

Motoaki Seki

List of Publications by Year in descending order

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303
papers

46,791
citations

2203

99
h-index

1895

208
g-index

310
all docs

310
docs citations

310
times ranked

28843
citing authors

#	ARTICLE	IF	CITATIONS
1	Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) Function as Transcriptional Activators in Abscisic Acid Signaling. <i>Plant Cell</i> , 2003, 15, 63-78.	3.1	1,905
2	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. <i>Plant Journal</i> , 2002, 31, 279-292.	2.8	1,697
3	Regulatory network of gene expression in the drought and cold stress responses. <i>Current Opinion in Plant Biology</i> , 2003, 6, 410-417.	3.5	1,616
4	OsDREB genes in rice, <i>Oryza sativa</i> L., encode transcription activators that function in drought-, high-salt- and cold-responsive gene expression. <i>Plant Journal</i> , 2003, 33, 751-763.	2.8	1,482
5	Isolation and Functional Analysis of Arabidopsis Stress-Inducible NAC Transcription Factors That Bind to a Drought-Responsive cis-Element in the early responsive to dehydration stress 1 Promoter[W]. <i>Plant Cell</i> , 2004, 16, 2481-2498.	3.1	1,329
6	Regulation of drought tolerance by gene manipulation of 9-cis-epoxycarotenoid dioxygenase, a key enzyme in abscisic acid biosynthesis in Arabidopsis. <i>Plant Journal</i> , 2001, 27, 325-333.	2.8	1,138
7	Important roles of drought- and cold-inducible genes for galactinol synthase in stress tolerance in Arabidopsis thaliana. <i>Plant Journal</i> , 2002, 29, 417-426.	2.8	1,002
8	Monitoring the Expression Pattern of 1300 Arabidopsis Genes under Drought and Cold Stresses by Using a Full-Length cDNA Microarray. <i>Plant Cell</i> , 2001, 13, 61-72.	3.1	986
9	Functional Analysis of an Arabidopsis Transcription Factor, DREB2A, Involved in Drought-Responsive Gene Expression. <i>Plant Cell</i> , 2006, 18, 1292-1309.	3.1	968
10	Monitoring Expression Profiles of Rice Genes under Cold, Drought, and High-Salinity Stresses and Abscisic Acid Application Using cDNA Microarray and RNA Gel-Blot Analyses. <i>Plant Physiology</i> , 2003, 133, 1755-1767.	2.3	906
11	A dehydration-induced NAC protein, RD26, is involved in a novel ABA-dependent stress-signaling pathway. <i>Plant Journal</i> , 2004, 39, 863-876.	2.8	877
12	Identification of CRE1 as a cytokinin receptor from Arabidopsis. <i>Nature</i> , 2001, 409, 1060-1063.	13.7	854
13	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
14	Functional Analysis of Rice DREB1/CBF-type Transcription Factors Involved in Cold-responsive Gene Expression in Transgenic Rice. <i>Plant and Cell Physiology</i> , 2006, 47, 141-153.	1.5	853
15	AREB1 Is a Transcription Activator of Novel ABRE-Dependent ABA Signaling That Enhances Drought Stress Tolerance in Arabidopsis. <i>Plant Cell</i> , 2005, 17, 3470-3488.	3.1	826
16	Regulatory metabolic networks in drought stress responses. <i>Current Opinion in Plant Biology</i> , 2007, 10, 296-302.	3.5	761
17	NAC Transcription Factors, NST1 and NST3, Are Key Regulators of the Formation of Secondary Walls in Woody Tissues of Arabidopsis. <i>Plant Cell</i> , 2007, 19, 270-280.	3.1	739
18	The NAC Transcription Factors NST1 and NST2 of Arabidopsis Regulate Secondary Wall Thickenings and Are Required for Anther Dehiscence. <i>Plant Cell</i> , 2005, 17, 2993-3006.	3.1	632

