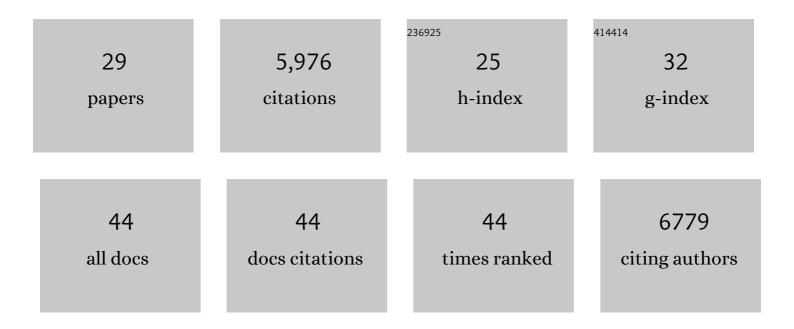
Shujun Ou

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/449221/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	LTR_retriever: A Highly Accurate and Sensitive Program for Identification of Long Terminal Repeat Retrotransposons. Plant Physiology, 2018, 176, 1410-1422.	4.8	694
2	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275.	8.8	579
3	Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. Nature Genetics, 2015, 47, 834-838.	21.4	527
4	Origin and evolution of the octoploid strawberry genome. Nature Genetics, 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. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10013-10018.	7.1	449
6	OsbZIP71, a bZIP transcription factor, confers salinity and drought tolerance in rice. Plant Molecular Biology, 2014, 84, 19-36.	3.9	311
7	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science, 2021, 373, 655-662.	12.6	282
8	Assessing genome assembly quality using the LTR Assembly Index (LAI). Nucleic Acids Research, 2018, 46, e126.	14.5	261
9	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. Cell, 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. Plant Cell, 2018, 30, 638-651.	6.6	227
11	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
12	Genomic basis of geographical adaptation to soil nitrogen in rice. Nature, 2021, 590, 600-605.	27.8	204
13	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. CigaScience, 2019, 8, .	6.4	167
14	Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. Nature Communications, 2018, 9, 3302.	12.8	155
15	Construction of a chromosome-scale long-read reference genome assembly for potato. GigaScience, 2020, 9, .	6.4	150
16	How the pan-genome is changing crop genomics and improvement. Genome Biology, 2021, 22, 3.	8.8	142
17	Variations in <scp><i>CYP</i></scp> <i>78</i> <scp><i>A</i></scp> <i>13</i> coding region influence grain size and yield in rice. Plant, Cell and Environment, 2015, 38, 800-811.	5.7	102
18	Gapless assembly of maize chromosomes using long-read technologies. Genome Biology, 2020, 21, 121.	8.8	101

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