Motoaki Seki

List of Publications by Year in Descending Order

298 papers	37,481 citations	91 h-index	191 g-index
310 ext. papers	43,040 ext. citations	6.4 avg, IF	6.85 L-index

#	Paper	IF	Citations
298	Transcriptional Association between mRNAs and Their Paired Natural Antisense Transcripts Following Fusarium oxysporum Inoculation in Brassica rapa L.. *Horticulturae*, **2022**, 8, 17	2.5	1
297	Jasmonates and Histone deacetylase 6 activate Arabidopsis genome-wide histone acetylation and methylation during the early acute stress response.. *BMC Biology*, **2022**, 20, 83	7.3	1
296	Suppressed expression of starch branching enzyme 1 and 2 increases resistant starch and amylose content and modifies amylopectin structure in cassava. *Plant Molecular Biology*, **2021**, 1	4.6	0
295	Agrobacterium-mediated cassava transformation for the Asian elite variety KU50. *Plant Molecular Biology*, **2021**, 1	4.6	
294	Acetic-acid-induced jasmonate signaling in root enhances drought avoidance in rice. *Scientific Reports*, **2021**, 11, 6280	4.9	6
293	Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in Brassica rapa. *PLoS ONE*, **2021**, 16, e0242530	3.7	3
292	Field-transcriptome analyses reveal developmental transitions during flowering in cassava (Manihot esculenta Crantz). *Plant Molecular Biology*, **2021**, 106, 285-296	4.6	0
291	Transcriptome Analysis of Plants Treated with a New Compound Natolen128, Enhancing Salt Stress Tolerance. *Plants*, **2021**, 10,	4.5	1
290	Characterization of Histone H3 Lysine 4 and 36 Tri-methylation in L. *Frontiers in Plant Science*, **2021**, 12, 659634	6.2	3
289	Advances in Chemical Priming to Enhance Abiotic Stress Tolerance in Plants. *Plant and Cell Physiology*, **2021**, 61, 1995-2003	4.9	13
288	Cassava mosaic disease and its management in Southeast Asia. *Plant Molecular Biology*, **2021**, 1	4.6	2
287	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	4.6	2
286	Exogenous ethanol treatment alleviates oxidative damage of under conditions of high-light stress. *Plant Biotechnology*, **2021**, 38, 339-344	1.3	1
285	Roles of subcellular metal homeostasis in crop improvement. *Journal of Experimental Botany*, **2021**, 72, 2083-2098	7	7
284	Inhibition of mitochondrial complex I by the novel compound FSL0260 enhances high salinity-stress tolerance in Arabidopsis thaliana. *Scientific Reports*, **2020**, 10, 8691	4.9	6
283	Cassava breeding and agronomy in Asia: 50 years of history and future directions. *Breeding Science*, **2020**, 70, 145-166	2	26
282	Metabolite and Phytohormone Profiling Illustrates Metabolic Reprogramming as an Escape Strategy of Deepwater Rice during Partially Submerged Stress. *Metabolites*, **2020**, 10,	5.6	6

