Shujun Ou

List of Publications by Year
in descending order

		236925	414414
29	5,976	25	32
papers	citations	h-index	g-index

44	44	44	6779
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	TEsorter: An accurate and fast method to classify LTR-retrotransposons in plant genomes. Horticulture Research, 2022, 9, .	6.3	70
2	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid Brassica napus. New Phytologist, 2021, 230, 354-371.	7.3	57
3	A Tutorial of EDTA: Extensive De Novo TE Annotator. Methods in Molecular Biology, 2021, 2250, 55-67.	0.9	22
4	How the pan-genome is changing crop genomics and improvement. Genome Biology, 2021, 22, 3.	8.8	142
5	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. Cell, 2021, 184, 3542-3558.e16.	28.9	237
6	Chromosome-Scale Genome for a Red-Fruited, Perpetual Flowering and Runnerless Woodland Strawberry (Fragaria vesca). Frontiers in Genetics, 2021, 12, 671371.	2.3	8
7	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. Plant Genome, 2021, 14, e20114.	2.8	14
8	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	12.6	282
9	Genomic basis of geographical adaptation to soil nitrogen in rice. Nature, 2021, 590, 600-605.	27.8	204
10	Large structural variations in the haplotypeâ€resolved African cassava genome. Plant Journal, 2021, 108, 1830-1848.	5.7	22
11	Construction of a chromosome-scale long-read reference genome assembly for potato. GigaScience, 2020, 9, .	6.4	150
12	Natural variations of SLG1 confer high-temperature tolerance in indica rice. Nature Communications, 2020, 11, 5441.	12.8	66
13	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. Nature Communications, 2020, 11, 2288.	12.8	39
14	Gapless assembly of maize chromosomes using long-read technologies. Genome Biology, 2020, 21, 121.	8.8	101
15	Origin and evolution of the octoploid strawberry genome. Nature Genetics, 2019, 51, 541-547.	21.4	469
16	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. GigaScience, 2019, 8, .	6.4	167
17	LTR_FINDER_parallel: parallelization of LTR_FINDER enabling rapid identification of long terminal repeat retrotransposons. Mobile DNA, 2019, 10, 48.	3.6	99
18	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275.	8.8	579

#	Article	IF	Citations
19	Expression of the Nitrate Transporter Gene OsNRT1.1A/OsNPF6.3 Confers High Yield and Early Maturation in Rice. Plant Cell, 2018, 30, 638-651.	6.6	227
20	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (Fragaria vesca) with chromosome-scale contiguity. GigaScience, 2018, 7, 1-7.	6.4	209
21	LTR_retriever: A Highly Accurate and Sensitive Program for Identification of Long Terminal Repeat Retrotransposons. Plant Physiology, 2018, 176, 1410-1422.	4.8	694
22	Extreme haplotype variation in the desiccation-tolerant clubmoss Selaginella lepidophylla. Nature Communications, 2018, 9, 13.	12.8	89
23	Integrating GWAS and gene expression data for functional characterization of resistance to white mould in soya bean. Plant Biotechnology Journal, 2018, 16, 1825-1835.	8.3	60
24	Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. Nature Communications, 2018, 9, 3302.	12.8	155
25	Assessing genome assembly quality using the LTR Assembly Index (LAI). Nucleic Acids Research, 2018, 46, e126.	14.5	261
26	Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. Nature Genetics, 2015, 47, 834-838.	21.4	527
27	Variations in <scp>CYP</scp>78<scp>A</scp>13 coding region influence grain size and yield in rice. Plant, Cell and Environment, 2015, 38, 800-811.	5.7	102
28	OsNAP connects abscisic acid and leaf senescence by fine-tuning abscisic acid biosynthesis and directly targeting senescence-associated genes in rice. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10013-10018.	7.1	449
29	OsbZIP71, a bZIP transcription factor, confers salinity and drought tolerance in rice. Plant Molecular Biology, 2014, 84, 19-36.	3.9	311