogenetic Analysis of Plant Cyclin-Like Proteins. Plant Physiology, 2004, 135, 1084-1099.	4.8	252
27	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Molecular Plant, 2018, 11, 414-428.	8.3	251
28	Expression of floral MADS-box genes in basal angiosperms: implications for the evolution of floral regulators. Plant Journal, 2005, 43, 724-744.	5.7	247
29	Manipulation of flower structure in transgenic tobacco. Cell, 1992, 71, 133-143.	28.9	244
30	The water lily genome and the early evolution of flowering plants. Nature, 2020, 577, 79-84.	27.8	238
31	The BAM1/BAM2 Receptor-Like Kinases Are Important Regulators of Arabidopsis Early Anther Development. Plant Cell, 2006, 18, 1667-1680.	6.6	226
32	Defective Pollen WallIs Required for Anther and Microspore Development in Rice and Encodes a Fatty Acyl Carrier Protein Reductase Â Â. Plant Cell, 2011, 23, 2225-2246.	6.6	226
33	Arabidopsis MALE STERILITY1 Encodes a PHD-Type Transcription Factor and Regulates Pollen and Tapetum Development. Plant Cell, 2007, 19, 3549-3562.	6.6	218
34	Type I MADS-box genes have experienced faster birth-and-death evolution than type II MADS-box genes in angiosperms. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1910-1915.	7.1	209
35	The NAC Family Transcription Factor OsNAP Confers Abiotic Stress Response Through the ABA Pathway. Plant and Cell Physiology, 2014, 55, 604-619.	3.1	207
36	The hornwort genome and early land plant evolution. Nature Plants, 2020, 6, 107-118.	9.3	203

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37	Evolution of Rosaceae Fruit Types Based on Nuclear Phylogeny in the Context of Geological Times and Genome Duplication. Molecular Biology and Evolution, 2017, 34, msw242.	8.9	200
38	The FLORAL ORGAN NUMBER4 Gene Encoding a Putative Ortholog of Arabidopsis CLAVATA3 Regulates Apical Meristem Size in Rice. Plant Physiology, 2006, 142, 1039-1052.	4.8	198
39	Specific interactions between the K domains of AG and AGLs, members of the MADS domain family of DNA binding proteins. Plant Journal, 1997, 12, 999-1010.	5.7	196
40	A mitogen-activated protein kinase of the corn leaf pathogen Cochliobolus heterostrophus is involved in conidiation, appressorium formation, and pathogenicity: Diverse roles for mitogen-activated protein kinase homologs in foliar pathogens. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 13542-13547.	7.1	192
41	Highly conserved lowâ€copy nuclear genes as effective markers for phylogenetic analyses in angiosperms. New Phytologist, 2012, 195, 923-937.	7.3	192
42	The unfolding drama of flower development: recent results from genetic and molecular analyses.. Genes and Development, 1994, 8, 745-756.	5.9	189
43	The Arabidopsis SKP1-LIKE1 gene is essential for male meiosis and may control homologue separation. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11416-11421.	7.1	184
44	Isolation of cDNAs encoding guanine nucleotide-binding protein beta-subunit homologues from maize (ZGB1) and Arabidopsis (AGB1).. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 9554-9558.	7.1	182
45	Flower Development under Drought Stress: Morphological and Transcriptomic Analyses Reveal Acute Responses and Long-Term Acclimation in Arabidopsis. Plant Cell, 2013, 25, 3785-3807.	6.6	176
46	Conservation and divergence in the AGAMOUS subfamily of MADS-box genes: evidence of independent sub- and neofunctionalization events. Evolution & Development, 2006, 8, 30-45.	2.0	172
47	The ABCs of Floral Evolution. Cell, 2000, 101, 5-8.	28.9	171
48	Plant fertility defects induced by the enhanced expression of microRNA167. Cell Research, 2006, 16, 457-465.	12.0	167
49	To B or Not to B a Flower: The Role of DEFICIENS and GLOBOSA Orthologs in the Evolution of the Angiosperms. Journal of Heredity, 2005, 96, 225-240.	2.4	166
