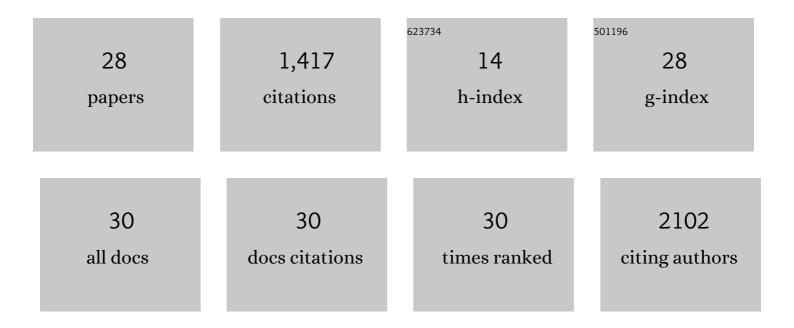
Cheng-Jun Zhang

List of Publications by Year in descending order

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CHENC-LUN ZHANC

#	Article	IF	CITATIONS
1	Rapid evolution of T2/S-RNase genes in Fragaria linked to multiple transitions from self-incompatibility to self-compatibility. Plant Diversity, 2023, 45, 219-228.	3.7	3
2	Temporal regulation of alternative splicing events in rice memory under drought stress. Plant Diversity, 2022, 44, 116-125.	3.7	10
3	Gene fusion as an important mechanism to generate new genes in the genus Oryza. Genome Biology, 2022, 23, .	8.8	7
4	Genetic innovations: Transposable element recruitment and de novo formation lead to the birth of orphan genes in the rice genome. Journal of Systematics and Evolution, 2021, 59, 341-351.	3.1	14
5	The new chimeric chiron genes evolved essential roles in zebrafish embryonic development by regulating NAD+ levels. Science China Life Sciences, 2021, 64, 1929-1948.	4.9	6
6	The Rhododendron Plant Genome Database (RPGD): a comprehensive online omics database for Rhododendron. BMC Genomics, 2021, 22, 376.	2.8	16
7	Highâ€quality evergreen azalea genome reveals tandem duplicationâ€facilitated lowâ€altitude adaptability and floral scent evolution. Plant Biotechnology Journal, 2021, 19, 2544-2560.	8.3	35
8	New Genes Interacted With Recent Whole-Genome Duplicates in the Fast Stem Growth of Bamboos. Molecular Biology and Evolution, 2021, 38, 5752-5768.	8.9	28
9	Rapid Genome Evolution and Adaptation of Thlaspi arvense Mediated by Recurrent RNA-Based and Tandem Gene Duplications. Frontiers in Plant Science, 2021, 12, 772655.	3.6	8
10	Divergence and hybridization in the desert plant Reaumuria soongarica. Journal of Systematics and Evolution, 2020, 58, 159-173.	3.1	5
11	Alternative splicing coupled to nonsense-mediated mRNA decay contributes to the high-altitude adaptation of maca (Lepidium meyenii). Gene, 2019, 694, 7-18.	2.2	10
12	Rapid evolution of protein diversity by de novo origination in Oryza. Nature Ecology and Evolution, 2019, 3, 679-690.	7.8	121
13	Physiological and Transcriptome Analyses Reveal Short-Term Responses and Formation of Memory Under Drought Stress in Rice. Frontiers in Genetics, 2019, 10, 55.	2.3	114
14	Evolutionary patterns of chimeric retrogenes in Oryza species. Scientific Reports, 2019, 9, 17733.	3.3	3
15	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
16	A survey of transcriptome complexity in Sus scrofa using single-molecule long-read sequencing. DNA Research, 2018, 25, 421-437.	3.4	83
17	Population size may shape the accumulation of functional mutations following domestication. BMC Evolutionary Biology, 2018, 18, 4.	3.2	15
18	Global transcriptome analysis reveals extensive gene remodeling, alternative splicing and differential transcription profiles in non-seed vascular plant Selaginella moellendorffii. BMC Genomics, 2017, 18, 1042.	2.8	34

CHENG-JUN ZHANG

#	Article	IF	CITATIONS
19	The draft genome assembly of Rhododendron delavayi Franch. var. delavayi. GigaScience, 2017, 6, 1-11.	6.4	64
20	Origination and Establishment of a Trigenic Reproductive Isolation System in Rice. Molecular Plant, 2016, 9, 1542-1545.	8.3	18
21	Evolutionary Character of Alternative Splicing in Plants. Bioinformatics and Biology Insights, 2015, 9s1, BBI.S33716.	2.0	51
22	Evolution of Gene Structural Complexity: An Alternative-Splicing-Based Model Accounts for Intron-Containing Retrogenes Â. Plant Physiology, 2014, 165, 412-423.	4.8	19
23	gKaKs: the pipeline for genome-level Ka/Ks calculation. Bioinformatics, 2013, 29, 645-646.	4.1	47
24	Natural variation in Ghd7.1 plays an important role in grain yield and adaptation in rice. Cell Research, 2013, 23, 969-971.	12.0	222
25	High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. Genome Biology and Evolution, 2013, 5, 1038-1048.	2.5	11
26	Complex evolution of <i>S5</i> , a major reproductive barrier regulator, in the cultivated rice <i>Oryza sativa</i> and its wild relatives. New Phytologist, 2011, 191, 275-287.	7.3	33
27	Dynamic programming procedure for searching optimal models to estimate substitution rates based on the maximum-likelihood method. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7860-7865.	7.1	15
28	Analysis of <i>MYB</i> genes in four plant species and the detection of genes associated with drought resistance. Botany, 0, , 1-14.	1.0	3