Motoaki Seki

List of Publications by Year
in descending order

303 papers	46,791 citations	2565 99 h-index	2196 208 g-index
310 all docs	310 docs citations	310 times ranked	31943 citing authors

#	Article	IF	Citations
1	SUPPRESSOR of MAX2 1 (SMAX1) and SMAX1-LIKE2 (SMXL2) Negatively Regulate Drought Resistance in Arabidopsis thaliana. Plant and Cell Physiology, 2023, 63, 1900-1913.	1.5	13
2	Integrative omics approaches revealed a crosstalk among phytohormones during tuberous root development in cassava. Plant Molecular Biology, 2022, 109, 249-269.	2.0	26
3	Field transcriptome analysis reveals a molecular mechanism for cassava-flowering in a mountainous environment in Southeast Asia. Plant Molecular Biology, 2022, 109, 233-248.	2.0	14
4	Cassava mosaic disease and its management in Southeast Asia. Plant Molecular Biology, 2022, 109, 301-311.	2.0	18
5	Suppressed expression of starch branching enzyme 1 and 2 increases resistant starch and amylose content and modifies amylopectin structure in cassava. Plant Molecular Biology, 2022, 108, 413-427.	2.0	8
6	Agrobacterium-mediated cassava transformation for the Asian elite variety KU50. Plant Molecular Biology, 2022, 109, 271-282.	2.0	0
7	Sustained defense response via volatile signaling and its epigenetic transcriptional regulation. Plant Physiology, 2022, 189, 922-933.	2.3	8
8	Transcriptional Association between mRNAs and Their Paired Natural Antisense Transcripts Following Fusarium oxysporum Inoculation in Brassica rapa L.. Horticulturae, 2022, 8, 17.	1.2	8
9	Jasmonates and Histone deacetylase 6 activate Arabidopsis genome-wide histone acetylation and methylation during the early acute stress response. BMC Biology, 2022, 20, 83.	1.7	5
10	Ethanol induces heat tolerance in plants by stimulating unfolded protein response. Plant Molecular Biology, 2022, 110, 131-145.	2.0	6
11	Advances in Chemical Priming to Enhance Abiotic Stress Tolerance in Plants. Plant and Cell Physiology, 2021, 61, 1995-2003.	1.5	46
12	Acetic-acid-induced jasmonate signaling in root enhances drought avoidance in rice. Scientific Reports, 2021, 11, 6280.	1.6	23
13	Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in Brassica rapa. PLoS ONE, 2021, 16, e0242530.	1.1	8
14	Field-transcriptome analyses reveal developmental transitions during flowering in cassava (Manihot) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	2
15	Transcriptome Analysis of Arabidopsis thaliana Plants Treated with a New Compound Natolen128, Enhancing Salt Stress Tolerance. Plants, 2021, 10, 978.	1.6	6
16	Characterization of Histone H3 Lysine 4 and 36 Tri-methylation in Brassica rapa L.. Frontiers in Plant Science, 2021, 12, 659634.	1.7	9
17	Overexpression of nicotinamidase 3 (NIC3) gene and the exogenous application of nicotinic acid (NA) enhance drought tolerance and increase biomass in Arabidopsis. Plant Molecular Biology, 2021, 107, 63-84.	2.0	14
18	Exogenous ethanol treatment alleviates oxidative damage of <i>Arabidopsis thaliana</i> under conditions of high-light stress. Plant Biotechnology, 2021, 38, 339-344.	0.5	8

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19	Roles of subcellular metal homeostasis in crop improvement. Journal of Experimental Botany, 2021, 72, 2083-2098.	2.4	15
20	Defective cytokinin signaling reprograms lipid and flavonoid gene-to-metabolite networks to mitigate high salinity in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
21	An efficient method of propagating cassava plants using aeroponic culture. Journal of Crop Improvement, 2020, 34, 64-83.	0.9	5
22	Raf-like kinases CBC1 and CBC2 negatively regulate stomatal opening by negatively regulating plasma membrane H+-ATPase phosphorylation in Arabidopsis. Photochemical and Photobiological Sciences, 2020, 19, 88-98.	1.6	16
23	Transcriptomic analysis of root specific drought mediated response of G. arboreum and G. hirsutum. Biologia (Poland), 2020, 75, 627-636.	0.8	3
