Tianyu Wang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic Variation in ZmPAT7 Contributes to Tassel Branch Number in Maize. International Journal of Molecular Sciences, 2022, 23, 2586.	4.1	5
2	Fine mapping qKRN5.04 provides a functional gene negatively regulating maize kernel row number. Theoretical and Applied Genetics, 2022, 135, 1997-2007.	3.6	5
3	HTPdb and HTPtools: Exploiting maize haplotype-tag polymorphisms for germplasm resource analyses and genomics-informed breeding. Plant Communications, 2022, 3, 100331.	7.7	2
4	Genomic insights into historical improvement of heterotic groups during modern hybrid maize breeding. Nature Plants, 2022, 8, 750-763.	9.3	36
5	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4
6	Genome-wide association studies of leaf angle in maize. Molecular Breeding, 2021, 41, 1.	2.1	9
7	The retromer protein ZmVPS29 regulates maize kernel morphology likely through an auxinâ€dependent process(es). Plant Biotechnology Journal, 2020, 18, 1004-1014.	8.3	25
8	Transcriptome and GWAS analyses reveal candidate gene for seminal root length of maize seedlings under drought stress. Plant Science, 2020, 292, 110380.	3.6	81
9	Genome-wide association studies and whole-genome prediction reveal the genetic architecture of KRN in maize. BMC Plant Biology, 2020, 20, 490.	3.6	14
10	Genetic mapping of northern corn leaf blight-resistant quantitative trait loci in maize. Medicine (United States), 2020, 99, e21326.	1.0	9
11	Fine mapping and candidate gene analysis of qKW7b, a major QTL for kernel width in maize. Molecular Breeding, 2020, 40, 1.	2.1	4
12	Genome-wide selection and genetic improvement during modern maize breeding. Nature Genetics, 2020, 52, 565-571.	21.4	146
13	Identification of genomic insertion and flanking sequences of the transgenic drought-tolerant maize line "SbSNAC1-382―using the single-molecule real-time (SMRT) sequencing method. PLoS ONE, 2020, 15, e0226455.	2.5	9
14	Genetic architecture of phenotypic means and plasticities of kernel size and weight in maize. Theoretical and Applied Genetics, 2019, 132, 3309-3320.	3.6	16
15	Characterization and fine mapping of qkrnw4, a major QTL controlling kernel row number in maize. Theoretical and Applied Genetics, 2019, 132, 3321-3331.	3.6	11
16	Candidate loci for the kernel row number in maize revealed by a combination of transcriptome analysis and regional association mapping. BMC Plant Biology, 2019, 19, 201.	3.6	10
17	High-density quantitative trait locus mapping revealed genetic architecture of leaf angle and tassel size in maize. Molecular Breeding, 2019, 39, 1.	2.1	10
18	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. Scientific Reports, 2018, 8, 6848.	3.3	16

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19	Characterization and fine mapping of qkc7.03: a major locus for kernel cracking in maize. Theoretical and Applied Genetics, 2018, 131, 437-448.	3.6	8
20	Genome-wide analysis of the pentatricopeptide repeat gene family in different maize genomes and its important role in kernel development. BMC Plant Biology, 2018, 18, 366.	3.6	26
21	Both major and minor QTL associated with plant height can be identified using near-isogenic lines in maize. Euphytica, 2017, 213, 1.	1.2	8
22	Candidate Loci for Yield-Related Traits in Maize Revealed by a Combination of MetaQTL Analysis and Regional Association Mapping. Frontiers in Plant Science, 2017, 8, 2190.	3.6	48
23	Genome-wide identification of gene expression in contrasting maize inbred lines under field drought conditions reveals the significance of transcription factors in drought tolerance. PLoS ONE, 2017, 12, e0179477.	2.5	45
24	Identification of genetic variants associated with maize flowering time using an extremely large multiâ€genetic background population. Plant Journal, 2016, 86, 391-402.	5.7	122
25	Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. Theoretical and Applied Genetics, 2016, 129, 1775-1784.	3.6	9
26	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. BMC Genomics, 2016, 17, 894.	2.8	63
27	Quantitative trait loci mapping of yield and related traits using a high-density genetic map of maize. Molecular Breeding, 2016, 36, 1.	2.1	22
28	Fine-mapping of qGW4.05, a major QTL for kernel weight and size in maize. BMC Plant Biology, 2016, 16, 81.	3.6	47
29	Fine mapping of qKW7, a major QTL for kernel weight and kernel width in maize, confirmed by the combined analytic approaches of linkage and association analysis. Euphytica, 2016, 210, 221-232.	1.2	21
30	Jointâ€ŀinkage mapping and <scp>GWAS</scp> reveal extensive genetic loci that regulate male inflorescence size in maize. Plant Biotechnology Journal, 2016, 14, 1551-1562.	8.3	121
31	Fine mapping of qKL1.07, a major QTL for kernel length in maize. Molecular Breeding, 2016, 36, 1.	2.1	21
32	Exploring Identity-By-Descent Segments and Putative Functions Using Different Foundation Parents in Maize. PLoS ONE, 2016, 11, e0168374.	2.5	18
33	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. BMC Biology, 2015, 13, 78.	3.8	40
34	Analysis of genetic differentiation and genomic variation to reveal potential regions of importance during maize improvement. BMC Plant Biology, 2015, 15, 256.	3.6	22
35	The Identification of Two Head Smut Resistance-Related QTL in Maize by the Joint Approach of Linkage Mapping and Association Analysis. PLoS ONE, 2015, 10, e0145549.	2.5	12
36	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. PLoS ONE, 2015, 10, e0121624.	2.5	69

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37	Contributions of Parental Inbreds and Heterosis to Morphology and Yield of Singleâ€Cross Maize Hybrids in China. Crop Science, 2014, 54, 76-88.	1.8	19
38	Fine genetic characterization of elite maize germplasm using high-throughput SNP genotyping. Theoretical and Applied Genetics, 2014, 127, 621-631.	3.6	78
39	Quantitative trait loci mapping for yield components and kernel-related traits in multiple connected RIL populations in maize. Euphytica, 2013, 193, 303-316.	1.2	80
40	Changes in Yield and Yield Components of Single ross Maize Hybrids Released in China between 1964 and 2001. Crop Science, 2011, 51, 512-525.	1.8	83
41	QTL analysis for yield components and kernel-related traits in maize across multi-environments. Theoretical and Applied Genetics, 2011, 122, 1305-1320.	3.6	143
42	Increasing Maize Productivity in China by Planting Hybrids with Germplasm that Responds Favorably to Higher Planting Densities. Crop Science, 2011, 51, 2391-2400.	1.8	68
43	Population structure and linkage disequilibrium of a mini core set of maize inbred lines in China. Theoretical and Applied Genetics, 2008, 117, 1141-1153.	3.6	83
44	Establishment of a core collection for maize germplasm preserved in Chinese National Genebank using geographic distribution and characterization data. Genetic Resources and Crop Evolution, 2005, 51, 845-852.	1.6	56

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