

Jianming Yu

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

19,487
citations

36203

51
h-index

27345

106
g-index

117
all docs

117
docs citations

117
times ranked

14708
citing authors

#	ARTICLE	IF	CITATIONS
1	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006, 38, 203-208.	9.4	3,622
2	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	9.4	2,022
3	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	6.0	1,284
4	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008, 1, .	1.6	1,118
5	Genetic Design and Statistical Power of Nested Association Mapping in Maize. <i>Genetics</i> , 2008, 178, 539-551.	1.2	939
6	Genetic association mapping and genome organization of maize. <i>Current Opinion in Biotechnology</i> , 2006, 17, 155-160.	3.3	869
7	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005, 44, 1054-1064.	2.8	821
8	Prospects for Genomewide Selection for Quantitative Traits in Maize. <i>Crop Science</i> , 2007, 47, 1082-1090.	0.8	712
9	Qualitative and quantitative analysis of lignocellulosic biomass using infrared techniques: A mini-review. <i>Applied Energy</i> , 2013, 104, 801-809.	5.1	677
10	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21760-21765.	3.3	469
11	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419
12	Parallel domestication of the Shattering1 genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724.	9.4	401
13	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
14	A deletion mutation in TaHRC confers Fhb1 resistance to Fusarium head blight in wheat. <i>Nature Genetics</i> , 2019, 51, 1099-1105.	9.4	258
15	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
16	Features of sweet sorghum juice and their performance in ethanol fermentation. <i>Industrial Crops and Products</i> , 2010, 31, 164-170.	2.5	221
17	Status and prospects of genome-wide association studies in plants. <i>Plant Genome</i> , 2021, 14, e20077.	1.6	200
18	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , 2016, 2, 16150.	4.7	179

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19	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 110-118.	3.5	166
20	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014, 12, 73.	1.7	160
21	Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a <i>GST</i> gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7339-7344.	3.3	157
22	Presence of tannins in sorghum grains is conditioned by different natural alleles of <i>Tannin1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10281-10286.	3.3	156
23	Increased Power To Dissect Adaptive Traits in Global Sorghum Diversity Using a Nested Association Mapping Population. <i>Genetics</i> , 2017, 206, 573-585.	1.2	152
24	Genomic and environmental determinants and their interplay underlying phenotypic plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6679-6684.	3.3	151
25	Cloning and Characterization of a Critical Regulator for Preharvest Sprouting in Wheat. <i>Genetics</i> , 2013, 195, 263-273.	1.2	148
26	Variation explained in mixed-model association mapping. <i>Heredity</i> , 2010, 105, 333-340.	1.2	133
27	Population structure and marker-trait association analysis of the US peanut (<i>Arachis hypogaea</i> L.) mini-core collection. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1307-1317.	1.8	128
28	Genetic diversity and population structure analysis of accessions in the US historic sweet sorghum collection. <i>Theoretical and Applied Genetics</i> , 2009, 120, 13-23.	1.8	127
29	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444.	2.4	125
30	Association Mapping for Grain Quality in a Diverse Sorghum Collection. <i>Plant Genome</i> , 2012, 5, .	1.6	113
31	Dissecting repulsion linkage in the dwarfing gene <i>Dw3</i> region for sorghum plant height provides insights into heterosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11823-11828.	3.3	110
32	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
33	Genetic Diversity, Population Structure, and Linkage Disequilibrium in U.S. Elite Winter Wheat. <i>Plant Genome</i> , 2010, 3, .	1.6	103
34	Nonmetric Multidimensional Scaling Corrects for Population Structure in Association Mapping With Different Sample Types. <i>Genetics</i> , 2009, 182, 875-888.	1.2	102
35	Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , 2015, 6, 8974.	5.8	100
36	Technological advances in maize breeding: past, present and future. <i>Theoretical and Applied Genetics</i> , 2019, 132, 817-849.	1.8	97

