

Motoaki Seki

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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	Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. <i>Plant Cell</i> , 2003 , 15, 63-78	11.6	1552
297	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, 279-92	6.9	1501
296	Regulatory network of gene expression in the drought and cold stress responses. <i>Current Opinion in Plant Biology</i> , 2003 , 6, 410-7	9.9	1398
295	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, 751-63	6.9	1152
294	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. <i>Plant Cell</i> , 2004 , 16, 2481-98	11.6	1040
293	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	11.6	910
292	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, 325-33	6.9	896
291	Important roles of drought- and cold-inducible genes for galactinol synthase in stress tolerance in Arabidopsis thaliana. <i>Plant Journal</i> , 2002 , 29, 417-26	6.9	835
290	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, 1755-67	6.6	799
289	Empirical analysis of transcriptional activity in the Arabidopsis genome. <i>Science</i> , 2003 , 302, 842-6	33.3	782
288	Functional analysis of an Arabidopsis transcription factor, DREB2A, involved in drought-responsive gene expression. <i>Plant Cell</i> , 2006 , 18, 1292-309	11.6	780
287	Identification of CRE1 as a cytokinin receptor from Arabidopsis. <i>Nature</i> , 2001 , 409, 1060-3	50.4	759
286	A dehydration-induced NAC protein, RD26, is involved in a novel ABA-dependent stress-signaling pathway. <i>Plant Journal</i> , 2004 , 39, 863-76	6.9	693
285	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, 141-53	4.9	671
284	AREB1 is a transcription activator of novel ABRE-dependent ABA signaling that enhances drought stress tolerance in Arabidopsis. <i>Plant Cell</i> , 2005 , 17, 3470-88	11.6	638
283	Regulatory metabolic networks in drought stress responses. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 296-302	9.9	636
282	Functional annotation of a full-length Arabidopsis cDNA collection. <i>Science</i> , 2002 , 296, 141-5	33.3	588

281	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, 270-80	11.6	576
280	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, 8821-6	11.5	529
279	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	11.6	514
278	Comparative genomics in salt tolerance between Arabidopsis and a Rabidopsis-related halophyte salt cress using Arabidopsis microarray. <i>Plant Physiology</i> , 2004 , 135, 1697-709	6.6	497
277	Identification of cold-inducible downstream genes of the Arabidopsis DREB1A/CBF3 transcriptional factor using two microarray systems. <i>Plant Journal</i> , 2004 , 38, 982-93	6.9	479
276	Derepression of ethylene-stabilized transcription factors (EIN3/EIL1) mediates jasmonate and ethylene signaling synergy in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12539-44	11.5	474
275	A transmembrane hybrid-type histidine kinase in Arabidopsis functions as an osmosensor. <i>Plant Cell</i> , 1999 , 11, 1743-54	11.6	464
274	Arabidopsis transcriptome analysis under drought, cold, high-salinity and ABA treatment conditions using a tiling array. <i>Plant and Cell Physiology</i> , 2008 , 49, 1135-49	4.9	407
273	OmicsAnalyses of regulatory networks in plant abiotic stress responses. <i>Current Opinion in Plant Biology</i> , 2010 , 13, 132-8	9.9	371
272	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, 851-6	11.5	370
271	Molecular responses to drought, salinity and frost: common and different paths for plant protection. <i>Current Opinion in Biotechnology</i> , 2003 , 14, 194-9	11.4	368
270	Antagonistic interaction between systemic acquired resistance and the abscisic acid-mediated abiotic stress response in Arabidopsis. <i>Plant Cell</i> , 2008 , 20, 1678-92	11.6	367
269	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, 282-91	3.8	353
268	Two different novel cis-acting elements of erd1, a clpA homologous Arabidopsis gene function in induction by dehydration stress and dark-induced senescence. <i>Plant Journal</i> , 2003 , 33, 259-70	6.9	334
267	Comparative genomics of Physcomitrella patens 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, 8007-12	11.5	301
266	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, 657-65	4.6	291
265	An Arabidopsis gene family encoding DRE/CRT binding proteins involved in low-temperature-responsive gene expression. <i>Biochemical and Biophysical Research Communications</i> , 1998 , 250, 161-70	3.4	267
264	TCP transcription factors regulate the activities of ASYMMETRIC LEAVES1 and miR164, as well as the auxin response, during differentiation of leaves in Arabidopsis. <i>Plant Cell</i> , 2010 , 22, 3574-88	11.6	266

