Jianming Yu

List of Publications by Year
in descending order

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108 papers	19,487 citations	41627 51 h-index	31191 106 g-index
117 all docs	117 docs citations	117 times ranked	16383 citing authors

#	Article	IF	Citations
1	Genetics-inspired data-driven approaches explain and predict crop performance fluctuations attributed to changing climatic conditions. Molecular Plant, 2022, 15, 203-206.	3.9	8
2	Unraveling the sorghum domestication. Molecular Plant, 2022, , .	3.9	1
3	Phenotypic plasticity in plant height shaped by interaction between genetic loci and diurnal temperature range. New Phytologist, 2022, 233, 1768-1779.	3.5	25
4	Maize Leaf Appearance Rates: A Synthesis From the United States Corn Belt. Frontiers in Plant Science, 2022, 13, 872738.	1.7	9
5	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. Methods in Molecular Biology, 2022, , 63-80.	0.4	2
6	Combining GWAS and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. Genetics, 2022, 221, .	1.2	15
7	Retrofitting elite cultivars with an ancestral allele for sustainable agriculture. Science China Life Sciences, 2021, 64, 1029-1030.	2.3	0
8	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. One Earth, 2021, 4, 372-383.	3.6	20
9	Registration of the sorghum nested association mapping (NAM) population in RTx430 background. Journal of Plant Registrations, 2021, 15, 395-402.	0.4	9
10	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. Trends in Plant Science, 2021, 26, 631-649.	4.3	244
11	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. Molecular Plant, 2021, 14, 874-887.	3.9	56
12	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	6.0	282
13	Genetic dissection of seasonal vegetation index dynamics in maize through aerial based highâ€throughput phenotyping. Plant Genome, 2021, 14, e20155.	1.6	7
14	Status and prospects of genomeâ€wide association studies in plants. Plant Genome, 2021, 14, e20077.	1.6	200
15	Comprehensive analytical and empirical evaluation of genomic prediction across diverse accessions in maize. Plant Genome, 2021, 14, e20160.	1.6	7
16	A Method for Identifying Environmental Stimuli and Genes Responsible for Genotype-by-Environment Interactions From a Large-Scale Multi-Environment Data Set. Frontiers in Genetics, 2021, 12, 803636.	1.1	7
17	An <i>Agrobacterium</i>â€delivered <scp>CRISPR</scp>/Cas9 system for targeted mutagenesis in sorghum. Plant Biotechnology Journal, 2020, 18, 319-321.	4.1	40
18	Peanut FAD2 Genotype and Growing Location Interactions Significantly Affect the Level of Oleic Acid in Seeds. JAOCS, Journal of the American Oil Chemists' Society, 2020, 97, 1001-1010.	0.8	6

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19	Coupling day length data and genomic prediction tools for predicting time-related traits under complex scenarios. Scientific Reports, 2020, 10, 13382.	1.6	9
20	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. Plant Biotechnology Journal, 2020, 18, 2456-2465.	4.1	20
21	A Large Transposon Insertion in the <i>stiff1</i> Promoter Increases Stalk Strength in Maize. Plant Cell, 2020, 32, 152-165.	3.1	40
22	Dynamic effects of interacting genes underlying rice flowering-time phenotypic plasticity and global adaptation. Genome Research, 2020, 30, 673-683.	2.4	46
23	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. Frontiers in Genetics, 2020, 11, 592769.	1.1	44
24	Optimal Designs for Genomic Selection in Hybrid Crops. Molecular Plant, 2019, 12, 390-401.	3.9	63
25	A deletion mutation in TaHRC confers Fhb1 resistance to Fusarium head blight in wheat. Nature Genetics, 2019, 51, 1099-1105.	9.4	258
26	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. Genome Biology, 2019, 20, 74.	3.8	13
27	Technological advances in maize breeding: past, present and future. Theoretical and Applied Genetics, 2019, 132, 817-849.	1.8	97
28	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. Genome Research, 2019, 29, 1962-1973.	2.4	35
29	Allelochemicals targeted to balance competing selections in African agroecosystems. Nature Plants, 2019, 5, 1229-1236.	4.7	41
30	Dissection of Leaf Angle Variation in Maize through Genetic Mapping and Metaâ€Analysis. Plant Genome, 2019, 12, 180024.	1.6	26
31	The genetic architecture of nodal root number in maize. Plant Journal, 2018, 93, 1032-1044.	2.8	57
32	Controlling population structure in the genomic prediction of tropical maize hybrids. Molecular Breeding, 2018, 38, 1.	1.0	15
33	Genetic Mapping of Foliar and Tassel Heat Stress Tolerance in Maize. Crop Science, 2018, 58, 2484-2493.	0.8	22
34	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. Molecular Biology and Evolution, 2018, 35, 2762-2772.	3.5	4
35	Genomic and environmental determinants and their interplay underlying phenotypic plasticity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6679-6684.	3.3	151
36	Increased Power To Dissect Adaptive Traits in Global Sorghum Diversity Using a Nested Association Mapping Population. Genetics, 2017, 206, 573-585.	1.2	152