24	CIPK23 regulates blue lightâ€dependent stomatal opening in Arabidopsis thaliana. Plant Journal, 2020, 104, 679-692.	2.8	18
25	Inhibition of mitochondrial complex I by the novel compound FSL0260 enhances high salinity-stress tolerance in Arabidopsis thaliana. Scientific Reports, 2020, 10, 8691.	1.6	11
26	Cassava breeding and agronomy in Asia: 50 years of history and future directions. Breeding Science, 2020, 70, 145-166.	0.9	67
27	Metabolite and Phytohormone Profiling Illustrates Metabolic Reprogramming as an Escape Strategy of Deepwater Rice during Partially Submerged Stress. Metabolites, 2020, 10, 68.	1.3	17
28	Comparative functional analyses of DWARF14 and KARRIKIN INSENSITIVEÂ2 in drought adaptation of Arabidopsis thaliana. Plant Journal, 2020, 103, 111-127.	2.8	58
29	Histone Modifications Form Epigenetic Regulatory Networks to Regulate Abiotic Stress Response. Plant Physiology, 2020, 182, 15-26.	2.3	132
30	Cytosolic GLUTAMINE SYNTHETASE1;1 Modulates Metabolism and Chloroplast Development in Roots. Plant Physiology, 2020, 182, 1894-1909.	2.3	25
31	The Dynamic Kaleidoscope of RNA Biology in Plants. Plant Physiology, 2020, 182, 1-9.	2.3	11
32	Editorial. Plant Molecular Biology, 2019, 100, 1-2.	2.0	0
33	Intracellular localization of histone deacetylase HDA6 in plants. Journal of Plant Research, 2019, 132, 629-640.	1.2	7
34	Long noncoding RNAs in Brassica rapa L. following vernalization. Scientific Reports, 2019, 9, 9302.	1.6	42
35	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.	1.5	25
36	Histone acetylation orchestrates wound-induced transcriptional activation and cellular reprogramming in Arabidopsis. Communications Biology, 2019, 2, 404.	2.0	65

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37	RNA-Mediated Plant Behavior. Plant and Cell Physiology, 2019, 60, 1893-1896.	1.5	3
38	Transcriptome analysis of soybean (Glycine max) root genes differentially expressed in rhizobial, arbuscular mycorrhizal, and dual symbiosis. Journal of Plant Research, 2019, 132, 541-568.	1.2	22
39	Recent advances in the characterization of plant transcriptomes in response to drought, salinity, heat, and cold stress. F1000Research, 2019, 8, 658.	0.8	74
40	Biological Function of Changes in RNA Metabolism in Plant Adaptation to Abiotic Stress. Plant and Cell Physiology, 2019, 60, 1897-1905.	1.5	27
41	Acetic Acid Treatment Enhances Drought Avoidance in Cassava (Manihot esculenta Crantz). Frontiers in Plant Science, 2019, 10, 521.	1.7	65
42	Primed histone demethylation regulates shoot regenerative competency. Nature Communications, 2019, 10, 1786.	5.8	52
43	The Involvement of Long Noncoding RNAs in Response to Plant Stress. Methods in Molecular Biology, 2019, 1933, 151-171.	0.4	15
44	Transcriptome Analysis of the Hierarchical Response of Histone Deacetylase Proteins That Respond in an Antagonistic Manner to Salinity Stress. Frontiers in Plant Science, 2019, 10, 1323.	1.7	13
45	The transport of essential micronutrients in rice. Molecular Breeding, 2019, 39, 1.	1.0	25
46	A regulatory module controlling stress-induced cell cycle arrest in Arabidopsis. ELife, 2019, 8, .	2.8	86
47	Cassava microRNAs and storage root development. Biologia Plantarum, 2019, 63, 193-199.	1.9	1
48	Identification of DNA methylated regions by using methylated DNA immunoprecipitation sequencing in Brassica rapa. Crop and Pasture Science, 2018, 69, 107.	0.7	16
49	Transcriptomic analysis of Arabidopsis thaliana plants treated with the Ky-9 and Ky-72 histone deacetylase inhibitors. Plant Signaling and Behavior, 2018, 13, e1448333.	1.2	19
50	Identifying the target genes of <scp>SUPPRESSOR OF GAMMA RESPONSE</scp> 1, a master transcription factor controlling <scp>DNA</scp> damage response in Arabidopsis. Plant Journal, 2018, 94, 439-453.	2.8	127
