

Jianbing Yan

List of Publications by Year in descending order

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Version: 2024-02-01

100
papers

11,115
citations

36303

51
h-index

33894

99
g-index

109
all docs

109
docs citations

109
times ranked

8260
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome optimization via virtual simulation to accelerate maize hybrid breeding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
2	Genome-wide association of the metabolic shifts underpinning dark-induced senescence in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2022, 34, 557-578.	6.6	29
3	Genetic variation in <i>YIG1</i> contributes to ear length and grain yield in maize. <i>New Phytologist</i> , 2022, 234, 513-526.	7.3	38
4	Enhancing crop diversity for food security in the face of climate uncertainty. <i>Plant Journal</i> , 2022, 109, 402-414.	5.7	60
5	gcaPDA: a haplotype-resolved diploid assembler. <i>BMC Bioinformatics</i> , 2022, 23, 68.	2.6	2
6	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	12.6	110
7	Target-oriented prioritization: targeted selection strategy by integrating organismal and molecular traits through predictive analytics in breeding. <i>Genome Biology</i> , 2022, 23, 80.	8.8	13
8	A reactive oxygen species burst causes haploid induction in maize. <i>Molecular Plant</i> , 2022, 15, 943-955.	8.3	39
9	Crop breeding “From experience-based selection to precision design. <i>Journal of Plant Physiology</i> , 2021, 256, 153313.	3.5	19
10	Phenotypic Plasticity Contributes to Maize Adaptation and Heterosis. <i>Molecular Biology and Evolution</i> , 2021, 38, 1262-1275.	8.9	32
11	<i>QDtbn1</i> , an <i>Box</i> gene affecting maize tassel branch number by a dominant model. <i>Plant Biotechnology Journal</i> , 2021, 19, 1183-1194.	8.3	14
12	The genetic architecture of the dynamic changes in grain moisture in maize. <i>Plant Biotechnology Journal</i> , 2021, 19, 1195-1205.	8.3	35
13	A high-throughput and low-cost maize ear traits scorer. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	2
14	Seeing is believing: a visualization toolbox to enhance selection efficiency in maize genome editing. <i>Plant Biotechnology Journal</i> , 2021, 19, 872-874.	8.3	10
15	New genomic approaches for enhancing maize genetic improvement. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101977.	7.1	9
16	Using precision phenotyping to inform de novo domestication. <i>Plant Physiology</i> , 2021, 186, 1397-1411.	4.8	7
17	The genetic mechanism of heterosis utilization in maize improvement. <i>Genome Biology</i> , 2021, 22, 148.	8.8	69
18	Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661.	8.8	60

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19	Natural Variation in Crops: Realized Understanding, Continuing Promise. <i>Annual Review of Plant Biology</i> , 2021, 72, 357-385.	18.7	73
20	Mining novel kernel size-related genes by pQTL mapping and multi-omics integrative analysis in developing maize kernels. <i>Plant Biotechnology Journal</i> , 2021, 19, 1489-1491.	8.3	14
21	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	8.8	47
22	NPF transporters in synaptic-like vesicles control delivery of iron and copper to seeds. <i>Science Advances</i> , 2021, 7, eabh2450.	10.3	29
23	LightGBM: accelerated genomically designed crop breeding through ensemble learning. <i>Genome Biology</i> , 2021, 22, 271.	8.8	76
24	Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292.	5.7	25
25	The Past, Present, and Future of Maize Improvement: Domestication, Genomics, and Functional Genomic Routes toward Crop Enhancement. <i>Plant Communications</i> , 2020, 1, 100010.	7.7	68
26	Application of deep learning in genomics. <i>Science China Life Sciences</i> , 2020, 63, 1860-1878.	4.9	25
27	The Kernel Size-Related Quantitative Trait Locus <i>qKW9</i> Encodes a Pentatricopeptide Repeat Protein That Affects Photosynthesis and Grain Filling. <i>Plant Physiology</i> , 2020, 183, 1696-1709.	4.8	29
28	Single-Cell Genomics and Epigenomics: Technologies and Applications in Plants. <i>Trends in Plant Science</i> , 2020, 25, 1030-1040.	8.8	37
29	Sustainable agriculture in the era of omics: knowledge-driven crop breeding. <i>Genome Biology</i> , 2020, 21, 154.	8.8	45
30	Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163.	8.8	76
31	ZEAMAP, a Comprehensive Database Adapted to the Maize Multi-Omics Era. <i>IScience</i> , 2020, 23, 101241.	4.1	63
32	MaizeCUBIC: a comprehensive variation database for a maize synthetic population. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	5
33	Targeting Key Genes to Tailor Old and New Crops for a Greener Agriculture. <i>Molecular Plant</i> , 2020, 13, 354-356.	8.3	9
34	CUBIC: an atlas of genetic architecture promises directed maize improvement. <i>Genome Biology</i> , 2020, 21, 20.	8.8	57
35	Crop Phenomics and High-Throughput Phenotyping: Past Decades, Current Challenges, and Future Perspectives. <i>Molecular Plant</i> , 2020, 13, 187-214.	8.3	423
36	Genetic variants and underlying mechanisms influencing variance heterogeneity in maize. <i>Plant Journal</i> , 2020, 103, 1089-1102.	5.7	7

