

Kang Yu

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

979
citations

1163117

8
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996975

15
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16
all docs

16
docs citations

16
times ranked

1570
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome resequencing of the wheat A subgenome progenitor <i>Triticum urartu</i> provides insights into its demographic history and geographic adaptation. <i>Plant Communications</i> , 2022, , 100345.	7.7	1
2	Compacting a synthetic yeast chromosome arm. <i>Genome Biology</i> , 2021, 22, 5.	8.8	28
3	The MYB family transcription factor TuODORANT1 from <i>Triticum urartu</i> and the homolog TaODORANT1 from <i>Triticum aestivum</i> inhibit seed storage protein synthesis in wheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 1863-1877.	8.3	15
4	De novo genome assembly of a foxtail millet cultivar Huagu11 uncovered the genetic difference to the cultivar Yugu1, and the genetic mechanism of imazethapyr tolerance. <i>BMC Plant Biology</i> , 2021, 21, 271.	3.6	9
5	Identification of QTL related to anther color and hull color by RAD sequencing in a RIL population of <i>Setaria italica</i> . <i>BMC Genomics</i> , 2021, 22, 556.	2.8	4
6	Genome-wide identification of seed storage protein gene regulators in wheat through coexpression analysis. <i>Plant Journal</i> , 2021, 108, 1704-1720.	5.7	9
7	Natural variations in the promoter of <i>Awn Length Inhibitor 1</i> (<i>ALI</i>) are associated with awn elongation and grain length in common wheat. <i>Plant Journal</i> , 2020, 101, 1075-1090.	5.7	32
8	Numerical Study on Bubble Rising in Complex Channels Saturated with Liquid Using a Phase-Field Lattice-Boltzmann Method. <i>Processes</i> , 2020, 8, 1608.	2.8	7
9	<i>TubZIP28</i> , a novel bZIP family transcription factor from <i>Triticum urartu</i> , and <i>TabZIP28</i> , its homologue from <i>Triticum aestivum</i> , enhance starch synthesis in wheat. <i>New Phytologist</i> , 2020, 226, 1384-1398.	7.3	46
10	Construction of a high-density genetic map of tree peony (<i>Paeonia suffruticosa</i> Andr. Moutan) using restriction site associated DNA sequencing (RADseq) approach. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	7
11	Unraveling the genetic architecture of grain size in einkorn wheat through linkage and homology mapping and transcriptomic profiling. <i>Journal of Experimental Botany</i> , 2019, 70, 4671-4688.	4.8	19
12	A wheat dominant dwarfing line with <i>Rht12</i> , which reduces stem cell length and affects gibberellic acid synthesis, is a 5AL terminal deletion line. <i>Plant Journal</i> , 2019, 97, 887-900.	5.7	65
13	Mechanisms, origin and heredity of Glu-1Ay silencing in wheat evolution and domestication. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1561-1575.	3.6	7
14	Development of an integrated linkage map of einkorn wheat and its application for QTL mapping and genome sequence anchoring. <i>Theoretical and Applied Genetics</i> , 2017, 130, 53-70.	3.6	30
15	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	27.8	700