Yuan-Ming Zhang

List of Publications by Year
in descending order

103 papers	4,573 citations	136740 32 h-index	118652 62 g-index
114 all docs	114 docs citations	114 times ranked	2643 citing authors

#	Article	IF	Citations
1	A compressed variance component mixed model framework for detecting small and linked QTL-by-environment interactions. Briefings in Bioinformatics, 2022, 23, .	3.2	5
2	A combinatorial strategy to identify various types of QTLs for quantitative traits using extreme phenotype individuals in an F2 population. Plant Communications, 2022, 3, 100319.	3.6	7
3	A compressed variance component mixed model for detecting QTNsÂand QTN-by-environment and QTN-by-QTN interactions in genome-wide association studies. Molecular Plant, 2022, 15, 630-650.	3.9	53
4	dQTG.seq: A comprehensive R tool for detecting all types of QTLs using extreme phenotype individuals in bi-parental segregation populations. Computational and Structural Biotechnology Journal, 2022, 20, 2332-2337.	1.9	1
5	Multi-faceted approaches for breeding nutrient-dense, disease-resistant, and climate-resilient crop varieties for food and nutritional security. Heredity, 2022, 128, 387-390.	1.2	5
6	Domestication and improvement genes reveal the differences of seed size- and oil-related traits in soybean domestication and improvement. Computational and Structural Biotechnology Journal, 2022, 20, 2951-2964.	1.9	7
7	IIIVmrMLM: The R and C++ tools associated with 3VmrMLM, a comprehensive GWAS method for dissecting quantitative traits. Molecular Plant, 2022, 15, 1251-1253.	3.9	36
8	Largeâ€fragment insertion activates gene *GaFZ* (*Ga08G0121*) and is associated with the fuzz and trichome reduction in cotton (*Gossypium arboreum*). Plant Biotechnology Journal, 2021, 19, 1110-1124.	4.1	17
9	Identification of QTNs and their candidate genes for flowering time and plant height in soybean using multi-locus genome-wide association studies. Molecular Breeding, 2021, 41, 1.	1.0	7
10	Integrated Transcriptomic and Bioinformatics Analyses Reveal the Molecular Mechanisms for the Differences in Seed Oil and Starch Content Between Glycine max and Cicer arietinum. Frontiers in Plant Science, 2021, 12, 743680.	1.7	4
11	Integrated Bioinformatics Analyses of PIN1, CKX, and Yield-Related Genes Reveals the Molecular Mechanisms for the Difference of Seed Number Per Pod Between Soybean and Cowpea. Frontiers in Plant Science, 2021, 12, 749902.	1.7	11
12	QTL.gCIMapping.GUI v2.0: An R software for detecting small-effect and linked QTLs for quantitative traits in bi-parental segregation populations. Computational and Structural Biotechnology Journal, 2020, 18, 59-65.	1.9	27
13	The improved FASTmrEMMA and GCIM algorithms for genome-wide association and linkage studies in large mapping populations. Crop Journal, 2020, 8, 723-732.	2.3	10
14	Inference of Chromosome-Length Haplotypes Using Genomic Data of Three or a Few More Single Gametes. Molecular Biology and Evolution, 2020, 37, 3684-3698.	3.5	11
15	DNA N6-Methyladenine Modification in Wild and Cultivated Soybeans Reveals Different Patterns in Nucleus and Cytoplasm. Frontiers in Genetics, 2020, 11, 736.	1.1	13
16	An evolutionary population structure model reveals pleiotropic effects of *GmPDAT* for traits related to seed size and oil content in soybean. Journal of Experimental Botany, 2020, 71, 6988-7002.	2.4	35
17	mrMLM v4.0.2: An R Platform for Multi-locus Genome-wide Association Studies. Genomics, Proteomics and Bioinformatics, 2020, 18, 481-487.	3.0	91
18	Casparian strip membrane domain proteins in Gossypium arboreum: genome-wide identification and negative regulation of lateral root growth. BMC Genomics, 2020, 21, 340.	1.2	4