51	Monitoring Transcriptomic Changes in Soil-Grown Roots and Shoots of Arabidopsis thaliana Subjected to a Progressive Drought Stress. Methods in Molecular Biology, 2018, 1761, 223-230.	0.4	3
52	Arabidopsis molybdenum cofactor sulfurase ABA3 contributes to anthocyanin accumulation and oxidative stress tolerance in ABA-dependent and independent ways. Scientific Reports, 2018, 8, 16592.	1.6	43
53	RNA Regulation in Plant Cold Stress Response. Advances in Experimental Medicine and Biology, 2018, 1081, 23-44.	0.8	11
54	PtWOX11 acts as master regulator conducting the expression of key transcription factors to induce de novo shoot organogenesis in poplar. Plant Molecular Biology, 2018, 98, 389-406.	2.0	21

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55	A rationally designed JAZ subtype-selective agonist of jasmonate perception. Nature Communications, 2018, 9, 3654.	5.8	47
56	The modulation of acetic acid pathway genes in Arabidopsis improves survival under drought stress. Scientific Reports, 2018, 8, 7831.	1.6	59
57	AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5810-5815.	3.3	89
58	Regulation and Modification of the Epigenome for Enhanced Salinity Tolerance in Crop Plants. , 2018, , 77-91.		10
59	The duration of ethanol-induced high-salinity stress tolerance in Arabidopsis thaliana. Plant Signaling and Behavior, 2018, 13, 1-3.	1.2	3
60	Versatility of HDA19-deficiency in increasing the tolerance of Arabidopsis to different environmental stresses. Plant Signaling and Behavior, 2018, 13, 1-4.	1.2	20
61	Genome-wide characterization of DNA methylation, small RNA expression, and histone H3 lysine nine di-methylation in Brassica rapa L.. DNA Research, 2018, 25, 511-520.	1.5	25
62	Sustainable Management of Invasive Cassava Pests in Vietnam, Cambodia, and Thailand. , 2018, , 131-157.		4
63	Overexpression of oligouridylate binding protein 1b results in ABA hypersensitivity. Plant Signaling and Behavior, 2017, 12, e1282591.	1.2	15
64	Paralogs and mutants show that one DMA synthase functions in iron homeostasis in rice. Journal of Experimental Botany, 2017, 68, 1785-1795.	2.4	47
65	Live imaging of H3K9 acetylation in plant cells. Scientific Reports, 2017, 7, 45894.	1.6	15
66	The Distinct Roles of Class I and II RPD3-Like Histone Deacetylases in Salinity Stress Response. Plant Physiology, 2017, 175, 1760-1773.	2.3	76
67	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in Arabidopsis thaliana Accessions. Molecular Biology and Evolution, 2017, 34, 3111-3122.	3.5	14
68	Novel Stress-Inducible Antisense RNAs of Protein-Coding Loci Are Synthesized by RNA-Dependent RNA Polymerase. Plant Physiology, 2017, 175, 457-472.	2.3	16
69	Acetate-mediated novel survival strategy against drought in plants. Nature Plants, 2017, 3, 17097.	4.7	232
70	Ethanol Enhances High-Salinity Stress Tolerance by Detoxifying Reactive Oxygen Species in Arabidopsis thaliana and Rice. Frontiers in Plant Science, 2017, 8, 1001.	1.7	86
71	Formation of friable embryogenic callus in cassava is enhanced under conditions of reduced nitrate, potassium and phosphate. PLoS ONE, 2017, 12, e0180736.	1.1	20
72	The karrikin receptor KAI2 promotes drought resistance in Arabidopsis thaliana. PLoS Genetics, 2017, 13, e1007076.	1.5	140

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73	Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress. Frontiers in Plant Science, 2016, 7, 180.	1.7	94
74	Oligouridylate Binding Protein 1b Plays an Integral Role in Plant Heat Stress Tolerance. Frontiers in Plant Science, 2016, 7, 853.	1.7	43
75	Sm-Like Protein-Mediated RNA Metabolism Is Required for Heat Stress Tolerance in Arabidopsis. Frontiers in Plant Science, 2016, 7, 1079.	1.7	26
76	Regulating Subcellular Metal Homeostasis: The Key to Crop Improvement. Frontiers in Plant Science, 2016, 7, 1192.	1.7	118