263	Arabidopsis HsfA1 transcription factors function as the main positive regulators in heat shock-responsive gene expression. <i>Molecular Genetics and Genomics</i> , 2011 , 286, 321-32	3.1	253
262	Transcriptional regulation of ABI3- and ABA-responsive genes including RD29B and RD29A in seeds, germinating embryos, and seedlings of Arabidopsis. <i>Plant Molecular Biology</i> , 2006 , 60, 51-68	4.6	249
261	Alterations of lysine modifications on the histone H3 N-tail under drought stress conditions in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2008 , 49, 1580-8	4.9	248
260	The AP2/ERF transcription factor WIND1 controls cell dedifferentiation in Arabidopsis. <i>Current Biology</i> , 2011 , 21, 508-14	6.3	246
259	Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. <i>Frontiers in Plant Science</i> , 2015 , 6, 114	6.2	245
258	Leucine-rich repeat receptor-like kinase1 is a key membrane-bound regulator of abscisic acid early signaling in Arabidopsis. <i>Plant Cell</i> , 2005 , 17, 1105-19	11.6	239
257	CYP707A3, a major ABA 8Rhydroxylase involved in dehydration and rehydration response in Arabidopsis thaliana. <i>Plant Journal</i> , 2006 , 46, 171-82	6.9	233
256	Monitoring expression profiles of Arabidopsis gene expression during rehydration process after dehydration using ca 7000 full-length cDNA microarray. <i>Plant Journal</i> , 2003 , 34, 868-87	6.9	223
255	Specific interactions between Dicer-like proteins and HYL1/DRB-family dsRNA-binding proteins in Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2005 , 57, 173-88	4.6	221
254	Epigenetic memory for stress response and adaptation in plants. <i>Plant and Cell Physiology</i> , 2014 , 55, 1859-63	4.9	218
253	Plants tolerant of high boron levels. <i>Science</i> , 2007 , 318, 1417	33.3	207
252	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, 810-22	6.9	203
251	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. <i>Genome Research</i> , 2007 , 17, 175-83	9.7	200
250	The FOX hunting system: an alternative gain-of-function gene hunting technique. <i>Plant Journal</i> , 2006 , 48, 974-85	6.9	199
249	Genome-wide analysis of alternative pre-mRNA splicing in Arabidopsis thaliana based on full-length cDNA sequences. <i>Nucleic Acids Research</i> , 2004 , 32, 5096-103	20.1	195
248	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. <i>Plant Journal</i> , 1998 , 15, 707-20	6.9	189
247	High humidity induces abscisic acid 8Rhydroxylase in stomata and vasculature to regulate local and systemic abscisic acid responses in Arabidopsis. <i>Plant Physiology</i> , 2009 , 149, 825-34	6.6	188
246	Crosstalk in the responses to abiotic and biotic stresses in Arabidopsis: analysis of gene expression in cytochrome P450 gene superfamily by cDNA microarray. <i>Plant Molecular Biology</i> , 2004 , 55, 327-42	4.6	184

