

Qian-Tao Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

2,087
citations

257450

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330143

37
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130
all docs

130
docs citations

130
times ranked

1614
citing authors

#	ARTICLE	IF	CITATIONS
1	A major vernalization-independent QTL for tiller angle on chromosome arm 2BL in bread wheat. <i>Crop Journal</i> , 2022, 10, 185-193.	5.2	6
2	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.	3.6	5
3	Exome Sequencing from Bulk Segregant Analysis Identifies a Gene for All-Stage Resistance to Stripe Rust on Chromosome 1AL in Chinese Wheat Landrace "Xiaohemai". <i>Plant Disease</i> , 2022, 106, 1209-1215.	1.4	4
4	Mapping a stable adult-plant stripe rust resistance QTL on chromosome 6AL in Chinese wheat landrace Yibinzhuermi. <i>Crop Journal</i> , 2022, , .	5.2	5
5	Editing of the starch synthase IIa gene led to transcriptomic and metabolomic changes and high amylose starch in barley. <i>Carbohydrate Polymers</i> , 2022, 285, 119238.	10.2	17
6	The PGS1 basic helix-loop-helix protein regulates <i>FL3</i> to impact seed growth and grain yield in cereals. <i>Plant Biotechnology Journal</i> , 2022, 20, 1311-1326.	8.3	23
7	Genome-Wide Association Study of Kernel Black Point Resistance in Chinese Wheat Landraces. <i>Plant Disease</i> , 2022, 106, 1428-1433.	1.4	2
8	Polyploidization affects the allelic variation of jasmonate-regulated protein Ta-JA1 belonging to the monocot chimeric jacalin (MCJ) family in wild emmer wheat. <i>Gene</i> , 2022, 825, 146399.	2.2	0
9	A major and stable QTL for wheat spikelet number per spike validated in different genetic backgrounds. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1551-1562.	3.5	15
10	Analysis of starch structure and functional properties of tetraploid wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387. <i>Agriculture</i> , 2022, 102, 5974-5983.	3.5	4
11	Identification and validation of a major QTL for kernel length in bread wheat based on two F3 biparental populations. <i>BMC Genomics</i> , 2022, 23, 386.	2.8	4
12	Reference genome assemblies reveal the origin and evolution of allohexaploid oat. <i>Nature Genetics</i> , 2022, 54, 1248-1258.	21.4	45
13	The Qc5 Allele Increases Wheat Bread-Making Quality by Regulating SPA and SPR. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7581.	4.1	2
14	Quick mapping and characterization of a co-located kernel length and thousand-kernel weight-related QTL in wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2849-2860.	3.6	16
15	QTL mapping and validation of bread wheat flag leaf morphology across multiple environments in different genetic backgrounds. <i>Theoretical and Applied Genetics</i> , 2021, 134, 261-278.	3.6	24
16	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.	1.4	6
17	Genome-wide association mapping reveals potential novel loci controlling stripe rust resistance in a Chinese wheat landrace diversity panel from the southern autumn-sown spring wheat zone. <i>BMC Genomics</i> , 2021, 22, 34.	2.8	18
18	Genome-wide transcriptome profiling indicates the putative mechanism underlying enhanced grain size in a wheat mutant. <i>3 Biotech</i> , 2021, 11, 54.	2.2	3