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37	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	5.8	105
38	Fast analysis of high heating value and elemental compositions of sorghum biomass using near-infrared spectroscopy. Energy, 2017, 118, 1353-1360.	4.5	26
39	Genetic diversity and population structure of castor (<i>Ricinus communis</i> L.) germplasm within the US collection assessed with EST-SSR markers. Genome, 2017, 60, 193-200.	0.9	17
40	Sorghum RILs Segregating for Stayâ€•Green QTL and Leaf Dhurrin Content Show Differential Reaction to Stalk Rot Diseases. Crop Science, 2016, 56, 2895-2903.	0.8	9
41	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. Nature Plants, 2016, 2, 16150.	4.7	179
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	QTL Mapping for Grain Yield, Flowering Time, and Stayâ€•Green Traits in Sorghum with Genotypingâ€•byâ€•Sequencing Markers. Crop Science, 2016, 56, 1429-1442.	0.8	73
44	Extremeâ€•phenotype genomeâ€•wide association study (<scp>XP</scp>â€•<scp>GWAS</scp>): a method for identifying traitâ€•associated variants by sequencing pools of individuals selected from a diversity panel. Plant Journal, 2015, 84, 587-596.	2.8	93
45	Genetic control of morphometric diversity in the maize shoot apical meristem. Nature Communications, 2015, 6, 8974.	5.8	100
46	Genome-Wide Association Study on Resistance to Stalk Rot Diseases in Grain Sorghum. G3: Genes, Genomes, Genetics, 2015, 5, 1165-1175.	0.8	63
47	Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. Nucleic Acids Research, 2015, 43, 3614-3625.	6.5	9
48	Genetic diversity and population structure in a rice drought stress panel. Plant Genetic Resources: Characterisation and Utilisation, 2015, 13, 195-205.	0.4	2
49	Rapid Determination of Both Structural Polysaccharides and Soluble Sugars in Sorghum Biomass Using Near-Infrared Spectroscopy. Bioenergy Research, 2015, 8, 130-136.	2.2	22
50	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. Current Opinion in Plant Biology, 2015, 24, 110-118.	3.5	166
51	Diversity of Maize Shoot Apical Meristem Architecture and Its Relationship to Plant Morphology. G3: Genes, Genomes, Genetics, 2015, 5, 819-827.	0.8	22
52	Dissecting repulsion linkage in the dwarfing gene <i>Dw3</i> region for sorghum plant height provides insights into heterosis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11823-11828.	3.3	110
53	Association Analysis of Stem Rust Resistance in U.S. Winter Wheat. PLoS ONE, 2014, 9, e103747.	1.1	75
54	A Simple Quantitative Model to Predict Leaf Area Index in Sorghum. Agronomy Journal, 2014, 106, 219-226.	0.9	7

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55	Genetic Control of Maize Shoot Apical Meristem Architecture. G3: Genes, Genomes, Genetics, 2014, 4, 1327-1337.	0.8	13
56	Enrichment of statistical power for genome-wide association studies. BMC Biology, 2014, 12, 73.	1.7	160
57	Genome-wide discovery and characterization of maize long non-coding RNAs. Genome Biology, 2014, 15, R40.	13.9	419
58	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
59	Cloning and Characterization of a Critical Regulator for Preharvest Sprouting in Wheat. Genetics, 2013, 195, 263-273.	1.2	148
60	Association Genetics Strategies and Resources. , 2013, , 187-203.		6
61	Qualitative and quantitative analysis of lignocellulosic biomass using infrared techniques: A mini-review. Applied Energy, 2013, 104, 801-809.	5.1	677
62	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. PLoS Genetics, 2013, 9, e1003202.	1.5	84
63	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
64	Association of candidate genes with drought tolerance traits in diverse perennial ryegrass accessions. Journal of Experimental Botany, 2013, 64, 1537-1551.	2.4	83
65	Water and Radiation Use Efficiencies in Sorghum. Agronomy Journal, 2013, 105, 649-656.	0.9	43
66	Genic and nongenic contributions to natural variation of quantitative traits in maize. Genome Research, 2012, 22, 2436-2444.	2.4	125
67	Ontogeny of the Maize Shoot Apical Meristem. Plant Cell, 2012, 24, 3219-3234.	3.1	72
68	Association Mapping for Grain Quality in a Diverse Sorghum Collection. Plant Genome, 2012, 5, .	1.6	113
69	Computer Simulation in Plant Breeding. Advances in Agronomy, 2012, 116, 219-264.	2.4	33
70	Presence of tannins in sorghum grains is conditioned by different natural alleles of <i>Tannin1</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10281-10286.	3.3	156
71	Parallel domestication of the Shattering1 genes in cereals. Nature Genetics, 2012, 44, 720-724.	9.4	401
72	Association Study of Resistance to <i>Soilborne wheat mosaic virus</i> in U.S. Winter Wheat. Phytopathology, 2011, 101, 1322-1329.	1.1	15

