

Zhaorong Hu

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

2,982
citations

147726

31
h-index

189801

50
g-index

73
all docs

73
docs citations

73
times ranked

2942
citing authors

#	ARTICLE	IF	CITATIONS
1	Stress granule-associated TaMBF1c confers thermotolerance through regulating specific mRNA translation in wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2022, 233, 1719-1731.	3.5	31
2	A single nucleotide deletion in the third exon of <i>FT-D1</i> increases the spikelet number and delays heading date in wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2022, 20, 920-933.	4.1	35
3	ggComp enables dissection of germplasm resources and construction of a multiscale germplasm network in wheat. <i>Plant Physiology</i> , 2022, 188, 1950-1965.	2.3	13
4	The genetic and molecular basis for improving heat stress tolerance in wheat. <i>ABIOTECH</i> , 2022, 3, 25-39.	1.8	3
5	Unprocessed wheat gliadin reduces gluten accumulation associated with the endoplasmic reticulum stress and elevated cell death. <i>New Phytologist</i> , 2022, 236, 146-164.	3.5	5
6	Histone acetyltransferase <i>TaHAG1</i> interacts with <i>TaPLATZ5</i> to activate <i>TaPAD4</i> expression and positively contributes to powdery mildew resistance in wheat. <i>New Phytologist</i> , 2022, 236, 590-607.	3.5	16
7	Histone acetyltransferase <i>TaHAG1</i> interacts with <i>TaNACL</i> to promote heat stress tolerance in wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1645-1647.	4.1	10
8	Genome-wide association study identifies QTL for thousand grain weight in winter wheat under normal- and late-sown stressed environments. <i>Theoretical and Applied Genetics</i> , 2021, 134, 143-157.	1.8	36
9	Phenotypic characterization of the glossy1 mutant and fine mapping of GLOSSY1 in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 835-847.	1.8	6
10	The endosperm-specific transcription factor <i>TaNAC019</i> regulates glutenin and starch accumulation and its elite allele improves wheat grain quality. <i>Plant Cell</i> , 2021, 33, 603-622.	3.1	88
11	Single-cell-type transcriptomic analysis reveals distinct gene expression profiles in wheat guard cells in response to abscisic acid. <i>Functional Plant Biology</i> , 2021, 48, 1087-1099.	1.1	2
12	Pleiotropic function of the SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE gene <i>TaSPL14</i> in wheat plant architecture. <i>Planta</i> , 2021, 253, 44.	1.6	26
13	Histone acetyltransferase <i>TaHAG1</i> acts as a crucial regulator to strengthen salt tolerance of hexaploid wheat. <i>Plant Physiology</i> , 2021, 186, 1951-1969.	2.3	69
14	Fine mapping of a powdery mildew resistance gene <i>MLIW39</i> derived from wild emmer wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	9
15	<i>FRIZZY PANICLE</i> defines a regulatory hub for simultaneously controlling spikelet formation and awn elongation in bread wheat. <i>New Phytologist</i> , 2021, 231, 814-833.	3.5	41
16	Fine Mapping of the Leaf Rust Resistance Gene <i>Lr65</i> in Spelt Wheat 'Altgold'. <i>Frontiers in Plant Science</i> , 2021, 12, 666921.	1.7	7
17	The decreased expression of <i>GW2</i> homologous genes contributed to the increased grain width and thousand grain weight in wheat- <i>Dasypyrum villosum</i> 6VSÀ-6DL translocation lines. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3873-3894.	1.8	7
18	Ectopic expression of <i>VRT-A2</i> underlies the origin of <i>Triticum polonicum</i> and <i>Triticum petropavlovskyi</i> with long outer glumes and grains. <i>Molecular Plant</i> , 2021, 14, 1472-1488.	3.9	32

