

Tianyu Wang

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

1,748
citations

361296

20
h-index

302012

39
g-index

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all docs

45
docs citations

45
times ranked

1633
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Variation in ZmPAT7 Contributes to Tassel Branch Number in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2586.	1.8	5
2	Fine mapping qKRN5.04 provides a functional gene negatively regulating maize kernel row number. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1997-2007.	1.8	5
3	HTPdb and HTPtools: Exploiting maize haplotype-tag polymorphisms for germplasm resource analyses and genomics-informed breeding. <i>Plant Communications</i> , 2022, 3, 100331.	3.6	2
4	Genomic insights into historical improvement of heterotic groups during modern hybrid maize breeding. <i>Nature Plants</i> , 2022, 8, 750-763.	4.7	36
5	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	1.2	4
6	Genome-wide association studies of leaf angle in maize. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	9
7	The retromer protein ZmVPS29 regulates maize kernel morphology likely through an auxin-dependent process(es). <i>Plant Biotechnology Journal</i> , 2020, 18, 1004-1014.	4.1	25
8	Transcriptome and GWAS analyses reveal candidate gene for seminal root length of maize seedlings under drought stress. <i>Plant Science</i> , 2020, 292, 110380.	1.7	81
9	Genome-wide association studies and whole-genome prediction reveal the genetic architecture of KRN in maize. <i>BMC Plant Biology</i> , 2020, 20, 490.	1.6	14
10	Genetic mapping of northern corn leaf blight-resistant quantitative trait loci in maize. <i>Medicine (United States)</i> , 2020, 99, e21326.	0.4	9
11	Fine mapping and candidate gene analysis of qKW7b, a major QTL for kernel width in maize. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	4
12	Genome-wide selection and genetic improvement during modern maize breeding. <i>Nature Genetics</i> , 2020, 52, 565-571.	9.4	146
13	Identification of genomic insertion and flanking sequences of the transgenic drought-tolerant maize line α SbSNAC1-382 using the single-molecule real-time (SMRT) sequencing method. <i>PLoS ONE</i> , 2020, 15, e0226455.	1.1	9
14	Genetic architecture of phenotypic means and plasticities of kernel size and weight in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3309-3320.	1.8	16
15	Characterization and fine mapping of qkrnw4, a major QTL controlling kernel row number in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3321-3331.	1.8	11
16	Candidate loci for the kernel row number in maize revealed by a combination of transcriptome analysis and regional association mapping. <i>BMC Plant Biology</i> , 2019, 19, 201.	1.6	10
17	High-density quantitative trait locus mapping revealed genetic architecture of leaf angle and tassel size in maize. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
18	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. <i>Scientific Reports</i> , 2018, 8, 6848.	1.6	16

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19	Characterization and fine mapping of qkc7.03: a major locus for kernel cracking in maize. <i>Theoretical and Applied Genetics</i> , 2018, 131, 437-448.	1.8	8
20	Genome-wide analysis of the pentatricopeptide repeat gene family in different maize genomes and its important role in kernel development. <i>BMC Plant Biology</i> , 2018, 18, 366.	1.6	26
21	Both major and minor QTL associated with plant height can be identified using near-isogenic lines in maize. <i>Euphytica</i> , 2017, 213, 1.	0.6	8
22	Candidate Loci for Yield-Related Traits in Maize Revealed by a Combination of MetaQTL Analysis and Regional Association Mapping. <i>Frontiers in Plant Science</i> , 2017, 8, 2190.	1.7	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. <i>PLoS ONE</i> , 2017, 12, e0179477.	1.1	45
24	Identification of genetic variants associated with maize flowering time using an extremely large multi-ethnic genetic background population. <i>Plant Journal</i> , 2016, 86, 391-402.	2.8	122
25	Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1775-1784.	1.8	9
26	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. <i>BMC Genomics</i> , 2016, 17, 894.	1.2	63
27	Quantitative trait loci mapping of yield and related traits using a high-density genetic map of maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	22
28	Fine-mapping of qGW4.05, a major QTL for kernel weight and size in maize. <i>BMC Plant Biology</i> , 2016, 16, 81.	1.6	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. <i>Euphytica</i> , 2016, 210, 221-232.	0.6	21
30	Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. <i>Plant Biotechnology Journal</i> , 2016, 14, 1551-1562.	4.1	121
31	Fine mapping of qKL1.07, a major QTL for kernel length in maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	21
32	Exploring Identity-By-Descent Segments and Putative Functions Using Different Foundation Parents in Maize. <i>PLoS ONE</i> , 2016, 11, e0168374.	1.1	18
33	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015, 13, 78.	1.7	40
34	Analysis of genetic differentiation and genomic variation to reveal potential regions of importance during maize improvement. <i>BMC Plant Biology</i> , 2015, 15, 256.	1.6	22
35	The Identification of Two Head Smut Resistance-Related QTL in Maize by the Joint Approach of Linkage Mapping and Association Analysis. <i>PLoS ONE</i> , 2015, 10, e0145549.	1.1	12
36	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. <i>PLoS ONE</i> , 2015, 10, e0121624.	1.1	69

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37	Contributions of Parental Inbreds and Heterosis to Morphology and Yield of Singleâ€Cross Maize Hybrids in China. <i>Crop Science</i> , 2014, 54, 76-88.	0.8	19
38	Fine genetic characterization of elite maize germplasm using high-throughput SNP genotyping. <i>Theoretical and Applied Genetics</i> , 2014, 127, 621-631.	1.8	78
39	Quantitative trait loci mapping for yield components and kernel-related traits in multiple connected RIL populations in maize. <i>Euphytica</i> , 2013, 193, 303-316.	0.6	80
40	Changes in Yield and Yield Components of Singleâ€Cross Maize Hybrids Released in China between 1964 and 2001. <i>Crop Science</i> , 2011, 51, 512-525.	0.8	83
41	QTL analysis for yield components and kernel-related traits in maize across multi-environments. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1305-1320.	1.8	143
42	Increasing Maize Productivity in China by Planting Hybrids with Germplasm that Responds Favorably to Higher Planting Densities. <i>Crop Science</i> , 2011, 51, 2391-2400.	0.8	68
43	Population structure and linkage disequilibrium of a mini core set of maize inbred lines in China. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1141-1153.	1.8	83
44	Establishment of a core collection for maize germplasm preserved in Chinese National Genebank using geographic distribution and characterization data. <i>Genetic Resources and Crop Evolution</i> , 2005, 51, 845-852.	0.8	56