

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-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. <i>Nature Genetics</i> , 2013, 45, 43-50. | 21.4 | 764 |
| 2 | Natural Genetic Variation in <i>Lycopene Epsilon Cyclase</i> Tapped for Maize Biofortification. <i>Science</i> , 2008, 319, 330-333. | 12.6 | 692 |
| 3 | Genetic variation in <i>ZmVPP1</i> contributes to drought tolerance in maize seedlings. <i>Nature Genetics</i> , 2016, 48, 1233-1241. | 21.4 | 438 |
| 4 | Crop Phenomics and High-Throughput Phenotyping: Past Decades, Current Challenges, and Future Perspectives. <i>Molecular Plant</i> , 2020, 13, 187-214. | 8.3 | 423 |
| 5 | 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 |
| 6 | Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. <i>Nature Communications</i> , 2014, 5, 3438. | 12.8 | 402 |
| 7 | 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 |
| 8 | Genome-wide Association Studies in Maize: Praise and Stargaze. <i>Molecular Plant</i> , 2017, 10, 359-374. | 8.3 | 334 |
| 9 | 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 |
| 10 | 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 |
| 11 | Association Mapping for Enhancing Maize (<i>Zea mays</i> L.) Genetic Improvement. <i>Crop Science</i> , 2011, 51, 433-449. | 1.8 | 305 |
| 12 | 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 |
| 13 | De Novo Domestication: An Alternative Route toward New Crops for the Future. <i>Molecular Plant</i> , 2019, 12, 615-631. | 8.3 | 267 |
| 14 | RNA sequencing reveals the complex regulatory network in the maize kernel. <i>Nature Communications</i> , 2013, 4, 2832. | 12.8 | 252 |
| 15 | A 4-bp Insertion at <i>ZmPLA1</i> Encoding a Putative Phospholipase A Generates Haploid Induction in Maize. <i>Molecular Plant</i> , 2017, 10, 520-522. | 8.3 | 219 |
| 16 | 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 |
| 17 | Relationship, evolutionary fate and function of two maize co-orthologs of rice <i>GW2</i> associated with kernel size and weight. <i>BMC Plant Biology</i> , 2010, 10, 143. | 3.6 | 179 |
| 18 | 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 |

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|----|--|------|-----------|
| 19 | 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 |
| 20 | Crop genome-wide association study: a harvest of biological relevance. <i>Plant Journal</i> , 2019, 97, 8-18. | 5.7 | 151 |
| 21 | 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 |
| 22 | High-Throughput CRISPR/Cas9 Mutagenesis Streamlines Trait Gene Identification in Maize. <i>Plant Cell</i> , 2020, 32, 1397-1413. | 6.6 | 148 |
| 23 | Genome-wide dissection of the maize ear genetic architecture using multiple populations. <i>New Phytologist</i> , 2016, 210, 1095-1106. | 7.3 | 142 |
| 24 | 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 |
| 25 | Natural variation in ZmFBL41 confers banded leaf and sheath blight resistance in maize. <i>Nature Genetics</i> , 2019, 51, 1540-1548. | 21.4 | 138 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985. | 12.6 | 110 |
| 31 | Contributions of <i>Zea mays</i> subspecies <i>mexicana</i> haplotypes to modern maize. <i>Nature Communications</i> , 2017, 8, 1874. | 12.8 | 102 |
| 32 | Dissecting meiotic recombination based on tetrad analysis by single-microspore sequencing in maize. <i>Nature Communications</i> , 2015, 6, 6648. | 12.8 | 97 |
| 33 | The Genetic Basis of Plant Architecture in 10 Maize Recombinant Inbred Line Populations. <i>Plant Physiology</i> , 2017, 175, 858-873. | 4.8 | 97 |
| 34 | Chromatin interaction maps reveal genetic regulation for quantitative traits in maize. <i>Nature Communications</i> , 2019, 10, 2632. | 12.8 | 93 |
| 35 | Genome-wide recombination dynamics are associated with phenotypic variation in maize. <i>New Phytologist</i> , 2016, 210, 1083-1094. | 7.3 | 88 |
| 36 | Multi-environment QTL analysis of grain morphology traits and fine mapping of a kernel-width QTL in Zheng58ASK maize population. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1465-1477. | 3.6 | 84 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | Mapping regulatory variants controlling gene expression in drought response and tolerance in maize. <i>Genome Biology</i> , 2020, 21, 163. | 8.8 | 76 |
| 40 | LightGBM: accelerated genomically designed crop breeding through ensemble learning. <i>Genome Biology</i> , 2021, 22, 271. | 8.8 | 76 |
| 41 | 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 |
| 42 | Natural Variation in Crops: Realized Understanding, Continuing Promise. <i>Annual Review of Plant Biology</i> , 2021, 72, 357-385. | 18.7 | 73 |
| 43 | Genomic, Transcriptomic, and Phenomic Variation Reveals the Complex Adaptation of Modern Maize Breeding. <i>Molecular Plant</i> , 2015, 8, 871-884. | 8.3 | 72 |
| 44 | 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 |
| 45 | 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 |
| 46 | The genetic mechanism of heterosis utilization in maize improvement. <i>Genome Biology</i> , 2021, 22, 148. | 8.8 | 69 |
| 47 | Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. <i>Scientific Reports</i> , 2016, 6, 18936. | 3.3 | 68 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | ZEAMAP, a Comprehensive Database Adapted to the Maize Multi-Omics Era. <i>IScience</i> , 2020, 23, 101241. | 4.1 | 63 |
| 52 | 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 |
| 53 | Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661. | 8.8 | 60 |
| 54 | Enhancing crop diversity for food security in the face of climate uncertainty. <i>Plant Journal</i> , 2022, 109, 402-414. | 5.7 | 60 |