50	Spatially and temporally regulated expression of the MADS-box gene AGL2 in wild-type and mutant arabidopsis flowers. Plant Molecular Biology, 1994, 26, 581-595.	3.9	156
51	Multiple Polyploidization Events across Asteraceae with Two Nested Events in the Early History Revealed by Nuclear Phylogenomics. Molecular Biology and Evolution, 2016, 33, 2820-2835.	8.9	149
52	Homolog interaction during meiotic prophase I in Arabidopsis requires the SOLO DANCERS gene encoding a novel cyclin-like protein. EMBO Journal, 2002, 21, 3081-3095.	7.8	148
53	Isolation and characterization of the binding sequences for the product of the Arabidopsis floral homeotic geneAGAMOUS. Nucleic Acids Research, 1993, 21, 4769-4776.	14.5	146
54	Arabidopsis TOE proteins convey a photoperiodic signal to antagonize CONSTANS and regulate flowering time. Genes and Development, 2015, 29, 975-987.	5.9	140

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55	Regulation of the Arabidopsis anther transcriptome by DYT1 for pollen development. Plant Journal, 2012, 72, 612-624.	5.7	138
56	Missing links: the genetic architecture of flower and floral diversification. Trends in Plant Science, 2002, 7, 22-31.	8.8	136
57	The <scp>DYT</scp>1â€interacting proteins b<scp>HLH</scp>010, b<scp>HLH</scp>089 and b<scp>HLH</scp>091 are redundantly required for <scp>A</scp>rabidopsis anther development and transcriptome. Plant Journal, 2015, 83, 976-990.	5.7	136
58	The transcriptome landscape of Arabidopsis male meiocytes from highâ€throughput sequencing: the complexity and evolution of the meiotic process. Plant Journal, 2011, 65, 503-516.	5.7	135
59	Regulation of Arabidopsis Early Anther Development by the Mitogen-Activated Protein Kinases, MPK3 and MPK6, and the ERECTA and Related Receptor-Like Kinases. Molecular Plant, 2008, 1, 645-658.	8.3	134
60	Resolution of deep eudicot phylogeny and their temporal diversification using nuclear genes from transcriptomic and genomic datasets. New Phytologist, 2017, 214, 1338-1354.	7.3	134
61	The Arabidopsis MADS-box gene AGL3 is widely expressed and encodes a sequence-specific DNA-binding protein. Plant Molecular Biology, 1995, 28, 549-567.	3.9	132
62	Dual Role of BKI1 and 14-3-3Âs in Brassinosteroid Signaling to Link Receptor with Transcription Factors. Developmental Cell, 2011, 21, 825-834.	7.0	130
63	AtPRK2 Promotes ROP1 Activation via RopGEFs in the Control of Polarized Pollen Tube Growth. Molecular Plant, 2013, 6, 1187-1201.	8.3	130
64	Tissue-Specific Transcriptomics Reveals an Important Role of the Unfolded Protein Response in Maintaining Fertility upon Heat Stress in Arabidopsis. Plant Cell, 2017, 29, 1007-1023.	6.6	130
65	Evolution of the RNA-dependent RNA polymerase (RdRP) genes: Duplications and possible losses before and after the divergence of major eukaryotic groups. Gene, 2009, 447, 29-39.	2.2	125
66	Analysis of Arabidopsis genome-wide variations before and after meiosis and meiotic recombination by resequencing Landsberg erecta and all four products of a single meiosis. Genome Research, 2012, 22, 508-518.	5.5	125
67	Antiquity and Evolution of the MADS-Box Gene Family Controlling Flower Development in Plants. Molecular Biology and Evolution, 2003, 20, 1435-1447.	8.9	122
68	Genome-Wide Comparative Analysis and Expression Pattern of TCP Gene Families in Arabidopsis thaliana and Oryza sativa. Journal of Integrative Plant Biology, 2007, 49, 885-897.	8.5	121
69	The ASK1 and ASK2 Genes Are Essential for Arabidopsis Early Development. Plant Cell, 2004, 16, 5-20.	6.6	117
70	Separation of AG function in floral meristem determinacy from that in reproductive organ identity by expressing antisense AG RNA. Plant Molecular Biology, 1995, 28, 767-784.	3.9	114
71	The Arabidopsis ROCKâ€Nâ€ROLLERS gene encodes a homolog of the yeast ATPâ€dependent DNA helicase MER3 and is required for normal meiotic crossover formation. Plant Journal, 2005, 43, 321-334.	5.7	113