281	Comparative functional analyses of DWARF14 and KARRIKIN INSENSITIVE2 in drought adaptation of Arabidopsis thaliana. *Plant Journal*, **2020**, 103, 111-127	6.9	19
280	Histone Modifications Form Epigenetic Regulatory Networks to Regulate Abiotic Stress Response. *Plant Physiology*, **2020**, 182, 15-26	6.6	72
279	Cytosolic GLUTAMINE SYNTHETASE1;1 Modulates Metabolism and Chloroplast Development in Roots. *Plant Physiology*, **2020**, 182, 1894-1909	6.6	12
278	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	4.2	5
277	Transcriptomic analysis of root specific drought mediated response of G. arboreum and G. hirsutum. *Biologia (Poland)*, **2020**, 75, 627-636	1.5	2
276	Integrative omics approaches revealed a crosstalk among phytohormones during tuberous root development in cassava. *Plant Molecular Biology*, **2020**, 1	4.6	7
275	CIPK23 regulates blue light-dependent stomatal opening in Arabidopsis thaliana. *Plant Journal*, **2020**, 104, 679-692	6.9	6
274	Field transcriptome analysis reveals a molecular mechanism for cassava-flowering in a mountainous environment in Southeast Asia. *Plant Molecular Biology*, **2020**, 1	4.6	7
273	An efficient method of propagating cassava plants using aeroponic culture. *Journal of Crop Improvement*, **2020**, 34, 64-83	1.4	2
272	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	2.6	13
271	Recent advances in the characterization of plant transcriptomes in response to drought, salinity, heat, and cold stress. *F1000Research*, **2019**, 8,	3.6	35
270	Biological Function of Changes in RNA Metabolism in Plant Adaptation to Abiotic Stress. *Plant and Cell Physiology*, **2019**, 60, 1897-1905	4.9	10
269	Acetic Acid Treatment Enhances Drought Avoidance in Cassava (Crantz). *Frontiers in Plant Science*, **2019**, 10, 521	6.2	24
268	Primed histone demethylation regulates shoot regenerative competency. *Nature Communications*, **2019**, 10, 1786	17.4	25
267	The Involvement of Long Noncoding RNAs in Response to Plant Stress. *Methods in Molecular Biology*, **2019**, 1933, 151-171	1.4	8
266	Intracellular localization of histone deacetylase HDA6 in plants. *Journal of Plant Research*, **2019**, 132, 629-640	2.6	4
265	Long noncoding RNAs in Brassica rapa L. following vernalization. *Scientific Reports*, **2019**, 9, 9302	4.9	19
264	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	4.5	12

263	Histone acetylation orchestrates wound-induced transcriptional activation and cellular reprogramming in Arabidopsis. *Communications Biology*, **2019**, 2, 404	6.7	33
262	A regulatory module controlling stress-induced cell cycle arrest in. *ELife*, **2019**, 8,	8.9	46
261	Cassava microRNAs and storage root development. *Biologia Plantarum*, **2019**, 63, 193-199	2.1	0
260	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	6.2	9
259	The transport of essential micronutrients in rice. *Molecular Breeding*, **2019**, 39, 1	3.4	14
258	Identification of DNA methylated regions by using methylated DNA immunoprecipitation sequencing in Brassica rapa. *Crop and Pasture Science*, **2018**, 69, 107	2.2	12
257	Transcriptomic analysis of Arabidopsis thaliana plants treated with the Ky-9 and Ky-72 histone deacetylase inhibitors. *Plant Signaling and Behavior*, **2018**, 13, e1448333	2.5	10
256	Identifying the target genes of SUPPRESSOR OF GAMMA RESPONSE 1, a master transcription factor controlling DNA damage response in Arabidopsis. *Plant Journal*, **2018**, 94, 439-453	6.9	77
255	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	1.4	1
254	The duration of ethanol-induced high-salinity stress tolerance in Arabidopsis thaliana. *Plant Signaling and Behavior*, **2018**, 13, e1500065	2.5	1
253	Versatility of HDA19-deficiency in increasing the tolerance of Arabidopsis to different environmental stresses. *Plant Signaling and Behavior*, **2018**, 13, e1475808	2.5	14
252	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	4.5	15
251	Sustainable Management of Invasive Cassava Pests in Vietnam, Cambodia, and Thailand **2018**, 131-157		2
250	Arabidopsis molybdenum cofactor sulfurase ABA3 contributes to anthocyanin accumulation and oxidative stress tolerance in ABA-dependent and independent ways. *Scientific Reports*, **2018**, 8, 16592	4.9	20
249	RNA Regulation in Plant Cold Stress Response. *Advances in Experimental Medicine and Biology*, **2018** , 1081, 23-44	3.6	1
248	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	4.6	6
247	A rationally designed JAZ subtype-selective agonist of jasmonate perception. *Nature Communications*, **2018**, 9, 3654	17.4	25
246	The modulation of acetic acid pathway genes in Arabidopsis improves survival under drought stress. *Scientific Reports*, **2018**, 8, 7831	4.9	26