77	Cassava (Manihot esculenta) transcriptome analysis in response to infection by the fungus Colletotrichum gloeosporioides using an oligonucleotide-DNA microarray. Journal of Plant Research, 2016, 129, 711-726.	1.2	28
78	Drought stress differentially regulates the expression of small open reading frames (sORFs) in Arabidopsis roots and shoots. Plant Signaling and Behavior, 2016, 11, e1215792.	1.2	13
79	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. Nature Communications, 2016, 7, 13295.	5.8	138
80	A Stress-Activated Transposon in Arabidopsis Induces Transgenerational Abscisic Acid Insensitivity. Scientific Reports, 2016, 6, 23181.	1.6	106
81	Control of root cap maturation and cell detachment by BEARSKIN transcription factors in Arabidopsis. Development (Cambridge), 2016, 143, 4063-4072.	1.2	45
82	Arabidopsis type B cytokinin response regulators ARR1, ARR10, and ARR12 negatively regulate plant responses to drought. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3090-3095.	3.3	186
83	Knocking down mitochondrial iron transporter (MIT) reprograms primary and secondary metabolism in rice plants. Journal of Experimental Botany, 2016, 67, 1357-1368.	2.4	36
84	Ky-2, a Histone Deacetylase Inhibitor, Enhances High-Salinity Stress Tolerance inArabidopsis thaliana. Plant and Cell Physiology, 2016, 57, 776-783.	1.5	58
85	The Histone Deacetylase Inhibitor Suberoylanilide Hydroxamic Acid Alleviates Salinity Stress in Cassava. Frontiers in Plant Science, 2016, 7, 2039.	1.7	47
86	Wheat germ-based protein libraries for the functional characterisation of the Arabidopsis E2 ubiquitin conjugating enzymes and the RING-type E3 ubiquitin ligase enzymes. BMC Plant Biology, 2015, 15, 275.	1.6	40
87	Comparative analysis of root transcriptomes from two contrasting drought-responsive Williams 82 and DT2008 soybean cultivars under normal and dehydration conditions. Frontiers in Plant Science, 2015, 6, 551.	1.7	37
88	Loss of Arabidopsis 5â€²â€“3â€² Exoribonuclease AtXRN4 Function Enhances Heat Stress Tolerance of Plants Subjected to Severe Heat Stress. Plant and Cell Physiology, 2015, 56, 1762-1772.	1.5	57
89	Members of the Plant CRK Superfamily Are Capable of Trans- and Autophosphorylation of Tyrosine Residues. Journal of Biological Chemistry, 2015, 290, 16665-16677.	1.6	46
90	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. Plant Molecular Biology, 2015, 88, 531-543.	2.0	46

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91	Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. Frontiers in Plant Science, 2015, 6, 114.	1.7	367
92	Gene Expression Profiles in Jatropha Under Drought Stress and During Recovery. Plant Molecular Biology Reporter, 2015, 33, 1075-1087.	1.0	9
93	Comparison of Leaf Sheath Transcriptome Profiles with Physiological Traits of Bread Wheat Cultivars under Salinity Stress. PLoS ONE, 2015, 10, e0133322.	1.1	33
94	Transcriptomic analysis of rice in response to iron deficiency and excess. Rice, 2014, 7, 18.	1.7	74
95	tasiRNA-ARF Pathway Moderates Floral Architecture inArabidopsisPlants Subjected to Drought Stress. BioMed Research International, 2014, 2014, 1-10.	0.9	44
96	Analysis of Differential Expression Patterns of mRNA and Protein During Cold-acclimation and De-acclimation in Arabidopsis. Molecular and Cellular Proteomics, 2014, 13, 3602-3611.	2.5	78
97	Positive regulatory role of strigolactone in plant responses to drought and salt stress. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 851-856.	3.3	555
98	Epigenetic Memory for Stress Response and Adaptation in Plants. Plant and Cell Physiology, 2014, 55, 1859-1863.	1.5	321
99	Proteomic Analysis of the 26S Proteasome Reveals Its Direct Interaction with Transit Peptides of Plastid Protein Precursors for Their Degradation. Journal of Proteome Research, 2014, 13, 3223-3230.	1.8	25
100	Highly Reproducible ChIP-on-Chip Analysis to Identify Genome-Wide Protein Binding and Chromatin Status in Arabidopsis thaliana. Methods in Molecular Biology, 2014, 1062, 405-426.	0.4	6
