

Heng Zhang

List of Publications by Year in descending order

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65
papers

6,495
citations

94433

37
h-index

123424

61
g-index

67
all docs

67
docs citations

67
times ranked

8514
citing authors

#	ARTICLE	IF	CITATIONS
1	Acetylproteomics analyses reveal critical features of lysine- μ -acetylation in Arabidopsis and a role of 14-3-3 protein acetylation in alkaline response. <i>Stress Biology</i> , 2022, 2, .	3.1	7
2	Transcriptome analyses of quinoa leaves revealed critical function of epidermal bladder cells in salt stress acclimation. <i>Plant Stress</i> , 2022, 3, 100061.	5.5	4
3	Liquid-liquid phase separation of RBGD2/4 is required for heat stress resistance in Arabidopsis. <i>Developmental Cell</i> , 2022, 57, 583-597.e6.	7.0	45
4	Stalk cell polar ion transport provide for bladder-based salinity tolerance in <i>Chenopodium quinoa</i> . <i>New Phytologist</i> , 2022, 235, 1822-1835.	7.3	8
5	Salinity Effects on Guard Cell Proteome in <i>Chenopodium quinoa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 428.	4.1	20
6	The receptor-like kinases BAM1 and BAM2 are required for root xylem patterning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
7	A histone H3K4me1-specific binding protein is required for siRNA accumulation and DNA methylation at a subset of loci targeted by RNA-directed DNA methylation. <i>Nature Communications</i> , 2021, 12, 3367.	12.8	21
8	Recognition of H3K9me1 by maize RNA-directed DNA methylation factor SHH2. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1091-1096.	8.5	6
9	Comparative physiological and transcriptomic analysis reveals salinity tolerance mechanisms in <i>Sorghum bicolor</i> (L.) Moench. <i>Planta</i> , 2021, 254, 98.	3.2	7
10	Mechanisms of Salinity Tolerance in Quinoa. , 2021, , 221-242.		0
11	Alleviating the effect of quinoa and the underlying mechanism on hepatic steatosis in high-fat diet-fed rats. <i>Nutrition and Metabolism</i> , 2021, 18, 106.	3.0	6
12	Identification of endogenous small peptides involved in rice immunity through transcriptomics and proteomics-based screening. <i>Plant Biotechnology Journal</i> , 2020, 18, 415-428.	8.3	33
13	It Takes NSUN2 to Beat the Heat in Rice. <i>Developmental Cell</i> , 2020, 53, 253-254.	7.0	1
14	Thriving under Stress: How Plants Balance Growth and the Stress Response. <i>Developmental Cell</i> , 2020, 55, 529-543.	7.0	283
15	Unveiling of active diazotrophs in a flooded rice soil by combination of NanoSIMS and $^{15}\text{N}_2$ -DNA-stable isotope probing. <i>Biology and Fertility of Soils</i> , 2020, 56, 1189-1199.	4.3	17
16	Mechanisms of Plant Responses and Adaptation to Soil Salinity. <i>Innovation(China)</i> , 2020, 1, 100017.	9.1	387
17	Developing and validating protocols for mechanical isolation of guard-cell enriched epidermal peels for omics studies. <i>Functional Plant Biology</i> , 2020, 47, 803.	2.1	8
18	RNA-directed DNA methylation has an important developmental function in Arabidopsis that is masked by the chromatin remodeler PICKLE. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1647-1652.	8.5	4

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19	Sugar Beet (<i>Beta vulgaris</i>) Guard Cells Responses to Salinity Stress: A Proteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2331.	4.1	16
20	Histone acetylation recruits the SWR1 complex to regulate active DNA demethylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16641-16650.	7.1	73
21	A Role for PICKLE in the Regulation of Cold and Salt Stress Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 900.	3.6	58
22	A large-scale screening of quinoa accessions reveals an important role of epidermal bladder cells and stomatal patterning in salinity tolerance. <i>Environmental and Experimental Botany</i> , 2019, 168, 103885.	4.2	39
23	HDAC1 and HDAC2 Regulate Intermediate Progenitor Positioning to Safeguard Neocortical Development. <i>Neuron</i> , 2019, 101, 1117-1133.e5.	8.1	37
24	The genome of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 436.	12.8	130
25	TMK1-mediated auxin signalling regulates differential growth of the apical hook. <i>Nature</i> , 2019, 568, 240-243.	27.8	156
26	Soil aluminum oxides determine biological nitrogen fixation and diazotrophic communities across major types of paddy soils in China. <i>Soil Biology and Biochemistry</i> , 2019, 131, 81-89.	8.8	61
27	Critical function of DNA methyltransferase 1 in tomato development and regulation of the DNA methylome and transcriptome. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1224-1242.	8.5	49
28	Global increase in DNA methylation during orange fruit development and ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1430-1436.	7.1	190
29	A virus-targeted plant receptor-like kinase promotes cell-to-cell spread of RNAi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1388-1393.	7.1	203
30	Complete Genome Sequence of <i>Bacillus megaterium</i> Strain TG1-E1, a Plant Drought Tolerance-Enhancing Bacterium. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
31	Developing naturally stress-resistant crops for a sustainable agriculture. <i>Nature Plants</i> , 2018, 4, 989-996.	9.3	186
32	Understanding the Molecular Basis of Salt Sequestration in Epidermal Bladder Cells of <i>Chenopodium quinoa</i> . <i>Current Biology</i> , 2018, 28, 3075-3085.e7.	3.9	98
33	Structural Basis for Recognition of a Unique Epitope by a Human Anti-tau Antibody. <i>Structure</i> , 2018, 26, 1626-1634.e4.	3.3	9
34	<i>Arabidopsis</i> AGDP1 links H3K9me2 to DNA methylation in heterochromatin. <i>Nature Communications</i> , 2018, 9, 4547.	12.8	66
35	The Chromatin Remodelers PKL and PIE1 Act in an Epigenetic Pathway That Determines H3K27me3 Homeostasis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2018, 30, 1337-1352.	6.6	97
36	Genome Sequence of <i>Bacillus megaterium</i> Strain YC4-R4, a Plant Growth-Promoting Rhizobacterium Isolated from a High-Salinity Environment. <i>Genome Announcements</i> , 2018, 6, .	0.8	8