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37	High-Throughput CRISPR/Cas9 Mutagenesis Streamlines Trait Gene Identification in Maize. <i>Plant Cell</i> , 2020, 32, 1397-1413.	6.6	148
38	Large-Scale Discovery of Non-conventional Peptides in Maize and Arabidopsis through an Integrated Peptidogenomic Pipeline. <i>Molecular Plant</i> , 2020, 13, 1078-1093.	8.3	58
39	Metabolomics analysis reveals differences in evolution between maize and rice. <i>Plant Journal</i> , 2020, 103, 1710-1722.	5.7	41
40	Structural variation in complex genome: detection, integration and function. <i>Science China Life Sciences</i> , 2019, 62, 1098-1100.	4.9	7
41	SEED CAROTENOID DEFICIENT Functions in Isoprenoid Biosynthesis via the Plastid MEP Pathway. <i>Plant Physiology</i> , 2019, 179, 1723-1738.	4.8	18
42	An allele of <i>ZmPORB2</i> encoding a protochlorophyllide oxidoreductase promotes tocopherol accumulation in both leaves and kernels of maize. <i>Plant Journal</i> , 2019, 100, 114-127.	5.7	21
43	Genome assembly of a tropical maize inbred line provides insights into structural variation and crop improvement. <i>Nature Genetics</i> , 2019, 51, 1052-1059.	21.4	202
44	Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632.	12.8	93
45	De Novo Domestication: An Alternative Route toward New Crops for the Future. <i>Molecular Plant</i> , 2019, 12, 615-631.	8.3	267
46	Large-scale metabolite quantitative trait locus analysis provides new insights for high-quality maize improvement. <i>Plant Journal</i> , 2019, 99, 216-230.	5.7	37
47	Leveraging GWAS data to identify metabolic pathways and networks involved in maize lipid biosynthesis. <i>Plant Journal</i> , 2019, 98, 853-863.	5.7	37
48	Single gametophyte sequencing reveals that crossover events differ between sexes in maize. <i>Nature Communications</i> , 2019, 10, 785.	12.8	36
49	Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. <i>Genome Biology</i> , 2019, 20, 243.	8.8	65
50	Natural variation in <i>ZmFBL41</i> confers banded leaf and sheath blight resistance in maize. <i>Nature Genetics</i> , 2019, 51, 1540-1548.	21.4	138
51	Crop genome-wide association study: a harvest of biological relevance. <i>Plant Journal</i> , 2019, 97, 8-18.	5.7	151
52	CRISPR-Local: a local single-guide RNA (sgRNA) design tool for non-reference plant genomes. <i>Bioinformatics</i> , 2019, 35, 2501-2503.	4.1	28
53	An integrated multi-layered analysis of the metabolic networks of different tissues uncovers key genetic components of primary metabolism in maize. <i>Plant Journal</i> , 2018, 93, 1116-1128.	5.7	38
54	Beyond pathways: genetic dissection of tocopherol content in maize kernels by combining linkage and association analyses. <i>Plant Biotechnology Journal</i> , 2018, 16, 1464-1475.	8.3	70