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73	Characterization of sorghum genotypes for traits related to drought tolerance. Field Crops Research, 2011, 123, 10-18.	2.3	91
74	Population structure and markerâ€“trait association analysis of the US peanut (Arachis hypogaea L.) mini-core collection. Theoretical and Applied Genetics, 2011, 123, 1307-1317.	1.8	128
75	Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. BMC Genomics, 2011, 12, 352.	1.2	82
76	Chromosome Size in Diploid Eukaryotic Species Centers on the Average Length with a Conserved Boundary. Molecular Biology and Evolution, 2011, 28, 1901-1911.	3.5	31
77	Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a <i>GST</i> gene. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7339-7344.	3.3	157
78	Integrating Rare-Variant Testing, Function Prediction, and Gene Network in Composite Resequencing-Based Genome-Wide Association Studies (CR-GWAS). G3: Genes, Genomes, Genetics, 2011, 1, 233-243.	0.8	16
79	Features of sweet sorghum juice and their performance in ethanol fermentation. Industrial Crops and Products, 2010, 31, 164-170.	2.5	221
80	Variation explained in mixed-model association mapping. Heredity, 2010, 105, 333-340.	1.2	133
81	Mixed linear model approach adapted for genome-wide association studies. Nature Genetics, 2010, 42, 355-360.	9.4	2,022
82	Genetic Diversity, Population Structure, and Linkage Disequilibrium in U.S. Elite Winter Wheat. Plant Genome, 2010, 3, .	1.6	103
83	Nonmetric Multidimensional Scaling Corrects for Population Structure in Association Mapping With Different Sample Types. Genetics, 2009, 182, 875-888.	1.2	102
84	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21760-21765.	3.3	469
85	Genetic diversity and population structure analysis of accessions in the US historic sweet sorghum collection. Theoretical and Applied Genetics, 2009, 120, 13-23.	1.8	127
86	Selection before backcross during exotic germplasm introgression. Field Crops Research, 2009, 112, 37-42.	2.3	5
87	Applications of Linkage Disequilibrium and Association Mapping in Maize. Biotechnology in Agriculture and Forestry, 2009, , 173-195.	0.2	41
88	The Genetic Architecture of Maize Flowering Time. Science, 2009, 325, 714-718.	6.0	1,284
89	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. Plant Genome, 2009, 2, .	1.6	66
90	Linkage Disequilibrium and Association Mapping in the Triticeae. , 2009, , 655-683.		16

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91	The Potential of Ultrahigh Throughput Genomic Technologies in Crop Improvement. Plant Genome, 2009, 2, .	1.6	6
92	Genetic Design and Statistical Power of Nested Association Mapping in Maize. Genetics, 2008, 178, 539-551.	1.2	939
93	Status and Prospects of Association Mapping in Plants. Plant Genome, 2008, 1, .	1.6	1,118
94	Features and Fermentation Performance of Sweet Sorghum Juice after Harvest. , 2008, , .		2
95	Major Regulatory Genes in Maize Contribute to Standing Variation in Teosinte (Zea mays ssp.) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.2	67
96	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. Genetics, 2007, 176, 563-570.	1.2	43
97	Prospects for Genomewide Selection for Quantitative Traits in Maize. Crop Science, 2007, 47, 1082-1090.	0.8	712
98	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. , 2007, , 97-119.		95
99	Multilocus epistasis, linkage, and genetic variance in breeding populations with few parents. Theoretical and Applied Genetics, 2007, 115, 335-342.	1.8	3
100	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nature Genetics, 2006, 38, 203-208.	9.4	3,622
101	Genetic association mapping and genome organization of maize. Current Opinion in Biotechnology, 2006, 17, 155-160.	3.3	869
102	Power of mixed-model QTL mapping from phenotypic, pedigree and marker data in self-pollinated crops. Theoretical and Applied Genetics, 2006, 112, 876-884.	1.8	13
103	Maize association population: a high-resolution platform for quantitative trait locus dissection. Plant Journal, 2005, 44, 1054-1064.	2.8	821
104	Power of in silico QTL mapping from phenotypic, pedigree, and marker data in a hybrid breeding program. Theoretical and Applied Genetics, 2005, 110, 1061-1067.	1.8	33
105	Changes in Genetic Variance during Advanced Cycle Breeding in Maize. Crop Science, 2004, 44, 405-410.	0.8	24
106	Metabolic control analysis as a mechanism that conserves genetic variance during advanced cycle breeding. Theoretical and Applied Genetics, 2004, 108, 1614-1619.	1.8	1
107	Analysis of cold tolerance in sorghum under controlled environment conditions. Field Crops Research, 2004, 85, 21-30.	2.3	37
108	Genetic Analysis of Seedling Growth under Cold Temperature Stress in Grain Sorghum. Crop Science, 2001, 41, 1438-1443.	0.8	53