101	Group A PP2Cs evolved in land plants as key regulators of intrinsic desiccation tolerance. Nature Communications, 2013, 4, 2219.	5.8	142
102	Arabidopsis AHP2, AHP3, and AHP5 histidine phosphotransfer proteins function as redundant negative regulators of drought stress response. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4840-4845.	3.3	191
103	A poly(A)-specific ribonuclease directly regulates the poly(A) status of mitochondrial mRNA in Arabidopsis. Nature Communications, 2013, 4, 2247.	5.8	43
104	Small open reading frames associated with morphogenesis are hidden in plant genomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2395-2400.	3.3	178
105	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. Trends in Plant Science, 2013, 18, 267-276.	4.3	229
106	Arabidopsis Non-Coding RNA Regulation in Abiotic Stress Responses. International Journal of Molecular Sciences, 2013, 14, 22642-22654.	1.8	47
107	The Cold Signaling Attenuator HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE1 Activates FLOWERING LOCUS C Transcription via Chromatin Remodeling under Short-Term Cold Stress in Arabidopsis Â Â. Plant Cell, 2013, 25, 4378-4390.	3.1	106
108	HsfA1d, a Protein Identified via FOX Hunting Using Thellungiella salsuginea cDNAs Improves Heat Tolerance by Regulating Heat-Stress-Responsive Gene Expression. Molecular Plant, 2013, 6, 411-422.	3.9	52

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109	Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. PLoS ONE, 2013, 8, e74056.	1.1	12
110	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. Bioinformatics, 2012, 28, 929-937.	1.8	6
111	Surveillance of 3â€² Noncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. G3: Genes, Genomes, Genetics, 2012, 2, 487-498.	0.8	47
112	Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. DNA Research, 2012, 19, 335-345.	1.5	101
113	Tissue-Specific Transcriptome Analysis Reveals Cell Wall Metabolism, Flavonol Biosynthesis and Defense Responses are Activated in the Endosperm of Germinating Arabidopsis thaliana Seeds. Plant and Cell Physiology, 2012, 53, 16-27.	1.5	58
114	Transition of Chromatin Status During the Process of Recovery from Drought Stress in Arabidopsis thaliana. Plant and Cell Physiology, 2012, 53, 847-856.	1.5	208
115	Structural Basis for Sequence-specific DNA Recognition by an Arabidopsis WRKY Transcription Factor. Journal of Biological Chemistry, 2012, 287, 7683-7691.	1.6	95
116	Genomeâ€wide biochemical analysis of Arabidopsis protein phosphatase using a wheat cellâ€free system. FEBS Letters, 2012, 586, 3134-3141.	1.3	9
117	An Epigenetic Integrator: New Insights into Genome Regulation, Environmental Stress Responses and Developmental Controls by HISTONE DEACETYLASE 6. Plant and Cell Physiology, 2012, 53, 794-800.	1.5	71
118	RNA regulation in plant abiotic stress responses. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 149-153.	0.9	57
119	Differential Gene Expression in Soybean Leaf Tissues at Late Developmental Stages under Drought Stress Revealed by Genome-Wide Transcriptome Analysis. PLoS ONE, 2012, 7, e49522.	1.1	162
120	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. Tropical Plant Biology, 2012, 5, 110-116.	1.0	12
121	Transcriptome Analyses of a Salt-Tolerant Cytokinin-Deficient Mutant Reveal Differential Regulation of Salt Stress Response by Cytokinin Deficiency. PLoS ONE, 2012, 7, e32124.	1.1	146
122	Identification and Expression Analysis of Cytokinin Metabolic Genes in Soybean under Normal and Drought Conditions in Relation to Cytokinin Levels. PLoS ONE, 2012, 7, e42411.	1.1	132
123	Derepression of ethylene-stabilized transcription factors (EIN3/EIL1) mediates jasmonate and ethylene signaling synergy in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12539-12544.	3.3	622