72	Os<scp>NAC</scp>2 encoding a <scp>NAC</scp> transcription factor that affects plant height through mediating the gibberellic acid pathway in rice. Plant Journal, 2015, 82, 302-314.	5.7	110

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73	Members of the Arabidopsis-SKP1-like Gene Family Exhibit a Variety of Expression Patterns and May Play Diverse Roles in Arabidopsis. Plant Physiology, 2003, 133, 203-217.	4.8	108
74	Reverse breeding: a novel breeding approach based on engineered meiosis. Plant Biotechnology Journal, 2009, 7, 837-845.	8.3	108
75	Optimized IMACâ˜IMAC Protocol for Phosphopeptide Recovery from Complex Biological Samples. Journal of Proteome Research, 2010, 9, 3561-3573.	3.7	106
76	The floral genome: an evolutionary history of gene duplication and shifting patterns of gene expression. Trends in Plant Science, 2007, 12, 358-367.	8.8	103
77	Specific expression of the AGL1 MADS-box gene suggests regulatory functions in Arabidopsis gynoecium and ovule development. Plant Journal, 1996, 10, 343-353.	5.7	101
78	The rice OsDIL gene plays a role in drought tolerance at vegetative and reproductive stages. Plant Molecular Biology, 2013, 82, 239-253.	3.9	100
79	Rice Male Development under Drought Stress: Phenotypic Changes and Stage-Dependent Transcriptomic Reprogramming. Molecular Plant, 2013, 6, 1630-1645.	8.3	99
80	Differential gene expression in Arabidopsis wildâ€type and mutant anthers: insights into anther cell differentiation and regulatory networks. Plant Journal, 2007, 52, 14-29.	5.7	98
81	Characterization of a novel putative zinc finger geneMIF1: involvement in multiple hormonal regulation of Arabidopsis development. Plant Journal, 2006, 45, 399-422.	5.7	94
82	The origins and early evolution of DNA mismatch repair genesâ€"multiple horizontal gene transfers and co-evolution. Nucleic Acids Research, 2007, 35, 7591-7603.	14.5	94
83	Arabidopsis GenesAS1,AS2, andJAGNegatively Regulate Boundary-Specifying Genes to Promote Sepal and Petal Development. Plant Physiology, 2008, 146, 323-324.	4.8	93
84	TheASK1 gene regulates development and interacts with theUFO gene to control floral organ identity inArabidopsis. , 1999, 25, 209-223.		92
85	Feedback Regulation of DYT1 by Interactions with Downstream bHLH Factors Promotes DYT1 Nuclear Localization and Anther Development. Plant Cell, 2016, 28, 1078-1093.	6.6	92
86	Phylotranscriptomics in Cucurbitaceae Reveal Multiple Whole-Genome Duplications and Key Morphological and Molecular Innovations. Molecular Plant, 2020, 13, 1117-1133.	8.3	89
87	The plant WNK gene family and regulation of flowering time in Arabidopsis. Plant Biology, 2008, 10, 548-562.	3.8	88
88	Evolution of Plant MADS Box Transcription Factors: Evidence for Shifts in Selection Associated with Early Angiosperm Diversification and Concerted Gene Duplications. Molecular Biology and Evolution, 2009, 26, 2229-2244.	8.9	88
89	Molecular control of microsporogenesis in Arabidopsis. Current Opinion in Plant Biology, 2011, 14, 66-73.	7.1	88
90	Nuclear phylotranscriptomics and phylogenomics support numerous polyploidization events and hypotheses for the evolution of rhizobial nitrogen-fixing symbiosis in Fabaceae. Molecular Plant, 2021, 14, 748-773.	8.3	86

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91	The Arabidopsis CALLOSE DEFECTIVE MICROSPORE1 Gene Is Required for Male Fertility through Regulating Callose Metabolism during Microsporogenesis. Plant Physiology, 2014, 164, 1893-1904.	4.8	85
92	Identification, sequence analysis and expression studies of novel anther-specific genes of Arabidopsis thaliana. Plant Molecular Biology, 1998, 37, 607-619.	3.9	84
93	Phylogenetic Analysis of the Plantâ€specificZinc Fingerâ€HomeoboxandMini Zinc FingerGene Families. Journal of Integrative Plant Biology, 2008, 50, 1031-1045.	8.5	82