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19	Introgression Leads to Genomic Divergence and Responsible for Important Traits in Upland Cotton. Frontiers in Plant Science, 2020, 11, 929.	1.7	15
20	Identification of QTNs and Their Candidate Genes for 100-Seed Weight in Soybean (Glycine max L.) Using Multi-Locus Genome-Wide Association Studies. Genes, 2020, 11, 714.	1.0	22
21	Threeâ€dimensional genetic networks among seed oilâ€related traits, metabolites and genes reveal the genetic foundations of oil synthesis in soybean. Plant Journal, 2020, 103, 1103-1124.	2.8	26
22	A Multi-Locus Association Model Framework for Nested Association Mapping With Discriminating QTL Effects in Various Subpopulations. Frontiers in Genetics, 2020, 11, 590012.	1.1	3
23	Integration of RNA-Seq profiling with genome-wide association study predicts candidate genes for oil accumulation in soybean. Crop and Pasture Science, 2020, 71, 996.	0.7	5
24	Genome-Wide Composite Interval Mapping (GCIM) of Expressional Quantitative Trait Loci in Backcross Population. Methods in Molecular Biology, 2020, 2082, 63-71.	0.4	1
25	QTG-Seq Accelerates QTL Fine Mapping through QTL Partitioning and Whole-Genome Sequencing of Bulked Segregant Samples. Molecular Plant, 2019, 12, 426-437.	3.9	75
26	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (Glycine max L.). Heredity, 2019, 123, 579-592.	1.2	41
27	Editorial: The Applications of New Multi-Locus GWAS Methodologies in the Genetic Dissection of Complex Traits. Frontiers in Plant Science, 2019, 10, 100.	1.7	121
28	Comparative transcriptome, physiological and biochemical analyses reveal response mechanism mediated by CBF4 and ICE2 in enhancing cold stress tolerance in Gossypium thurberi. AoB PLANTS, 2019, 11, plz045.	1.2	27
29	An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. Briefings in Bioinformatics, 2019, 20, 1913-1924.	3.2	74
30	pKWmEB: integration of Kruskalâ€"Wallis test with empirical Bayes under polygenic background control for multi-locus genome-wide association study. Heredity, 2018, 120, 208-218.	1.2	175
31	Methodological implementation of mixed linear models in multi-locus genome-wide association studies. Briefings in Bioinformatics, 2018, 19, 700-712.	3.2	315
32	An integrated omics analysis reveals molecular mechanisms that are associated with differences in seed oil content between Glycine max and Brassica napus. BMC Plant Biology, 2018, 18, 328.	1.6	23
33	*Bradyrhizobium diazoefficiens* USDA 110â€"*Glycine max* Interactome Provides Candidate Proteins Associated with Symbiosis. Journal of Proteome Research, 2018, 17, 3061-3074.	1.8	9
34	Epigenetic game theory and its application in plants. Physics of Life Reviews, 2017, 20, 158-160.	1.5	1
35	pLARmEB: integration of least angle regression with empirical Bayes for multilocus genome-wide association studies. Heredity, 2017, 118, 517-524.	1.2	231
36	Whole-genome resequencing reveals candidate mutations for pig prolificacy. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20172437.	1.2	17

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37	Iterative sure independence screening EM-Bayesian LASSO algorithm for multi-locus genome-wide association studies. PLoS Computational Biology, 2017, 13, e1005357.	1.5	280
38	EcoTILLING revealed SNPs in GhSus genes that are associated with fiber- and seed-related traits in upland cotton. Scientific Reports, 2016, 6, 29250.	1.6	18
39	Identification and Validation of Candidate Genes Associated with Domesticated and Improved Traits in Soybean. Plant Genome, 2016, 9, plantgenome2015.09.0090.	1.6	21
40	Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. Scientific Reports, 2016, 5, 18376.	1.6	34
41	Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. Scientific Reports, 2016, 6, 19444.	1.6	479
42	Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. Scientific Reports, 2016, 6, 29951.	1.6	51
43	An Integrated Bioinformatics Analysis Reveals Divergent Evolutionary Pattern of Oil Biosynthesis in High- and Low-Oil Plants. PLoS ONE, 2016, 11, e0154882.	1.1	21
44	Interacted QTL Mapping in Partial NCII Design Provides Evidences for Breeding by Design. PLoS ONE, 2015, 10, e0121034.	1.1	12
45	Identification of domestication-related loci associated with flowering time and seed size in soybean with the RAD-seq genotyping method. Scientific Reports, 2015, 5, 9350.	1.6	62
46	Genomewide mapping reveals a combination of different genetic effects causing the genetic basis of heterosis in two elite rice hybrids. Journal of Genetics, 2015, 94, 261-270.	0.4	8
47	Epistatic Association Mapping for Alkaline and Salinity Tolerance Traits in the Soybean Germination Stage. PLoS ONE, 2014, 9, e84750.	1.1	33
48	Fine mapping of quantitative trait loci for seed size traits in soybean. Molecular Breeding, 2014, 34, 2165-2178.	1.0	36
49	Enrichment of statistical power for genome-wide association studies. BMC Biology, 2014, 12, 73.	1.7	160
50	Linkage group correction using epistatic distorted markers in F2 and backcross populations. Heredity, 2014, 112, 479-488.	1.2	10
51	Multi-QTL mapping for quantitative traits using distorted markers. Molecular Breeding, 2013, 31, 395-404.	1.0	6
52	Association mapping for seed size and shape traits in soybean cultivars. Molecular Breeding, 2013, 31, 785-794.	1.0	93
53	Comparative Genomics Suggests That an Ancestral Polyploidy Event Leads to Enhanced Root Nodule Symbiosis in the Papilionoideae. Molecular Biology and Evolution, 2013, 30, 2602-2611.	3.5	42
54	The origin and functional transition of P34. Heredity, 2013, 110, 259-266.	1.2	4

