

Miki Fujita

List of Publications by Year in descending order

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42
papers

13,325
citations

136950

32
h-index

302126

39
g-index

45
all docs

45
docs citations

45
times ranked

12013
citing authors

#	ARTICLE	IF	CITATIONS
1	Inter-tissue and inter-organ signaling in drought stress response and phenotyping of drought tolerance. <i>Plant Journal</i> , 2022, 109, 342-358.	5.7	50
2	High affinity promoter binding of STOP1 is essential for early expression of novel aluminum-induced resistance genes <i>GDH1</i> and <i>GDH2</i> in Arabidopsis. <i>Journal of Experimental Botany</i> , 2021, 72, 2769-2789.	4.8	28
3	The genotype-dependent phenotypic landscape of quinoa in salt tolerance and key growth traits. <i>DNA Research</i> , 2020, 27, .	3.4	15
4	CRISPR/Cas9-targeted mutagenesis of OsERA1 confers enhanced responses to abscisic acid and drought stress and increased primary root growth under nonstressed conditions in rice. <i>PLoS ONE</i> , 2020, 15, e0243376.	2.5	73
5	Extracellular Spermine Triggers a Rapid Intracellular Phosphatidic Acid Response in Arabidopsis, Involving PLD γ Activation and Stimulating Ion Flux. <i>Frontiers in Plant Science</i> , 2019, 10, 601.	3.6	19
6	Casein kinase 2 β and γ subunits inversely modulate ABA signal output in Arabidopsis protoplasts. <i>Planta</i> , 2018, 248, 571-578.	3.2	14
7	RIPPS: A Plant Phenotyping System for Quantitative Evaluation of Growth Under Controlled Environmental Stress Conditions. <i>Plant and Cell Physiology</i> , 2018, 59, 2030-2038.	3.1	26
8	Overexpression of AtABCG25 enhances the abscisic acid signal in guard cells and improves plant water use efficiency. <i>Plant Science</i> , 2016, 251, 75-81.	3.6	45
9	SNACs, stress-responsive NAC transcription factors, mediate ABA-inducible leaf senescence. <i>Plant Journal</i> , 2015, 84, 1114-1123.	5.7	202
10	Polyamine Transport Systems in Plants. , 2015, , 179-185.		6
11	Identification of Polyamine Transporters in Plants: Paraquat Transport Provides Crucial Clues. <i>Plant and Cell Physiology</i> , 2014, 55, 855-861.	3.1	72
12	STOP2 Activates Transcription of Several Genes for Al- and Low pH-Tolerance that Are Regulated by STOP1 in Arabidopsis. <i>Molecular Plant</i> , 2014, 7, 311-322.	8.3	120
13	Characterization of the Promoter Region of an Arabidopsis Gene for 9-cis-Epoxycarotenoid Dioxygenase Involved in Dehydration-Inducible Transcription. <i>DNA Research</i> , 2013, 20, 315-324.	3.4	93
14	Natural variation in a polyamine transporter determines paraquat tolerance in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6343-6347.	7.1	115
15	FOX-superroots of <i>Lotus corniculatus</i> , overexpressing Arabidopsis full-length cDNA, show stable variations in morphological traits. <i>Journal of Plant Physiology</i> , 2011, 168, 181-187.	3.5	13
16	ABA-mediated transcriptional regulation in response to osmotic stress in plants. <i>Journal of Plant Research</i> , 2011, 124, 509-525.	2.4	860
17	Efficient Yeast One-/Two-Hybrid Screening Using a Library Composed Only of Transcription Factors in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2010, 51, 2145-2151.	3.1	104
18	STOP1 Regulates Multiple Genes That Protect Arabidopsis from Proton and Aluminum Toxicities. <i>Plant Physiology</i> , 2009, 150, 281-294.	4.8	283

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19	Systematic approaches to using the FOX hunting system to identify useful rice genes. <i>Plant Journal</i> , 2009, 57, 883-894.	5.7	121
20	Three SnRK2 Protein Kinases are the Main Positive Regulators of Abscisic Acid Signaling in Response to Water Stress in Arabidopsis. <i>Plant and Cell Physiology</i> , 2009, 50, 2123-2132.	3.1	599
21	Metabolic Pathways Involved in Cold Acclimation Identified by Integrated Analysis of Metabolites and Transcripts Regulated by DREB1A and DREB2A. <i>Plant Physiology</i> , 2009, 150, 1972-1980.	4.8	315
22	Arabidopsis DREB2A-Interacting Proteins Function as RING E3 Ligases and Negatively Regulate Plant Drought Stress-Responsive Gene Expression. <i>Plant Cell</i> , 2008, 20, 1693-1707.	6.6	477
23	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.	2.1	112
24	Functional analysis of a NAC-type transcription factor OsNAC6 involved in abiotic and biotic stress-responsive gene expression in rice. <i>Plant Journal</i> , 2007, 51, 617-630.	5.7	996
25	A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. <i>Plant Molecular Biology</i> , 2007, 65, 357-371.	3.9	103
26	The FOX hunting system: an alternative gain-of-function gene hunting technique. <i>Plant Journal</i> , 2006, 48, 974-985.	5.7	244
27	Engineering drought tolerance in plants: discovering and tailoring genes to unlock the future. <i>Current Opinion in Biotechnology</i> , 2006, 17, 113-122.	6.6	683
28	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. <i>Functional and Integrative Genomics</i> , 2006, 6, 212-234.	3.5	137
29	Crosstalk between abiotic and biotic stress responses: a current view from the points of convergence in the stress signaling networks. <i>Current Opinion in Plant Biology</i> , 2006, 9, 436-442.	7.1	1,595
30	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.	6.6	826
31	A dehydration-induced NAC protein, RD26, is involved in a novel ABA-dependent stress-signaling pathway. <i>Plant Journal</i> , 2004, 39, 863-876.	5.7	877
32	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.	6.6	1,329
33	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, 868-887.	5.7	263
34	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.	4.8	94
35	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.	3.1	161
36	Expression Profiles of Arabidopsis Phospholipase A IIA Gene in Response to Biotic and Abiotic Stresses. <i>Plant and Cell Physiology</i> , 2003, 44, 1246-1252.	3.1	50

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37	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.	3.5	394
38	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.	5.7	1,697
39	Interactions and Nuclear Import of the N and P Proteins of Sonchus Yellow Net Virus, a Plant Nucleorhabdovirus. <i>Journal of Virology</i> , 2001, 75, 9393-9406.	3.4	69
40	Bromovirus Movement Protein Conditions for the Host Specificity of Virus Movement Through the Vascular System and Affects Pathogenicity in Cowpea. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 1195-1203.	2.6	12
41	Transcriptome analysis in abiotic stress conditions in higher plants. <i>Topics in Current Genetics</i> , 0, , 271-308.	0.7	16
42	Transcription Factors Involved in the Crosstalk between Abiotic and Biotic Stress-Signaling Networks. , 0, , 43-58.		10