

Feng Qin

List of Publications by Year in descending order

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48
papers

8,090
citations

136885

32
h-index

233338

45
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48
all docs

48
docs citations

48
times ranked

7580
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional Analysis of an Arabidopsis Transcription Factor, DREB2A, Involved in Drought-Responsive Gene Expression. <i>Plant Cell</i> , 2006, 18, 1292-1309.	3.1	968
2	Dual function of an Arabidopsis transcription factor DREB2A in water-stress-responsive and heat-stress-responsive gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18822-18827.	3.3	694
3	Plant abiotic stress response and nutrient use efficiency. <i>Science China Life Sciences</i> , 2020, 63, 635-674.	2.3	689
4	Functional analysis of AHK1/ATHK1 and cytokinin receptor histidine kinases in response to abscisic acid, drought, and salt stress in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20623-20628.	3.3	592
5	<i>Arabidopsis</i> 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.	3.1	477
6	Achievements and Challenges in Understanding Plant Abiotic Stress Responses and Tolerance. <i>Plant and Cell Physiology</i> , 2011, 52, 1569-1582.	1.5	451
7	Regulation and functional analysis of ZmDREB2A in response to drought and heat stresses in <i>Zea mays</i> L. <i>Plant Journal</i> , 2007, 50, 54-69.	2.8	447
8	Genetic variation in ZmVPP1 contributes to drought tolerance in maize seedlings. <i>Nature Genetics</i> , 2016, 48, 1233-1241.	9.4	438
9	A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. <i>Nature Communications</i> , 2015, 6, 8326.	5.8	392
10	Cloning and Functional Analysis of a Novel DREB1/CBF Transcription Factor Involved in Cold-Responsive Gene Expression in <i>Zea mays</i> L. <i>Plant and Cell Physiology</i> , 2004, 45, 1042-1052.	1.5	336
11	Genome-Wide Analysis of ZmDREB Genes and Their Association with Natural Variation in Drought Tolerance at Seedling Stage of <i>Zea mays</i> L. <i>PLoS Genetics</i> , 2013, 9, e1003790.	1.5	280
12	Co-expression of the stress-inducible zinc finger homeodomain ZFHD1 and NAC transcription factors enhances expression of the ERD1 gene in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2006, 49, 46-63.	2.8	256
13	Functional analysis of an Arabidopsis heat-shock transcription factor HsfA3 in the transcriptional cascade downstream of the DREB2A stress-regulatory system. <i>Biochemical and Biophysical Research Communications</i> , 2008, 368, 515-521.	1.0	209
14	<i>Arabidopsis</i> Cys2/His2 Zinc-Finger Proteins AZF1 and AZF2 Negatively Regulate Abscisic Acid-Repressive and Auxin-Inducible Genes under Abiotic Stress Conditions. <i>Plant Physiology</i> , 2011, 157, 742-756.	2.3	165
15	<i>Arabidopsis</i> DPB3-1, a DREB2A Interactor, Specifically Enhances Heat Stress-Induced Gene Expression by Forming a Heat Stress-Specific Transcriptional Complex with NF-Y Subunits. <i>Plant Cell</i> , 2014, 26, 4954-4973.	3.1	143
16	<i>Arabidopsis</i> RZFP34/CHYR1, a Ubiquitin E3 Ligase, Regulates Stomatal Movement and Drought Tolerance via SnRK2.6-Mediated Phosphorylation. <i>Plant Cell</i> , 2015, 27, 3228-3244.	3.1	129
17	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	6.0	110
18	Deletion of an Endoplasmic Reticulum Stress Response Element in a ZmPP2C-A Gene Facilitates Drought Tolerance of Maize Seedlings. <i>Molecular Plant</i> , 2017, 10, 456-469.	3.9	107

