

Shujun Ou

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

5,976
citations

236925

25
h-index

414414

32
g-index

44
all docs

44
docs citations

44
times ranked

6779
citing authors

#	ARTICLE	IF	CITATIONS
1	LTR_retriever: A Highly Accurate and Sensitive Program for Identification of Long Terminal Repeat Retrotransposons. <i>Plant Physiology</i> , 2018, 176, 1410-1422.	4.8	694
2	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. <i>Genome Biology</i> , 2019, 20, 275.	8.8	579
3	Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. <i>Nature Genetics</i> , 2015, 47, 834-838.	21.4	527
4	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	21.4	469
5	OsNAP connects abscisic acid and leaf senescence by fine-tuning abscisic acid biosynthesis and directly targeting senescence-associated genes in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10013-10018.	7.1	449
6	OsZIP71, a bZIP transcription factor, confers salinity and drought tolerance in rice. <i>Plant Molecular Biology</i> , 2014, 84, 19-36.	3.9	311
7	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	12.6	282
8	Assessing genome assembly quality using the LTR Assembly Index (LAI). <i>Nucleic Acids Research</i> , 2018, 46, e126.	14.5	261
9	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16.	28.9	237
10	Expression of the Nitrate Transporter Gene <i>OsNRT1.1A/OsNPF6.3</i> Confers High Yield and Early Maturation in Rice. <i>Plant Cell</i> , 2018, 30, 638-651.	6.6	227
11	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (<i>Fragaria vesca</i>) with chromosome-scale contiguity. <i>GigaScience</i> , 2018, 7, 1-7.	6.4	209
12	Genomic basis of geographical adaptation to soil nitrogen in rice. <i>Nature</i> , 2021, 590, 600-605.	27.8	204
13	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. <i>GigaScience</i> , 2019, 8, .	6.4	167
14	Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. <i>Nature Communications</i> , 2018, 9, 3302.	12.8	155
15	Construction of a chromosome-scale long-read reference genome assembly for potato. <i>GigaScience</i> , 2020, 9, .	6.4	150
16	How the pan-genome is changing crop genomics and improvement. <i>Genome Biology</i> , 2021, 22, 3.	8.8	142
17	Variations in <i>CYP78A13</i> coding region influence grain size and yield in rice. <i>Plant, Cell and Environment</i> , 2015, 38, 800-811.	5.7	102
18	Gapless assembly of maize chromosomes using long-read technologies. <i>Genome Biology</i> , 2020, 21, 121.	8.8	101

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19	LTR_FINDER_parallel: parallelization of LTR_FINDER enabling rapid identification of long terminal repeat retrotransposons. <i>Mobile DNA</i> , 2019, 10, 48.	3.6	99
20	Extreme haplotype variation in the desiccation-tolerant clubmoss <i>Selaginella lepidophylla</i> . <i>Nature Communications</i> , 2018, 9, 13.	12.8	89
21	TEsorter: An accurate and fast method to classify LTR-retrotransposons in plant genomes. <i>Horticulture Research</i> , 2022, 9, .	6.3	70
22	Natural variations of SLG1 confer high-temperature tolerance in indica rice. <i>Nature Communications</i> , 2020, 11, 5441.	12.8	66
23	Integrating GWAS and gene expression data for functional characterization of resistance to white mould in soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 1825-1835.	8.3	60
24	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 230, 354-371.	7.3	57
25	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. <i>Nature Communications</i> , 2020, 11, 2288.	12.8	39
26	A Tutorial of EDTA: Extensive De Novo TE Annotator. <i>Methods in Molecular Biology</i> , 2021, 2250, 55-67.	0.9	22
27	Large structural variations in the haplotype-resolved African cassava genome. <i>Plant Journal</i> , 2021, 108, 1830-1848.	5.7	22
28	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
29	Chromosome-Scale Genome for a Red-Fruited, Perpetual Flowering and Runnerless Woodland Strawberry (<i>Fragaria vesca</i>). <i>Frontiers in Genetics</i> , 2021, 12, 671371.	2.3	8