

Yuan-Ming Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

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	Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. <i>Scientific Reports</i> , 2016, 6, 19444.	1.6	479
2	Methodological implementation of mixed linear models in multi-locus genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2018, 19, 700-712.	3.2	315
3	Iterative sure independence screening EM-Bayesian LASSO algorithm for multi-locus genome-wide association studies. <i>PLoS Computational Biology</i> , 2017, 13, e1005357.	1.5	280
4	pLARmEB: integration of least angle regression with empirical Bayes for multilocus genome-wide association studies. <i>Heredity</i> , 2017, 118, 517-524.	1.2	231
5	pKWmEB: integration of Kruskal-Wallis test with empirical Bayes under polygenic background control for multi-locus genome-wide association study. <i>Heredity</i> , 2018, 120, 208-218.	1.2	175
6	QTL mapping of yield and fiber traits based on a four-way cross population in <i>Gossypium hirsutum</i> L.. <i>Theoretical and Applied Genetics</i> , 2008, 117, 883-894.	1.8	167
7	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014, 12, 73.	1.7	160
8	Bayesian Shrinkage Estimation of Quantitative Trait Loci Parameters. <i>Genetics</i> , 2005, 170, 465-480.	1.2	145
9	Mapping Quantitative Trait Loci Using Naturally Occurring Genetic Variance Among Commercial Inbred Lines of Maize (<i>Zea mays</i> L.). <i>Genetics</i> , 2005, 169, 2267-2275.	1.2	138
10	Variations and Transmission of QTL Alleles for Yield and Fiber Qualities in Upland Cotton Cultivars Developed in China. <i>PLoS ONE</i> , 2013, 8, e57220.	1.1	137
11	Editorial: The Applications of New Multi-Locus GWAS Methodologies in the Genetic Dissection of Complex Traits. <i>Frontiers in Plant Science</i> , 2019, 10, 100.	1.7	121
12	Association mapping for seed size and shape traits in soybean cultivars. <i>Molecular Breeding</i> , 2013, 31, 785-794.	1.0	93
13	mrMLM v4.0.2: An R Platform for Multi-locus Genome-wide Association Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 481-487.	3.0	91
14	Mapping quantitative trait loci for seed size traits in soybean (<i>Glycine max</i> L. Merr.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 581-594.	1.8	82
15	QTC-Seq Accelerates QTL Fine Mapping through QTL Partitioning and Whole-Genome Sequencing of Bulk Segregant Samples. <i>Molecular Plant</i> , 2019, 12, 426-437.	3.9	75
16	An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. <i>Briefings in Bioinformatics</i> , 2019, 20, 1913-1924.	3.2	74
17	A penalized maximum likelihood method for estimating epistatic effects of QTL. <i>Heredity</i> , 2005, 95, 96-104.	1.2	73
18	A quantitative genetics model for viability selection. <i>Heredity</i> , 2005, 94, 347-355.	1.2	70

