Haiming Xu

List of Publications by Year
in descending order

19 papers	343 citations	1040056 9 h-index	839539 18 g-index
23 all docs	23 docs citations	23 times ranked	476 citing authors

#	Article	IF	Citations
1	Establishment of Chinese soybean Glycine max core collections with agronomic traits and SSR markers. Euphytica, 2006, 151, 215-223.	1.2	71
2	Dissection of genetic architecture of rice plant height and heading date by multiple-strategy-based association studies. Scientific Reports, 2016, 6, 29718.	3.3	49
3	Genomic evidence of human selection on Vavilovian mimicry. Nature Ecology and Evolution, 2019, 3, 1474-1482.	7.8	38
4	Long-read sequencing unveils high-resolution HPV integration and its oncogenic progression in cervical cancer. Nature Communications, 2022, 13, 2563.	12.8	34
5	Sampling a Core Collection of Island Cotton (Gossypium barbadense L.) Based on the Genotypic Values of Fiber Traits. Genetic Resources and Crop Evolution, 2006, 53, 515-521.	1.6	29
6	Diagnostic and clinical utility of whole genome sequencing in a cohort of undiagnosed Chinese families with rare diseases. Scientific Reports, 2019, 9, 19365.	3.3	28
7	Genomic insights into the evolution of Echinochloa species as weed and orphan crop. Nature Communications, 2022, 13, 689.	12.8	26
8	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. BMC Genomics, 2018, 19, 451.	2.8	22
9	Statistical approaches in QTL mapping and molecular breeding for complex traits. Science Bulletin, 2012, 57, 2637-2644.	1.7	12
10	Detection of Epistatic and Gene-Environment Interactions Underlying Three Quality Traits in Rice Using High-Throughput Genome-Wide Data. BioMed Research International, 2015, 2015, 1-7.	1.9	9
11	Genetic dissection of yield traits in super hybrid rice Xieyou9308 using both unconditional and conditional genome-wide association mapping. Scientific Reports, 2017, 7, 824.	3.3	7
12	Statistical method for mapping QTLs for complex traits based on two backcross populations. Science Bulletin, 2012, 57, 2645-2654.	1.7	4
13	Dissecting Genetic Architecture Underlying Seed Traits in Multiple Environments. Genetics, 2015, 199, 61-71.	2.9	4
14	Conditional and unconditional genome-wide association study reveal complicate genetic architecture of human body weight and impacts of smoking. Scientific Reports, 2020, 10, 12136.	3.3	2
15	EigenGWAS: An online visualizing and interactive application for detecting genomic signatures of natural selection. Molecular Ecology Resources, 2021, 21, 1732-1744.	4.8	2
16	Functional mapping of tillering QTLs using the Wangâ€"Lanâ€"Ding model and a SSSL population. Molecular Genetics and Genomics, 2021, 296, 1279-1286.	2.1	2
17	Dissection of additive, epistatic and <scp>QTL</scp> Ã— environment effects involved in oil content variations in rapeseed. Plant Breeding, 2017, 136, 728-737.	1.9	1
18	Robustification of Linear Regression and Its Application in Genome-Wide Association Studies. Frontiers in Genetics, 2020, 11, 549.	2.3	1

#	Article	IF	Citations
19	Genome-wide conditional association study reveals the influences of lifestyle cofactors on genetic regulation of body surface area in MESA population. PLoS ONE, 2021, 16, e0253167.	2.5	0