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55	Multi-QTL Mapping for Quantitative Traits Using Epistatic Distorted Markers. PLoS ONE, 2013, 8, e68510.	1.1	3
56	Variations and Transmission of QTL Alleles for Yield and Fiber Qualities in Upland Cotton Cultivars Developed in China. PLoS ONE, 2013, 8, e57220.	1.1	137
57	An Efficient Hierarchical Generalized Linear Mixed Model for Mapping QTL of Ordinal Traits in Crop Cultivars. PLoS ONE, 2013, 8, e59541.	1.1	10
58	Genetic Basics of Seed Traits in Soybean with Bayes Hierarchical Generalized Linear Model Method. Acta Agronomica Sinica(China), 2013, 39, 258.	0.1	1
59	Fine Mapping of Quantitative Trait Loci for Seed Shape Traits in Soybean. Acta Agronomica Sinica(China), 2013, 39, 609.	0.1	4
60	Association of molecular markers with cold tolerance and green period in zoysiagrass (<i>Zoysia</i> Willd.). Breeding Science, 2012, 62, 320-327.	0.9	17
61	Bias correction for estimated QTL effects using the penalized maximum likelihood method. Heredity, 2012, 108, 396-402.	1.2	9
62	Divergent Evolutionary Pattern of Starch Biosynthetic Pathway Genes in Grasses and Dicots. Molecular Biology and Evolution, 2012, 29, 3227-3236.	3.5	36
63	Transmission of important chromosomal regions under selection revealed in rice pedigree breeding programs. Molecular Breeding, 2012, 30, 717-729.	1.0	1
64	F2 Designs for QTL Analysis. Methods in Molecular Biology, 2012, 871, 17-29.	0.4	5
65	Genome-wide mapping of QTL associated with heterosis in the RIL-based NCIII design. Science Bulletin, 2012, 57, 2655-2665.	1.7	9
66	Gene duplication and an accelerated evolutionary rate in 11S globulin genes are associated with higher protein synthesis in dicots as compared to monocots. BMC Evolutionary Biology, 2012, 12, 15.	3.2	13
67	Quantitative trait loci mapping for yield and its components by using two immortalized populations of a heterotic hybrid in Gossypium hirsutum L.. Molecular Breeding, 2012, 29, 297-311.	1.0	57
68	Molecular Mechanisms of Fiber Differential Development between G. barbadense and G. hirsutum Revealed by Genetical Genomics. PLoS ONE, 2012, 7, e30056.	1.1	43
69	Relationships between differential gene expression and heterosis in cotton hybrids developed from the foundation parent CRI-12 and its pedigree-derived lines. Plant Science, 2011, 180, 221-227.	1.7	13
70	A Complete Solution for Dissecting Pure Main and Epistatic Effects of QTL in Triple Testcross Design. PLoS ONE, 2011, 6, e24575.	1.1	10
71	Molecular evolution of glycinin and β-conglycinin gene families in soybean (Glycine max L. Merr.). Heredity, 2011, 106, 633-641.	1.2	37
72	Mapping of epistatic quantitative trait loci in four-way crosses. Theoretical and Applied Genetics, 2011, 122, 33-48.	1.8	13

