

Jian

List of Publications by Year in descending order

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78
papers

1,632
citations

304368

22
h-index

360668

35
g-index

80
all docs

80
docs citations

80
times ranked

1382
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide association study of 23 agronomic traits in Chinese wheat landraces. <i>Plant Journal</i> , 2017, 91, 861-873.	2.8	152
2	A 55K SNP array-based genetic map and its utilization in QTL mapping for productive tiller number in common wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2439-2450.	1.8	95
3	Identification and validation of a major and stably expressed QTL for spikelet number per spike in bread wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3155-3167.	1.8	70
4	Genome-wide identification and analysis of the MADS-box gene family in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 69	1.1	69
5	Sequence-Based Analysis of Translocations and Inversions in Bread Wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013, 8, e79329.	1.1	62
6	Identification of QTL for flag leaf length in common wheat and their pleiotropic effects. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	61
7	Flag leaf size and posture of bread wheat: genetic dissection, QTL validation and their relationships with yield-related traits. <i>Theoretical and Applied Genetics</i> , 2020, 133, 297-315.	1.8	53
8	<i>Myb10</i> confers <i>PHS3D</i> resistance to pre-harvest sprouting by regulating <i>NCED</i> in ABA biosynthesis pathway of wheat. <i>New Phytologist</i> , 2021, 230, 1940-1952.	3.5	53
9	Identification and validation of a novel major QTL for all-stage stripe rust resistance on 1BL in the winter wheat line 20828. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1363-1373.	1.8	49
10	Identification of quantitative trait loci for kernel traits in a wheat cultivar Chuannong16. <i>BMC Genetics</i> , 2019, 20, 77.	2.7	42
11	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. <i>PLoS ONE</i> , 2014, 9, e113309.	1.1	42
12	Molecular Mapping of the Stripe Rust Resistance Gene <i>Yr69</i> on Wheat Chromosome 2AS. <i>Plant Disease</i> , 2016, 100, 1717-1724.	0.7	41
13	Genome-Wide Association Study for Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landraces (<i>Triticum aestivum</i> L.) From the Yellow and Huai River Valleys. <i>Frontiers in Plant Science</i> , 2019, 10, 596.	1.7	41
14	A novel, major, and validated QTL for the effective tiller number located on chromosome arm 1BL in bread wheat. <i>Plant Molecular Biology</i> , 2020, 104, 173-185.	2.0	36
15	A genome-wide analysis of the auxin/indole-3-acetic acid gene family in hexaploid bread wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Ov	1.7	34
16	Comprehensive transcriptomics, proteomics, and metabolomics analyses of the mechanisms regulating tiller production in low-tillering wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2181-2193.	1.8	33
17	Identification of Quantitative Trait Loci Controlling Agronomic Traits Indicates Breeding Potential of Tibetan Semiwild Wheat (<i>Triticum aestivum</i> ssp. <i>tibetanum</i>). <i>Crop Science</i> , 2016, 56, 2410-2420.	0.8	32
18	Mutation of the d-hordein gene by RNA-guided Cas9 targeted editing reducing the grain size and changing grain compositions in barley. <i>Food Chemistry</i> , 2020, 311, 125892.	4.2	32