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19	Identification of domestication-related loci associated with flowering time and seed size in soybean with the RAD-seq genotyping method. <i>Scientific Reports</i> , 2015, 5, 9350.	1.6	62
20	Modeling segregation distortion for viability selection I. Reconstruction of linkage maps with distorted markers. <i>Theoretical and Applied Genetics</i> , 2006, 114, 295-305.	1.8	59
21	Quantitative trait loci mapping for yield and its components by using two immortalized populations of a heterotic hybrid in <i>Gossypium hirsutum</i> L.. <i>Molecular Breeding</i> , 2012, 29, 297-311.	1.0	57
22	Epistatic Association Mapping in Homozygous Crop Cultivars. <i>PLoS ONE</i> , 2011, 6, e17773.	1.1	57
23	A compressed variance component mixed model for detecting QTNs and QTN-by-environment and QTN-by-QTN interactions in genome-wide association studies. <i>Molecular Plant</i> , 2022, 15, 630-650.	3.9	53
24	Mapping small-effect and linked quantitative trait loci for complex traits in backcross or DH populations via a multi-locus GWAS methodology. <i>Scientific Reports</i> , 2016, 6, 29951.	1.6	51
25	Molecular Mechanisms of Fiber Differential Development between <i>G. barbadense</i> and <i>G. hirsutum</i> Revealed by Genetical Genomics. <i>PLoS ONE</i> , 2012, 7, e30056.	1.1	43
26	Comparative Genomics Suggests That an Ancestral Polyploidy Event Leads to Enhanced Root Nodule Symbiosis in the Papilionoideae. <i>Molecular Biology and Evolution</i> , 2013, 30, 2602-2611.	3.5	42
27	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. <i>Genetics</i> , 2004, 166, 1981-1993.	1.2	41
28	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (<i>Glycine max</i> L.). <i>Heredity</i> , 2019, 123, 579-592.	1.2	41
29	Molecular evolution of glycinin and β^2 -conglycinin gene families in soybean (<i>Glycine max</i> L. Merr.). <i>Heredity</i> , 2011, 106, 633-641.	1.2	37
30	The EIM algorithm in the joint segregation analysis of quantitative traits. <i>Genetical Research</i> , 2003, 81, 157-163.	0.3	36
31	Divergent Evolutionary Pattern of Starch Biosynthetic Pathway Genes in Grasses and Dicots. <i>Molecular Biology and Evolution</i> , 2012, 29, 3227-3236.	3.5	36
32	Fine mapping of quantitative trait loci for seed size traits in soybean. <i>Molecular Breeding</i> , 2014, 34, 2165-2178.	1.0	36
33	IIIvMrMLM: The R and C++ tools associated with 3VmrMLM, a comprehensive GWAS method for dissecting quantitative traits. <i>Molecular Plant</i> , 2022, 15, 1251-1253.	3.9	36
34	An evolutionary population structure model reveals pleiotropic effects of <i>GmPDAT</i> for traits related to seed size and oil content in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 6988-7002.	2.4	35
35	Genetic dissection of heterosis using epistatic association mapping in a partial NCII mating design. <i>Scientific Reports</i> , 2016, 5, 18376.	1.6	34
36	Epistatic Association Mapping for Alkaline and Salinity Tolerance Traits in the Soybean Germination Stage. <i>PLoS ONE</i> , 2014, 9, e84750.	1.1	33

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37	Comparative transcriptome, physiological and biochemical analyses reveal response mechanism mediated by CBF4 and ICE2 in enhancing cold stress tolerance in <i>Gossypium thurberi</i> . <i>AoB PLANTS</i> , 2019, 11, plz045.	1.2	27
38	QTL.gCIMapping.GUI v2.0: An R software for detecting small-effect and linked QTLs for quantitative traits in bi-parental segregation populations. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 59-65.	1.9	27
39	Three-dimensional genetic networks among seed oil-related traits, metabolites and genes reveal the genetic foundations of oil synthesis in soybean. <i>Plant Journal</i> , 2020, 103, 1103-1124.	2.8	26
40	An integrated omics analysis reveals molecular mechanisms that are associated with differences in seed oil content between <i>Glycine max</i> and <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2018, 18, 328.	1.6	23
41	Identification of QTNs and Their Candidate Genes for 100-Seed Weight in Soybean (<i>Glycine max</i> L.) Using Multi-Locus Genome-Wide Association Studies. <i>Genes</i> , 2020, 11, 714.	1.0	22
42	Identification and Validation of Candidate Genes Associated with Domesticated and Improved Traits in Soybean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0090.	1.6	21
43	An Integrated Bioinformatics Analysis Reveals Divergent Evolutionary Pattern of Oil Biosynthesis in High- and Low-Oil Plants. <i>PLoS ONE</i> , 2016, 11, e0154882.	1.1	21
44	Identification of Quantitative Trait Loci Associated with Aluminum Tolerance in Rice (<i>Oryza Sativa</i> L.). <i>Euphytica</i> , 2006, 150, 37-45.	0.6	20
45	Functional mapping of quantitative trait loci associated with rice tillering. <i>Molecular Genetics and Genomics</i> , 2010, 284, 263-271.	1.0	18
46	EcoTILLING revealed SNPs in GhSus genes that are associated with fiber- and seed-related traits in upland cotton. <i>Scientific Reports</i> , 2016, 6, 29250.	1.6	18
47	Association of molecular markers with cold tolerance and green period in zoysiagrass (<i>Zoysia</i> Willd.). <i>Breeding Science</i> , 2012, 62, 320-327.	0.9	17
48	Whole-genome resequencing reveals candidate mutations for pig prolificacy. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20172437.	1.2	17
49	Large fragment insertion activates gene <i>GaFZ</i> (<i>Ga08G0121</i>) and is associated with the fuzz and trichome reduction in cotton (<i>Gossypium arboreum</i>). <i>Plant Biotechnology Journal</i> , 2021, 19, 1110-1124.	4.1	17
50	An EM algorithm for mapping segregation distortion loci. <i>BMC Genetics</i> , 2007, 8, 82.	2.7	15
51	Introgression Leads to Genomic Divergence and Responsible for Important Traits in Upland Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 929.	1.7	15
52	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. <i>Genetics</i> , 2004, 166, 1981-1993.	1.2	15
53	Methodologies for segregation analysis and QTL mapping in plants. <i>Genetica</i> , 2009, 136, 311-318.	0.5	14
54	An EM algorithm for mapping quantitative resistance loci. <i>Heredity</i> , 2005, 94, 119-128.	1.2	13

