

Jianming Yu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

105
papers

13,350
citations

45
h-index

115
g-index

117
ext. papers

17,349
ext. citations

8.4
avg, IF

6.3
L-index

#	Paper	IF	Citations
105	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006 , 38, 203-8	36.3	2595
104	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010 , 42, 355-60	36.3	1259
103	The genetic architecture of maize flowering time. <i>Science</i> , 2009 , 325, 714-8	33.3	1043
102	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008 , 1,	4.4	818
101	Genetic design and statistical power of nested association mapping in maize. <i>Genetics</i> , 2008 , 178, 539-514		753
100	Genetic association mapping and genome organization of maize. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 155-60	11.4	659
99	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005 , 44, 1054-64	6.9	633
98	Prospects for Genomewide Selection for Quantitative Traits in Maize. <i>Crop Science</i> , 2007 , 47, 1082-1090	2.4	576
97	Qualitative and quantitative analysis of lignocellulosic biomass using infrared techniques: A mini-review. <i>Applied Energy</i> , 2013 , 104, 801-809	10.7	479
96	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, 21760-5	11.5	354
95	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014 , 15, R40	18.3	308
94	Parallel domestication of the Shattering1 genes in cereals. <i>Nature Genetics</i> , 2012 , 44, 720-4	36.3	287
93	Features of sweet sorghum juice and their performance in ethanol fermentation. <i>Industrial Crops and Products</i> , 2010 , 31, 164-170	5.9	182
92	A deletion mutation in TaHRC confers Fhb1 resistance to Fusarium head blight in wheat. <i>Nature Genetics</i> , 2019 , 51, 1099-1105	36.3	127
91	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , 2016 , 2, 16150	11.5	125
90	Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a GST gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7339-44	11.5	115
89	Presence of tannins in sorghum grains is conditioned by different natural alleles of Tannin1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10281-6	11.5	111

88	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	6	108
87	Cloning and characterization of a critical regulator for preharvest sprouting in wheat. <i>Genetics</i> , 2013 , 195, 263-73	4	105
86	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012 , 22, 2436-44	9.7	96
85	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, 110-8	9.9	94
84	Nonmetric multidimensional scaling corrects for population structure in association mapping with different sample types. <i>Genetics</i> , 2009 , 182, 875-88	4	89
83	Variation explained in mixed-model association mapping. <i>Heredity</i> , 2010 , 105, 333-40	3.6	87
82	Increased Power To Dissect Adaptive Traits in Global Sorghum Diversity Using a Nested Association Mapping Population. <i>Genetics</i> , 2017 , 206, 573-585	4	85
81	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, 1307-17	6	82
80	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants 2007 , 97-119		75
79	Association Mapping for Grain Quality in a Diverse Sorghum Collection. <i>Plant Genome</i> , 2012 , 5,	4.4	74
78	Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. <i>BMC Genomics</i> , 2011 , 12, 352	4.5	73
77	Dissecting repulsion linkage in the dwarfing gene Dw3 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, 11823-8	11.5	69
76	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021 , 26, 631-649	13.1	68
75	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	11.5	67
74	Mendelian and non-Mendelian regulation of gene expression in maize. <i>PLoS Genetics</i> , 2013 , 9, e10032026		66
73	Association of candidate genes with drought tolerance traits in diverse perennial ryegrass accessions. <i>Journal of Experimental Botany</i> , 2013 , 64, 1537-51	7	65
72	Characterization of sorghum genotypes for traits related to drought tolerance. <i>Field Crops Research</i> , 2011 , 123, 10-18	5.5	65
71	Genetic Diversity, Population Structure, and Linkage Disequilibrium in U.S. Elite Winter Wheat. <i>Plant Genome</i> , 2010 , 3,	4.4	65