94	The AWPM-19 Family Protein OsPM1 Mediates Abscisic Acid Influx and Drought Response in Rice. Plant Cell, 2018, 30, 1258-1276.	6.6	82
95	Asterid Phylogenomics/Phylotranscriptomics Uncover Morphological Evolutionary Histories and Support Phylogenetic Placement for Numerous Whole-Genome Duplications. Molecular Biology and Evolution, 2020, 37, 3188-3210.	8.9	82
96	A well-resolved fern nuclear phylogeny reveals the evolution history of numerous transcription factor families. Molecular Phylogenetics and Evolution, 2018, 127, 961-977.	2.7	80
97	Wholeâ€genome DNA methylation patterns and complex associations with gene structure and expression during flower development in Arabidopsis. Plant Journal, 2015, 81, 268-281.	5.7	76
98	Stable and dynamic nucleosome states during a meiotic developmental process. Genome Research, 2011, 21, 875-884.	5.5	75
99	The DNA Replication Factor RFC1 Is Required for Interference-Sensitive Meiotic Crossovers in Arabidopsis thaliana. PLoS Genetics, 2012, 8, e1003039.	3.5	75
100	Development of Flowering Plant Gametophytes. Current Topics in Developmental Biology, 2010, 91, 379-412.	2.2	73
101	Regulation of Flower Development in Arabidopsis by SCF Complexes. Plant Physiology, 2004, 134, 1574-1585.	4.8	69
102	Gene duplications and phylogenomic conflict underlie major pulses of phenotypic evolution in gymnosperms. Nature Plants, 2021, 7, 1015-1025.	9.3	68
103	The Amborella genome: an evolutionary reference for plant biology. Genome Biology, 2008, 9, 402.	9.6	67
104	Expansion and Functional Divergence of Jumonji C-Containing Histone Demethylases: Significance of Duplications in Ancestral Angiosperms and Vertebrates. Plant Physiology, 2015, 168, 1321-1337.	4.8	67
105	Genome-wide expression profiling and identification of gene activities during early flower development in Arabidopsis. Plant Molecular Biology, 2005, 58, 401-419.	3.9	65
106	Complex evolutionary history and diverse domain organization of SET proteins suggest divergent regulatory interactions. New Phytologist, 2012, 195, 248-263.	7.3	65
107	Proteomic and phosphoproteomic analyses reveal extensive phosphorylation of regulatory proteins in developing rice anthers. Plant Journal, 2015, 84, 527-544.	5.7	62
108	The Compositae Tree of Life in the age of phylogenomics. Journal of Systematics and Evolution, 2017, 55, 405-410.	3.1	61

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109	Signaling and Transcriptional Control ofÂReproductive Development in Arabidopsis. Current Biology, 2010, 20, R988-R997.	3.9	60
110	Elevated temperature increases meiotic crossover frequency via the interfering (Type I) pathway in Arabidopsis thaliana. PLoS Genetics, 2018, 14, e1007384.	3.5	60
111	OsERF101, an ERF family transcription factor, regulates drought stress response in reproductive tissues. Plant Molecular Biology, 2018, 98, 51-65.	3.9	59
112	Deep mRNA Sequencing Analysis to Capture the Transcriptome Landscape of Zebrafish Embryos and Larvae. PLoS ONE, 2013, 8, e64058.	2.5	57
113	Detection of genomic variations and DNA polymorphisms and impact on analysis of meiotic recombination and genetic mapping. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10007-10012.	7.1	55
114	Arabidopsis Cell Division Cycle 20.1 Is Required for Normal Meiotic Spindle Assembly and Chromosome Segregation. Plant Cell, 2015, 27, 3367-3382.	6.6	55
115	Phylotranscriptomic insights into Asteraceae diversity, polyploidy, and morphological innovation. Journal of Integrative Plant Biology, 2021, 63, 1273-1293.	8.5	55
116	Stimulated Raman scattering microscopy and spectroscopy with a rapid scanning optical delay line. Optics Letters, 2017, 42, 659.	3.3	52
117	To be, or not to be, a flower â€" control of floral meristem identity. Trends in Genetics, 1998, 14, 26-32.	6.7	51
118	Towards a comprehensive integration of morphological and genetic studies of floral development. Trends in Plant Science, 2004, 9, 164-173.	8.8	51