124	Genome-Wide Analysis of RNA Degradation in Arabidopsis. , 2011, , 79-89.		0
125	Arabidopsis HDA6 is required for freezing tolerance. Biochemical and Biophysical Research Communications, 2011, 406, 414-419.	1.0	133
126	FOX-superroots of Lotus corniculatus, overexpressing Arabidopsis full-length cDNA, show stable variations in morphological traits. Journal of Plant Physiology, 2011, 168, 181-187.	1.6	13

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127	Generation of chimeric repressors that confer salt tolerance in Arabidopsis and rice. Plant Biotechnology Journal, 2011, 9, 736-746.	4.1	67
128	The AP2/ERF Transcription Factor WIND1 Controls Cell Dedifferentiation in Arabidopsis. Current Biology, 2011, 21, 508-514.	1.8	369
129	Arabidopsis HsfA1 transcription factors function as the main positive regulators in heat shock-responsive gene expression. Molecular Genetics and Genomics, 2011, 286, 321-332.	1.0	377
130	Construction and EST sequencing of full-length, drought stress cDNA libraries for common beans (Phaseolus vulgaris L.). BMC Plant Biology, 2011, 11, 171.	1.6	28
131	ABA 9â€²-hydroxylation is catalyzed by CYP707A in Arabidopsis. Phytochemistry, 2011, 72, 717-722.	1.4	52
132	Autophosphorylation profiling of Arabidopsis protein kinases using the cell-free system. Phytochemistry, 2011, 72, 1136-1144.	1.4	51
133	ARTADE2DB: Improved Statistical Inferences for Arabidopsis Gene Functions and Structure Predictions by Dynamic Structure-Based Dynamic Expression (DSDE) Analyses. Plant and Cell Physiology, 2011, 52, 254-264.	1.5	15
134	Arabidopsis RPT2a Encoding the 26S Proteasome Subunit is Required for Various Aspects of Root Meristem Maintenance, and Regulates Gametogenesis Redundantly with its Homolog, RPT2b. Plant and Cell Physiology, 2011, 52, 1628-1640.	1.5	23
135	Expression profile and 5â€™-terminal structure of Arabidopsis antisense transcripts expressed in seeds. Plant Signaling and Behavior, 2011, 6, 691-693.	1.2	4
136	Arabidopsis HDA6 Regulates Locus-Directed Heterochromatin Silencing in Cooperation with MET1. PLoS Genetics, 2011, 7, e1002055.	1.5	148
137	Arabidopsis Tiling Array Analysis to Identify the Stress-Responsive Genes. Methods in Molecular Biology, 2010, 639, 141-155.	0.4	27
138	â€˜Omicsâ€™ analyses of regulatory networks in plant abiotic stress responses. Current Opinion in Plant Biology, 2010, 13, 132-138.	3.5	477
139	Comparative genomic analysis of 1047 completely sequenced cDNAs from an Arabidopsis-related model halophyte, Thellungiella halophila. BMC Plant Biology, 2010, 10, 261.	1.6	38
140	Chromatin regulation functions in plant abiotic stress responses. Plant, Cell and Environment, 2010, 33, 604-611.	2.8	194
141	Genome-wide analysis of endogenous abscisic acid-mediated transcription in dry and imbibed seeds of Arabidopsis using tiling arrays. Plant Journal, 2010, 62, 39-51.	2.8	109
142	Transduction of RNA-directed DNA methylation signals to repressive histone marks in Arabidopsis thaliana. EMBO Journal, 2010, 29, 352-362.	3.5	49
143	TCP Transcription Factors Regulate the Activities of ASYMMETRIC LEAVES1 and miR164, as Well as the Auxin Response, during Differentiation of Leaves inArabidopsisÂ Â. Plant Cell, 2010, 22, 3574-3588.	3.1	335
144	Microarray Analysis for Studying the Abiotic Stress Responses in Plants. , 2010, , 333-355.		4

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145	Construction of a Protein Library of Arabidopsis Transcription Factors Using a Wheat Cell-Free Protein Production System and Its Application for DNA Binding Analysis. Bioscience, Biotechnology and Biochemistry, 2009, 73, 1661-1664.	0.6	11
146	Genome-wide suppression of aberrant mRNA-like noncoding RNAs by NMD in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2453-2458.	3.3	165
147	PosMed-plus: An Intelligent Search Engine that Inferentially Integrates Cross-Species Information Resources for Molecular Breeding of Plants. Plant and Cell Physiology, 2009, 50, 1249-1259.	1.5	17