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55	Reconstruction of linkage maps in the distorted segregation populations of backcross, doubled haploid and recombinant inbred lines. <i>Science Bulletin</i> , 2007, 52, 1648-1653.	1.7	13
56	Relationships between differential gene expression and heterosis in cotton hybrids developed from the foundation parent CRI-12 and its pedigree-derived lines. <i>Plant Science</i> , 2011, 180, 221-227.	1.7	13
57	Mapping of epistatic quantitative trait loci in four-way crosses. <i>Theoretical and Applied Genetics</i> , 2011, 122, 33-48.	1.8	13
58	Gene duplication and an accelerated evolutionary rate in 11S globulin genes are associated with higher protein synthesis in dicots as compared to monocots. <i>BMC Evolutionary Biology</i> , 2012, 12, 15.	3.2	13
59	DNA N6-Methyladenine Modification in Wild and Cultivated Soybeans Reveals Different Patterns in Nucleus and Cytoplasm. <i>Frontiers in Genetics</i> , 2020, 11, 736.	1.1	13
60	Advances on methods for mapping QTL in plant. <i>Science Bulletin</i> , 2006, 51, 2809-2818.	1.7	12
61	Interacted QTL Mapping in Partial NCII Design Provides Evidences for Breeding by Design. <i>PLoS ONE</i> , 2015, 10, e0121034.	1.1	12
62	Inference of Chromosome-Length Haplotypes Using Genomic Data of Three or a Few More Single Gametes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3684-3698.	3.5	11
63	A Genetic Linkage Map of Nonheading Chinese Cabbage. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 816-823.	0.5	11
64	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. <i>Frontiers in Plant Science</i> , 2021, 12, 749902.	1.7	11
65	Mapping epistatic quantitative trait loci underlying endosperm traits using all markers on the entire genome in a random hybridization design. <i>Heredity</i> , 2008, 101, 39-47.	1.2	10
66	A Complete Solution for Dissecting Pure Main and Epistatic Effects of QTL in Triple Testcross Design. <i>PLoS ONE</i> , 2011, 6, e24575.	1.1	10
67	Linkage group correction using epistatic distorted markers in F2 and backcross populations. <i>Heredity</i> , 2014, 112, 479-488.	1.2	10
68	The improved FASTmrEMMA and GCIM algorithms for genome-wide association and linkage studies in large mapping populations. <i>Crop Journal</i> , 2020, 8, 723-732.	2.3	10
69	An Efficient Hierarchical Generalized Linear Mixed Model for Mapping QTL of Ordinal Traits in Crop Cultivars. <i>PLoS ONE</i> , 2013, 8, e59541.	1.1	10
70	Bias correction for estimated QTL effects using the penalized maximum likelihood method. <i>Heredity</i> , 2012, 108, 396-402.	1.2	9
71	Genome-wide mapping of QTL associated with heterosis in the RIL-based NCIII design. <i>Science Bulletin</i> , 2012, 57, 2655-2665.	1.7	9
72	<i>Bradyrhizobium diazoefficiens</i> USDA 110â€™ <i>Glycine max</i> Interactome Provides Candidate Proteins Associated with Symbiosis. <i>Journal of Proteome Research</i> , 2018, 17, 3061-3074.	1.8	9