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19	Functional Annotation of a Full-Length Arabidopsis cDNA Collection. <i>Science</i> , 2002, 296, 141-145.	6.0	631
20	Derepression of ethylene-stabilized transcription factors (EIN3/EIL1) mediates jasmonate and ethylene signaling synergy in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12539-12544.	3.3	622
21	In planta functions of the Arabidopsis cytokinin receptor family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8821-8826.	3.3	610
22	Positive regulatory role of strigolactone in plant responses to drought and salt stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 851-856.	3.3	555
23	Identification of cold-inducible downstream genes of the Arabidopsis DREB1A/CBF3 transcriptional factor using two microarray systems. <i>Plant Journal</i> , 2004, 38, 982-993.	2.8	546
24	Comparative Genomics in Salt Tolerance between Arabidopsis and Arabidopsis-Related Halophyte Salt Cress Using Arabidopsis Microarray. <i>Plant Physiology</i> , 2004, 135, 1697-1709.	2.3	542
25	A Transmembrane Hybrid-Type Histidine Kinase in Arabidopsis Functions as an Osmosensor. <i>Plant Cell</i> , 1999, 11, 1743-1754.	3.1	501
26	Omics analyses of regulatory networks in plant abiotic stress responses. <i>Current Opinion in Plant Biology</i> , 2010, 13, 132-138.	3.5	477
27	Arabidopsis Transcriptome Analysis under Drought, Cold, High-Salinity and ABA Treatment Conditions using a Tiling Array. <i>Plant and Cell Physiology</i> , 2008, 49, 1135-1149.	1.5	475
28	Antagonistic Interaction between Systemic Acquired Resistance and the Abscisic Acid-Mediated Abiotic Stress Response in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 1678-1692.	3.1	465
29	Molecular responses to drought, salinity and frost: common and different paths for plant protection. <i>Current Opinion in Biotechnology</i> , 2003, 14, 194-199.	3.3	417
30	Two different novel cis-acting elements of <i>erd1</i> , a homologous Arabidopsis gene function in induction by dehydration stress and dark-induced senescence. <i>Plant Journal</i> , 2003, 33, 259-270.	2.8	402
31	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. <i>Functional and Integrative Genomics</i> , 2002, 2, 282-291.	1.4	394
32	Arabidopsis HsfA1 transcription factors function as the main positive regulators in heat shock-responsive gene expression. <i>Molecular Genetics and Genomics</i> , 2011, 286, 321-332.	1.0	377
33	The AP2/ERF Transcription Factor WIND1 Controls Cell Dedifferentiation in Arabidopsis. <i>Current Biology</i> , 2011, 21, 508-514.	1.8	369
34	Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. <i>Frontiers in Plant Science</i> , 2015, 6, 114.	1.7	367
35	Organization and expression of two Arabidopsis DREB2 genes encoding DRE-binding proteins involved in dehydration- and high-salinity-responsive gene expression. <i>Plant Molecular Biology</i> , 2000, 42, 657-665.	2.0	341
36	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and Arabidopsis thaliana: Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.	3.3	341

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37	TCP Transcription Factors Regulate the Activities of ASYMMETRIC LEAVES1 and miR164, as Well as the Auxin Response, during Differentiation of Leaves in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 3574-3588.	3.1	335
38	Epigenetic Memory for Stress Response and Adaptation in Plants. <i>Plant and Cell Physiology</i> , 2014, 55, 1859-1863.	1.5	321
39	Leucine-Rich Repeat Receptor-Like Kinase1 Is a Key Membrane-Bound Regulator of Abscisic Acid Early Signaling in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2005, 17, 1105-1119.	3.1	313
40	An <i>Arabidopsis</i> Gene Family Encoding DRE/CRT Binding Proteins Involved in Low-Temperature-Responsive Gene Expression. <i>Biochemical and Biophysical Research Communications</i> , 1998, 250, 161-170.	1.0	309
41	Alterations of Lysine Modifications on the Histone H3 N-Tail under Drought Stress Conditions in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2008, 49, 1580-1588.	1.5	308
42	CYP707A3, a major ABA 8 α -hydroxylase involved in dehydration and rehydration response in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2006, 46, 171-182.	2.8	294
43	Transcriptional Regulation of ABI3- and ABA-responsive Genes Including RD29B and RD29A in Seeds, Germinating Embryos, and Seedlings of <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2006, 60, 51-68.	2.0	293
44	A Novel Zinc-binding Motif Revealed by Solution Structures of DNA-binding Domains of <i>Arabidopsis</i> SBP-family Transcription Factors. <i>Journal of Molecular Biology</i> , 2004, 337, 49-63.	2.0	267
45	Monitoring expression profiles of <i>Arabidopsis</i> gene expression during rehydration process after dehydration using ca. 7000 full-length cDNA microarray. <i>Plant Journal</i> , 2003, 34, 868-887.	2.8	263
46	Specific interactions between Dicer-like proteins and HYL1/DRB- family dsRNA-binding proteins in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2005, 57, 173-188.	2.0	259
47	Plants Tolerant of High Boron Levels. <i>Science</i> , 2007, 318, 1417-1417.	6.0	256
48	Drought tolerance established by enhanced expression of the CC-NBS-LRR gene, ADR1, requires salicylic acid, EDS1 and ABI1. <i>Plant Journal</i> , 2004, 38, 810-822.	2.8	253
49	The FOX hunting system: an alternative gain-of-function gene hunting technique. <i>Plant Journal</i> , 2006, 48, 974-985.	2.8	244
50	Genome-wide analysis of alternative pre-mRNA splicing in <i>Arabidopsis thaliana</i> based on full-length cDNA sequences. <i>Nucleic Acids Research</i> , 2004, 32, 5096-5103.	6.5	235
51	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017, 3, 17097.	4.7	232
52	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013, 18, 267-276.	4.3	229
53	Crosstalk in the responses to abiotic and biotic stresses in <i>Arabidopsis</i> : Analysis of gene expression in cytochrome P450 gene superfamily by cDNA microarray. <i>Plant Molecular Biology</i> , 2004, 55, 327-342.	2.0	225
54	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218