245	A novel zinc-binding motif revealed by solution structures of DNA-binding domains of Arabidopsis SBP-family transcription factors. <i>Journal of Molecular Biology</i> , 2004 , 337, 49-63	6.5	178
244	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013 , 18, 267-76	13.1	167
243	Identification of Arabidopsis genes regulated by high light-stress using cDNA microarray. <i>Photochemistry and Photobiology</i> , 2003 , 77, 226-33	3.6	166
242	Chromatin regulation functions in plant abiotic stress responses. <i>Plant, Cell and Environment</i> , 2010 , 33, 604-11	8.4	163
241	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	8.4	161
240	Vacuolar processing enzymes are essential for proper processing of seed storage proteins in Arabidopsis thaliana. <i>Journal of Biological Chemistry</i> , 2003 , 278, 32292-9	5.4	160
239	Genome-wide suppression of aberrant mRNA-like noncoding RNAs by NMD in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2453-8	11.5	145
238	Solution structure of an Arabidopsis WRKY DNA binding domain. <i>Plant Cell</i> , 2005 , 17, 944-56	11.6	143
237	Transition of chromatin status during the process of recovery from drought stress in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2012 , 53, 847-56	4.9	142
236	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, 873-88	6.9	140
235	Arabidopsis 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, 4840-5	11.5	137
234	Toxicity of free proline revealed in an arabidopsis T-DNA-tagged mutant deficient in proline dehydrogenase. <i>Plant and Cell Physiology</i> , 2003 , 44, 541-8	4.9	136
233	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, 1525-39	4.9	136
232	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	3.7	133
231	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, 709-19	6.6	133
230	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017 , 3, 17097	11.5	129
229	Classification and expression analysis of Arabidopsis F-box-containing protein genes. <i>Plant and Cell Physiology</i> , 2002 , 43, 1073-85	4.9	129
228	Arabidopsis HDA6 regulates locus-directed heterochromatin silencing in cooperation with MET1. <i>PLoS Genetics</i> , 2011 , 7, e1002055	6	119

227	Arabidopsis 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, 3090-5	11.5	118
226	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. <i>Functional and Integrative Genomics</i> , 2006 , 6, 212-34	3.8	118
225	Identification of plant promoter constituents by analysis of local distribution of short sequences. <i>BMC Genomics</i> , 2007 , 8, 67	4.5	117
224	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, 2395-400	11.5	116
223	Analysis of ABA hypersensitive germination2 revealed the pivotal functions of PARN in stress response in Arabidopsis. <i>Plant Journal</i> , 2005 , 44, 972-84	6.9	116
222	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, 633-43	2.6	115
221	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	4.6	115
220	RARTF: database and tools for complete sets of Arabidopsis transcription factors. <i>DNA Research</i> , 2005 , 12, 247-56	4.5	115
219	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	3.7	112
218	A plant locus essential for phyloquinone (vitamin K1) biosynthesis originated from a fusion of four eubacterial genes. <i>Journal of Biological Chemistry</i> , 2006 , 281, 17189-17196	5.4	101
217	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, 250-7	3.4	100
216	Systematic approaches to using the FOX hunting system to identify useful rice genes. <i>Plant Journal</i> , 2009 , 57, 883-94	6.9	99
215	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, 1496-501	11.5	99
214	A genome-wide gain-of function analysis of rice genes using the FOX-hunting system. <i>Plant Molecular Biology</i> , 2007 , 65, 357-71	4.6	96
213	Arabidopsis HDA6 is required for freezing tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 406, 414-9	3.4	95
212	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	6.9	95
211	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, 852-64	6.9	95
210	Group A PP2Cs evolved in land plants as key regulators of intrinsic desiccation tolerance. <i>Nature Communications</i> , 2013 , 4, 2219	17.4	94