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19	<i>SPINDLY</i> , a Negative Regulator of Gibberellic Acid Signaling, Is Involved in the Plant Abiotic Stress Response. <i>Plant Physiology</i> , 2011, 157, 1900-1913.	2.3	93
20	Induced over-expression of AtDREB2A CA improves drought tolerance in sugarcane. <i>Plant Science</i> , 2014, 221-222, 59-68.	1.7	91
21	Genetic variation in <i>ZmTIP1</i> contributes to root hair elongation and drought tolerance in maize. <i>Plant Biotechnology Journal</i> , 2020, 18, 1271-1283.	4.1	85
22	BPM-CUL3 E3 ligase modulates thermotolerance by facilitating negative regulatory domain-mediated degradation of DREB2A in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8528-E8536.	3.3	82
23	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163.	3.8	76
24	Genome-Wide Association Study Reveals Natural Variations Contributing to Drought Resistance in Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 1110.	1.7	72
25	Heat-induced inhibition of phosphorylation of the stress-protective transcription factor DREB2A promotes thermotolerance of <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 902-917.	1.6	62
26	Contribution of Genomics to Gene Discovery in Plant Abiotic Stress Responses. <i>Molecular Plant</i> , 2012, 5, 1176-1178.	3.9	59
27	A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. <i>Nature Communications</i> , 2022, 13, 2222.	5.8	55
28	Stabilization of <i>Arabidopsis</i> DREB2A Is Required but Not Sufficient for the Induction of Target Genes under Conditions of Stress. <i>PLoS ONE</i> , 2013, 8, e80457.	1.1	52
29	Genetic dissection of maize drought tolerance for trait improvement. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	49
30	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	3.8	47
31	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	3.5	46
32	Genomic basis underlying the metabolome-mediated drought adaptation of maize. <i>Genome Biology</i> , 2021, 22, 260.	3.8	44
33	The classical <i>SOS</i> pathway confers natural variation of salt tolerance in maize. <i>New Phytologist</i> , 2022, 236, 479-494.	3.5	39
34	Characterization of Proteome Variation During Modern Maize Breeding*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 263-276.	2.5	36
35	MAPK-like protein 1 positively regulates maize seedling drought sensitivity by suppressing ABA biosynthesis. <i>Plant Journal</i> , 2020, 102, 747-760.	2.8	33
36	Manipulating <i>ZmEXPA4</i> expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. <i>Plant Cell</i> , 2021, 33, 2058-2071.	3.1	33

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37	Measuring specific interaction of transcription factor ZmDREB1A with its DNA responsive element at the molecular level. <i>Nucleic Acids Research</i> , 2004, 32, e101-e101.	6.5	25
38	Late Pliocene vegetation and climate of Zhangcun region, Shanxi, North China. <i>Global Change Biology</i> , 2011, 17, 1850-1870.	4.2	24
39	IntAssoPlot: An R Package for Integrated Visualization of Genome-Wide Association Study Results With Gene Structure and Linkage Disequilibrium Matrix. <i>Frontiers in Genetics</i> , 2020, 11, 260.	1.1	22
40	COP1 positively regulates ABA signaling during Arabidopsis seedling growth in darkness by mediating ABA-induced ABI5 accumulation. <i>Plant Cell</i> , 2022, 34, 2286-2308.	3.1	17
41	AFLP and RFLP linkage map in Coix. <i>Genetic Resources and Crop Evolution</i> , 2005, 52, 209-214.	0.8	15
42	Quantitative Profiling of Arabidopsis Polar Glycerolipids under Two Types of Heat Stress. <i>Plants</i> , 2020, 9, 693.	1.6	11
43	Heat shock protein 101 (HSP101) promotes flowering under nonstress conditions. <i>Plant Physiology</i> , 2021, 186, 407-419.	2.3	11
44	The transcription factor ZmMYB69 represses lignin biosynthesis by activating <i>ZmMYB31/42</i> expression in maize. <i>Plant Physiology</i> , 2022, 189, 1916-1919.	2.3	11
45	Utility of Surface Pollen Assemblages to Delimit Eastern Eurasian Steppe Types. <i>PLoS ONE</i> , 2015, 10, e0119412.	1.1	8
46	ABA Regulation of Plant Responses to Drought and Salt Stresses. , 2014, , 315-336.		7
47	Transcription Factors Involved in Environmental Stress Responses in Plants. , 2012, , 279-295.		2
48	Genome-Wide Association Analyses to Identify SNPs Related to. <i>Methods in Molecular Biology</i> , 2022, 2462, 201-219.	0.4	0