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19	A Stable Quantitative Trait Locus on Chromosome 5BL Combined with <i>Yr18</i> Conferring High-Level Adult Plant Resistance to Stripe Rust in Chinese Wheat Landrace Anyuehong. <i>Phytopathology</i> , 2021, 111, 1594-1601.	2.2	11
20	<i>Myb10a</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.	7.3	53
21	Genome-wide identification of bZIP transcription factor genes related to starch synthesis in barley (<i>Hordeum vulgare</i> L.). <i>Genome</i> , 2021, 64, 1067-1080.	2.0	8
22	Genetic Mapping and Validation of Loci for Kernel-Related Traits in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 667493.	3.6	17
23	Post-translational cleavage of HMW-GS Dy10 allele improves the cookie-making quality in common wheat (<i>Triticum aestivum</i>). <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	5
24	Major Facilitator Superfamily Transporter Gene <i>FgMFS1</i> Is Essential for <i>Fusarium graminearum</i> to Deal with Salicylic Acid Stress and for Its Pathogenicity towards Wheat. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8497.	4.1	6
25	The 55K SNP-Based Exploration of QTLs for Spikelet Number Per Spike in a Tetraploid Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Over 12, 732837.	3.6	6
26	Selenium and anthocyanins share the same transcription factors R2R3MYB and bHLH in wheat. <i>Food Chemistry</i> , 2021, 356, 129699.	8.2	11
27	Genetic identification and characterization of chromosomal regions for kernel length and width increase from tetraploid wheat. <i>BMC Genomics</i> , 2021, 22, 706.	2.8	6
28	A single base change at exon of <i>Wxa1</i> caused gene inactivation and starch properties modified in a wheat EMS mutant line. <i>Journal of the Science of Food and Agriculture</i> , 2021, , .	3.5	3
29	Genetic dissection of wheat uppermost-internode diameter and its association with agronomic traits in five recombinant inbred line populations at various field environments. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2849-2861.	3.5	3
30	Re-examination of the APETALA2/Ethylene-Responsive Factor Gene Family in Barley (<i>Hordeum vulgare</i> L.) Indicates a Role in the Regulation of Starch Synthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 791584.	3.6	4
31	Molecular Mapping and Analysis of an Excellent Quantitative Trait Loci Conferring Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landrace Gaoxianguangtoumai. <i>Frontiers in Plant Science</i> , 2021, 12, 756557.	3.6	2
32	Genome-Wide Association Analysis of Stable Stripe Rust Resistance Loci in a Chinese Wheat Landrace Panel Using the 660K SNP Array. <i>Frontiers in Plant Science</i> , 2021, 12, 783830.	3.6	9
33	Spike Density Quantitative Trait Loci Detection and Analysis in Tetraploid and Hexaploid Wheat Recombinant Inbred Line Populations. <i>Frontiers in Plant Science</i> , 2021, 12, 796397.	3.6	9
34	Quantitative trait loci for seeding root traits and the relationships between root and agronomic traits in common wheat. <i>Genome</i> , 2020, 63, 27-36.	2.0	15
35	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.	3.6	53
36	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.	1.6	9

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37	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.	8.2	32
38	Several stably expressed QTL for spike density of common wheat (<i>Triticum aestivum</i>) in multiple environments. <i>Plant Breeding</i> , 2020, 139, 284-294.	1.9	18
39	The production of wheat <i>Aegilops sharonensis</i> 1S ^{sh} chromosome substitution lines harboring alien novel high-molecular-weight glutenin subunits. <i>Genome</i> , 2020, 63, 155-167.	2.0	3
40	Population structure and genetic basis of the stripe rust resistance of 140 Chinese wheat landraces revealed by a genome-wide association study. <i>Plant Science</i> , 2020, 301, 110688.	3.6	15
41	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.	3.9	36
42	A novel, validated, and plant height-independent QTL for spike extension length is associated with yield-related traits in wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3381-3393.	3.6	29
43	Transfer of the <i>ph1b</i> gene of "Chinese Spring" into a common wheat cultivar with excellent traits. <i>Cereal Research Communications</i> , 2020, 48, 283-291.	1.6	3
44	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.	3.6	8
45	EMS induced SNP changes led to mutation of Wx protein in common wheat. <i>Cereal Research Communications</i> , 2020, 48, 233-238.	1.6	2
46	Identification and characterization of mRNAs and lncRNAs of a barley shrunken endosperm mutant using RNA-seq. <i>Genetica</i> , 2020, 148, 55-68.	1.1	5
47	Transcriptome analysis of near-isogenic lines for glume hairiness of wheat. <i>Gene</i> , 2020, 739, 144517.	2.2	7
48	Effects of the 1BL/1RS translocation on 24 traits in a recombinant inbred line population. <i>Cereal Research Communications</i> , 2020, 48, 225-232.	1.6	11
49	Mapping and characterization of major QTL for spike traits in common wheat. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1295-1307.	3.1	15
50	Genome-wide association study reveals new loci for yield-related traits in Sichuan wheat germplasm under stripe rust stress. <i>BMC Genomics</i> , 2019, 20, 640.	2.8	19
51	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. <i>Plant Science</i> , 2019, 287, 110204.	3.6	22
52	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.	3.6	70
53	Identification of quantitative trait loci for kernel traits in a wheat cultivar Chuannong16. <i>BMC Genetics</i> , 2019, 20, 77.	2.7	42
54	<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.	3.4	5