209	Identification of photorespiratory glutamate:glyoxylate aminotransferase (GGAT) gene in Arabidopsis. <i>Plant Journal</i> , 2003 , 33, 975-87	6.9	94
208	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, 749-62	3.6	93
207	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016 , 7, 13295	17.4	91
206	Solution structure of the B3 DNA binding domain of the Arabidopsis cold-responsive transcription factor RAV1. <i>Plant Cell</i> , 2004 , 16, 3448-59	11.6	91
205	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, 1695-9	6.6	91
204	The karrikin receptor KAI2 promotes drought resistance in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2017 , 13, e1007076	6	87
203	Sequencing and analysis of approximately 40,000 soybean cDNA clones from a full-length-enriched cDNA library. <i>DNA Research</i> , 2008 , 15, 333-46	4.5	86
202	Armadillo repeat-containing kinesins and a NIMA-related kinase are required for epidermal-cell morphogenesis in Arabidopsis. <i>Plant Journal</i> , 2008 , 53, 157-71	6.9	85
201	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	3.7	82
200	Development of 5006 full-length cDNAs in barley: a tool for accessing cereal genomics resources. <i>DNA Research</i> , 2009 , 16, 81-9	4.5	81
199	Heterogeneity of Arabidopsis core promoters revealed by high-density TSS analysis. <i>Plant Journal</i> , 2009 , 60, 350-62	6.9	81
198	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, 6753-8	11.5	81
197	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, 355-68	3.1	80
196	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, 335-45	4.5	79
195	Plastidic RNA polymerase sigma factors in Arabidopsis. <i>Plant and Cell Physiology</i> , 1999 , 40, 832-42	4.9	79
194	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	5.3	78
193	Identifying the target genes of SUPPRESSOR OF GAMMA RESPONSE 1, a master transcription factor controlling DNA damage response in Arabidopsis. <i>Plant Journal</i> , 2018 , 94, 439-453	6.9	77
192	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. <i>Plant Cell</i> , 2013 , 25, 4378-90	11.6	76

191	The cDNA microarray analysis using an Arabidopsis pad3 mutant reveals the expression profiles and classification of genes induced by <i>Alternaria brassicicola</i> attack. <i>Plant and Cell Physiology</i> , 2003 , 44, 377-387	4.9	76
190	Regulating Subcellular Metal Homeostasis: The Key to Crop Improvement. <i>Frontiers in Plant Science</i> , 2016 , 7, 1192	6.2	76
189	Gene-specific expression and calcium activation of Arabidopsis thaliana phospholipase C isoforms. <i>New Phytologist</i> , 2004 , 162, 643-654	9.8	74
188	Identification of ASK and clock-associated proteins as molecular partners of LKP2 (LOV kelch protein 2) in Arabidopsis. <i>Journal of Experimental Botany</i> , 2004 , 55, 2015-27	7	73
187	Histone Modifications Form Epigenetic Regulatory Networks to Regulate Abiotic Stress Response. <i>Plant Physiology</i> , 2020 , 182, 15-26	6.6	72
186	RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions. <i>Journal of Experimental Botany</i> , 2004 , 55, 213-23	7	72
185	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, 806-15	3.4	72
184	Solution structure of the major DNA-binding domain of Arabidopsis thaliana ethylene-insensitive3-like3. <i>Journal of Molecular Biology</i> , 2005 , 348, 253-64	6.5	68
183	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, 813-6	6	68
182	A Stress-Activated Transposon in Arabidopsis Induces Transgenerational Abscisic Acid Insensitivity. <i>Scientific Reports</i> , 2016 , 6, 23181	4.9	67
181	A novel Arabidopsis gene TONSOKU is required for proper cell arrangement in root and shoot apical meristems. <i>Plant Journal</i> , 2004 , 38, 673-84	6.9	67
180	RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenome. <i>Nucleic Acids Research</i> , 2005 , 33, D647-50	20.1	66
179	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	4.5	64
178	Expression and interaction analysis of Arabidopsis Skp1-related genes. <i>Plant and Cell Physiology</i> , 2004 , 45, 83-91	4.9	64
177	AtXTH27 plays an essential role in cell wall modification during the development of tracheary elements. <i>Plant Journal</i> , 2005 , 42, 525-34	6.9	64
176	Structural basis for sequence-specific DNA recognition by an Arabidopsis WRKY transcription factor. <i>Journal of Biological Chemistry</i> , 2012 , 287, 7683-91	5.4	62
175	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, 453-61	6.9	62
174	Structures and evolutionary origins of plant-specific transcription factor DNA-binding domains. <i>Plant Physiology and Biochemistry</i> , 2008 , 46, 394-401	5.4	58