245	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	11.5	49
244	Regulation and Modification of the Epigenome for Enhanced Salinity Tolerance in Crop Plants **2018**, 77-91		3
243	Overexpression of oligouridylate binding protein 1b results in ABA hypersensitivity. *Plant Signaling and Behavior*, **2017**, 12, e1282591	2.5	11
242	Paralogs and mutants show that one DMA synthase functions in iron homeostasis in rice. *Journal of Experimental Botany*, **2017**, 68, 1785-1795	7	26
241	Live imaging of H3K9 acetylation in plant cells. *Scientific Reports*, **2017**, 7, 45894	4.9	7
240	The Distinct Roles of Class I and II RPD3-Like Histone Deacetylases in Salinity Stress Response. *Plant Physiology*, **2017**, 175, 1760-1773	6.6	45
239	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	8.3	5
238	Formation of friable embryogenic callus in cassava is enhanced under conditions of reduced nitrate, potassium and phosphate. *PLoS ONE*, **2017**, 12, e0180736	3.7	14
237	The karrikin receptor KAI2 promotes drought resistance in Arabidopsis thaliana. *PLoS Genetics*, **2017**, 13, e1007076	6	87
236	Novel Stress-Inducible Antisense RNAs of Protein-Coding Loci Are Synthesized by RNA-Dependent RNA Polymerase. *Plant Physiology*, **2017**, 175, 457-472	6.6	12
235	Acetate-mediated novel survival strategy against drought in plants. *Nature Plants*, **2017**, 3, 17097	11.5	129
234	Ethanol Enhances High-Salinity Stress Tolerance by Detoxifying Reactive Oxygen Species in and Rice. *Frontiers in Plant Science*, **2017**, 8, 1001	6.2	47
233	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. *Nature Communications* , **2016**, 7, 13295	17.4	91
232	A Stress-Activated Transposon in Arabidopsis Induces Transgenerational Abscisic Acid Insensitivity. *Scientific Reports*, **2016**, 6, 23181	4.9	67
231	Control of root cap maturation and cell detachment by BEARSKIN transcription factors in Arabidopsis. *Development (Cambridge)*, **2016**, 143, 4063-4072	6.6	25
230	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, 3090-5	11.5	118
229	Knocking down mitochondrial iron transporter (MIT) reprograms primary and secondary metabolism in rice plants. *Journal of Experimental Botany*, **2016**, 67, 1357-68	7	26
228	Ky-2, a Histone Deacetylase Inhibitor, Enhances High-Salinity Stress Tolerance in Arabidopsis thaliana. *Plant and Cell Physiology*, **2016**, 57, 776-83	4.9	35

227	The Histone Deacetylase Inhibitor Suberoylanilide Hydroxamic Acid Alleviates Salinity Stress in Cassava. *Frontiers in Plant Science*, **2016**, 7, 2039	6.2	29
226	Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress. *Frontiers in Plant Science*, **2016**, 7, 180	6.2	58
225	Oligouridylate Binding Protein 1b Plays an Integral Role in Plant Heat Stress Tolerance. *Frontiers in Plant Science*, **2016**, 7, 853	6.2	26
224	Sm-Like Protein-Mediated RNA Metabolism Is Required for Heat Stress Tolerance in Arabidopsis. *Frontiers in Plant Science*, **2016**, 7, 1079	6.2	14
223	Regulating Subcellular Metal Homeostasis: The Key to Crop Improvement. *Frontiers in Plant Science*, **2016**, 7, 1192	6.2	76
222	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	2.6	21
221	Drought stress differentially regulates the expression of small open reading frames (sORFs) in Arabidopsis roots and shoots. *Plant Signaling and Behavior*, **2016**, 11, e1215792	2.5	7
220	Loss of Arabidopsis 5R3RExoribonuclease AtXRN4 Function Enhances Heat Stress Tolerance of Plants Subjected to Severe Heat Stress. *Plant and Cell Physiology*, **2015**, 56, 1762-72	4.9	43
219	Members of the Plant CRK Superfamily Are Capable of Trans- and Autophosphorylation of Tyrosine Residues. *Journal of Biological Chemistry*, **2015**, 290, 16665-77	5.4	34
218	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. *Plant Molecular Biology*, **2015**, 88, 531-43	4.6	29
217	Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. *Frontiers in Plant Science*, **2015**, 6, 114	6.2	245
216	Gene Expression Profiles in Jatropha Under Drought Stress and During Recovery. *Plant Molecular Biology Reporter*, **2015**, 33, 1075-1087	1.7	8
215	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	5.3	24
214	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	6.2	29
213	Comparison of Leaf Sheath Transcriptome Profiles with Physiological Traits of Bread Wheat Cultivars under Salinity Stress. *PLoS ONE*, **2015**, 10, e0133322	3.7	26
212	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, 851-6	11.5	370
211	Epigenetic memory for stress response and adaptation in plants. *Plant and Cell Physiology*, **2014**, 55, 1859-63	4.9	218
210	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, 3223-30	5.6	19

