

Yu Lin

List of Publications by Year in descending order

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18
papers

487
citations

933447

10
h-index

839539

18
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18
all docs

18
docs citations

18
times ranked

431
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide association study of 23 agronomic traits in Chinese wheat landraces. <i>Plant Journal</i> , 2017, 91, 861-873.	5.7	152
2	Identification and validation of novel low-tiller number QTL in common wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 603-612.	3.6	71
3	Genome-wide association study of drought-related resistance traits in <i>Aegilops tauschii</i> . <i>Genetics and Molecular Biology</i> , 2016, 39, 398-407.	1.3	46
4	Dissection of Phenotypic and Genetic Variation of Drought-Related Traits in Diverse Chinese Wheat Landraces. <i>Plant Genome</i> , 2019, 12, 1-14.	2.8	44
5	Genome-wide association study of pre-harvest sprouting resistance in Chinese wheat founder parents. <i>Genetics and Molecular Biology</i> , 2017, 40, 620-629.	1.3	19
6	Phenotypic and genetic variation in phosphorus-deficiency-tolerance traits in Chinese wheat landraces. <i>BMC Plant Biology</i> , 2020, 20, 330.	3.6	19
7	QTL mapping for grain number per spikelet in wheat using a high-density genetic map. <i>Crop Journal</i> , 2021, 9, 1108-1114.	5.2	19
8	Mapping of QTL for total spikelet number per spike on chromosome 2D in wheat using a high-density genetic map. <i>Genetics and Molecular Biology</i> , 2019, 42, 603-610.	1.3	15
9	Quantitative trait loci analysis for root traits in synthetic hexaploid wheat under drought stress conditions. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1947-1960.	3.5	15
10	A Genome-Wide Association Study of Coleoptile Length in Different Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2020, 11, 677.	3.6	14
11	Identification and Validation of a Novel Major Quantitative Trait Locus for Plant Height in Common Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2020, 11, 602495.	2.3	13
12	Identification and validation of stable quantitative trait loci for grain filling rate in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 2377-2385.	3.6	13
13	Quantitative trait loci analysis of root traits under phosphorus deficiency at the seedling stage in wheat. <i>Genome</i> , 2018, 61, 209-215.	2.0	12
14	Fine mapping of the tiller inhibition gene <i>TIN4</i> contributing to ideal plant architecture in common wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 527-535.	3.6	12
15	Quantitative trait locus mapping for panicle exertion length in common wheat using two related recombinant inbred line populations. <i>Euphytica</i> , 2019, 215, 1.	1.2	11
16	Multi-Locus Genome-Wide Association Study of Four Yield-Related Traits in Chinese Wheat Landraces. <i>Frontiers in Plant Science</i> , 2021, 12, 665122.	3.6	5
17	Genome-Wide Association Study of Kernel Traits in <i>Aegilops tauschii</i> . <i>Frontiers in Genetics</i> , 2021, 12, 651785.	2.3	4
18	Identification and Validation of Quantitative Trait Loci Mapping for Spike-Layer Uniformity in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1052.	4.1	3