

Feng Qin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1051945/publications.pdf>

Version: 2024-02-01

48
papers

8,090
citations

136950

32
h-index

233421

45
g-index

48
all docs

48
docs citations

48
times ranked

7580
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Analyses to Identify SNPs Related to. <i>Methods in Molecular Biology</i> , 2022, 2462, 201-219.	0.9	0
2	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.	6.6	17
3	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	12.6	110
4	A dirigent family protein confers variation of Casparian strip thickness and salt tolerance in maize. <i>Nature Communications</i> , 2022, 13, 2222.	12.8	55
5	The classical <sc>SOS</sc> pathway confers natural variation of salt tolerance in maize. <i>New Phytologist</i> , 2022, 236, 479-494.	7.3	39
6	The transcription factor ZmMYB69 represses lignin biosynthesis by activating <i>ZmMYB31/42</i> expression in maize. <i>Plant Physiology</i> , 2022, 189, 1916-1919.	4.8	11
7	Genetic dissection of maize drought tolerance for trait improvement. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	49
8	Heat shock protein 101 (HSP101) promotes flowering under nonstress conditions. <i>Plant Physiology</i> , 2021, 186, 407-419.	4.8	11
9	Manipulating <i>ZmEXPA4</i> expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. <i>Plant Cell</i> , 2021, 33, 2058-2071.	6.6	33
10	Metabolomics-driven gene mining and genetic improvement of tolerance to salt-induced osmotic stress in maize. <i>New Phytologist</i> , 2021, 230, 2355-2370.	7.3	46
11	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	8.8	47
12	Genomic basis underlying the metabolome-mediated drought adaptation of maize. <i>Genome Biology</i> , 2021, 22, 260.	8.8	44
13	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.	8.3	85
14	MAPK-like protein 1 positively regulates maize seedling drought sensitivity by suppressing ABA biosynthesis. <i>Plant Journal</i> , 2020, 102, 747-760.	5.7	33
15	Quantitative Profiling of Arabidopsis Polar Glycerolipids under Two Types of Heat Stress. <i>Plants</i> , 2020, 9, 693.	3.5	11
16	Plant abiotic stress response and nutrient use efficiency. <i>Science China Life Sciences</i> , 2020, 63, 635-674.	4.9	689
17	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.	2.3	22
18	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163.	8.8	76

#	ARTICLE	IF	CITATIONS
19	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.	3.4	62
20	Characterization of Proteome Variation During Modern Maize Breeding*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 263-276.	3.8	36
21	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.	7.1	82
22	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.	8.3	107
23	Genome-Wide Association Study Reveals Natural Variations Contributing to Drought Resistance in Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 1110.	3.6	72
24	Genetic variation in ZmVPP1 contributes to drought tolerance in maize seedlings. <i>Nature Genetics</i> , 2016, 48, 1233-1241.	21.4	438
25	Utility of Surface Pollen Assemblages to Delimit Eastern Eurasian Steppe Types. <i>PLoS ONE</i> , 2015, 10, e0119412.	2.5	8
26	A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. <i>Nature Communications</i> , 2015, 6, 8326.	12.8	392
27	<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.	6.6	129
28	<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.	6.6	143
29	ABA Regulation of Plant Responses to Drought and Salt Stresses. , 2014, , 315-336.		7
30	Induced over-expression of AtDREB2A CA improves drought tolerance in sugarcane. <i>Plant Science</i> , 2014, 221-222, 59-68.	3.6	91
31	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.	3.5	280
32	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.	2.5	52
33	Contribution of Genomics to Gene Discovery in Plant Abiotic Stress Responses. <i>Molecular Plant</i> , 2012, 5, 1176-1178.	8.3	59
34	Transcription Factors Involved in Environmental Stress Responses in Plants. , 2012, , 279-295.		2
35	Achievements and Challenges in Understanding Plant Abiotic Stress Responses and Tolerance. <i>Plant and Cell Physiology</i> , 2011, 52, 1569-1582.	3.1	451
36	Late Pliocene vegetation and climate of Zhangcun region, Shanxi, North China. <i>Global Change Biology</i> , 2011, 17, 1850-1870.	9.5	24

#	ARTICLE	IF	CITATIONS
37	Arabidopsis Cys2/His2 Zinc-Finger Proteins AZF1 and AZF2 Negatively Regulate Abscisic Acid-Repressive and Auxin-Inducible Genes under Abiotic Stress Conditions Å Å. Plant Physiology, 2011, 157, 742-756.	4.8	165
38	<i>SPINDLY</i>, a Negative Regulator of Gibberellic Acid Signaling, Is Involved in the Plant Abiotic Stress Response Å Å. Plant Physiology, 2011, 157, 1900-1913.	4.8	93
39	Functional analysis of an Arabidopsis heat-shock transcription factor HsfA3 in the transcriptional cascade downstream of the DREB2A stress-regulatory system. Biochemical and Biophysical Research Communications, 2008, 368, 515-521.	2.1	209
40	<i>Arabidopsis</i> DREB2A-Interacting Proteins Function as RING E3 Ligases and Negatively Regulate Plant Drought Stressâ€Responsive Gene Expression. Plant Cell, 2008, 20, 1693-1707.	6.6	477
41	Functional analysis of AHK1/ATHK1 and cytokinin receptor histidine kinases in response to abscisic acid, drought, and salt stress in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20623-20628.	7.1	592
42	Regulation and functional analysis of ZmDREB2A in response to drought and heat stresses in Zea mays L. Plant Journal, 2007, 50, 54-69.	5.7	447
43	Co-expression of the stress-inducible zinc finger homeodomain ZFHD1 and NAC transcription factors enhances expression of the ERD1 gene in Arabidopsis. Plant Journal, 2006, 49, 46-63.	5.7	256
44	Functional Analysis of an Arabidopsis Transcription Factor, DREB2A, Involved in Drought-Responsive Gene Expression. Plant Cell, 2006, 18, 1292-1309.	6.6	968
45	Dual function of an Arabidopsis transcription factor DREB2A in water-stress-responsive and heat-stress-responsive gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18822-18827.	7.1	694
46	AFLP and RFLP linkage map in Coix. Genetic Resources and Crop Evolution, 2005, 52, 209-214.	1.6	15
47	Measuring specific interaction of transcription factor ZmDREB1A with its DNA responsive element at the molecular level. Nucleic Acids Research, 2004, 32, e101-e101.	14.5	25
48	Cloning and Functional Analysis of a Novel DREB1/CBF Transcription Factor Involved in Cold-Responsive Gene Expression in Zea mays L.. Plant and Cell Physiology, 2004, 45, 1042-1052.	3.1	336