209	Transcriptomic analysis of rice in response to iron deficiency and excess. *Rice*, **2014**, 7, 18	5.8	53
208	tasiRNA-ARF pathway moderates floral architecture in Arabidopsis plants subjected to drought stress. *BioMed Research International*, **2014**, 2014, 303451	3	40
207	Analysis of differential expression patterns of mRNA and protein during cold-acclimation and de-acclimation in Arabidopsis. *Molecular and Cellular Proteomics*, **2014**, 13, 3602-11	7.6	47
206	Highly reproducible ChIP-on-chip analysis to identify genome-wide protein binding and chromatin status in Arabidopsis thaliana. *Methods in Molecular Biology*, **2014**, 1062, 405-26	1.4	6
205	Group A PP2Cs evolved in land plants as key regulators of intrinsic desiccation tolerance. *Nature Communications*, **2013**, 4, 2219	17.4	94
204	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, 4840-5	11.5	137
203	A poly(A)-specific ribonuclease directly regulates the poly(A) status of mitochondrial mRNA in Arabidopsis. *Nature Communications*, **2013**, 4, 2247	17.4	31
202	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, 2395-400	11.5	116
201	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. *Trends in Plant Science*, **2013**, 18, 267-76	13.1	167
200	Arabidopsis non-coding RNA regulation in abiotic stress responses. *International Journal of Molecular Sciences*, **2013**, 14, 22642-54	6.3	41
199	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. *Plant Cell*, **2013**, 25, 4378-90	11.6	76
198	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, 411-22	14.4	28
197	Genome-wide discovery and information resource development of DNA polymorphisms in cassava. *PLoS ONE*, **2013**, 8, e74056	3.7	10
196	Genome-wide biochemical analysis of Arabidopsis protein phosphatase using a wheat cell-free system. *FEBS Letters*, **2012**, 586, 3134-41	3.8	8
195	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	4.9	52
194	RNA regulation in plant abiotic stress responses. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2012**, 1819, 149-53	6	51
193	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	3.7	133
192	Cassava Genetic Improvement: Omics Approaches for Facing Global Challenges **2012**, 1049-1065		

191	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. *Tropical Plant Biology*, **2012**, 5, 110-116	1.6	9
190	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. *Bioinformatics*, **2012**, 28, 929-37	7.2	6
189	Surveillance of 3′Noncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. *G3: Genes, Genomes, Genetics*, **2012**, 2, 487-98	3.2	33
188	Transcriptome analysis using a high-density oligomicroarray under drought stress in various genotypes of cassava: an important tropical crop. *DNA Research*, **2012**, 19, 335-45	4.5	79
187	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	4.9	47
186	Transition of chromatin status during the process of recovery from drought stress in Arabidopsis thaliana. *Plant and Cell Physiology*, **2012**, 53, 847-56	4.9	142
185	Structural basis for sequence-specific DNA recognition by an Arabidopsis WRKY transcription factor. *Journal of Biological Chemistry*, **2012**, 287, 7683-91	5.4	62
184	Transcriptome analyses of a salt-tolerant cytokinin-deficient mutant reveal differential regulation of salt stress response by cytokinin deficiency. *PLoS ONE*, **2012**, 7, e32124	3.7	112
183	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	3.7	82
182	Genome-Wide Analysis of RNA Degradation in Arabidopsis **2011**, 79-89		
181	Arabidopsis HDA6 is required for freezing tolerance. *Biochemical and Biophysical Research Communications*, **2011**, 406, 414-9	3.4	95
180	FOX-superroots of Lotus corniculatus, overexpressing Arabidopsis full-length cDNA, show stable variations in morphological traits. *Journal of Plant Physiology*, **2011**, 168, 181-7	3.6	12
179	Generation of chimeric repressors that confer salt tolerance in Arabidopsis and rice. *Plant Biotechnology Journal*, **2011**, 9, 736-46	11.6	42
178	The AP2/ERF transcription factor WIND1 controls cell dedifferentiation in Arabidopsis. *Current Biology*, **2011**, 21, 508-14	6.3	246
177	Arabidopsis HsfA1 transcription factors function as the main positive regulators in heat shock-responsive gene expression. *Molecular Genetics and Genomics*, **2011**, 286, 321-32	3.1	253
176	Construction and EST sequencing of full-length, drought stress cDNA libraries for common beans (Phaseolus vulgaris L.). *BMC Plant Biology*, **2011**, 11, 171	5.3	25
175	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, 12539-44	11.5	474
174	ABA 9′hydroxylation is catalyzed by CYP707A in Arabidopsis. *Phytochemistry*, **2011**, 72, 717-22	4	43