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19	Dissection of genetic factors underlying grain size and fine mapping of QTgw.cau-7D in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 149-162.	1.8	42
20	Heat shock transcription factor A1b regulates heat tolerance in wheat and <i>Arabidopsis</i> through <i>OPR3</i> and jasmonate signalling pathway. <i>Plant Biotechnology Journal</i> , 2020, 18, 1109-1111.	4.1	36
21	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
22	Changes in Alternative Splicing in Response to Domestication and Polyploidization in Wheat. <i>Plant Physiology</i> , 2020, 184, 1955-1968.	2.3	34
23	Fine Mapping of the Wheat Leaf Rust Resistance Gene <i>LrLC10</i> (<i>Lr13</i>) and Validation of Its Co-segregation Markers. <i>Frontiers in Plant Science</i> , 2020, 11, 470.	1.7	14
24	Genome-wide linkage mapping of QTL for root hair length in a Chinese common wheat population. <i>Crop Journal</i> , 2020, 8, 1049-1056.	2.3	6
25	Dissection and validation of a QTL cluster linked to <i>Rht-B1</i> locus controlling grain weight in common wheat (<i>Triticum aestivum</i> L.) using near-isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2639-2653.	1.8	26
26	A Single Amino Acid Substitution in <i>STKc_GSK3</i> Kinase Conferring Semispherical Grains and Its Implications for the Origin of <i>Triticum sphaerococcum</i> . <i>Plant Cell</i> , 2020, 32, 923-934.	3.1	78
27	The semidominant mutation <i>w5</i> impairs epicuticular wax deposition in common wheat (<i>Triticum</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overloc</i>	1.8	6
28	Pleiotropic QTL influencing spikelet number and heading date in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1825-1838.	1.8	53
29	Identification of <i>AflR</i> Binding Sites in the Genome of <i>Aspergillus flavus</i> by ChIP-Seq. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 52.	1.5	9
30	Histone acetyltransferase <i>GCN5</i> contributes to cell wall integrity and salt stress tolerance by altering the expression of cellulose synthesis genes. <i>Plant Journal</i> , 2019, 97, 587-602.	2.8	99
31	Histone acetyltransferase <i>GCN5</i> -mediated regulation of long non-coding RNA <i>At4</i> contributes to phosphate starvation response in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6337-6348.	2.4	30
32	Characterization of a new hexaploid triticale 6D(6A) substitution line with increased grain weight and decreased spikelet number. <i>Crop Journal</i> , 2019, 7, 598-607.	2.3	4
33	High Molecular Weight Glutenin Subunits 1Bx7 and 1By9 Encoded by <i>Glu-B1</i> Locus Affect Wheat Dough Properties and Sponge Cake Quality. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 11796-11804.	2.4	23
34	Identification of <i>HSP90C</i> as a substrate of E3 ligase <i>TaSAP5</i> through ubiquitylome profiling. <i>Plant Science</i> , 2019, 287, 110170.	1.7	14
35	Wheat <i>TaSPL8</i> Modulates Leaf Angle Through Auxin and Brassinosteroid Signaling. <i>Plant Physiology</i> , 2019, 181, 179-194.	2.3	69
36	Use of near-isogenic lines to precisely map and validate a major QTL for grain weight on chromosome 4AL in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2367-2379.	1.8	32

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37	Btr1-A Induces Grain Shattering and Affects Spike Morphology and Yield-Related Traits in Wheat. <i>Plant and Cell Physiology</i> , 2019, 60, 1342-1353.	1.5	31
38	Dissection of two quantitative trait loci with pleiotropic effects on plant height and spike length linked in coupling phase on the short arm of chromosome 2D of common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 1815-1831.	1.8	22
39	GCN5 contributes to stem cuticular wax biosynthesis by histone acetylation of CER3 in Arabidopsis. <i>Journal of Experimental Botany</i> , 2018, 69, 2911-2922.	2.4	36
40	Genomic Imprinting Was Evolutionarily Conserved during Wheat Polyploidization. <i>Plant Cell</i> , 2018, 30, 37-47.	3.1	26
41	Wheat miR9678 Affects Seed Germination by Generating Phased siRNAs and Modulating Abscisic Acid/Gibberellin Signaling. <i>Plant Cell</i> , 2018, 30, 796-814.	3.1	75
42	Genetic improvement of heat tolerance in wheat: Recent progress in understanding the underlying molecular mechanisms. <i>Crop Journal</i> , 2018, 6, 32-41.	2.3	103
43	Global profiling of alternative splicing landscape responsive to drought, heat and their combination in wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2018, 16, 714-726.	4.1	161
44	A novel allele of TaGW2-A1 is located in a finely mapped QTL that increases grain weight but decreases grain number in wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 539-553.	1.8	121
45	Dissection of two quantitative trait loci with pleiotropic effects on plant height and spike length linked in coupling phase on the short arm of chromosome 2D of common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 2621-2637.	1.8	51
46	Unconventional splicing of wheat TabZIP60 confers heat tolerance in transgenic Arabidopsis. <i>Plant Science</i> , 2018, 274, 252-260.	1.7	33
47	Three genomes differentially contribute to the seedling lateral root number in allohexaploid wheat: evidence from phenotype evolution and gene expression. <i>Plant Journal</i> , 2018, 95, 976-987.	2.8	35
48	Global QTL Analysis Identifies Genomic Regions on Chromosomes 4A and 4B Harboring Stable Loci for Yield-Related Traits Across Different Environments in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 529.	1.7	132
49	TaWRKY51 promotes lateral root formation through negative regulation of ethylene biosynthesis in wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2018, 96, 372-388.	2.8	55
50	Ectopic expression of TaOEP16-2-5B, a wheat plastid outer envelope protein gene, enhances heat and drought stress tolerance in transgenic Arabidopsis plants. <i>Plant Science</i> , 2017, 258, 1-11.	1.7	42
51	Isolation and characterization of heat-responsive gene TaGASR1 from wheat (<i>Triticum aestivum</i> L.). <i>Journal of Plant Biology</i> , 2017, 60, 57-65.	0.9	39
52	The E3 Ligase TaSAP5 Alters Drought Stress Responses by Promoting the Degradation of DRIP Proteins. <i>Plant Physiology</i> , 2017, 175, 1878-1892.	2.3	64
53	Altered expression of the TaRSL2 gene contributed to variation in root hair length during allopolyploid wheat evolution. <i>Planta</i> , 2017, 246, 1019-1028.	1.6	14
54	Molecular and Functional Characterization of Wheat ARGOS Genes Influencing Plant Growth and Stress Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 170.	1.7	20