173	DNA microarray analysis of plastid gene expression in an Arabidopsis mutant deficient in a plastid transcription factor sigma, SIG2. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004 , 68, 694-704	2.1	58
172	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	6.2	58
171	Catalysis, subcellular localization, expression and evolution of the targeting peptides degrading protease, AtPreP2. <i>Plant and Cell Physiology</i> , 2005 , 46, 985-96	4.9	55
170	Transcriptomic analysis of rice in response to iron deficiency and excess. <i>Rice</i> , 2014 , 7, 18	5.8	53
169	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	4.9	52
168	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, Thellungiella halophila. <i>BMC Plant Biology</i> , 2008 , 8, 115	5.3	52
167	A resource of 5,814 dissociation transposon-tagged and sequence-indexed lines of Arabidopsis transposed from start loci on chromosome 5. <i>Plant and Cell Physiology</i> , 2005 , 46, 1149-53	4.9	52
166	RNA regulation in plant abiotic stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012 , 1819, 149-53	6	51
165	Isolation and identification of ubiquitin-related proteins from Arabidopsis seedlings. <i>Journal of Experimental Botany</i> , 2009 , 60, 3067-73	7	51
164	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	6.9	51
163	Identification of the candidate genes regulated by RNA-directed DNA methylation in Arabidopsis. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 376, 553-7	3.4	49
162	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	11.5	49
161	Arabidopsis Rad51B is important for double-strand DNA breaks repair in somatic cells. <i>Plant Molecular Biology</i> , 2005 , 57, 819-33	4.6	48
160	Ethanol Enhances High-Salinity Stress Tolerance by Detoxifying Reactive Oxygen Species in and Rice. <i>Frontiers in Plant Science</i> , 2017 , 8, 1001	6.2	47
159	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, 3602-11	7.6	47
158	Tissue-specific transcriptome analysis reveals cell wall metabolism, flavonol biosynthesis and defense responses are activated in the endosperm of germinating Arabidopsis thaliana seeds. <i>Plant and Cell Physiology</i> , 2012 , 53, 16-27	4.9	47
157	Expression profiles of Arabidopsis phospholipase A IIA gene in response to biotic and abiotic stresses. <i>Plant and Cell Physiology</i> , 2003 , 44, 1246-52	4.9	47
156	Genome-scale, biochemical annotation method based on the wheat germ cell-free protein synthesis system. <i>Phytochemistry</i> , 2004 , 65, 1549-55	4	46

155	A regulatory module controlling stress-induced cell cycle arrest in. <i>ELife</i> , 2019 , 8,	8.9	46
154	The Distinct Roles of Class I and II RPD3-Like Histone Deacetylases in Salinity Stress Response. <i>Plant Physiology</i> , 2017 , 175, 1760-1773	6.6	45
153	Construction of a full-length cDNA library from young spikelets of hexaploid wheat and its characterization by large-scale sequencing of expressed sequence tags. <i>Genes and Genetic Systems</i> , 2004 , 79, 227-32	1.4	44
152	Loss of Arabidopsis 5R3RExoribonuclease AtXRN4 Function Enhances Heat Stress Tolerance of Plants Subjected to Severe Heat Stress. <i>Plant and Cell Physiology</i> , 2015 , 56, 1762-72	4.9	43
151	Transduction of RNA-directed DNA methylation signals to repressive histone marks in Arabidopsis thaliana. <i>EMBO Journal</i> , 2010 , 29, 352-62	13	43
150	A simple and high-sensitivity method for analysis of ubiquitination and polyubiquitination based on wheat cell-free protein synthesis. <i>BMC Plant Biology</i> , 2009 , 9, 39	5.3	43
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