173	Autophosphorylation profiling of Arabidopsis protein kinases using the cell-free system. *Phytochemistry*, **2011**, 72, 1136-44	4	40
172	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, 254-64	4.9	12
171	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, 1628-40	4.9	20
170	Expression profile and 5Rterminal structure of Arabidopsis antisense transcripts expressed in seeds. *Plant Signaling and Behavior*, **2011**, 6, 691-3	2.5	4
169	Arabidopsis HDA6 regulates locus-directed heterochromatin silencing in cooperation with MET1. *PLoS Genetics*, **2011**, 7, e1002055	6	119
168	Chromatin regulation functions in plant abiotic stress responses. *Plant, Cell and Environment*, **2010**, 33, 604-11	8.4	163
167	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	6.9	95
166	Transduction of RNA-directed DNA methylation signals to repressive histone marks in Arabidopsis thaliana. *EMBO Journal*, **2010**, 29, 352-62	13	43
165	TCP transcription factors regulate the activities of ASYMMETRIC LEAVES1 and miR164, as well as the auxin response, during differentiation of leaves in Arabidopsis. *Plant Cell*, **2010**, 22, 3574-88	11.6	266
164	Arabidopsis tiling array analysis to identify the stress-responsive genes. *Methods in Molecular Biology*, **2010**, 639, 141-55	1.4	26
163	ROmicsRanalyses of regulatory networks in plant abiotic stress responses. *Current Opinion in Plant Biology*, **2010**, 13, 132-8	9.9	371
162	Comparative genomic analysis of 1047 completely sequenced cDNAs from an Arabidopsis-related model halophyte, Thellungiella halophila. *BMC Plant Biology*, **2010**, 10, 261	5.3	36
161	Microarray Analysis for Studying the Abiotic Stress Responses in Plants **2010**, 333-355		3
160	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, 1661-4	2.1	9
159	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, 2453-8	11.5	145
158	PosMed-plus: an intelligent search engine that inferentially integrates cross-species information resources for molecular breeding of plants. *Plant and Cell Physiology*, **2009**, 50, 1249-59	4.9	14
157	Analysis of multiple occurrences of alternative splicing events in Arabidopsis thaliana using novel sequenced full-length cDNAs. *DNA Research*, **2009**, 16, 155-64	4.5	12
156	High humidity induces abscisic acid 8Rhydroxylase in stomata and vasculature to regulate local and systemic abscisic acid responses in Arabidopsis. *Plant Physiology*, **2009**, 149, 825-34	6.6	188