70	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. <i>Plant Genome</i> , 2009 , 2,	4.4	62
69	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014 , 12, 73	7.3	60
68	Ontogeny of the maize shoot apical meristem. <i>Plant Cell</i> , 2012 , 24, 3219-34	11.6	60
67	Major regulatory genes in maize contribute to standing variation in teosinte (<i>Zea mays</i> ssp. <i>parviglumis</i>). <i>Genetics</i> , 2007 , 177, 2349-59	4	60
66	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017 , 8, 134817.4	5.8	58
65	Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , 2015 , 6, 8974	17.4	58
64	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. <i>Plant Journal</i> , 2015 , 84, 587-96	6.9	57
63	Identification of a novel gene, H34, in wheat using recombinant inbred lines and single nucleotide polymorphism markers. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2065-71	6	47
62	Genetic Analysis of Seedling Growth under Cold Temperature Stress in Grain Sorghum. <i>Crop Science</i> , 2001 , 41, 1438-1443	2.4	47
61	Genome-wide association analysis on pre-harvest sprouting resistance and grain color in U.S. winter wheat. <i>BMC Genomics</i> , 2016 , 17, 794	4.5	45
60	Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 2085-94	3.2	45
59	Status and prospects of genome-wide association studies in plants. <i>Plant Genome</i> , 2021 , 14, e20077	4.4	43
58	Optimal Designs for Genomic Selection in Hybrid Crops. <i>Molecular Plant</i> , 2019 , 12, 390-401	14.4	41
57	Power to detect higher-order epistatic interactions in a metabolic pathway using a new mapping strategy. <i>Genetics</i> , 2007 , 176, 563-70	4	41
56	Association analysis of stem rust resistance in U.S. winter wheat. <i>PLoS ONE</i> , 2014 , 9, e103747	3.7	40
55	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021 , 373, 655-662	33.3	40
54	Technological advances in maize breeding: past, present and future. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 817-849	6	39
53	Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , 2009 , 173-195		35

52	Water and Radiation Use Efficiencies in Sorghum. <i>Agronomy Journal</i> , 2013 , 105, 649-656	2.2	33
51	Analysis of cold tolerance in sorghum under controlled environment conditions. <i>Field Crops Research</i> , 2004 , 85, 21-30	5.5	32
50	The genetic architecture of nodal root number in maize. <i>Plant Journal</i> , 2018 , 93, 1032-1044	6.9	31
49	Genome-Wide Association Study on Resistance to Stalk Rot Diseases in Grain Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1165-75	3.2	30
48	QTL Mapping for Grain Yield, Flowering Time, and Stay-Green Traits in Sorghum with Genotyping-by-Sequencing Markers. <i>Crop Science</i> , 2016 , 56, 1429-1442	2.4	28
47	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, 1061-7	6	27
46	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019 , 29, 1962-1973	9.7	26
45	Computer Simulation in Plant Breeding. <i>Advances in Agronomy</i> , 2012 , 116, 219-264	7.7	23
44	An Agrobacterium-delivered CRISPR/Cas9 system for targeted mutagenesis in sorghum. <i>Plant Biotechnology Journal</i> , 2020 , 18, 319-321	11.6	22
43	Association Mapping of Genetic Resources: Achievements and Future Perspectives 2014 , 207-235		21
42	Rapid Determination of Both Structural Polysaccharides and Soluble Sugars in Sorghum Biomass Using Near-Infrared Spectroscopy. <i>Bioenergy Research</i> , 2015 , 8, 130-136	3.1	20
41	Changes in Genetic Variance during Advanced Cycle Breeding in Maize. <i>Crop Science</i> , 2004 , 44, 405-410	2.4	20
40	Chromosome size in diploid eukaryotic species centers on the average length with a conserved boundary. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1901-11	8.3	19
39	Allelochemicals targeted to balance competing selections in African agroecosystems. <i>Nature Plants</i> , 2019 , 5, 1229-1236	11.5	17
38	Fast analysis of high heating value and elemental compositions of sorghum biomass using near-infrared spectroscopy. <i>Energy</i> , 2017 , 118, 1353-1360	7.9	16
37	Dissection of Leaf Angle Variation in Maize through Genetic Mapping and Meta-Analysis. <i>Plant Genome</i> , 2019 , 12, 180024	4.4	15
36	Dynamic effects of interacting genes underlying rice flowering-time phenotypic plasticity and global adaptation. <i>Genome Research</i> , 2020 , 30, 673-683	9.7	15
35	Diversity of maize shoot apical meristem architecture and its relationship to plant morphology. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 819-27	3.2	14

