

Aimin Zhang

List of Publications by Year in descending order

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55
papers

2,729
citations

236833

25
h-index

189801

50
g-index

56
all docs

56
docs citations

56
times ranked

3248
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	13.7	700
2	Genome sequence of the progenitor of wheat A subgenome <i>Triticum urartu</i> . <i>Nature</i> , 2018, 557, 424-428.	13.7	354
3	Enhancing Genetic Gain through Genomic Selection: From Livestock to Plants. <i>Plant Communications</i> , 2020, 1, 100005.	3.6	147
4	Major quantitative trait loci for seminal root morphology of wheat seedlings. <i>Molecular Breeding</i> , 2012, 30, 139-148.	1.0	123
5	Awns play a dominant role in carbohydrate production during the grain-filling stages in wheat (<i>Triticum aestivum</i>). <i>Physiologia Plantarum</i> , 2006, 127, 701-709.	2.6	92
6	TaFlo2-A1, an ortholog of rice Flo2, is associated with thousand grain weight in bread wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 164.	1.6	90
7	New Insights into the Organization, Recombination, Expression and Functional Mechanism of Low Molecular Weight Glutenin Subunit Genes in Bread Wheat. <i>PLoS ONE</i> , 2010, 5, e13548.	1.1	74
8	Comparative analysis of mitochondrial genomes between a wheat K-type cytoplasmic male sterility (CMS) line and its maintainer line. <i>BMC Genomics</i> , 2011, 12, 163.	1.2	73
9	Composition and functional analysis of low-molecular-weight glutenin alleles with Aroona near-isogenic lines of bread wheat. <i>BMC Plant Biology</i> , 2012, 12, 243.	1.6	68
10	Characterization of the temporal and spatial expression of wheat (<i>Triticum aestivum</i> L.) plant height at the QTL level and their influence on yield-related traits. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1235-1252.	1.8	68
11	A wheat dominant dwarfing line with <i>Rht12</i> , which reduces stem cell length and affects gibberellic acid synthesis, is a 5AL terminal deletion line. <i>Plant Journal</i> , 2019, 97, 887-900.	2.8	65
12	Characterization of QTLs for Root Traits of Wheat Grown under Different Nitrogen and Phosphorus Supply Levels. <i>Frontiers in Plant Science</i> , 2017, 8, 2096.	1.7	50
13	<i>TubZIP28</i> , a novel bZIP family transcription factor from <i>Triticum urartu</i> , and <i>TabZIP28</i> , its homologue from <i>Triticum aestivum</i> , enhance starch synthesis in wheat. <i>New Phytologist</i> , 2020, 226, 1384-1398.	3.5	46
14	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. <i>Scientific Reports</i> , 2018, 8, 15338.	1.6	45
15	Novel Natural Allelic Variations at the <i>Rht1</i> Loci in Wheat. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1026-1037.	4.1	41
16	Novel insights into the composition, variation, organization, and expression of the low-molecular-weight glutenin subunit gene family in common wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 2027-2040.	2.4	39
17	Wheat <i>FRIZZY PANICLE</i> activates <i>VERNALIZATION1</i> and <i>HOMEBOX4</i> to regulate spike development in wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 1141-1154.	4.1	37
18	Effects of stem structure and cell wall components on bending strength in wheat. <i>Science Bulletin</i> , 2006, 51, 815-823.	4.3	36

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19	Development of a new marker system for identifying the complex members of the low-molecular-weight glutenin subunit gene family in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 1503-1516.	1.8	35
20	Dissecting and Enhancing the Contributions of High-Molecular-Weight Glutenin Subunits to Dough Functionality and Bread Quality. <i>Molecular Plant</i> , 2015, 8, 332-334.	3.9	32
21	Genetic diversity, population structure and marker-trait associations for agronomic and grain traits in wild diploid wheat <i>Triticum urartu</i> . <i>BMC Plant Biology</i> , 2017, 17, 112.	1.6	32
22	Natural variations in the promoter of <i>Awn Length Inhibitor 1</i> (<i>ALI1</i>) are associated with awn elongation and grain length in common wheat. <i>Plant Journal</i> , 2020, 101, 1075-1090.	2.8	32
23	Development of an integrated linkage map of einkorn wheat and its application for QTL mapping and genome sequence anchoring. <i>Theoretical and Applied Genetics</i> , 2017, 130, 53-70.	1.8	30
24	Characterization and Genetic Analysis of a Novel Light-Dependent Lesion Mimic Mutant, <i>lm3</i> , Showing Adult-Plant Resistance to Powdery Mildew in Common Wheat. <i>PLoS ONE</i> , 2016, 11, e0155358.	1.1	29
25	Diversity, distribution of Puroindoline genes and their effect on kernel hardness in a diverse panel of Chinese wheat germplasm. <i>BMC Plant Biology</i> , 2017, 17, 158.	1.6	28
26	Genome-, Transcriptome- and Proteome-Wide Analyses of the Gliadin Gene Families in <i>Triticum urartu</i> . <i>PLoS ONE</i> , 2015, 10, e0131559.	1.1	26
27	Isolation of a gibberellin-insensitive dwarfing gene, <i>Rht-B1e</i> , and development of an allele-specific PCR marker. <i>Molecular Breeding</i> , 2012, 30, 1443-1451.	1.0	24
28	A novel NAC family transcription factor <i>SPR</i> suppresses seed storage protein synthesis in wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 992-1007.	4.1	24
29	Pattern analysis on grain yield performance of Chinese and CIMMYT spring wheat cultivars sown in China and CIMMYT. <i>Euphytica</i> , 2006, 147, 409-420.	0.6	23
30	Genetic diversity of wheat gene pool of recurrent selection assessed by microsatellite markers and morphological traits. <i>Euphytica</i> , 2007, 155, 249-258.	0.6	23
31	High-throughput mining of genome-specific SNPs for characterizing <i>Thinopyrum elongatum</i> introgressions in common wheat. <i>Molecular Ecology Resources</i> , 2017, 17, 1318-1329.	2.2	22
32	PCR-based isolation and identification of full-length low-molecular-weight glutenin subunit genes in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 1293-1305.	1.8	21
33	Unraveling the genetic architecture of grain size in einkorn wheat through linkage and homology mapping and transcriptomic profiling. <i>Journal of Experimental Botany</i> , 2019, 70, 4671-4688.	2.4	19
34	Composition, variation, expression and evolution of low-molecular-weight glutenin subunit genes in <i>Triticum urartu</i> . <i>BMC Plant Biology</i> , 2015, 15, 68.	1.6	18
35	Genome-wide identification and expression analysis of new cytokinin metabolic genes in bread wheat (<i>Triticum aestivum</i> L.). <i>PeerJ</i> , 2019, 7, e6300.	0.9	18
36	Allelic variation, sequence determination and microsatellite screening at the XGWM261 locus in Chinese hexaploid wheat (<i>Triticum aestivum</i>) varieties. <i>Euphytica</i> , 2005, 145, 103-112.	0.6	17

