Zhenhai Cui

List of Publications by Year
in descending order

14 papers	312 citations	1478505 6 h-index	1199594 12 g-index
14 all docs	14 docs citations	14 times ranked	428 citing authors

#	Article	IF	Citations
1	A Genome-Wide Association Study Dissects the Genetic Architecture of the Metaxylem Vessel Number in Maize Brace Roots. Frontiers in Plant Science, 2022, 13, 847234.	3.6	5
2	Genetic analysis of maize shank length by QTL mapping in three recombinant inbred line populations. Plant Science, 2021, 303, 110767.	3.6	4
3	Genetic analysis of three maize husk traits by QTL mapping in a maize-teosinte population. BMC Genomics, 2021, 22, 386.	2.8	4
4	Genetic basis of maize ear angle revealed by high-density single nucleotide polymorphism markers in four recombinant inbred line populations. Euphytica, 2020, 216, 1.	1.2	0
5	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. G3: Genes, Genomes, Genetics, 2020, 10, 3741-3749.	1.8	16
6	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. Scientific Reports, 2020, 10, 8165.	3.3	12
7	Genome-Wide Association Study Dissects the Genetic Architecture of Maize Husk Tightness. Frontiers in Plant Science, 2020, 11, 861.	3.6	17
8	miRNA expression profiling and zeatin dynamic changes in a new model system of in vivo indirect regeneration of tomato. PLoS ONE, 2020, 15, e0237690.	2.5	6
9	ZmRAD51C Is Essential for Double-Strand Break Repair and Homologous Recombination in Maize Meiosis. International Journal of Molecular Sciences, 2019, 20, 5513.	4.1	17
10	Linkage mapping combined with association analysis reveals QTL and candidate genes for three husk traits in maize. Theoretical and Applied Genetics, 2018, 131, 2131-2144.	3.6	19
11	Identification of maize brace-root quantitative trait loci in a recombinant inbred line population. Euphytica, 2018, 214, 1.	1.2	7
12	Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. Frontiers in Plant Science, 2017, 8, 1916.	3.6	145
13	Genome-wide association study (GWAS) reveals the genetic architecture of four husk traits in maize. BMC Genomics, 2016, 17, 946.	2.8	59
14	Transcriptional analyses of maize leaves in response to high‐density planting. Agronomy Journal, 0, , .	1.8	1