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55	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. <i>Plant Journal</i> , 1998, 15, 707-720.	2.8	217
56	High Humidity Induces Abscisic Acid 8â€²-Hydroxylase in Stomata and Vasculature to Regulate Local and Systemic Abscisic Acid Responses in Arabidopsis. <i>Plant Physiology</i> , 2009, 149, 825-834.	2.3	216
57	Transition of Chromatin Status During the Process of Recovery from Drought Stress in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2012, 53, 847-856.	1.5	208
58	Chromatin regulation functions in plant abiotic stress responses. <i>Plant, Cell and Environment</i> , 2010, 33, 604-611.	2.8	194
59	Identification of Arabidopsis Genes Regulated by High Lightâ€“Stress Using cDNA Microarray. <i>Photochemistry and Photobiology</i> , 2003, 77, 226.	1.3	193
60	Characterization of Arabidopsis genes involved in biosynthesis of polyamines in abiotic stress responses and developmental stages. <i>Plant, Cell and Environment</i> , 2003, 26, 1917-1926.	2.8	191
61	<i>Arabidopsis</i> AHP2, AHP3, and AHP5 histidine phosphotransfer proteins function as redundant negative regulators of drought stress response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4840-4845.	3.3	191
62	Vacuolar Processing Enzymes Are Essential for Proper Processing of Seed Storage Proteins in Arabidopsis thaliana. <i>Journal of Biological Chemistry</i> , 2003, 278, 32292-32299.	1.6	189
63	The Effect of Overexpression of Two Brassica CBF/DREB1-like Transcription Factors on Photosynthetic Capacity and Freezing Tolerance in Brassica napus. <i>Plant and Cell Physiology</i> , 2005, 46, 1525-1539.	1.5	186
64	<i>Arabidopsis</i> type B cytokinin response regulators ARR1, ARR10, and ARR12 negatively regulate plant responses to drought. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3090-3095.	3.3	186
65	Solution Structure of an Arabidopsis WRKY DNA Binding Domain. <i>Plant Cell</i> , 2005, 17, 944-956.	3.1	185
66	Small open reading frames associated with morphogenesis are hidden in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2395-2400.	3.3	178
67	Genome-wide suppression of aberrant mRNA-like noncoding RNAs by NMD in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2453-2458.	3.3	165
68	A single amino acid insertion in the WRKY domain of the Arabidopsis TIR-NBS-LRR-WRKY-type disease resistance protein SLH1 (sensitive to low humidity 1) causes activation of defense responses and hypersensitive cell death. <i>Plant Journal</i> , 2005, 43, 873-888.	2.8	164
69	Differential Gene Expression in Soybean Leaf Tissues at Late Developmental Stages under Drought Stress Revealed by Genome-Wide Transcriptome Analysis. <i>PLoS ONE</i> , 2012, 7, e49522.	1.1	162
70	Toxicity of Free Proline Revealed in an Arabidopsis T-DNA-Tagged Mutant Deficient in Proline Dehydrogenase. <i>Plant and Cell Physiology</i> , 2003, 44, 541-548.	1.5	161
71	ACTCAT, a Novel cis-Acting Element for Proline- and Hypoosmolarity-Responsive Expression of the ProDH Gene Encoding Proline Dehydrogenase in Arabidopsis. <i>Plant Physiology</i> , 2002, 130, 709-719.	2.3	159
72	Classification and Expression Analysis of Arabidopsis F-Box-Containing Protein Genes. <i>Plant and Cell Physiology</i> , 2002, 43, 1073-1085.	1.5	158

