

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	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
2	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
3	Histone acetyltransferase <i>GCN5</i> is essential for heat stress-responsive gene activation and thermotolerance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 1178-1191.	2.8	126
4	A novel allele of <i>TaGW2-A1</i> 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
5	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
6	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
7	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
8	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
9	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
10	Characterization of wheat MYB genes responsive to high temperatures. <i>BMC Plant Biology</i> , 2017, 17, 208.	1.6	75
11	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
12	Epigenetic modification contributes to the expression divergence of three <i>TaEXPA1</i> homoeologs in hexaploid wheat (<i>Triticum turgidum</i> L. × <i>Triticum aestivum</i> L.). <i>Overlook 10</i>	3.1	75
13	Altered expression of <i>TaRSL4</i> gene by genome interplay shapes root hair length in allopolyploid wheat. <i>New Phytologist</i> , 2016, 209, 721-732.	3.5	71
14	Comparative Proteomic Analysis of Embryos between a Maize Hybrid and Its Parental Lines during Early Stages of Seed Germination. <i>PLoS ONE</i> , 2013, 8, e65867.	1.1	71
15	Wheat <i>TaSPL8</i> Modulates Leaf Angle Through Auxin and Brassinosteroid Signaling. <i>Plant Physiology</i> , 2019, 181, 179-194.	2.3	69
16	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
17	The E3 Ligase <i>TaSAP5</i> Alters Drought Stress Responses by Promoting the Degradation of DRIP Proteins. <i>Plant Physiology</i> , 2017, 175, 1878-1892.	2.3	64
18	The Wheat NAC Transcription Factor <i>TaNAC2L</i> Is Regulated at the Transcriptional and Post-Translational Levels and Promotes Heat Stress Tolerance in Transgenic <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2015, 10, e0135667.	1.1	57

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19	GENERAL CONTROL NONREPRESSED PROTEIN5-Mediated Histone Acetylation of <i>FERRIC REDUCTASE DEFECTIVE3</i> Contributes to Iron Homeostasis in Arabidopsis. <i>Plant Physiology</i> , 2015, 168, 1309-1320.	2.3	56
20	Ta ^{WRKY} 51 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
21	Mapping QTLs associated with root traits using two different populations in wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 10	0.8	53
22	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
23	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
24	Genome-Wide Mapping of Targets of Maize Histone Deacetylase HDA101 Reveals Its Function and Regulatory Mechanism during Seed Development. <i>Plant Cell</i> , 2016, 28, 629-645.	3.1	49
25	The wheat transcription factor Ta ^{GAM} yb recruits histone acetyltransferase and activates the expression of a high-molecular-weight glutenin subunit gene. <i>Plant Journal</i> , 2015, 84, 347-359.	2.8	46
26	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
27	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
28	<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
29	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
30	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
31	Heat shock transcription factor A1b regulates heat tolerance in wheat and Arabidopsis through ^{OPR} 3 and jasmonate signalling pathway. <i>Plant Biotechnology Journal</i> , 2020, 18, 1109-1111.	4.1	36
32	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
33	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
34	A single nucleotide deletion in the third exon of <i>FTaED1</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
35	Changes in Alternative Splicing in Response to Domestication and Polyploidization in Wheat. <i>Plant Physiology</i> , 2020, 184, 1955-1968.	2.3	34
36	Unconventional splicing of wheat TabZIP60 confers heat tolerance in transgenic Arabidopsis. <i>Plant Science</i> , 2018, 274, 252-260.	1.7	33

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37	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
38	Ectopic expression of VRT-A2 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
39	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
40	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
41	Histone acetyltransferase general control non-repressed protein 5 (GCN5) affects the fatty acid composition of <i>Arabidopsis thaliana</i> seeds by acetylating fatty acid desaturase3 (FAD3). <i>Plant Journal</i> , 2016, 88, 794-808.	2.8	30
42	Histone acetyltransferase GCN5-mediated regulation of long non-coding RNA At4 contributes to phosphate starvation response in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6337-6348.	2.4	30
43	Expression divergence of TaMBD2 homoeologous genes encoding methyl CpG-binding domain proteins in wheat (<i>Triticum aestivum</i> L.). <i>Gene</i> , 2011, 471, 13-18.	1.0	26
44	Genomic Imprinting Was Evolutionarily Conserved during Wheat Polyploidization. <i>Plant Cell</i> , 2018, 30, 37-47.	3.1	26
45	Dissection and validation of a QTL cluster linked to Rht-B1 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
46	Pleiotropic function of the SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE gene TaSPL14 in wheat plant architecture. <i>Planta</i> , 2021, 253, 44.	1.6	26
47	Overexpression of a wheat stearyl-ACP desaturase (SACPD) gene TaSSI2 in <i>Arabidopsis ssi2</i> mutant compromise its resistance to powdery mildew. <i>Gene</i> , 2013, 524, 220-227.	1.0	25
48	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
49	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
50	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
51	Overexpression of Three TaEXPA1 Homoeologous Genes with Distinct Expression Divergence in Hexaploid Wheat Exhibit Functional Retention in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2013, 8, e63667.	1.1	16
52	Histone acetyltransferase TaHAG1 interacts with TaPLATZ5 to activate TaPAD4 expression and positively contributes to powdery mildew resistance in wheat. <i>New Phytologist</i> , 2022, 236, 590-607.	3.5	16
53	Temporal small RNA transcriptome profiling unraveled partitioned miRNA expression in developing maize endosperms between reciprocal crosses. <i>Frontiers in Plant Science</i> , 2015, 6, 744.	1.7	14
54	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

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55	Identification of HSP90C as a substrate of E3 ligase TaSAP5 through ubiquitylome profiling. <i>Plant Science</i> , 2019, 287, 110170.	1.7	14
56	Fine Mapping of the Wheat Leaf Rust Resistance Gene LrLC10 (Lr13) and Validation of Its Co-segregation Markers. <i>Frontiers in Plant Science</i> , 2020, 11, 470.	1.7	14
57	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
58	Ectopic Expression of a Maize Hybrid Down-Regulated Gene ZmARF25 Decreases Organ Size by Affecting Cellular Proliferation in Arabidopsis. <i>PLoS ONE</i> , 2014, 9, e94830.	1.1	12
59	Histone acetyltransferase <scp>TaHAG1</scp> interacts with <scp>TaNAACL</scp> to promote heat stress tolerance in wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1645-1647.	4.1	10
60	Identification of AfIR 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
61	Fine mapping of a powdery mildew resistance gene MliW39 derived from wild emmer wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 1.8 ggBT /Overl	1.8	9
62	Fine Mapping of the Leaf Rust Resistance Gene Lr65 in Spelt Wheat "Altgold"™. <i>Frontiers in Plant Science</i> , 2021, 12, 666921.	1.7	7
63	The decreased expression of CW2 homologous genes contributed to the increased grain width and thousand-grain weight in wheat- <i>Dasyphyrum villosum</i> 6VS-6DL translocation lines. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3873-3894.	1.8	7
64	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
65	The semidominant mutation w5 impairs epicuticular wax deposition in common wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 1.8 rgBT /Overl	1.8	6
66	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
67	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
68	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
69	The genetic and molecular basis for improving heat stress tolerance in wheat. <i>ABIOTECH</i> , 2022, 3, 25-39.	1.8	3
70	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