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55	Characterization of wheat MYB genes responsive to high temperatures. BMC Plant Biology, 2017, 17, 208.	1.6	75
56	Genome-Wide Mapping of Targets of Maize Histone Deacetylase HDA101 Reveals Its Function and Regulatory Mechanism during Seed Development. Plant Cell, 2016, 28, 629-645.	3.1	49
57	Histone acetyltransferase general control non-repressed protein 5 (<sc>GCN</sc>5) affects the fatty acid composition of <i>Arabidopsis thaliana</i> seeds by acetylating <i>fatty acid desaturase3</i> (<i><sc>FAD</sc>3</i>). Plant Journal, 2016, 88, 794-808.	2.8	30
58	Altered expression of <i>Ta<sc>RSL</sc>4</i> gene by genome interplay shapes root hair length in allopolyploid wheat. New Phytologist, 2016, 209, 721-732.	3.5	71
59	Histone acetyltransferase <sc>GCN</sc>5 is essential for heat stress-responsive gene activation and thermotolerance in Arabidopsis. Plant Journal, 2015, 84, 1178-1191.	2.8	126
60	The wheat transcription factor Ta<sc>GAM</sc>yb recruits histone acetyltransferase and activates the expression of a high-molecular-weight glutenin subunit gene. Plant Journal, 2015, 84, 347-359.	2.8	46
61	Temporal small RNA transcriptome profiling unraveled partitioned miRNA expression in developing maize endosperms between reciprocal crosses. Frontiers in Plant Science, 2015, 6, 744.	1.7	14
62	GENERAL CONTROL NONREPRESSED PROTEIN5-Mediated Histone Acetylation of <i>FERRIC REDUCTASE DEFECTIVE3</i> Contributes to Iron Homeostasis in Arabidopsis. Plant Physiology, 2015, 168, 1309-1320.	2.3	56
63	Mapping QTLs associated with root traits using two different populations in wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	53
64	The Wheat NAC Transcription Factor TaNAC2L Is Regulated at the Transcriptional and Post-Translational Levels and Promotes Heat Stress Tolerance in Transgenic Arabidopsis. PLoS ONE, 2015, 10, e0135667.	1.1	57
65	Ectopic Expression of a Maize Hybrid Down-Regulated Gene ZmARF25 Decreases Organ Size by Affecting Cellular Proliferation in Arabidopsis. PLoS ONE, 2014, 9, e94830.	1.1	12
66	Overexpression of a wheat stearyl-ACP desaturase (SACPD) gene TaSSI2 in Arabidopsis ssi2 mutant compromise its resistance to powdery mildew. Gene, 2013, 524, 220-227.	1.0	25
67	Epigenetic modification contributes to the expression divergence of three <i><sc>T</sc>a<sc>EXPA</sc>1</i> homoeologs in hexaploid wheat (<i><sc>T</sc>riticum) Tj ETQq1 1 0.784314 rgBT /Over	0.8	53
68	Overexpression of Three TaEXPA1 Homoeologous Genes with Distinct Expression Divergence in Hexaploid Wheat Exhibit Functional Retention in Arabidopsis. PLoS ONE, 2013, 8, e63667.	1.1	16
69	Comparative Proteomic Analysis of Embryos between a Maize Hybrid and Its Parental Lines during Early Stages of Seed Germination. PLoS ONE, 2013, 8, e65867.	1.1	71
70	Expression divergence of TaMBD2 homoeologous genes encoding methyl CpG-binding domain proteins in wheat (Triticum aestivum L.). Gene, 2011, 471, 13-18.	1.0	26