155	Development of 5006 full-length CDNAs in barley: a tool for accessing cereal genomics resources. *DNA Research*, **2009**, 16, 81-9	4.5	81
154	Transcriptome analyses revealed diverse expression changes in ago1 and hyl1 Arabidopsis mutants. *Plant and Cell Physiology*, **2009**, 50, 1715-20	4.9	18
153	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	4.5	40
152	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	5.3	43
151	Functional genomics using RIKEN Arabidopsis thaliana full-length cDNAs. *Journal of Plant Research*, **2009**, 122, 355-66	2.6	20
150	DEAR1, a transcriptional repressor of DREB protein that mediates plant defense and freezing stress responses in Arabidopsis. *Journal of Plant Research*, **2009**, 122, 633-43	2.6	115
149	Systematic approaches to using the FOX hunting system to identify useful rice genes. *Plant Journal*, **2009**, 57, 883-94	6.9	99
148	Heterogeneity of Arabidopsis core promoters revealed by high-density TSS analysis. *Plant Journal*, **2009**, 60, 350-62	6.9	81
147	CNI1/ATL31, a RING-type ubiquitin ligase that functions in the carbon/nitrogen response for growth phase transition in Arabidopsis seedlings. *Plant Journal*, **2009**, 60, 852-64	6.9	95
146	Generation of full-length cDNA libraries: focus on plants. *Methods in Molecular Biology*, **2009**, 533, 49-68	1.4	1
145	Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings. *Journal of Experimental Botany*, **2009**, 60, 3067-73	7	51
144	Characterization of growth-phase-specific responses to cold in Arabidopsis thaliana suspension-cultured cells. *Plant, Cell and Environment*, **2008**, 31, 354-65	8.4	12
143	Armadillo repeat-containing kinesins and a NIMA-related kinase are required for epidermal-cell morphogenesis in Arabidopsis. *Plant Journal*, **2008**, 53, 157-71	6.9	85
142	Characterization of expressed sequence tags from a full-length enriched cDNA library of Cryptomeria japonica male strobili. *BMC Genomics*, **2008**, 9, 383	4.5	64
141	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, Thellungiella halophila. *BMC Plant Biology*, **2008**, 8, 115	5.3	52
140	Arabidopsis transcriptome analysis under drought, cold, high-salinity and ABA treatment conditions using a tiling array. *Plant and Cell Physiology*, **2008**, 49, 1135-49	4.9	407
139	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, 355-68	3.1	80
138	Antagonistic interaction between systemic acquired resistance and the abscisic acid-mediated abiotic stress response in Arabidopsis. *Plant Cell*, **2008**, 20, 1678-92	11.6	367

137	Identification of the candidate genes regulated by RNA-directed DNA methylation in Arabidopsis. *Biochemical and Biophysical Research Communications*, **2008**, 376, 553-7	3.4	49
136	Alterations of lysine modifications on the histone H3 N-tail under drought stress conditions in Arabidopsis thaliana. *Plant and Cell Physiology*, **2008**, 49, 1580-8	4.9	248
135	Sequencing and analysis of approximately 40,000 soybean cDNA clones from a full-length-enriched cDNA library. *DNA Research*, **2008**, 15, 333-46	4.5	86
134	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	1	14
133	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. *Plant Physiology and Biochemistry*, **2008**, 46, 394-401	5.4	58
132	Transcriptome Analysis of Plant Drought and Salt Stress Response **2007**, 261-283		5
131	Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. *BMC Plant Biology*, **2007**, 7, 66	5.3	78
130	Identification of plant promoter constituents by analysis of local distribution of short sequences. *BMC Genomics*, **2007**, 8, 67	4.5	117
129	Regulatory metabolic networks in drought stress responses. *Current Opinion in Plant Biology*, **2007**, 10, 296-302	9.9	636
128	DRL1 regulates adaxial leaf patterning and shoot apical meristem activity inArabidopsis **2007**, 50, 467-474		2
127	A genome-wide gain-of function analysis of rice genes using the FOX-hunting system. *Plant Molecular Biology*, **2007**, 65, 357-71	4.6	96
126	NAC transcription factors, NST1 and NST3, are key regulators of the formation of secondary walls in woody tissues of Arabidopsis. *Plant Cell*, **2007**, 19, 270-80	11.6	576
125	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. *Genome Research*, **2007**, 17, 175-83	9.7	200
124	Identification of stress-tolerance-related transcription-factor genes via mini-scale Full-length cDNA Over-eXpressor (FOX) gene hunting system. *Biochemical and Biophysical Research Communications*, **2007**, 364, 250-7	3.4	100
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