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19	Functional Analysis of FgNahG Clarifies the Contribution of Salicylic Acid to Wheat (Triticum) Tj ETQq1 1 0.784314,rgBT /Overlock 10	1.8	30
20	A novel, validated, and plant height-independent QTL for spike extension length is associated with yield-related traits in wheat. Theoretical and Applied Genetics, 2020, 133, 3381-3393.	1.8	29
21	Extensive Pericentric Rearrangements in the Bread Wheat (Triticum aestivum L.) Genotype "Chinese Spring" Revealed from Chromosome Shotgun Sequence Data. Genome Biology and Evolution, 2014, 6, 3039-3048.	1.1	27
22	Characterization and expression analysis of WOX5 genes from wheat and its relatives. Gene, 2014, 537, 63-69.	1.0	25
23	QTL mapping and validation of bread wheat flag leaf morphology across multiple environments in different genetic backgrounds. Theoretical and Applied Genetics, 2021, 134, 261-278.	1.8	24
24	Structure and expression of barley starch phosphorylase genes. Planta, 2013, 238, 1081-1093.	1.6	23
25	Dissection of loci conferring resistance to stripe rust in Chinese wheat landraces from the middle and lower reaches of the Yangtze River via genome-wide association study. Plant Science, 2019, 287, 110204.	1.7	22
26	Putative interchromosomal rearrangements in the hexaploid wheat (Triticum aestivum L.) genotype "Chinese Spring" revealed by gene locations on homoeologous chromosomes. BMC Evolutionary Biology, 2015, 15, 37.	3.2	21
27	Characterization and expression analysis of waxy alleles in barley accessions. Genetica, 2013, 141, 227-238.	0.5	19
28	QTL mapping for grain number per spikelet in wheat using a high-density genetic map. Crop Journal, 2021, 9, 1108-1114.	2.3	19
29	Several stably expressed QTL for spike density of common wheat (<i>Triticum aestivum</i>) in multiple environments. Plant Breeding, 2020, 139, 284-294.	1.0	18
30	A single-base change at a splice site in Wx-A1 caused incorrect RNA splicing and gene inactivation in a wheat EMS mutant line. Theoretical and Applied Genetics, 2019, 132, 2097-2109.	1.8	17
31	Population structure and genetic basis of the stripe rust resistance of 140 Chinese wheat landraces revealed by a genome-wide association study. Plant Science, 2020, 301, 110688.	1.7	15
32	Mapping and characterization of major QTL for spike traits in common wheat. Physiology and Molecular Biology of Plants, 2020, 26, 1295-1307.	1.4	15
33	Conserved structure and varied expression reveal key roles of phosphoglucan phosphatase gene starch excess 4 in barley. Planta, 2014, 240, 1179-1190.	1.6	14
34	Transposon insertion resulted in the silencing of Wx-B1n in Chinese wheat landraces. Theoretical and Applied Genetics, 2017, 130, 1321-1330.	1.8	14
35	SSRMMD: A Rapid and Accurate Algorithm for Mining SSR Feature Loci and Candidate Polymorphic SSRs Based on Assembled Sequences. Frontiers in Genetics, 2020, 11, 706.	1.1	14
36	Characterization and expression analyses of the H ⁺ -pyrophosphatase gene in rye. Journal of Genetics, 2016, 95, 565-572.	0.4	13

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37	Identification of major quantitative trait loci for root diameter in synthetic hexaploid wheat under phosphorus-deficient conditions. <i>Journal of Applied Genetics</i> , 2017, 58, 437-447.	1.0	13
38	Identification and validation of stable quantitative trait loci for grain filling rate in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 2377-2385.	1.8	13
39	Characterization of barley Prp1 gene and its expression during seed development and under abiotic stress. <i>Genetica</i> , 2011, 139, 1283-1292.	0.5	12
40	Characterization of shrunken endosperm mutants in barley. <i>Gene</i> , 2014, 539, 15-20.	1.0	12
41	Characterization of high-molecular-weight glutenin subunits from <i>Eremopyrum bonaepartis</i> and identification of a novel variant with unusual high molecular weight and altered cysteine residues. <i>Planta</i> , 2014, 239, 865-875.	1.6	12
42	Identification of lncRNAs involved in wheat tillering development in two pairs of near-isogenic lines. <i>Functional and Integrative Genomics</i> , 2020, 20, 669-679.	1.4	11
43	Effects of the 1BL/1RS translocation on 24 traits in a recombinant inbred line population. <i>Cereal Research Communications</i> , 2020, 48, 225-232.	0.8	11
44	Genetic analysis of glume hairiness (Hg) gene in bread wheat (<i>Triticum aestivum</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2016, 63, 763-769.	0.8	10
45	A QTL located on chromosome 3D enhances the selenium concentration of wheat grain by improving phytoavailability and root structure. <i>Plant and Soil</i> , 2018, 425, 287-296.	1.8	10
46	Characterization of HMW-GSs and their gene inaction in tetraploid wheat. <i>Genetica</i> , 2012, 140, 325-335.	0.5	9
47	Structure and expression of the TaGW7 in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Growth Regulation</i> , 2017, 82, 281-291.	1.8	9
48	Production of waxy tetraploid wheat (<i>Triticum turgidum durum</i> L.) by EMS mutagenesis. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 433-443.	0.8	9
49	Identification of QTLs associated with tissue culture response of mature wheat embryos. <i>SpringerPlus</i> , 2016, 5, 1552.	1.2	8
50	A Novel QTL Conferring Fusarium Crown Rot Resistance Located on Chromosome Arm 6HL in Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 1206.	1.7	8
51	Genome-Wide Association Study Reveals the Genetic Architecture of Stripe Rust Resistance at the Adult Plant Stage in Chinese Endemic Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 625.	1.7	8
52	Identification of loci and candidate genes controlling kernel weight in barley based on a population for which whole genome assemblies are available for both parents. <i>Crop Journal</i> , 2021, 9, 854-861.	2.3	8
53	Characterization of intergeneric hybrid between common wheat and <i>Aegilops sharonensis</i> (Eig) and transfer of alien high molecular weight glutenin subunits into wheat. <i>Cereal Research Communications</i> , 2014, 42, 640-647.	0.8	8
54	Amphidiploids between tetraploid wheat and <i>Aegilops sharonensis</i> Eig exhibit variations in high-molecular-weight glutenin subunits. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 299-305.	0.8	7

