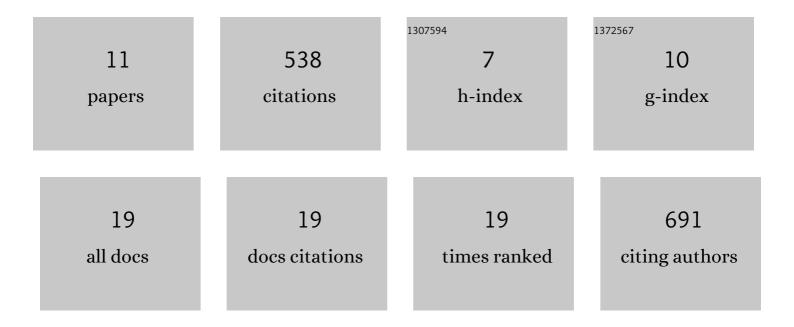
Yinjie Qiu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2674286/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	12.6	282
2	How the pan-genome is changing crop genomics and improvement. Genome Biology, 2021, 22, 3.	8.8	142
3	Whole-genome variation of transposable element insertions in a maize diversity panel. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	16
4	DNA content and ploidy estimation of <i>Festuca ovina</i> accessions by flow cytometry. Crop Science, 2020, 60, 2757-2767.	1.8	15
5	Towards Improved Molecular Identification Tools in Fine Fescue (Festuca L., Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. Frontiers in Genetics, 2019, 10, 1223.	2.3	14
6	WFhb1-1 plays an important role in resistance against Fusarium head blight in wheat. Scientific Reports, 2020, 10, 7794.	3.3	13
7	The Genetics and Genome-Wide Screening of Regrowth Loci, a Key Component of Perennialism in <i>Zea diploperennis</i> . G3: Genes, Genomes, Genetics, 2019, 9, 1393-1403.	1.8	11
8	Wholeâ€genome assembly and annotation of northern wild rice, <i>Zizania palustris</i> L., supports a wholeâ€genome duplication in the <i>Zizania</i> genus. Plant Journal, 2021, 107, 1802-1818.	5.7	7
9	The fungal endophyte <i>Epichloë festucae</i> var. <i>lolii</i> plays a limited role in mediating crown rust severity in perennial ryegrass. Crop Science, 2020, 60, 1090-1104.	1.8	6
10	Building a reference transcriptome for the hexaploid hard fescue turfgrass (<i>Festuca brevipila</i>) using a combination of PacBio Isoseq and Illumina sequencing. Crop Science, 2021, 61, 2798-2811.	1.8	3
11	Assessing fine fescue mixtures and plant growth regulator applications to determine their effect on traffic tolerance and divot recovery. Itsrj, 2022, 14, 502-515.	0.3	1