Ning Jiang

List of Publications by Year
in descending order

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45 papers	10,136 citations	159525 30 h-index	206029 48 g-index
52 all docs	52 docs citations	52 times ranked	11077 citing authors

#	Article	IF	Citations
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	6.0	3,612
2	Plant transposable elements: where genetics meets genomics. Nature Reviews Genetics, 2002, 3, 329-341.	7.7	854
3	LTR_retriever: A Highly Accurate and Sensitive Program for Identification of Long Terminal Repeat Retrotransposons. Plant Physiology, 2018, 176, 1410-1422.	2.3	694
4	Benchmarking transposable element annotation methods for creation of a streamlined, comprehensive pipeline. Genome Biology, 2019, 20, 275.	3.8	579
5	Pack-MULE transposable elements mediate gene evolution in plants. Nature, 2004, 431, 569-573.	13.7	495
6	Origin and evolution of the octoploid strawberry genome. Nature Genetics, 2019, 51, 541-547.	9.4	469
7	An active DNA transposon family in rice. Nature, 2003, 421, 163-167.	13.7	415
8	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	13.9	329
9	Assessing genome assembly quality using the LTR Assembly Index (LAI). Nucleic Acids Research, 2018, 46, e126.	6.5	261
10	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. Cell, 2021, 184, 3542-3558.e16.	13.5	237
11	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. Plant Journal, 2012, 71, 492-502.	2.8	209
12	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (Fragaria vesca) with chromosome-scale contiguity. GigaScience, 2018, 7, 1-7.	3.3	209
13	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. GigaScience, 2019, 8, .	3.3	167
14	Using rice to understand the origin and amplification of miniature inverted repeat transposable elements (MITEs). Current Opinion in Plant Biology, 2004, 7, 115-119.	3.5	162
15	Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. Plant Genome, 2011, 4, 191-203.	1.6	131
16	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genusOryza. Plant Journal, 2007, 52, 342-351.	2.8	99
17	LTR_FINDER_parallel: parallelization of LTR_FINDER enabling rapid identification of long terminal repeat retrotransposons. Mobile DNA, 2019, 10, 48.	1.3	99
18	The Functional Role of Pack-MULEs in Rice Inferred from Purifying Selection and Expression Profile. Plant Cell, 2009, 21, 25-38.	3.1	91

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19	Extreme haplotype variation in the desiccation-tolerant clubmoss Selaginella lepidophylla. Nature Communications, 2018, 9, 13.	5.8	89
20	The Transposable Element Landscape of the Model Legume Lotus japonicus. Genetics, 2006, 174, 2215-2228.	1.2	87
21	Arabidopsis KLU homologue GmCYP78A72 regulates seed size in soybean. Plant Molecular Biology, 2016, 90, 33-47.	2.0	84
22	Pack- Mutator â€“like transposable elements (Pack-MULEs) induce directional modification of genes through biased insertion and DNA acquisition. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1537-1542.	3.3	74
23	What makes up plant genomes: The vanishing line between transposable elements and genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 366-380.	0.9	67
24	Genome organization of the tomato sun locus and characterization of the unusual retrotransposon Rider. Plant Journal, 2009, 60, 181-193.	2.8	64
25	Identification and Characterization of Lineage-Specific Genes within the Poaceae. Plant Physiology, 2007, 145, 1311-1322.	2.3	63
26	Dasheng and RIRE2. A Nonautonomous Long Terminal Repeat Element and Its Putative Autonomous Partner in the Rice Genome. Plant Physiology, 2002, 130, 1697-1705.	2.3	59
27	Automated Update, Revision, and Quality Control of the Maize Genome Annotations Using MAKER-P Improves the B73 RefGen_v3 Gene Models and Identifies New Genes Â. Plant Physiology, 2014, 167, 25-39.	2.3	53
28	Transposons play an important role in the evolution and diversification of centromeres among closely related species. Frontiers in Plant Science, 2015, 6, 216.	1.7	51
29	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus Oryza. Plant Journal, 2010, 63, 430-442.	2.8	48
30	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. G3: Genes, Genomes, Genetics, 2017, 7, 203-219.	0.8	43
31	Duplication of host genes by transposable elements. Current Opinion in Genetics and Development, 2018, 49, 63-69.	1.5	39
32	GmILPA1, Encoding an anaphase-promoting complex-like Protein, affects Leaf Petiole Angle. Plant Physiology, 2017, 174, pp.00074.2017.	2.3	33
33	Selective Acquisition and Retention of Genomic Sequences by Pack-Mutator-Like Elements Based on Guanine-Cytosine Content and the Breadth of Expression. Plant Physiology, 2013, 163, 1419-1432.	2.3	25
34	A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. DNA Research, 2016, 23, 241-251.	1.5	18
35	The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. Nucleic Acids Research, 2018, 46, 2380-2397.	6.5	14
36	Overview of Repeat Annotation and De Novo Repeat Identification. Methods in Molecular Biology, 2013, 1057, 275-287.	0.4	12

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37	Evolution and Expression Divergence of the CYP78A Subfamily Genes in Soybean. Genes, 2018, 9, 611.	1.0	12
38	Transposition of a Rice Mutator-Like Element in the Yeast Saccharomyces cerevisiae. Plant Cell, 2015, 27, 132-148.	3.1	11
39	Mutator-Like Elements with Multiple Long Terminal Inverted Repeats in Plants. Comparative and Functional Genomics, 2012, 2012, 1-14.	2.0	9
40	GingerRoot: A Novel DNA Transposon Encoding Integrase-Related Transposase in Plants and Animals. Genome Biology and Evolution, 2019, 11, 3181-3193.	1.1	8
41	Dynamics of a Novel Highly Repetitive CACTA Family in Common Bean (Phaseolus vulgaris). G3: Genes, Genomes, Genetics, 2016, 6, 2091-2101.	0.8	5
42	AnnoSINE: a short interspersed nuclear elements annotation tool for plant genomes. Plant Physiology, 2022, 188, 955-970.	2.3	5
43	Nested Insertions and Accumulation of Indels Are Negatively Correlated with Abundance of Mutator-Like Transposable Elements in Maize and Rice. PLoS ONE, 2014, 9, e87069.	1.1	4
44	Computational Methods for Identification of DNA Transposons. Methods in Molecular Biology, 2013, 1057, 289-304.	0.4	2
45	Retrotransposon â€œQianâ€•mediated segmental duplication in silkworm, Bombyx mori. Insect Biochemistry and Molecular Biology, 2014, 46, 9-16.	1.2	1