148	Analysis of Multiple Occurrences of Alternative Splicing Events in Arabidopsis thaliana Using Novel Sequenced Full-Length cDNAs. DNA Research, 2009, 16, 155-164.	1.5	17
149	High Humidity Induces Abscisic Acid 8â€²-Hydroxylase in Stomata and Vasculature to Regulate Local and Systemic Abscisic Acid Responses in Arabidopsis. Plant Physiology, 2009, 149, 825-834.	2.3	216
150	Development of 5006 Full-Length CDNAs in Barley: A Tool for Accessing Cereal Genomics Resources. DNA Research, 2009, 16, 81-89.	1.5	99
151	Transcriptome Analyses Revealed Diverse Expression Changes in ago1 and hyl1 Arabidopsis Mutants. Plant and Cell Physiology, 2009, 50, 1715-1720.	1.5	18
152	Assessment of adaptive evolution between wheat and rice as deduced from full-length common wheat cDNA sequence data and expression patterns. BMC Genomics, 2009, 10, 271.	1.2	44
153	A simple and high-sensitivity method for analysis of ubiquitination and polyubiquitination based on wheat cell-free protein synthesis. BMC Plant Biology, 2009, 9, 39.	1.6	48
154	Functional genomics using RIKEN Arabidopsis thaliana full-length cDNAs. Journal of Plant Research, 2009, 122, 355-366.	1.2	22
155	DEAR1, a transcriptional repressor of DREB protein that mediates plant defense and freezing stress responses in Arabidopsis. Journal of Plant Research, 2009, 122, 633-643.	1.2	154
156	Systematic approaches to using the FOX hunting system to identify useful rice genes. Plant Journal, 2009, 57, 883-894.	2.8	121
157	Heterogeneity of Arabidopsis core promoters revealed by highâ€density TSS analysis. Plant Journal, 2009, 60, 350-362.	2.8	99
158	CNI1/ATL31, a RINGâ€type ubiquitin ligase that functions in the carbon/nitrogen response for growth phase transition in Arabidopsis seedlings. Plant Journal, 2009, 60, 852-864.	2.8	135
159	Solution structure of the rhodanese homology domain At4g01050(175-295) from Arabidopsis thaliana. Protein Science, 2009, 14, 224-230.	3.1	24
160	Generation of Full-Length cDNA Libraries: Focus on Plants. Methods in Molecular Biology, 2009, 533, 49-68.	0.4	2
161	Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings. Journal of Experimental Botany, 2009, 60, 3067-3073.	2.4	61
162	Gene coding for SigA-binding protein from Arabidopsis appears to be transcriptionally up-regulated by salicylic acid and NPR1-dependent mechanisms. Journal of General Plant Pathology, 2008, 74, 345-354.	0.6	18

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163	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. Plant Physiology and Biochemistry, 2008, 46, 394-401.	2.8	80
164	Characterization of growth-phase-specific responses to cold in Arabidopsis thaliana suspension-cultured cells. Plant, Cell and Environment, 2008, 31, 354-365.	2.8	14
165	Armadillo repeatâ€containing kinesins and a NIMAâ€related kinase are required for epidermalâ€cell morphogenesis in Arabidopsis. Plant Journal, 2008, 53, 157-171.	2.8	100
166	Characterization of expressed sequence tags from a full-length enriched cDNA library of Cryptomeria japonica male strobili. BMC Genomics, 2008, 9, 383.	1.2	70
167	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, Thellungiella halophila. BMC Plant Biology, 2008, 8, 115.	1.6	57
168	Arabidopsis Transcriptome Analysis under Drought, Cold, High-Salinity and ABA Treatment Conditions using a Tiling Array. Plant and Cell Physiology, 2008, 49, 1135-1149.	1.5	475
169	The Arabidopsis SDG4 contributes to the regulation of pollen tube growth by methylation of histone H3 lysines 4 and 36 in mature pollen. Developmental Biology, 2008, 315, 355-368.	0.9	109
170	Antagonistic Interaction between Systemic Acquired Resistance and the Abscisic Acidâ€“Mediated Abiotic Stress Response in Arabidopsis Â. Plant Cell, 2008, 20, 1678-1692.	3.1	465
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