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|----|---|------|-----------|
| 55 | 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 |
| 56 | CUBIC: an atlas of genetic architecture promises directed maize improvement. <i>Genome Biology</i> , 2020, 21, 20. | 8.8 | 57 |
| 57 | Maize orthologs of rice <i>CS5</i> and their trans-regulator are associated with kernel development. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 943-953. | 8.5 | 55 |
| 58 | Natural variation in the sequence of PSY1 and frequency of favorable polymorphisms among tropical and temperate maize germplasm. <i>Theoretical and Applied Genetics</i> , 2013, 126, 923-935. | 3.6 | 53 |
| 59 | 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 |
| 60 | Sustainable agriculture in the era of omics: knowledge-driven crop breeding. <i>Genome Biology</i> , 2020, 21, 154. | 8.8 | 45 |
| 61 | 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 |
| 62 | Metabolomics analysis reveals differences in evolution between maize and rice. <i>Plant Journal</i> , 2020, 103, 1710-1722. | 5.7 | 41 |
| 63 | 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 |
| 64 | A reactive oxygen species burst causes haploid induction in maize. <i>Molecular Plant</i> , 2022, 15, 943-955. | 8.3 | 39 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | Single-Cell Genomics and Epigenomics: Technologies and Applications in Plants. <i>Trends in Plant Science</i> , 2020, 25, 1030-1040. | 8.8 | 37 |
| 70 | 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 |
| 71 | Validation of DGAT1-2 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 |
| 72 | Single gametophyte sequencing reveals that crossover events differ between sexes in maize. <i>Nature Communications</i> , 2019, 10, 785. | 12.8 | 36 |

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|----|---|------|-----------|
| 73 | The genetic architecture of the dynamic changes in grain moisture in maize. <i>Plant Biotechnology Journal</i> , 2021, 19, 1195-1205. | 8.3 | 35 |
| 74 | Phenotypic Plasticity Contributes to Maize Adaptation and Heterosis. <i>Molecular Biology and Evolution</i> , 2021, 38, 1262-1275. | 8.9 | 32 |
| 75 | 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 |
| 76 | NPF transporters in synaptic-like vesicles control delivery of iron and copper to seeds. <i>Science Advances</i> , 2021, 7, eabh2450. | 10.3 | 29 |
| 77 | 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 |
| 78 | 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 |
| 79 | Broadening Our Portfolio in the Genetic Improvement of Maize Chemical Composition. <i>Trends in Genetics</i> , 2016, 32, 459-469. | 6.7 | 25 |
| 80 | Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292. | 5.7 | 25 |
| 81 | Application of deep learning in genomics. <i>Science China Life Sciences</i> , 2020, 63, 1860-1878. | 4.9 | 25 |
| 82 | 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 |
| 83 | 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 |
| 84 | Crop breeding “From experience-based selection to precision design. <i>Journal of Plant Physiology</i> , 2021, 256, 153313. | 3.5 | 19 |
| 85 | Multiple loci not only <i>Rf3</i> involved in the restoration ability of pollen fertility, anther exertion and pollen shedding to S type cytoplasmic male sterile in maize. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2341-2350. | 3.6 | 18 |
| 86 | SEED CAROTENOID DEFICIENT Functions in Isoprenoid Biosynthesis via the Plastid MEP Pathway. <i>Plant Physiology</i> , 2019, 179, 1723-1738. | 4.8 | 18 |
| 87 | <i>Q^{Dtbn1}</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 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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| 91 | Targeting Key Genes to Tailor Old and New Crops for a Greener Agriculture. <i>Molecular Plant</i> , 2020, 13, 354-356. | 8.3 | 9 |
| 92 | New genomic approaches for enhancing maize genetic improvement. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101977. | 7.1 | 9 |
| 93 | Structural variation in complex genome: detection, integration and function. <i>Science China Life Sciences</i> , 2019, 62, 1098-1100. | 4.9 | 7 |
| 94 | Genetic variants and underlying mechanisms influencing variance heterogeneity in maize. <i>Plant Journal</i> , 2020, 103, 1089-1102. | 5.7 | 7 |
| 95 | Using precision phenotyping to inform de novo domestication. <i>Plant Physiology</i> , 2021, 186, 1397-1411. | 4.8 | 7 |
| 96 | 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 |
| 97 | De Novo Domestication in the Multi-Omics Era. <i>Plant and Cell Physiology</i> , 0, , . | 3.1 | 4 |
| 98 | Genome optimization via virtual simulation to accelerate maize hybrid breeding. <i>Briefings in Bioinformatics</i> , 2022, 23, . | 6.5 | 3 |
| 99 | A high-throughput and low-cost maize ear traits scorer. <i>Molecular Breeding</i> , 2021, 41, 1. | 2.1 | 2 |
| 100 | gcaPDA: a haplotype-resolved diploid assembler. <i>BMC Bioinformatics</i> , 2022, 23, 68. | 2.6 | 2 |