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73	Genomewide mapping reveals a combination of different genetic effects causing the genetic basis of heterosis in two elite rice hybrids. <i>Journal of Genetics</i> , 2015, 94, 261-270.	0.4	8
74	Mapping Binary Trait Loci in the F2:3 Design. <i>Journal of Heredity</i> , 2007, 98, 337-344.	1.0	7
75	QTL Analysis for Dynamic Expression of Chlorophyll Content in Soybean (<i>Glycine max</i> L. Merr.). <i>Acta Agronomica Sinica</i> , 2010, 36, 242-248.	0.3	7
76	Identification of QTNs and their candidate genes for flowering time and plant height in soybean using multi-locus genome-wide association studies. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	7
77	A combinatorial strategy to identify various types of QTLs for quantitative traits using extreme phenotype individuals in an F2 population. <i>Plant Communications</i> , 2022, 3, 100319.	3.6	7
78	Domestication and improvement genes reveal the differences of seed size- and oil-related traits in soybean domestication and improvement. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2951-2964.	1.9	7
79	Multiple quantitative trait loci Haseman-Elston regression using all markers on the entire genome. <i>Theoretical and Applied Genetics</i> , 2008, 117, 683-690.	1.8	6
80	Multi-QTL mapping for quantitative traits using distorted markers. <i>Molecular Breeding</i> , 2013, 31, 395-404.	1.0	6
81	Further mapping of quantitative trait loci for female sterility in wheat (<i>Triticum aestivum</i> L.). <i>Genetical Research</i> , 2010, 92, 63-70.	0.3	5
82	F2 Designs for QTL Analysis. <i>Methods in Molecular Biology</i> , 2012, 871, 17-29.	0.4	5
83	Integration of RNA-Seq profiling with genome-wide association study predicts candidate genes for oil accumulation in soybean. <i>Crop and Pasture Science</i> , 2020, 71, 996.	0.7	5
84	A compressed variance component mixed model framework for detecting small and linked QTL-by-environment interactions. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
85	Multi-faceted approaches for breeding nutrient-dense, disease-resistant, and climate-resilient crop varieties for food and nutritional security. <i>Heredity</i> , 2022, 128, 387-390.	1.2	5
86	A mixture model approach to the mapping of QTL controlling endosperm traits with bulked samples. <i>Genetica</i> , 2007, 132, 59-70.	0.5	4
87	The origin and functional transition of P34. <i>Heredity</i> , 2013, 110, 259-266.	1.2	4
88	Casparian strip membrane domain proteins in <i>Gossypium arboreum</i> : genome-wide identification and negative regulation of lateral root growth. <i>BMC Genomics</i> , 2020, 21, 340.	1.2	4
89	Fine Mapping of Quantitative Trait Loci for Seed Shape Traits in Soybean. <i>Acta Agronomica Sinica</i> (China), 2013, 39, 609.	0.1	4
90	Integrated Transcriptomic and Bioinformatics Analyses Reveal the Molecular Mechanisms for the Differences in Seed Oil and Starch Content Between <i>Glycine max</i> and <i>Cicer arietinum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 743680.	1.7	4

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91	Multiple loci in silico mapping in inbred lines. <i>Heredity</i> , 2009, 103, 346-354.	1.2	3
92	Multi-QTL Mapping for Quantitative Traits Using Epistatic Distorted Markers. <i>PLoS ONE</i> , 2013, 8, e68510.	1.1	3
93	A Multi-Locus Association Model Framework for Nested Association Mapping With Discriminating QTL Effects in Various Subpopulations. <i>Frontiers in Genetics</i> , 2020, 11, 590012.	1.1	3
94	QTL Analysis for Dynamic Expression of Chlorophyll Content in Soybean (<l>Glycine max</l> L. Merri.). <i>Acta Agronomica Sinica(China)</i> , 2010, 36, 242-248.	0.1	2
95	Transmission of important chromosomal regions under selection revealed in rice pedigree breeding programs. <i>Molecular Breeding</i> , 2012, 30, 717-729.	1.0	1
96	Epigenetic game theory and its application in plants. <i>Physics of Life Reviews</i> , 2017, 20, 158-160.	1.5	1
97	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (<i>Glycine max L.</i>). , 0, .		1
98	Genetic Basics of Seed Traits in Soybean with Bayes Hierarchical Generalized Linear Model Method. <i>Acta Agronomica Sinica(China)</i> , 2013, 39, 258.	0.1	1
99	Genome-Wide Composite Interval Mapping (GCIM) of Expressional Quantitative Trait Loci in Backcross Population. <i>Methods in Molecular Biology</i> , 2020, 2082, 63-71.	0.4	1
100	dQTG.seq: A comprehensive R tool for detecting all types of QTLs using extreme phenotype individuals in bi-parental segregation populations. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2332-2337.	1.9	1
101	Shrinkage Estimation Method for Mapping Multiple Quantitative Trait Loci. <i>Journal of Genetics and Genomics</i> , 2006, 33, 861-869.	0.3	0
102	Mapping quantitative trait loci for binary trait in the F2:3 design. <i>Journal of Genetics</i> , 2008, 87, 201-207.	0.4	0
103	Linkage graph analysis: A linkage-group-based QTL synthesis analysis approach. <i>Science Bulletin</i> , 2011, 56, 1092-1099.	1.7	0