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55	Enriching LMW-GS alleles and strengthening gluten properties of common wheat through wide hybridization with wild emmer. <i>3 Biotech</i> , 2019, 9, 355.	2.2	3
56	Functional Analysis of FgNahG Clarifies the Contribution of Salicylic Acid to Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	3.4	30
57	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.	3.6	49
58	Transcriptional reference map of hormone responses in wheat spikes. <i>BMC Genomics</i> , 2019, 20, 390.	2.8	22
59	Reâ€acquisition of the brittle rachis trait via a transposon insertion in domestication gene Q during wheat deâ€domestication. <i>New Phytologist</i> , 2019, 224, 961-973.	7.3	37
60	Genome-Wide Association Study for Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landraces (Triticum aestivum L.) From the Yellow and Huai River Valleys. <i>Frontiers in Plant Science</i> , 2019, 10, 596.	3.6	41
61	A single-base change at a splice site in Wx-A1 caused incorrect RNA splicing and gene inactivation in a wheat EMS mutant line. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2097-2109.	3.6	17
62	Genome-wide association study of resistance to stripe rust (Puccinia striiformis f. sp. tritici) in Sichuan wheat. <i>BMC Plant Biology</i> , 2019, 19, 147.	3.6	39
63	Characterization of molecular diversity and genome-wide association study of stripe rust resistance at the adult plant stage in Northern Chinese wheat landraces. <i>BMC Genetics</i> , 2019, 20, 38.	2.7	56
64	Stable expression and heredity of alien Glu-1Ssh in wheat-Aegilops sharonensis hybrid progenies. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 619-632.	1.6	4
65	Expression of the high molecular weight glutenin 1Ay gene from Triticum urartu in barley. <i>Transgenic Research</i> , 2019, 28, 225-235.	2.4	6
66	Alternative splicing results in a lack of starch synthase IIa-D in Chinese wheat landrace. <i>Genome</i> , 2018, 61, 201-208.	2.0	5
67	An Overexpressed <i>Q</i> Allele Leads to Increased Spike Density and Improved Processing Quality in Common Wheat (<i>Triticum aestivum</i>). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 771-778.	1.8	27
68	Analysis of contributors to grain yield in wheat at the individual quantitative trait locus level. <i>Plant Breeding</i> , 2018, 137, 35-49.	1.9	29
69	Uncovering the dispersion history, adaptive evolution and selection of wheat in China. <i>Plant Biotechnology Journal</i> , 2018, 16, 280-291.	8.3	62
70	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.	2.0	4
71	Molecular characterization of the TaWTG1 in bread wheat (Triticum aestivum L.). <i>Gene</i> , 2018, 678, 23-32.	2.2	5
72	Mechanisms of wheat (Triticum aestivum) grain storage proteins in response to nitrogen application and its impacts on processing quality. <i>Scientific Reports</i> , 2018, 8, 11928.	3.3	38

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73	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.	3.6	95
74	<i>Fusarium graminearum</i> ATP-Binding Cassette Transporter Gene FgABCC9 Is Required for Its Transportation of Salicylic Acid, Fungicide Resistance, Mycelial Growth and Pathogenicity towards Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2351.	4.1	20
75	Molecular mapping of a stripe rust resistance gene in Chinese wheat landrace "Hejiangyizai" using SSR, RGAP, TRAP, and SRAP markers. <i>Crop Protection</i> , 2017, 94, 178-184.	2.1	7
76	Structure and expression of the TaGW7 in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Growth Regulation</i> , 2017, 82, 281-291.	3.4	9
77	Linoleic acid isomerase gene FgLAI12 affects sensitivity to salicylic acid, mycelial growth and virulence of <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2017, 7, 46129.	3.3	14
78	Transposon insertion resulted in the silencing of Wx-B1n in Chinese wheat landraces. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1321-1330.	3.6	14
79	Identification of quantitative trait loci for seedling root traits from Tibetan semi-wild wheat (<i>Triticum aestivum</i> subsp. <i>tibetanum</i>). <i>Genome</i> , 2017, 60, 1068-1075.	2.0	22
80	Identification and characterization of genes on a single subgenome in the hexaploid wheat (<i>Triticum aestivum</i> L.) genotype "Chinese Spring". <i>Genome</i> , 2017, 60, 208-215.	2.0	4
81	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.	1.5	2
82	Genome-Wide Association Study for Pre-harvest Sprouting Resistance in a Large Germplasm Collection of Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2017, 08, 401.	3.6	98
83	Genome-wide association study of pre-harvest sprouting resistance in Chinese wheat founder parents. <i>Genetics and Molecular Biology</i> , 2017, 40, 620-629.	1.3	19
84	Genome-wide identification and analysis of the MADS-box gene family in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 30	2.5	69
85	Inheritance analysis and mapping of quantitative trait loci (QTL) controlling individual anthocyanin compounds in purple barley (<i>Hordeum vulgare</i> L.) grains. <i>PLoS ONE</i> , 2017, 12, e0183704.	2.5	17
86	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.	1.8	32
87	Structure and expression of phosphoglucan phosphatase genes of Like Sex Four1 and Like Sex Four2 in barley. <i>Genetica</i> , 2016, 144, 313-323.	1.1	3
88	Inheritance and Molecular Mapping of an All-Stage Stripe Rust Resistance Gene Derived from the Chinese Common Wheat Landrace "Yilongtuomai". <i>Journal of Heredity</i> , 2016, 107, 463-470.	2.4	16
89	Structure and expression analysis of genes encoding ADP-glucose pyrophosphorylase large subunit in wheat and its relatives. <i>Genome</i> , 2016, 59, 501-507.	2.0	8
90	A super twin T-DNA vector that allows independent gene expression during <i>Agrobacterium</i> -mediated transformation. <i>Plasmid</i> , 2016, 87-88, 58-64.	1.4	2