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73	DEAR1, a transcriptional repressor of DREB protein that mediates plant defense and freezing stress responses in Arabidopsis. <i>Journal of Plant Research</i> , 2009, 122, 633-643.	1.2	154
74	Arabidopsis HDA6 Regulates Locus-Directed Heterochromatin Silencing in Cooperation with MET1. <i>PLoS Genetics</i> , 2011, 7, e1002055.	1.5	148
75	Transcriptome Analyses of a Salt-Tolerant Cytokinin-Deficient Mutant Reveal Differential Regulation of Salt Stress Response by Cytokinin Deficiency. <i>PLoS ONE</i> , 2012, 7, e32124.	1.1	146
76	Identification of plant promoter constituents by analysis of local distribution of short sequences. <i>BMC Genomics</i> , 2007, 8, 67.	1.2	142
77	Group A PP2Cs evolved in land plants as key regulators of intrinsic desiccation tolerance. <i>Nature Communications</i> , 2013, 4, 2219.	5.8	142
78	The karrikin receptor KAI2 promotes drought resistance in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2017, 13, e1007076.	1.5	140
79	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
80	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. <i>Functional and Integrative Genomics</i> , 2006, 6, 212-234.	1.4	137
81	CNI1/ATL31, a RING-type ubiquitin ligase that functions in the carbon/nitrogen response for growth phase transition in Arabidopsis seedlings. <i>Plant Journal</i> , 2009, 60, 852-864.	2.8	135
82	Arabidopsis HDA6 is required for freezing tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 414-419.	1.0	133
83	Histone Modifications Form Epigenetic Regulatory Networks to Regulate Abiotic Stress Response. <i>Plant Physiology</i> , 2020, 182, 15-26.	2.3	132
84	Identification and Expression Analysis of Cytokinin Metabolic Genes in Soybean under Normal and Drought Conditions in Relation to Cytokinin Levels. <i>PLoS ONE</i> , 2012, 7, e42411.	1.1	132
85	Analysis of ABA Hypersensitive Germination2 revealed the pivotal functions of PARN in stress response in Arabidopsis. <i>Plant Journal</i> , 2005, 44, 972-984.	2.8	131
86	Monitoring the expression profiles of genes induced by hyperosmotic, high salinity, and oxidative stress and abscisic acid treatment in Arabidopsis cell culture using a full-length cDNA microarray. <i>Plant Molecular Biology</i> , 2004, 56, 29-55.	2.0	130
87	RARTF: Database and Tools for Complete Sets of Arabidopsis Transcription Factors. <i>DNA Research</i> , 2005, 12, 247-256.	1.5	130
88	Identifying the target genes of <i>SUPPRESSOR OF GAMMA RESPONSE</i> 1, a master transcription factor controlling DNA damage response in Arabidopsis. <i>Plant Journal</i> , 2018, 94, 439-453.	2.8	127
89	A Plant Locus Essential for Phylloquinone (Vitamin K1) Biosynthesis Originated from a Fusion of Four Eubacterial Genes*. <i>Journal of Biological Chemistry</i> , 2006, 281, 17189-17196.	1.6	126
90	RCH1, a Locus in Arabidopsis That Confers Resistance to the Hemibiotrophic Fungal Pathogen <i>Colletotrichum higginsianum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 749-762.	1.4	123