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37	The developmental regulator PKL is required to maintain correct DNA methylation patterns at RNA-directed DNA methylation loci. <i>Genome Biology</i> , 2017, 18, 103.	8.8	44
38	A pair of transposon-derived proteins function in a histone acetyltransferase complex for active DNA demethylation. <i>Cell Research</i> , 2017, 27, 226-240.	12.0	80
39	Circulating tumour DNA methylation markers for diagnosis and prognosis of hepatocellular carcinoma. <i>Nature Materials</i> , 2017, 16, 1155-1161.	27.5	641
40	A protein complex regulates RNA processing of intronic heterochromatin-containing genes in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7377-E7384.	7.1	74
41	A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value. <i>Cell Research</i> , 2017, 27, 1327-1340.	12.0	170
42	DNA methylation markers for diagnosis and prognosis of common cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7414-7419.	7.1	387
43	Genome sequencing and analysis of <i>Ralstonia solanacearum</i> phylotype I strains FJAT-91, FJAT-452 and FJAT-462 isolated from tomato, eggplant, and chili pepper in China. <i>Standards in Genomic Sciences</i> , 2017, 12, 29.	1.5	1
44	Methylation interactions in <i>Arabidopsis</i> hybrids require RNA-directed DNA methylation and are influenced by genetic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4248-56.	7.1	79
45	Cross-Talk Between Sporophyte and Gametophyte Generations Is Promoted by CHD3 Chromatin Remodelers in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2016, 203, 817-829.	2.9	16
46	The <i>Vigna unguiculata</i> Gene Expression Atlas (VuGEA) from <i>de novo</i> assembly and quantification of RNA-seq data provides insights into seed maturation mechanisms. <i>Plant Journal</i> , 2016, 88, 318-327.	5.7	64
47	The DNA demethylase ROS1 targets genomic regions with distinct chromatin modifications. <i>Nature Plants</i> , 2016, 2, 16169.	9.3	147
48	The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. <i>Cell Discovery</i> , 2016, 2, 16027.	6.7	55
49	Dicer-independent RNA-directed DNA methylation in <i>Arabidopsis</i> . <i>Cell Research</i> , 2016, 26, 66-82.	12.0	95
50	Protecting genes from RNA silencing by destroying aberrant transcripts. <i>Science China Life Sciences</i> , 2015, 58, 613-615.	4.9	0
51	Comparative physiological, metabolomic, and transcriptomic analyses reveal mechanisms of improved abiotic stress resistance in bermudagrass [<i>Cynodon dactylon</i> (L.) Pers.] by exogenous melatonin. <i>Journal of Experimental Botany</i> , 2015, 66, 681-694.	4.8	425
52	Involvement of Multiple Gene-Silencing Pathways in a Paramutation-like Phenomenon in <i>Arabidopsis</i> . <i>Cell Reports</i> , 2015, 11, 1160-1167.	6.4	13
53	<i>Arabidopsis</i> EDM2 promotes IBM1 distal polyadenylation and regulates genome DNA methylation patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 527-532.	7.1	102
54	The CRISPR/Cas9 system produces specific and homozygous targeted gene editing in rice in one generation. <i>Plant Biotechnology Journal</i> , 2014, 12, 797-807.	8.3	726

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55	An Rrp6-like Protein Positively Regulates Noncoding RNA Levels and DNA Methylation in Arabidopsis. <i>Molecular Cell</i> , 2014, 54, 418-430.	9.7	45
56	PICKLE is a CHD subfamily II ATP-dependent chromatin remodeling factor. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 199-210.	1.9	61
57	DTF1 is a core component of RNA-directed DNA methylation and may assist in the recruitment of Pol IV. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8290-8295.	7.1	158
58	A Pre-mRNA-Splicing Factor Is Required for RNA-Directed DNA Methylation in Arabidopsis. <i>PLoS Genetics</i> , 2013, 9, e1003779.	3.5	58
59	RNA-directed DNA methylation in plants. <i>RNA Biology</i> , 2013, 10, 1593-1596.	3.1	31
60	The CHD3 Remodeler PICKLE Associates with Genes Enriched for Trimethylation of Histone H3 Lysine 27 Å. <i>Plant Physiology</i> , 2012, 159, 418-432.	4.8	144
61	A Histone Acetyltransferase Regulates Active DNA Demethylation in <i>Arabidopsis</i> . <i>Science</i> , 2012, 336, 1445-1448.	12.6	224
62	An Epigenetic Perspective on Developmental Regulation of Seed Genes. <i>Molecular Plant</i> , 2009, 2, 610-627.	8.3	61
63	The CHD3 Remodeler PICKLE Promotes Trimethylation of Histone H3 Lysine 27. <i>Journal of Biological Chemistry</i> , 2008, 283, 22637-22648.	3.4	131
64	PICKLE acts during germination to repress expression of embryonic traits. <i>Plant Journal</i> , 2005, 44, 1010-1022.	5.7	85
65	Genome-Wide Analysis of CqCrRLK1L and CqRALF Gene Families in <i>Chenopodium quinoa</i> and Their Roles in Salt Stress Response. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5