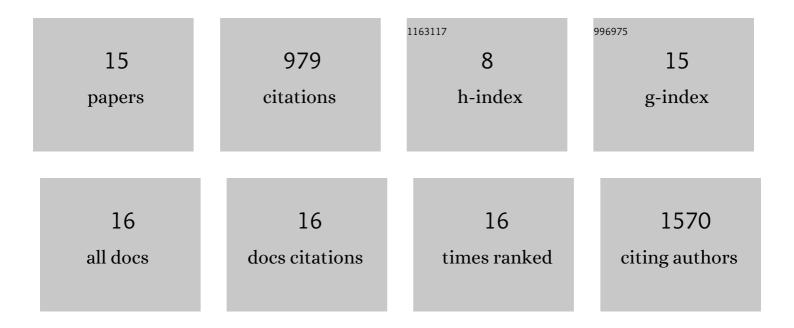


List of Publications by Year in descending order

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KANC YU

#	Article	IF	CITATIONS
1	Whole-genome resequencing of the wheat A subgenome progenitor Triticum urartu provides insights into its demographic history and geographic adaptation. Plant Communications, 2022, , 100345.	7.7	1
2	Compacting a synthetic yeast chromosome arm. Genome Biology, 2021, 22, 5.	8.8	28
3	The MYB family transcription factor TuODORANT1 from Triticum urartu and the homolog TaODORANT1 from Triticum aestivum inhibit seed storage protein synthesis in wheat. Plant Biotechnology Journal, 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. BMC Plant Biology, 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 Setaria italica. BMC Genomics, 2021, 22, 556.	2.8	4
6	Genomeâ€wide identification of seed storage protein gene regulators in wheat through coexpression analysis. Plant Journal, 2021, 108, 1704-1720.	5.7	9
7	Natural variations in the promoter of <scp><i>Awn Length Inhibitor 1</i></scp> (<scp><i>ALlâ€I </i></scp>) are associated with awn elongation and grain length in common wheat. Plant Journal, 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. Processes, 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. New Phytologist, 2020, 226, 1384-1398.	7.3	46
10	Construction of a high-density genetic map of tree peony (Paeonia suffruticosa Andr. Moutan) using restriction site associated DNA sequencing (RADseq) approach. Tree Genetics and Genomes, 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. Journal of Experimental Botany, 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. Plant Journal, 2019, 97, 887-900.	5.7	65
13	Mechanisms, origin and heredity of Glu-1Ay silencing in wheat evolution and domestication. Theoretical and Applied Genetics, 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. Theoretical and Applied Genetics, 2017, 130, 53-70.	3.6	30
15	Draft genome of the wheat A-genome progenitor Triticum urartu. Nature, 2013, 496, 87-90.	27.8	700