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37	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. , 2007, , 97-119.		95
38	Extreme phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. Plant Journal, 2015, 84, 587-596.	2.8	93
39	Characterization of sorghum genotypes for traits related to drought tolerance. Field Crops Research, 2011, 123, 10-18.	2.3	91
40	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. PLoS Genetics, 2013, 9, e1003202.	1.5	84
41	Association of candidate genes with drought tolerance traits in diverse perennial ryegrass accessions. Journal of Experimental Botany, 2013, 64, 1537-1551.	2.4	83
42	Genome-wide association analysis on pre-harvest sprouting resistance and grain color in U.S. winter wheat. BMC Genomics, 2016, 17, 794.	1.2	83
43	Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. BMC Genomics, 2011, 12, 352.	1.2	82
44	Association Analysis of Stem Rust Resistance in U.S. Winter Wheat. PLoS ONE, 2014, 9, e103747.	1.1	75
45	QTL Mapping for Grain Yield, Flowering Time, and Stay-Green Traits in Sorghum with Genotyping-by-Sequencing Markers. Crop Science, 2016, 56, 1429-1442.	0.8	73
46	Ontogeny of the Maize Shoot Apical Meristem. Plant Cell, 2012, 24, 3219-3234.	3.1	72
47	Identification of a novel gene, H34, in wheat using recombinant inbred lines and single nucleotide polymorphism markers. Theoretical and Applied Genetics, 2013, 126, 2065-2071.	1.8	69
48	Major Regulatory Genes in Maize Contribute to Standing Variation in Teosinte (Zea mays ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302	1.2	67
49	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. Plant Genome, 2009, 2, .	1.6	66
50	Dissecting Genome-Wide Association Signals for Loss-of-Function Phenotypes in Sorghum Flavonoid Pigmentation Traits. G3: Genes, Genomes, Genetics, 2013, 3, 2085-2094.	0.8	65
51	Genome-Wide Association Study on Resistance to Stalk Rot Diseases in Grain Sorghum. G3: Genes, Genomes, Genetics, 2015, 5, 1165-1175.	0.8	63
52	Optimal Designs for Genomic Selection in Hybrid Crops. Molecular Plant, 2019, 12, 390-401.	3.9	63
53	The genetic architecture of nodal root number in maize. Plant Journal, 2018, 93, 1032-1044.	2.8	57
54	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. Molecular Plant, 2021, 14, 874-887.	3.9	56

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55	Genetic Analysis of Seedling Growth under Cold Temperature Stress in Grain Sorghum. <i>Crop Science</i> , 2001, 41, 1438-1443.	0.8	53
56	Dynamic effects of interacting genes underlying rice flowering-time phenotypic plasticity and global adaptation. <i>Genome Research</i> , 2020, 30, 673-683.	2.4	46
57	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	1.1	44
58	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. <i>Genetics</i> , 2007, 176, 563-570.	1.2	43
59	Water and Radiation Use Efficiencies in Sorghum. <i>Agronomy Journal</i> , 2013, 105, 649-656.	0.9	43
60	Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 173-195.	0.2	41
61	Allelochemicals targeted to balance competing selections in African agroecosystems. <i>Nature Plants</i> , 2019, 5, 1229-1236.	4.7	41
62	An <i>Agrobacterium</i> -delivered CRISPR/Cas9 system for targeted mutagenesis in sorghum. <i>Plant Biotechnology Journal</i> , 2020, 18, 319-321.	4.1	40
63	A Large Transposon Insertion in the <i>stiff1</i> Promoter Increases Stalk Strength in Maize. <i>Plant Cell</i> , 2020, 32, 152-165.	3.1	40
64	Analysis of cold tolerance in sorghum under controlled environment conditions. <i>Field Crops Research</i> , 2004, 85, 21-30.	2.3	37
65	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	2.4	35
66	Power of in silico QTL mapping from phenotypic, pedigree, and marker data in a hybrid breeding program. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1061-1067.	1.8	33
67	Computer Simulation in Plant Breeding. <i>Advances in Agronomy</i> , 2012, 116, 219-264.	2.4	33
68	Chromosome Size in Diploid Eukaryotic Species Centers on the Average Length with a Conserved Boundary. <i>Molecular Biology and Evolution</i> , 2011, 28, 1901-1911.	3.5	31
69	Fast analysis of high heating value and elemental compositions of sorghum biomass using near-infrared spectroscopy. <i>Energy</i> , 2017, 118, 1353-1360.	4.5	26
70	Dissection of Leaf Angle Variation in Maize through Genetic Mapping and Meta-Analysis. <i>Plant Genome</i> , 2019, 12, 180024.	1.6	26
71	Phenotypic plasticity in plant height shaped by interaction between genetic loci and diurnal temperature range. <i>New Phytologist</i> , 2022, 233, 1768-1779.	3.5	25
72	Changes in Genetic Variance during Advanced Cycle Breeding in Maize. <i>Crop Science</i> , 2004, 44, 405-410.	0.8	24