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55	Intraspecific variation of residual heterozygosity and its utility for quantitative genetic studies in maize. <i>BMC Plant Biology</i> , 2018, 18, 66.	3.6	22
56	Genome-Wide Association Analyses Reveal the Importance of Alternative Splicing in Diversifying Gene Function and Regulating Phenotypic Variation in Maize. <i>Plant Cell</i> , 2018, 30, 1404-1423.	6.6	66
57	Distant eQTLs and Non-coding Sequences Play Critical Roles in Regulating Gene Expression and Quantitative Trait Variation in Maize. <i>Molecular Plant</i> , 2017, 10, 414-426.	8.3	137
58	A 4-bp Insertion at ZmPLA1 Encoding a Putative Phospholipase A Generates Haploid Induction in Maize. <i>Molecular Plant</i> , 2017, 10, 520-522.	8.3	219
59	The genetic architecture of amino acids dissection by association and linkage analysis in maize. <i>Plant Biotechnology Journal</i> , 2017, 15, 1250-1263.	8.3	72
60	High-Throughput Phenotyping and QTL Mapping Reveals the Genetic Architecture of Maize Plant Growth. <i>Plant Physiology</i> , 2017, 173, 1554-1564.	4.8	179
61	Genome-wide Association Studies in Maize: Praise and Stargaze. <i>Molecular Plant</i> , 2017, 10, 359-374.	8.3	334
62	The Genetic Basis of Plant Architecture in 10 Maize Recombinant Inbred Line Populations. <i>Plant Physiology</i> , 2017, 175, 858-873.	4.8	97
63	The Conserved and Unique Genetic Architecture of Kernel Size and Weight in Maize and Rice. <i>Plant Physiology</i> , 2017, 175, 774-785.	4.8	114
64	Contributions of Zea mays subspecies mexicana haplotypes to modern maize. <i>Nature Communications</i> , 2017, 8, 1874.	12.8	102
65	Genome-wide recombination dynamics are associated with phenotypic variation in maize. <i>New Phytologist</i> , 2016, 210, 1083-1094.	7.3	88
66	Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. <i>Scientific Reports</i> , 2016, 6, 18936.	3.3	68
67	Broadening Our Portfolio in the Genetic Improvement of Maize Chemical Composition. <i>Trends in Genetics</i> , 2016, 32, 459-469.	6.7	25
68	Multi-environment QTL analysis of grain morphology traits and fine mapping of a kernel-width QTL in Zheng58 Maize population. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1465-1477.	3.6	84
69	Genetic variation in ZmVPP1 contributes to drought tolerance in maize seedlings. <i>Nature Genetics</i> , 2016, 48, 1233-1241.	21.4	438
70	MODEM: multi-omics data envelopment and mining in maize. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw117.	3.0	39
71	Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. <i>Plant Physiology</i> , 2016, 170, 136-146.	4.8	62
72	Genome-wide dissection of the maize ear genetic architecture using multiple populations. <i>New Phytologist</i> , 2016, 210, 1095-1106.	7.3	142

