

# Yang Zhao

## List of Publications by Year in descending order

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30  
papers

1,167  
citations

567281

15  
h-index

477307

29  
g-index

30  
all docs

30  
docs citations

30  
times ranked

1478  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and characterization of heat-responsive miRNAs and their regulatory network in maize. <i>Plant Growth Regulation</i> , 2022, 96, 195-208.	3.4	4
2	Identification and characterization of heat-responsive lncRNAs in maize inbred line CM1. <i>BMC Genomics</i> , 2022, 23, 208.	2.8	6
3	Comparative Transcriptomics Reveals the Molecular Mechanism of the Parental Lines of Maize Hybrid Anâ€™nong876 in Response to Salt Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5231.	4.1	5
4	Identification and Characterization of the Core Region of ZmDi19-5 Promoter Activity and Its Upstream Regulatory Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7390.	4.1	0
5	Transcriptome Analysis of Tolerant and Susceptible Maize Genotypes Reveals Novel Insights about the Molecular Mechanisms Underlying Drought Responses in Leaves. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6980.	4.1	36
6	Genome-wide analysis of the maize superoxide dismutase (SOD) gene family reveals important roles in drought and salt responses. <i>Genetics and Molecular Biology</i> , 2021, 44, e20210035.	1.3	16
7	Genome-wide association study leads to novel genetic insights into resistance to <i>Aspergillus flavus</i> in maize kernels. <i>BMC Plant Biology</i> , 2020, 20, 206.	3.6	8
8	Comparative transcriptome analysis reveals important roles of nonadditive genes in maize hybrid Anâ€™nong 591 under heat stress. <i>BMC Plant Biology</i> , 2019, 19, 273.	3.6	43
9	Comparative genome analysis of the SPL gene family reveals novel evolutionary features in maize. <i>Genetics and Molecular Biology</i> , 2019, 42, 380-394.	1.3	13
10	A maize NAC transcription factor, ZmNAC34, negatively regulates starch synthesis in rice. <i>Plant Cell Reports</i> , 2019, 38, 1473-1484.	5.6	21
11	A maize stress-responsive Di19 transcription factor, ZmDi19-1, confers enhanced tolerance to salt in transgenic <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2019, 38, 1563-1578.	5.6	14
12	Systematic identification and characterization of candidate genes for the regulation of plant height in maize. <i>Euphytica</i> , 2019, 215, 1.	1.2	4
13	A Moso Bamboo Drought-Induced 19 Protein, PeDi19-4, Enhanced Drought and Salt Tolerance in Plants via the ABA-Dependent Signaling Pathway. <i>Plant and Cell Physiology</i> , 2019, 60, e1-e14.	3.1	7
14	Genome-wide association study of maize plant architecture using F1 populations. <i>Plant Molecular Biology</i> , 2019, 99, 1-15.	3.9	17
15	Global transcriptome and weighted gene co-expression network analyses reveal hybrid-specific modules and candidate genes related to plant height development in maize. <i>Plant Molecular Biology</i> , 2018, 98, 187-203.	3.9	23
16	Functional analysis of the HD-Zip I gene ZmHDZ1 in ABA-mediated salt tolerance in rice. <i>Journal of Plant Biology</i> , 2017, 60, 207-214.	2.1	13
17	A novel GRAS transcription factor, ZmGRAS20, regulates starch biosynthesis in rice endosperm. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 143-154.	3.1	18
18	Transcriptome analysis reveals critical genes and key pathways involved in early phyllotaxy development in maize. <i>Genes and Genomics</i> , 2017, 39, 15-26.	1.4	1

#	ARTICLE	IF	CITATIONS
19	The maize WRKY transcription factor ZmWRKY17 negatively regulates salt stress tolerance in transgenic Arabidopsis plants. <i>Planta</i> , 2017, 246, 1215-1231.	3.2	124
20	Genome-wide analysis of the IQD gene family in maize. <i>Molecular Genetics and Genomics</i> , 2016, 291, 543-558.	2.1	35
21	Significant Microsynteny with New Evolutionary Highlights Is Detected through Comparative Genomic Sequence Analysis of Maize CCCH IX Gene Subfamily. <i>International Journal of Genomics</i> , 2015, 2015, 1-12.	1.6	4
22	Systematic Analysis of the Maize PHD-Finger Gene Family Reveals a Subfamily Involved in Abiotic Stress Response. <i>International Journal of Molecular Sciences</i> , 2015, 16, 23517-23544.	4.1	35
23	Systematic analysis of maize class III peroxidase gene family reveals a conserved subfamily involved in abiotic stress response. <i>Gene</i> , 2015, 566, 95-108.	2.2	109
24	Identification and characterization of the RCI2 gene family in maize ( <i>Zea mays</i> ). <i>Journal of Genetics</i> , 2014, 93, 655-666.	0.7	15
25	A Novel Maize Homeodomain-“Leucine Zipper (HD-Zip) I Gene, Zmhdz10, Positively Regulates Drought and Salt Tolerance in Both Rice and Arabidopsis. <i>Plant and Cell Physiology</i> , 2014, 55, 1142-1156.	3.1	171
26	Overexpression of a maize WRKY58 gene enhances drought and salt tolerance in transgenic rice. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 565-577.	2.3	104
27	Downregulation of caffeoyl-CoA O-methyltransferase (CCoAOMT) by RNA interference leads to reduced lignin production in maize straw. <i>Genetics and Molecular Biology</i> , 2013, 36, 540-546.	1.3	82
28	Systematic Analysis of Sequences and Expression Patterns of Drought-Responsive Members of the HD-Zip Gene Family in Maize. <i>PLoS ONE</i> , 2011, 6, e28488.	2.5	123
29	Whole-genome survey and characterization of MADS-box gene family in maize and sorghum. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 105, 159-173.	2.3	74
30	Identification and characterization of NBS-encoding disease resistance genes in <i>Lotus japonicus</i> . <i>Plant Systematics and Evolution</i> , 2010, 289, 101-110.	0.9	42