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91	Systematic approaches to using the FOX hunting system to identify useful rice genes. <i>Plant Journal</i> , 2009, 57, 883-894.	2.8	121
92	Regulating Subcellular Metal Homeostasis: The Key to Crop Improvement. <i>Frontiers in Plant Science</i> , 2016, 7, 1192.	1.7	118
93	Identification of stress-tolerance-related transcription-factor genes via mini-scale Full-length cDNA Over-eXpressor (FOX) gene hunting system. <i>Biochemical and Biophysical Research Communications</i> , 2007, 364, 250-257.	1.0	112
94	Folate synthesis in plants: The p-aminobenzoate branch is initiated by a bifunctional PabA-PabB protein that is targeted to plastids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1496-1501.	3.3	111
95	Identification of photorespiratory glutamate:glyoxylate aminotransferase (GGAT) gene in Arabidopsis. <i>Plant Journal</i> , 2003, 33, 975-987.	2.8	109
96	The Arabidopsis SDG4 contributes to the regulation of pollen tube growth by methylation of histone H3 lysines 4 and 36 in mature pollen. <i>Developmental Biology</i> , 2008, 315, 355-368.	0.9	109
97	Genome-wide analysis of endogenous abscisic acid-mediated transcription in dry and imbibed seeds of Arabidopsis using tiling arrays. <i>Plant Journal</i> , 2010, 62, 39-51.	2.8	109
98	Solution Structure of the B3 DNA Binding Domain of the Arabidopsis Cold-Responsive Transcription Factor RAV1 [W]. <i>Plant Cell</i> , 2004, 16, 3448-3459.	3.1	107
99	The Cold Signaling Attenuator HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE1 Activates <i>FLOWERING LOCUS C</i> Transcription via Chromatin Remodeling under Short-Term Cold Stress in Arabidopsis. <i>Plant Cell</i> , 2013, 25, 4378-4390.	3.1	106
100	A Stress-Activated Transposon in Arabidopsis Induces Transgenerational Abscisic Acid Insensitivity. <i>Scientific Reports</i> , 2016, 6, 23181.	1.6	106
101	A New Resource of Locally Transposed Dissociation Elements for Screening Gene-Knockout Lines in Silico on the Arabidopsis Genome. <i>Plant Physiology</i> , 2002, 129, 1695-1699.	2.3	103
102	A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. <i>Plant Molecular Biology</i> , 2007, 65, 357-371.	2.0	103
103	Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. <i>DNA Research</i> , 2012, 19, 335-345.	1.5	101
104	Armadillo repeat-containing kinesins and a NIMA-related kinase are required for epidermal cell morphogenesis in Arabidopsis. <i>Plant Journal</i> , 2008, 53, 157-171.	2.8	100
105	Development of 5006 Full-Length CDNAs in Barley: A Tool for Accessing Cereal Genomics Resources. <i>DNA Research</i> , 2009, 16, 81-89.	1.5	99
106	Heterogeneity of Arabidopsis core promoters revealed by high-density TSS analysis. <i>Plant Journal</i> , 2009, 60, 350-362.	2.8	99
107	Sequencing and Analysis of Approximately 40 000 Soybean cDNA Clones from a Full-Length-Enriched cDNA Library. <i>DNA Research</i> , 2008, 15, 333-346.	1.5	98
108	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. <i>Journal of Biological Chemistry</i> , 2012, 287, 7683-7691.	1.6	95