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73	Maize orthologs of rice <i>GS5</i> and their trans-regulator are associated with kernel development. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 943-953.	8.5	55
74	Genomic, Transcriptomic, and Phenomic Variation Reveals the Complex Adaptation of Modern Maize Breeding. <i>Molecular Plant</i> , 2015, 8, 871-884.	8.3	72
75	Genetic Determinants of the Network of Primary Metabolism and Their Relationships to Plant Performance in a Maize Recombinant Inbred Line Population. <i>Plant Cell</i> , 2015, 27, 1839-1856.	6.6	149
76	A rare SNP mutation in <i>Brachytic2</i> moderately reduces plant height and increases yield potential in maize. <i>Journal of Experimental Botany</i> , 2015, 66, 3791-3802.	4.8	79
77	Dissecting meiotic recombination based on tetrad analysis by single-microspore sequencing in maize. <i>Nature Communications</i> , 2015, 6, 6648.	12.8	97
78	A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. <i>Nature Communications</i> , 2015, 6, 8326.	12.8	392
79	Genome-wide association mapping reveals novel sources of resistance to northern corn leaf blight in maize. <i>BMC Plant Biology</i> , 2015, 15, 206.	3.6	74
80	Multiple loci not only <i>Rf3</i> involved in the restoration ability of pollen fertility, anther exertion and pollen shedding to <i>S</i> type cytoplasmic male sterile in maize. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2341-2350.	3.6	18
81	Genome Wide Association Studies Using a New Nonparametric Model Reveal the Genetic Architecture of 17 Agronomic Traits in an Enlarged Maize Association Panel. <i>PLoS Genetics</i> , 2014, 10, e1004573.	3.5	307
82	Genetic basis of grain yield heterosis in an immortalized F2-maize population. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2149-2158.	3.6	83
83	Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. <i>Nature Communications</i> , 2014, 5, 3438.	12.8	402
84	Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. <i>Nature Genetics</i> , 2013, 45, 43-50.	21.4	764
85	Natural variation in the sequence of <i>PSY1</i> and frequency of favorable polymorphisms among tropical and temperate maize germplasm. <i>Theoretical and Applied Genetics</i> , 2013, 126, 923-935.	3.6	53
86	RNA sequencing reveals the complex regulatory network in the maize kernel. <i>Nature Communications</i> , 2013, 4, 2832.	12.8	252
87	CACTA-like transposable element in <i>ZmCCT</i> attenuated photoperiod sensitivity and accelerated the postdomestication spread of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16969-16974.	7.1	296
88	Genome-Wide Association Studies Identified Three Independent Polymorphisms Associated with γ -Tocopherol Content in Maize Kernels. <i>PLoS ONE</i> , 2012, 7, e36807.	2.5	140
89	Validation of <i>DGAT1-2</i> polymorphisms associated with oil content and development of functional markers for molecular breeding of high-oil maize. <i>Molecular Breeding</i> , 2012, 29, 939-949.	2.1	36
90	An 11-bp Insertion in <i>Zea mays fatb</i> Reduces the Palmitic Acid Content of Fatty Acids in Maize Grain. <i>PLoS ONE</i> , 2011, 6, e24699.	2.5	42

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91	Association Mapping for Enhancing Maize (<i>Zea mays</i> L.) Genetic Improvement. <i>Crop Science</i> , 2011, 51, 433-449.	1.8	305
92	Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. <i>Molecular Breeding</i> , 2011, 28, 511-526.	2.1	324
93	Major and minor QTL and epistasis contribute to fatty acid compositions and oil concentration in high-oil maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 665-678.	3.6	125
94	Nucleotide diversity and molecular evolution of the PSY1 gene in <i>Zea mays</i> compared to some other grass species. <i>Theoretical and Applied Genetics</i> , 2010, 120, 709-720.	3.6	36
95	Cloning and characterization of a putative GS3 ortholog involved in maize kernel development. <i>Theoretical and Applied Genetics</i> , 2010, 120, 753-763.	3.6	126
96	Genetic analysis and characterization of a new maize association mapping panel for quantitative trait loci dissection. <i>Theoretical and Applied Genetics</i> , 2010, 121, 417-431.	3.6	176
97	Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight. <i>BMC Plant Biology</i> , 2010, 10, 143.	3.6	179
98	Rare genetic variation at <i>Zea mays crtRB1</i> increases β^2 -carotene in maize grain. <i>Nature Genetics</i> , 2010, 42, 322-327.	21.4	421
99	Natural Genetic Variation in <i>Lycopene Epsilon Cyclase</i> Tapped for Maize Biofortification. <i>Science</i> , 2008, 319, 330-333.	12.6	692
100	De Novo Domestication in the Multi-Omics Era. <i>Plant and Cell Physiology</i> , 0, , .	3.1	4