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37	Molecular Characterization of Three GIBBERELLIN-INSENSITIVE DWARF2 Homologous Genes in Common Wheat. <i>PLoS ONE</i> , 2016, 11, e0157642.	1.1	16
38	The MYB family transcription factor TuODORANT1 from <i>Triticum urartu</i> and the homolog TaODORANT1 from <i>Triticum aestivum</i> inhibit seed storage protein synthesis in wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 1863-1877.	4.1	15
39	Molecular and Functional Characterization of Sphingosine-1-Phosphate Lyase Homolog from Higher Plants. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 323-335.	4.1	12
40	Isolation and characterisation of six putative wheat cell wall-associated kinases. <i>Functional Plant Biology</i> , 2006, 33, 811.	1.1	10
41	Genome-wide identification of seed storage protein gene regulators in wheat through coexpression analysis. <i>Plant Journal</i> , 2021, 108, 1704-1720.	2.8	9
42	Isolation of Six Novel Aquaporin Genes from <i>Triticum aestivum</i> L. and Functional Analysis of TaAQP6 in Water Redistribution. <i>Plant Molecular Biology Reporter</i> , 2008, 26, 32-45.	1.0	8
43	Alien cytoplasm effects on phytosiderophore release in two spring wheats (<i>Triticum aestivum</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2003, 50, 767-772.	0.8	7
44	Mechanisms, origin and heredity of Glu-1Ay silencing in wheat evolution and domestication. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1561-1575.	1.8	7
45	Combined Transcriptome and Proteome Analysis of Anthers of AL-type Cytoplasmic Male Sterile Line and Its Maintainer Line Reveals New Insights into Mechanism of Male Sterility in Common Wheat. <i>Frontiers in Genetics</i> , 2021, 12, 762332.	1.1	7
46	Dynamic changes in flag leaf angle contribute to high photosynthetic capacity. <i>Science Bulletin</i> , 2009, 54, 3045-3052.	1.7	6
47	Identification of new T1BL.1RS translocation lines derived from wheat (<i>Triticum aestivum</i> L. cultivar) Tj ETQq1 1 0.784314 rgBT /Over	1.0	5
48	TaCKX gene family, at large, is associated with thousand-grain weight and plant height in common wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3151-3163.	1.8	5
49	Characterization of the Mitochondrial Genome of a Wheat AL-Type Male Sterility Line and the Candidate CMS Gene. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6388.	1.8	5
50	Genetic Mapping of ms1s, a Recessive Gene for Male Sterility in Common Wheat. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8541.	1.8	5
51	A wheat "Thinopyrum ponticum" rye trigenic germplasm line with resistance to powdery mildew and stripe rust. <i>Euphytica</i> , 2012, 188, 199-207.	0.6	4
52	The Carotenoid Cleavage Dioxygenase Gene CCD7-B, at Large, Is Associated with Tillering in Common Wheat. <i>Agriculture (Switzerland)</i> , 2022, 12, 306.	1.4	4
53	Low molecular weight glutenin subunit gene composition at Glu-D3 loci of <i>Aegilops tauschii</i> and common wheat and a further view of wheat evolution. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2745-2763.	1.8	1
54	Dissecting and enhancing the contributions of high-molecular-weight glutenin subunits to dough functionality and bread quality. <i>Molecular Plant</i> , 2014, , .	3.9	1

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55	Whole-genome resequencing of the wheat A subgenome progenitor <i>Triticum urartu</i> provides insights into its demographic history and geographic adaptation. <i>Plant Communications</i> , 2022, , 100345.	3.6	1