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109	RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions. <i>Journal of Experimental Botany</i> , 2003, 55, 213-223.	2.4	94
110	Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 180.	1.7	94
111	Gene-specific expression and calcium activation of Arabidopsis thaliana phospholipase C isoforms. <i>New Phytologist</i> , 2004, 162, 643-654.	3.5	92
112	Genes for the peptidoglycan synthesis pathway are essential for chloroplast division in moss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6753-6758.	3.3	92
113	Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. <i>BMC Plant Biology</i> , 2007, 7, 66.	1.6	91
114	AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5810-5815.	3.3	89
115	Plastidic RNA polymerase \hat{A} factors in Arabidopsis. <i>Plant and Cell Physiology</i> , 1999, 40, 832-842.	1.5	87
116	Folate synthesis in plants: the last step of the p-aminobenzoate branch is catalyzed by a plastidial aminodeoxychorismate lyase. <i>Plant Journal</i> , 2004, 40, 453-461.	2.8	86
117	Ethanol Enhances High-Salinity Stress Tolerance by Detoxifying Reactive Oxygen Species in Arabidopsis thaliana and Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1001.	1.7	86
118	A regulatory module controlling stress-induced cell cycle arrest in Arabidopsis. <i>ELife</i> , 2019, 8, .	2.8	86
119	The cDNA Microarray Analysis Using an Arabidopsis pad3 Mutant Reveals the Expression Profiles and Classification of Genes Induced by Alternaria brassicicola Attack. <i>Plant and Cell Physiology</i> , 2003, 44, 377-387.	1.5	83
120	Identification of ASK and clock-associated proteins as molecular partners of LKP2 (LOV kelch protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.4	83
121	Solution Structure of the Major DNA-binding Domain of Arabidopsis thaliana Ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005, 348, 253-264.	2.0	82
122	Overexpression of Arabidopsis response regulators, ARR4/ATRR1/IBC7 and ARR8/ATRR3, alters cytokinin responses differentially in the shoot and in callus formation. <i>Biochemical and Biophysical Research Communications</i> , 2002, 293, 806-815.	1.0	81
123	Overexpression of LSH1, a member of an uncharacterised gene family, causes enhanced light regulation of seedling development. <i>Plant Journal</i> , 2004, 37, 694-706.	2.8	80
124	AtXTH27 plays an essential role in cell wall modification during the development of tracheary elements. <i>Plant Journal</i> , 2005, 42, 525-534.	2.8	80
125	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 394-401.	2.8	80
126	Analysis of Differential Expression Patterns of mRNA and Protein During Cold-acclimation and De-acclimation in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3602-3611.	2.5	78

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127	A novel <i>Arabidopsis</i> gene <i>TONSOKU1</i> is required for proper cell arrangement in root and shoot apical meristems. <i>Plant Journal</i> , 2004, 38, 673-684.	2.8	76
128	The Distinct Roles of Class I and II RPD3-Like Histone Deacetylases in Salinity Stress Response. <i>Plant Physiology</i> , 2017, 175, 1760-1773.	2.3	76
129	Gene delivery into cultured plant cells by DNA-coated gold particles accelerated by a pneumatic particle gun. <i>Theoretical and Applied Genetics</i> , 1990, 80, 813-816.	1.8	74
130	Transcriptomic analysis of rice in response to iron deficiency and excess. <i>Rice</i> , 2014, 7, 18.	1.7	74
131	Recent advances in the characterization of plant transcriptomes in response to drought, salinity, heat, and cold stress. <i>F1000Research</i> , 2019, 8, 658.	0.8	74
132	RARGE: a large-scale database of RIKEN <i>Arabidopsis</i> resources ranging from transcriptome to phenome. <i>Nucleic Acids Research</i> , 2004, 33, D647-D650.	6.5	73
133	An Epigenetic Integrator: New Insights into Genome Regulation, Environmental Stress Responses and Developmental Controls by HISTONE DEACETYLASE 6. <i>Plant and Cell Physiology</i> , 2012, 53, 794-800.	1.5	71
134	Characterization of expressed sequence tags from a full-length enriched cDNA library of <i>Cryptomeria japonica</i> male strobili. <i>BMC Genomics</i> , 2008, 9, 383.	1.2	70
135	Expression and Interaction Analysis of <i>Arabidopsis</i> Skp1-Related Genes. <i>Plant and Cell Physiology</i> , 2004, 45, 83-91.	1.5	67
136	Generation of chimeric repressors that confer salt tolerance in <i>Arabidopsis</i> and rice. <i>Plant Biotechnology Journal</i> , 2011, 9, 736-746.	4.1	67
137	Cassava breeding and agronomy in Asia: 50 years of history and future directions. <i>Breeding Science</i> , 2020, 70, 145-166.	0.9	67
138	Histone acetylation orchestrates wound-induced transcriptional activation and cellular reprogramming in <i>Arabidopsis</i> . <i>Communications Biology</i> , 2019, 2, 404.	2.0	65
139	Acetic Acid Treatment Enhances Drought Avoidance in Cassava (<i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 2019, 10, 521.	1.7	65
140	DNA Microarray Analysis of Plastid Gene Expression in an <i>Arabidopsis</i> Mutant Deficient in a Plastid Transcription Factor Sigma, SIG2. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004, 68, 694-704.	0.6	64
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