

# Chuanxiao Xie

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

2,718  
citations

201674

27  
h-index

243625

44  
g-index

44  
all docs

44  
docs citations

44  
times ranked

3294  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>hlh122</i> is important for drought and osmotic stress resistance in <i>A. rabidopsis</i> and in the repression of ABA catabolism. <i>New Phytologist</i> , 2014, 201, 1192-1204.	7.3	242
2	An alternative strategy for targeted gene replacement in plants using a dual-sgRNA/Cas9 design. <i>Scientific Reports</i> , 2016, 6, 23890.	3.3	212
3	Joint linkage disequilibrium mapping is a powerful approach to detecting quantitative trait loci underlying drought tolerance in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19585-19590.	7.1	202
4	Enhancing genetic gain in the era of molecular breeding. <i>Journal of Experimental Botany</i> , 2017, 68, 2641-2666.	4.8	197
5	CRISPR/Cas9: A powerful tool for crop genome editing. <i>Crop Journal</i> , 2016, 4, 75-82.	5.2	150
6	Genome-Wide Identification of MicroRNAs in Response to Low Nitrate Availability in Maize Leaves and Roots. <i>PLoS ONE</i> , 2011, 6, e28009.	2.5	146
7	Whole-genome strategies for marker-assisted plant breeding. <i>Molecular Breeding</i> , 2012, 29, 833-854.	2.1	129
8	Genome-Wide Association Study Identifies Candidate Genes That Affect Plant Height in Chinese Elite Maize ( <i>Zea mays</i> L.) Inbred Lines. <i>PLoS ONE</i> , 2011, 6, e29229.	2.5	110
9	Large-scale screening for maize drought resistance using multiple selection criteria evaluated under water-stressed and well-watered environments. <i>Field Crops Research</i> , 2011, 124, 37-45.	5.1	92
10	Meta-analysis of constitutive and adaptive QTL for drought tolerance in maize. <i>Euphytica</i> , 2010, 174, 165-177.	1.2	89
11	Comparative LD mapping using single SNPs and haplotypes identifies QTL for plant height and biomass as secondary traits of drought tolerance in maize. <i>Molecular Breeding</i> , 2012, 30, 407-418.	2.1	83
12	RNA-guided Cas9 as an <i>in vivo</i> desired target mutator in maize. <i>Plant Biotechnology Journal</i> , 2017, 15, 1566-1576.	8.3	82
13	Combined small RNA and degradome sequencing reveals novel miRNAs and their targets in response to low nitrate availability in maize. <i>Annals of Botany</i> , 2013, 112, 633-642.	2.9	73
14	Genetic Contribution to Advanced Yield for Maize Hybrids Released from 1970 to 2000 in China. <i>Crop Science</i> , 2011, 51, 13-20.	1.8	69
15	Genetic architecture of the maize kernel row number revealed by combining QTL mapping using a high-density genetic map and bulked segregant RNA sequencing. <i>BMC Genomics</i> , 2016, 17, 915.	2.8	63
16	Genome Editing and Double-Fluorescence Proteins Enable Robust Maternal Haploid Induction and Identification in Maize. <i>Molecular Plant</i> , 2018, 11, 1214-1217.	8.3	61
17	Precise base editing of non-allelic acetolactate synthase genes confers sulfonylurea herbicide resistance in maize. <i>Crop Journal</i> , 2020, 8, 449-456.	5.2	55
18	Genome-wide association study dissects yield components associated with low-phosphorus stress tolerance in maize. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1699-1714.	3.6	53

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19	Identification of Functional Genetic Variations Underlying Drought Tolerance in Maize Using SNP Markers. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 641-652.	8.5	52
20	Supersweet and waxy: meeting the diverse demands for specialty maize by genome editing. <i>Plant Biotechnology Journal</i> , 2019, 17, 1853-1855.	8.3	52
21	Inferring Genome Ancestry and Estimating Molecular Relatedness Among 187 Chinese Maize Inbred Lines. <i>Journal of Genetics and Genomics</i> , 2007, 34, 738-748.	3.9	48
22	Trends of grain yield and plant traits in Chinese maize cultivars from the 1950s to the 2000s. <i>Euphytica</i> , 2012, 185, 395-406.	1.2	46
23	CRISPR/Cas9-mediated genome editing in plants. <i>Methods</i> , 2017, 121-122, 94-102.	3.8	46
24	Meta-analysis and candidate gene mining of low-phosphorus tolerance in maize. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 262-270.	8.5	44
25	Genome Editing Enables Next-Generation Hybrid Seed Production Technology. <i>Molecular Plant</i> , 2020, 13, 1262-1269.	8.3	42
26	Low-nitrogen stress tolerance and nitrogen agronomic efficiency among maize inbreds: comparison of multiple indices and evaluation of genetic variation. <i>Euphytica</i> , 2011, 180, 281.	1.2	41
27	Creation of targeted inversion mutations in plants using an RNA-guided endonuclease. <i>Crop Journal</i> , 2017, 5, 83-88.	5.2	35
28	Systematic identification of endogenous RNA polymerase III promoters for efficient RNA guide-based genome editing technologies in maize. <i>Crop Journal</i> , 2018, 6, 314-320.	5.2	26
29	Molecular Mapping of the Major Resistance Quantitative Trait Locus <i>qHS2.09</i> with Simple Sequence Repeat and Single Nucleotide Polymorphism Markers in Maize. <i>Phytopathology</i> , 2012, 102, 692-699.	2.2	22
30	Fine mapping of a quantitative trait locus conferring resistance to maize rough dwarf disease. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2333-2342.	3.6	20
31	Large-Scale Evaluation of Maize Germplasm for Low-Phosphorus Tolerance. <i>PLoS ONE</i> , 2015, 10, e0124212.	2.5	18
32	Association Analysis of the <i>nced</i> and <i>rab28</i> Genes with Phenotypic Traits Under Water Stress in Maize. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 714-722.	1.8	17
33	A field-deployable method for single and multiplex detection of DNA or RNA from pathogens using Cas12 and Cas13. <i>Science China Life Sciences</i> , 2022, 65, 1456-1465.	4.9	16
34	Establishment of an efficient seed fluorescence reporter-assisted CRISPR/Cas9 gene editing in maize. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1671-1680.	8.5	14
35	Targeted generation of Null Mutants in <i>ZmGDI1</i> confers resistance against maize rough dwarf disease without agronomic penalty. <i>Plant Biotechnology Journal</i> , 2022, 20, 803-805.	8.3	14
36	Identification and functional characterization of the <i>AGO1</i> ortholog in maize. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 749-758.	8.5	12

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37	Zea mays (L.) P1 locus for cob glume color identified as a post-domestication selection target with an effect on temperate maize genomes. <i>Crop Journal</i> , 2013, 1, 15-24.	5.2	10
38	An analysis of the polymorphisms in a gene for being involved in drought tolerance in maize. <i>Genetica</i> , 2011, 139, 479-487.	1.1	9
39	Linkage mapping combined with GWAS revealed the genetic structural relationship and candidate genes of maize flowering time-related traits. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	6
40	Kernel lysine content does not increase in some maize opaque2 mutants. <i>Planta</i> , 2012, 235, 205-215.	3.2	5
41	A simple way to visualize detailed phylogenetic tree of huge genome-wide SNP data constructed by SNPhylo. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1972-1978.	3.5	5
42	Comparative QTL mapping of resistance to sugarcane mosaic virus in maize based on bioinformatics. <i>Frontiers of Agriculture in China</i> , 2008, 2, 365-371.	0.2	4