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73	Mapping quantitative trait loci for seed size traits in soybean (Glycine max L. Merr.). Theoretical and Applied Genetics, 2011, 122, 581-594.	1.8	82
74	Linkage graph analysis: A linkage-group-based QTL synthesis analysis approach. Science Bulletin, 2011, 56, 1092-1099.	1.7	0
75	Epistatic Association Mapping in Homozygous Crop Cultivars. PLoS ONE, 2011, 6, e17773.	1.1	57
76	Further mapping of quantitative trait loci for female sterility in wheat (Triticum aestivum L.). Genetical Research, 2010, 92, 63-70.	0.3	5
77	Functional mapping of quantitative trait loci associated with rice tillering. Molecular Genetics and Genomics, 2010, 284, 263-271.	1.0	18
78	QTL Analysis for Dynamic Expression of Chlorophyll Content in Soybean (Glycine max L. Merr.). Acta Agronomica Sinica, 2010, 36, 242-248.	0.3	7
79	QTL Analysis for Dynamic Expression of Chlorophyll Content in Soybean (<I>Glycine max</I> L. Merri.). Acta Agronomica Sinica(China), 2010, 36, 242-248.	0.1	2
80	Methodologies for segregation analysis and QTL mapping in plants. Genetica, 2009, 136, 311-318.	0.5	14
81	Multiple loci in silico mapping in inbred lines. Heredity, 2009, 103, 346-354.	1.2	3
82	Multiple quantitative trait loci Haseman–Elston regression using all markers on the entire genome. Theoretical and Applied Genetics, 2008, 117, 683-690.	1.8	6
83	QTL mapping of yield and fiber traits based on a four-way cross population in Gossypium hirsutum L.. Theoretical and Applied Genetics, 2008, 117, 883-894.	1.8	167
84	Mapping quantitative trait loci for binary trait in the F2:3 design. Journal of Genetics, 2008, 87, 201-207.	0.4	0
85	Mapping epistatic quantitative trait loci underlying endosperm traits using all markers on the entire genome in a random hybridization design. Heredity, 2008, 101, 39-47.	1.2	10
86	Mapping Binary Trait Loci in the F2:3 Design. Journal of Heredity, 2007, 98, 337-344.	1.0	7
87	An EM algorithm for mapping segregation distortion loci. BMC Genetics, 2007, 8, 82.	2.7	15
88	A mixture model approach to the mapping of QTL controlling endosperm traits with bulked samples. Genetica, 2007, 132, 59-70.	0.5	4
89	Reconstruction of linkage maps in the distorted segregation populations of backcross, doubled haploid and recombinant inbred lines. Science Bulletin, 2007, 52, 1648-1653.	1.7	13
90	A Genetic Linkage Map of Nonheading Chinese Cabbage. Journal of the American Society for Horticultural Science, 2007, 132, 816-823.	0.5	11

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91	Identification of Quantitative Trait Loci Associated with Aluminum Tolerance in Rice (Oryza Sativa L.). Euphytica, 2006, 150, 37-45.	0.6	20
92	Modeling segregation distortion for viability selection I. Reconstruction of linkage maps with distorted markers. Theoretical and Applied Genetics, 2006, 114, 295-305.	1.8	59
93	Advances on methods for mapping QTL in plant. Science Bulletin, 2006, 51, 2809-2818.	1.7	12
94	Shrinkage Estimation Method for Mapping Multiple Quantitative Trait Loci. Journal of Genetics and Genomics, 2006, 33, 861-869.	0.3	0
95	An EM algorithm for mapping quantitative resistance loci. Heredity, 2005, 94, 119-128.	1.2	13
96	A quantitative genetics model for viability selection. Heredity, 2005, 94, 347-355.	1.2	70
97	A penalized maximum likelihood method for estimating epistatic effects of QTL. Heredity, 2005, 95, 96-104.	1.2	73
98	Bayesian Shrinkage Estimation of Quantitative Trait Loci Parameters. Genetics, 2005, 170, 465-480.	1.2	145
99	Mapping Quantitative Trait Loci Using Naturally Occurring Genetic Variance Among Commercial Inbred Lines of Maize (Zea mays L.). Genetics, 2005, 169, 2267-2275.	1.2	138
100	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. Genetics, 2004, 166, 1981-1993.	1.2	41
101	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. Genetics, 2004, 166, 1981-1993.	1.2	15
102	The EIM algorithm in the joint segregation analysis of quantitative traits. Genetical Research, 2003, 81, 157-163.	0.3	36
103	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (Glycine max L.). , 0, .		1