119	Double-stranded DNA breaks and gene functions in recombination and meiosis. Cell Research, 2006, 16, 402-412.	12.0	51
120	Phosphorylation of SPOROCYTELESS/NOZZLE by the MPK3/6 Kinase Is Required for Anther Development. Plant Physiology, 2017, 173, 2265-2277.	4.8	51
121	The soybean root-specific protein kinase GmWNK1 regulates stress-responsive ABA signaling on the root system architecture. Plant Journal, 2010, 64, 230-242.	5.7	50
122	SKP1 is involved in abscisic acid signalling to regulate seed germination, stomatal opening and root growth in Arabidopsis thaliana. Plant, Cell and Environment, 2012, 35, 952-965.	5.7	50
123	TheArabidopsis SKP1homologASK1controls meiotic chromosome remodeling and release of chromatin from the nuclear membrane and nucleolus. Journal of Cell Science, 2006, 119, 3754-3763.	2.0	49
124	Comprehensive Analysis of Genic Male Sterility-Related Genes in Brassica rapa Using a Newly Developed Br300K Oligomeric Chip. PLoS ONE, 2013, 8, e72178.	2.5	49
125	MID1 plays an important role in response to drought stress during reproductive development. Plant Journal, 2016, 88, 280-293.	5.7	49
126	A well-supported nuclear phylogeny of Poaceae and implications for the evolution of C4 photosynthesis. Molecular Plant, 2022, 15, 755-777.	8.3	47

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127	The Arabidopsis thaliana DSB formation (AtDFO) gene is required for meiotic doubleâ€strand break formation. Plant Journal, 2012, 72, 271-281.	5.7	46
128	The PHD Finger Protein MMD1/DUET Ensures the Progression of Male Meiotic Chromosome Condensation and Directly Regulates the Expression of the Condensin Gene CAP-D3. Plant Cell, 2016, 28, 1894-1909.	6.6	46
129	Alternative splicing during Arabidopsis flower development results in constitutive and stage-regulated isoforms. Frontiers in Genetics, 2014, 5, 25.	2.3	45
130	Isolation, sequence analysis, and expression studies of florally expressed cDNAs in Arabidopsis. Plant Molecular Biology, 2003, 53, 545-563.	3.9	43
131	ASK1, a SKP1 homolog, is required for nuclear reorganization, presynaptic homolog juxtaposition and the proper distribution of cohesin during meiosis in Arabidopsis. Plant Molecular Biology, 2006, 62, 99-110.	3.9	43
132	Recurrent genome duplication events likely contributed to both the ancient and recent rise of ferns. Journal of Integrative Plant Biology, 2020, 62, 433-455.	8.5	43
133	The G protein Î± subunit (GPÎ±1) is associated with the ER and the plasma membrane in meristematic cells ofArabidopsisand cauliflower. FEBS Letters, 1997, 407, 361-367.	2.8	42
134	Conservation and divergence of ASK1 and ASK2 gene functions during male meiosis in Arabidopsis thaliana. Plant Molecular Biology, 2003, 53, 163-173.	3.9	42
135	Protein phosphorylation in plants: enzymes, substrates and regulators. Trends in Genetics, 1993, 9, 228-230.	6.7	39
136	Regulated Expression of the Arabidopsis G Protein Î± Subunit Gene GPA1. International Journal of Plant Sciences, 1994, 155, 3-14.	1.3	39
137	EST database for early flower development in California poppy (Eschscholzia californica Cham.,) Tj ETQq1 1 0.784314 rgBT /Overlock	3.9	38
138	AMS-dependent and independent regulation of anther transcriptome and comparison with those affected by other Arabidopsis anther genes. BMC Plant Biology, 2012, 12, 23.	3.6	38
139	Moderate drought causes dramatic floral transcriptomic reprogramming to ensure successful reproductive development in Arabidopsis. BMC Plant Biology, 2014, 14, 164.	3.6	38
140	Phylogenomic analyses of large-scale nuclear genes provide new insights into the evolutionary relationships within the rosids. Molecular Phylogenetics and Evolution, 2016, 105, 166-176.	2.7	38
141	Molecular genetic analyses of abiotic stress responses during plant reproductive development. Journal of Experimental Botany, 2020, 71, 2870-2885.	4.8	38