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55	Transcriptome analysis of near-isogenic lines for glume hairiness of wheat. <i>Gene</i> , 2020, 739, 144517.	1.0	7
56	Molecular characterization and comparative analysis of two waxy alleles in barley. <i>Genes and Genomics</i> , 2010, 32, 513-520.	0.5	6
57	Characterization of starch morphology, composition, physicochemical properties and gene expressions in oat. <i>Journal of Integrative Agriculture</i> , 2015, 14, 20-28.	1.7	6
58	Expression of the high molecular weight glutenin 1Ay gene from <i>Triticum urartu</i> in barley. <i>Transgenic Research</i> , 2019, 28, 225-235.	1.3	6
59	A 1BL/1RS translocation contributing to kernel length increase in three wheat recombinant inbred line populations. <i>Czech Journal of Genetics and Plant Breeding</i> , 2020, 56, 43-51.	0.4	6
60	Molecular Mapping of a Novel Quantitative Trait Locus Conferring Adult Plant Resistance to Stripe Rust in Chinese Wheat Landrace Guangtoumai. <i>Plant Disease</i> , 2021, 105, 1919-1925.	0.7	6
61	A major vernalization-independent QTL for tiller angle on chromosome arm 2BL in bread wheat. <i>Crop Journal</i> , 2022, 10, 185-193.	2.3	6
62	Genetic identification and characterization of chromosomal regions for kernel length and width increase from tetraploid wheat. <i>BMC Genomics</i> , 2021, 22, 706.	1.2	6
63	Molecular characterization of the TaWTC1 in bread wheat (<i>Triticum aestivum</i> L.). <i>Gene</i> , 2018, 678, 23-32.	1.0	5
64	<i>Fusarium graminearum</i> FgCWM1 Encodes a Cell Wall Mannoprotein Conferring Sensitivity to Salicylic Acid and Virulence to Wheat. <i>Toxins</i> , 2019, 11, 628.	1.5	5
65	Identification and characterization of mRNAs and lncRNAs of a barley shrunken endosperm mutant using RNA-seq. <i>Genetica</i> , 2020, 148, 55-68.	0.5	5
66	Multi-Locus Genome-Wide Association Study of Four Yield-Related Traits in Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2021, 12, 665122.	1.7	5
67	Characterization and fine mapping of a lesion mimic mutant (Lm5) with enhanced stripe rust and powdery mildew resistance in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2022, 135, 421-438.	1.8	5
68	Variation and diversity of the breakpoint sequences on 4AL for the 4AL/5AL translocation in <i>Triticum</i> . <i>Genome</i> , 2018, 61, 635-641.	0.9	4
69	Stable expression and heredity of alien Glu-1Ssh in wheat- <i>Aegilops sharonensis</i> hybrid progenies. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 619-632.	0.8	4
70	Structure and expression of phosphoglucan phosphatase genes of Like Sex Four1 and Like Sex Four2 in barley. <i>Genetica</i> , 2016, 144, 313-323.	0.5	3
71	Genetic mapping and a new PCR-based marker linked to a dwarfing gene in oat (<i>Avena sativa</i> L.). <i>Genome</i> , 2018, 61, 497-503.	0.9	3
72	Transfer of the ph1b gene of "Chinese Spring" into a common wheat cultivar with excellent traits. <i>Cereal Research Communications</i> , 2020, 48, 283-291.	0.8	3

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73	Cloning and characterization of Agp1, the gene encoding the small subunit of ADP-glucose pyrophosphorylase from wheat and its relatives. <i>Biologia (Poland)</i> , 2017, 72, 1446-1453.	0.8	2
74	A simple and effective ND-FISH probe design for identifying barley (<i>Hordeum vulgare</i>) chromosomes. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 2189-2198.	0.8	2
75	EMS induced SNP changes led to mutation of Wx protein in common wheat. <i>Cereal Research Communications</i> , 2020, 48, 233-238.	0.8	2
76	Structural Organization and Functional Activity of the Orthologous TaGLW7 Genes in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Russian Journal of Genetics</i> , 2019, 55, 571-579.	0.2	1
77	The development and validation of new DNA markers linked to the thousand-grain weight QTL in bread wheat (<i>Triticum aestivum</i> L.). <i>Czech Journal of Genetics and Plant Breeding</i> , 2020, 56, 52-61.	0.4	0
78	Identification of quantitative trait loci for seedling habit, grain color and cuticular wax from Tibetan semi-wild wheat (<i>Triticum aestivum</i> ssp. <i>tibetanum</i>). <i>Indian Journal of Genetics and Plant Breeding</i> , 2017, 77, 228.	0.2	0