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91	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.	1.6	10
92	Chitin synthase gene FgCHS8 affects virulence and fungal cell wall sensitivity to environmental stress in <i>Fusarium graminearum</i> . <i>Fungal Biology</i> , 2016, 120, 764-774.	2.5	29
93	Genetic analyses of Glu-1S sh in wheat/ <i>Aegilops sharonensis</i> hybrid progenies and development of alien HMW-GSs gene-specific markers. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	5
94	Quantitative trait locus mapping for seed dormancy in different post-ripening stages in a Tibetan semi-wild wheat (<i>Triticum aestivum</i> ssp. <i>tibetanum</i> Shao). <i>Euphytica</i> , 2015, 203, 557-567.	1.2	6
95	Characterization of starch branching enzyme I (SBE I) gene in two <i>Triticum monococcum</i> accessions with different starch content. <i>Starch/Staerke</i> , 2015, 67, 663-672.	2.1	4
96	Characterization of genes encoding Starch Branching Enzyme I from <i>Triticum monococcum</i> and its diploid wheat relatives. <i>Biologia (Poland)</i> , 2015, 70, 1193-1200.	1.5	0
97	Identification of genes bordering breakpoints of the pericentric inversions on 2B, 4B, and 5A in bread wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2015, 58, 385-390.	2.0	8
98	Genome-Wide Quantitative Trait Locus Mapping Identifies Multiple Major Loci for Brittle Rachis and Threshability in Tibetan Semi-Wild Wheat (<i>Triticum aestivum</i> ssp. <i>tibetanum</i> Shao). <i>PLoS ONE</i> , 2014, 9, e114066.	2.5	29
99	Conserved structure and varied expression reveal key roles of phosphoglucan phosphatase gene starch excess 4 in barley. <i>Planta</i> , 2014, 240, 1179-1190.	3.2	14
100	Characterization of shrunken endosperm mutants in barley. <i>Gene</i> , 2014, 539, 15-20.	2.2	12
101	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.	3.2	12
102	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.	1.6	7
103	Characterization and expression analysis of waxy alleles in barley accessions. <i>Genetica</i> , 2013, 141, 227-238.	1.1	19
104	Structure and expression of barley starch phosphorylase genes. <i>Planta</i> , 2013, 238, 1081-1093.	3.2	23
105	Novel variants of HMW glutenin subunits from <i>Aegilops</i> section <i>Sitopsis</i> species in relation to evolution and wheat breeding. <i>BMC Plant Biology</i> , 2012, 12, 73.	3.6	28
106	Characterization of barley Prp1 gene and its expression during seed development and under abiotic stress. <i>Genetica</i> , 2011, 139, 1283-1292.	1.1	12
107	Genome-wide identification and evaluation of novel internal control genes for Q-PCR based transcript normalization in wheat. <i>Plant Molecular Biology</i> , 2010, 74, 307-311.	3.9	106
108	Characterization and comparative analysis of HMW glutenin 1Ay alleles with differential expressions. <i>BMC Plant Biology</i> , 2009, 9, 16.	3.6	53

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109	Analysis of the starch properties in tetraploid wheat“ <i>Aegilops sharonensis</i> amphidiploid. <i>Cereal Research Communications</i> , 0, , 1.	1.6	1
110	Temporal transcriptomes unravel the effects of heat stress on seed germination during wheat grain filling. <i>Journal of Agronomy and Crop Science</i> , 0, , .	3.5	0