142	The <scp>A</scp>rabidopsis <scp>RAD</scp>51 paralogs <scp>RAD</scp>51B,<scp>RAD</scp>51<scp>D</scp> and <scp>XRCC</scp>2 play partially redundant roles in somatic <scp>DNA</scp> repair and gene regulation. New Phytologist, 2014, 201, 292-304.	7.3	37
143	Meiocyte-Specific and AtSPO11-1â€“Dependent Small RNAs and Their Association with Meiotic Gene Expression and Recombination. Plant Cell, 2019, 31, 444-464.	6.6	37
144	Arabidopsis RAD51, RAD51C and XRCC3 proteins form a complex and facilitate RAD51 localization on chromosomes for meiotic recombination. PLoS Genetics, 2017, 13, e1006827.	3.5	37

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145	Cell Biological Characterization of Male Meiosis and Pollen Development in Rice. Journal of Integrative Plant Biology, 2005, 47, 734-744.	8.5	34
146	Functional divergence of the duplicated AtKIN14a and AtKIN14b genes: critical roles in Arabidopsis meiosis and gametophyte development. Plant Journal, 2008, 53, 1013-1026.	5.7	34
147	Abundant protein phosphorylation potentially regulates Arabidopsis anther development. Journal of Experimental Botany, 2016, 67, 4993-5008.	4.8	34
148	Functional conservation of the meiotic genes SDS and RCK in male meiosis in the monocot rice. Cell Research, 2009, 19, 768-782.	12.0	33
149	CbCBF from Capsella bursa-pastoris enhances cold tolerance and restrains growth in Nicotiana tabacum by antagonizing with gibberellin and affecting cell cycle signaling. Plant Molecular Biology, 2014, 85, 259-275.	3.9	33
150	Stepâ€wise and lineageâ€specific diversification of plant <scp>RNA</scp> polymerase genes and origin of the largest plantâ€specific subunits. New Phytologist, 2015, 207, 1198-1212.	7.3	32
151	An EST database for Liriodendron tulipifera L. floral buds: the first EST resource for functional and comparative genomics in Liriodendron. Tree Genetics and Genomes, 2008, 4, 419-433.	1.6	31
152	Phylogenetic Resolution of Deep Eukaryotic and Fungal Relationships Using Highly Conserved Low-Copy Nuclear Genes. Genome Biology and Evolution, 2016, 8, 2683-2701.	2.5	31
153	BKI1 Regulates Plant Architecture through Coordinated Inhibition of the Brassinosteroid and ERECTA Signaling Pathways in Arabidopsis. Molecular Plant, 2017, 10, 297-308.	8.3	31
154	Phylotranscriptomics Resolves the Phylogeny of Pooideae and Uncovers Factors for Their Adaptive Evolution. Molecular Biology and Evolution, 2022, 39, .	8.9	31
155	Vectors for plant transformation and cosmid libraries. Gene, 1992, 117, 161-167.	2.2	30
156	Proteomic analysis of lysine acetylation provides strong evidence for involvement of acetylated proteins in plant meiosis and tapetum function. Plant Journal, 2018, 93, 142-154.	5.7	30
157	Orderâ€level fern plastome phylogenomics: new insights from Hymenophyllales. American Journal of Botany, 2018, 105, 1545-1555.	1.7	30
158	Comparative Analysis of Proteome-Wide Lysine Acetylation in Juvenile and Adult Schistosoma japonicum. Frontiers in Microbiology, 2017, 8, 2248.	3.5	29
159	The Largest Subunit of DNA Polymerase Delta Is Required for Normal Formation of Meiotic Type I Crossovers. Plant Physiology, 2019, 179, 446-459.	4.8	29
160	A terminator of floral stem cells: Figure 1.. Genes and Development, 2009, 23, 1705-1708.	5.9	28
161	Lys-C/Arg-C, a More Specific and Efficient Digestion Approach for Proteomics Studies. Analytical Chemistry, 2018, 90, 9700-9707.	6.5	28
162	Plant G proteins: The different faces of GPA1. Current Biology, 2001, 11, R869-R871.	3.9	27

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163	The GAOLAOZHUANGREN1 Gene Encodes a Putative Glycosyltransferase that is Critical for Normal Development and Carbohydrate Metabolism. Plant and Cell Physiology, 2004, 45, 1453-1460.	3.1	27
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