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73	Rapid Determination of Both Structural Polysaccharides and Soluble Sugars in Sorghum Biomass Using Near-Infrared Spectroscopy. <i>Bioenergy Research</i> , 2015, 8, 130-136.	2.2	22
74	Diversity of Maize Shoot Apical Meristem Architecture and Its Relationship to Plant Morphology. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 819-827.	0.8	22
75	Genetic Mapping of Foliar and Tassel Heat Stress Tolerance in Maize. <i>Crop Science</i> , 2018, 58, 2484-2493.	0.8	22
76	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. <i>Plant Biotechnology Journal</i> , 2020, 18, 2456-2465.	4.1	20
77	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. <i>One Earth</i> , 2021, 4, 372-383.	3.6	20
78	Genetic diversity and population structure of castor (<i>Ricinus communis</i> L.) germplasm within the US collection assessed with EST-SSR markers. <i>Genome</i> , 2017, 60, 193-200.	0.9	17
79	Integrating Rare-Variant Testing, Function Prediction, and Gene Network in Composite Resequencing-Based Genome-Wide Association Studies (CR-GWAS). <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 233-243.	0.8	16
80	Linkage Disequilibrium and Association Mapping in the Triticeae. , 2009, , 655-683.		16
81	Association Study of Resistance to <i>Soilborne wheat mosaic virus</i> in U.S. Winter Wheat. <i>Phytopathology</i> , 2011, 101, 1322-1329.	1.1	15
82	Controlling population structure in the genomic prediction of tropical maize hybrids. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	15
83	Combining GWAS and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. <i>Genetics</i> , 2022, 221, .	1.2	15
84	Power of mixed-model QTL mapping from phenotypic, pedigree and marker data in self-pollinated crops. <i>Theoretical and Applied Genetics</i> , 2006, 112, 876-884.	1.8	13
85	Genetic Control of Maize Shoot Apical Meristem Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1327-1337.	0.8	13
86	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019, 20, 74.	3.8	13
87	Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. <i>Nucleic Acids Research</i> , 2015, 43, 3614-3625.	6.5	9
88	Sorghum RILs Segregating for Stay-Green QTL and Leaf Dhurrin Content Show Differential Reaction to Stalk Rot Diseases. <i>Crop Science</i> , 2016, 56, 2895-2903.	0.8	9
89	Coupling day length data and genomic prediction tools for predicting time-related traits under complex scenarios. <i>Scientific Reports</i> , 2020, 10, 13382.	1.6	9
90	Registration of the sorghum nested association mapping (NAM) population in RTx430 background. <i>Journal of Plant Registrations</i> , 2021, 15, 395-402.	0.4	9

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91	Maize Leaf Appearance Rates: A Synthesis From the United States Corn Belt. <i>Frontiers in Plant Science</i> , 2022, 13, 872738.	1.7	9
92	Genetics-inspired data-driven approaches explain and predict crop performance fluctuations attributed to changing climatic conditions. <i>Molecular Plant</i> , 2022, 15, 203-206.	3.9	8
93	A Simple Quantitative Model to Predict Leaf Area Index in Sorghum. <i>Agronomy Journal</i> , 2014, 106, 219-226.	0.9	7
94	Genetic dissection of seasonal vegetation index dynamics in maize through aerial based high-throughput phenotyping. <i>Plant Genome</i> , 2021, 14, e20155.	1.6	7
95	Comprehensive analytical and empirical evaluation of genomic prediction across diverse accessions in maize. <i>Plant Genome</i> , 2021, 14, e20160.	1.6	7
96	A Method for Identifying Environmental Stimuli and Genes Responsible for Genotype-by-Environment Interactions From a Large-Scale Multi-Environment Data Set. <i>Frontiers in Genetics</i> , 2021, 12, 803636.	1.1	7
97	Association Genetics Strategies and Resources. , 2013, , 187-203.		6
98	Peanut FAD2 Genotype and Growing Location Interactions Significantly Affect the Level of Oleic Acid in Seeds. <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2020, 97, 1001-1010.	0.8	6
99	The Potential of Ultrahigh Throughput Genomic Technologies in Crop Improvement. <i>Plant Genome</i> , 2009, 2, .	1.6	6
100	Selection before backcross during exotic germplasm introgression. <i>Field Crops Research</i> , 2009, 112, 37-42.	2.3	5
101	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018, 35, 2762-2772.	3.5	4
102	Multilocus epistasis, linkage, and genetic variance in breeding populations with few parents. <i>Theoretical and Applied Genetics</i> , 2007, 115, 335-342.	1.8	3
103	Features and Fermentation Performance of Sweet Sorghum Juice after Harvest. , 2008, , .		2
104	Genetic diversity and population structure in a rice drought stress panel. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015, 13, 195-205.	0.4	2
105	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 63-80.	0.4	2
106	Metabolic control analysis as a mechanism that conserves genetic variance during advanced cycle breeding. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1614-1619.	1.8	1
107	Unraveling the sorghum domestication. <i>Molecular Plant</i> , 2022, , .	3.9	1
108	Retrofitting elite cultivars with an ancestral allele for sustainable agriculture. <i>Science China Life Sciences</i> , 2021, 64, 1029-1030.	2.3	0