34	A Large Transposon Insertion in the Promoter Increases Stalk Strength in Maize. <i>Plant Cell</i> , 2020 , 32, 152-165	11.6	14
33	Linkage Disequilibrium and Association Mapping in the Triticeae 2009 , 655-683		14
32	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, 233-43	3.2	12
31	Power of mixed-model QTL mapping from phenotypic, pedigree and marker data in self-pollinated crops. <i>Theoretical and Applied Genetics</i> , 2006 , 112, 876-84	6	12
30	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	4.5	11
29	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	2.4	10
28	Association study of resistance to Soilborne wheat mosaic virus in U.S. winter wheat. <i>Phytopathology</i> , 2011 , 101, 1322-9	3.8	10
27	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes		9
26	Controlling population structure in the genomic prediction of tropical maize hybrids. <i>Molecular Breeding</i> , 2018 , 38, 1	3.4	9
25	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2456-2465	11.6	8
24	Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. <i>Nucleic Acids Research</i> , 2015 , 43, 3614-25	20.1	8
23	Genetic control of maize shoot apical meristem architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1327-37	3.7	8
22	Genetic Mapping of Foliar and Tassel Heat Stress Tolerance in Maize. <i>Crop Science</i> , 2018 , 58, 2484-2493	2.4	8
21	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021 , 14, 874-887	14.4	7
20	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019 , 20, 74	18.3	6
19	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	2.4	6
18	Association Genetics Strategies and Resources 2013 , 187-203		6
17	Coupling day length data and genomic prediction tools for predicting time-related traits under complex scenarios. <i>Scientific Reports</i> , 2020 , 10, 13382	4.9	6

16	Selection before backcross during exotic germplasm introgression. <i>Field Crops Research</i> , 2009 , 112, 37-43	3.5	5
15	A Simple Quantitative Model to Predict Leaf Area Index in Sorghum. <i>Agronomy Journal</i> , 2014 , 106, 219-226		3
14	Multilocus epistasis, linkage, and genetic variance in breeding populations with few parents. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 335-42	6	3
13	Peanut FAD2 Genotype and Growing Location Interactions Significantly Affect the Level of Oleic Acid in Seeds. <i>JAACS, Journal of the American Oil Chemists Society</i> , 2020 , 97, 1001-1010	1.8	3
12	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. <i>One Earth</i> , 2021 , 4, 372-383	8.1	3
11	Registration of the sorghum nested association mapping (NAM) population in RTx430 background. <i>Journal of Plant Registrations</i> , 2021 , 15, 395-402	0.7	3
10	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2762-2772	8.3	2
9	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	4.5	2
8	Genetic diversity and population structure in a rice drought stress panel. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015 , 13, 195-205	1	1
7	Metabolic control analysis as a mechanism that conserves genetic variance during advanced cycle breeding. <i>Theoretical and Applied Genetics</i> , 2004 , 108, 1614-9	6	1
6	Coupling Day Length Data and Genomic Prediction tools for Predicting Time-Related Traits under Complex Scenarios		1
5	Genetic dissection of seasonal vegetation index dynamics in maize through aerial based high-throughput phenotyping. <i>Plant Genome</i> , 2021 , 14, e20155	4.4	1
4	Comprehensive analytical and empirical evaluation of genomic prediction across diverse accessions in maize. <i>Plant Genome</i> , 2021 , 14, e20160	4.4	0
3	Maize Leaf Appearance Rates: A Synthesis From the United States Corn Belt.. <i>Frontiers in Plant Science</i> , 2022 , 13, 872738	6.2	0
2	Retrofitting elite cultivars with an ancestral allele for sustainable agriculture. <i>Science China Life Sciences</i> , 2021 , 64, 1029-1030	8.5	
1	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022 , 63-80	1.4	