Long Wang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Parent–progeny sequencing indicates higher mutation rates in heterozygotes. Nature, 2015, 523, 463-467.	27.8	157
2	Contributions of Zea mays subspecies mexicana haplotypes to modern maize. Nature Communications, 2017, 8, 1874.	12.8	102
3	The architecture of intra-organism mutation rate variation in plants. PLoS Biology, 2019, 17, e3000191.	5.6	89
4	Great majority of recombination events in <i>Arabidopsis</i> are gene conversion events. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20992-20997.	7.1	69
5	Mutation rate analysis via parent–progeny sequencing of the perennial peach. I. A low rate in woody perennials and a higher mutagenicity in hybrids. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161016.	2.6	64
6	Large-scale identification and functional analysis of <i>NLR</i> genes in blast resistance in the Tetep rice genome sequence. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18479-18487.	7.1	63
7	Identifying a large number of high-yield genes in rice by pedigree analysis, whole-genome sequencing, and CRISPR-Cas9 gene knockout. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7559-E7567.	7.1	50
8	Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice ERECTA Genes. Frontiers in Plant Science, 2018, 9, 473.	3.6	33
9	Selective sweep with significant positive selection serves as the driving force for the differentiation of japonica and indica rice cultivars. BMC Genomics, 2017, 18, 307.	2.8	25
10	Repeat-induced point mutation in Neurospora crassa causes the highest known mutation rate and mutational burden of any cellular life. Genome Biology, 2020, 21, 142.	8.8	24
11	Cloning of novel rice blast resistance genes from two rapidly evolving NBS-LRR gene families in rice. Plant Molecular Biology, 2016, 90, 95-105.	3.9	19
12	Mutation rate analysis via parent–progeny sequencing of the perennial peach. II. No evidence for recombination-associated mutation. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161785.	2.6	17
13	Genome-Wide Survey of Pseudogenes in 80 Fully Re-sequenced Arabidopsis thaliana Accessions. PLoS ONE, 2012, 7, e51769.	2.5	14
14	Chromosomal-level genome assembly of the semi-dwarf rice Taichung Native 1, an initiator of Green Revolution. Genomics, 2021, 113, 2656-2674.	2.9	11
15	Deletion of PDK1 in oligodendrocyte lineage cells causes white matter abnormality and myelination defect in the central nervous system. Neurobiology of Disease, 2021, 148, 105212.	4.4	10
16	Somatic mutation analysis in Salix suchowensis reveals early segregated cell lineages. Molecular Biology and Evolution, 2021, 38, 5292-5308.	8.9	10
17	Impaired Spatial Learning is Associated with Disrupted Integrity of the White Matter in Akt3 Knockout Mice. CNS Neuroscience and Therapeutics, 2017, 23, 99-102.	3.9	9
18	Highâ€resolution insight into recombination events at the <i><scp>SD</scp>1</i> locus in rice. Plant Journal, 2019, 97, 683-692.	5.7	8

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19	Insertions/Deletions-Associated Nucleotide Polymorphism in Arabidopsis thaliana. Frontiers in Plant Science, 2016, 7, 1792.	3.6	4
20	Limited accumulation of high-frequency somatic mutations in a 1700-year-old <i>Osmanthus fragrans</i> tree. Tree Physiology, 0, , .	3.1	4
21	Fitness benefits play a vital role in the retention of the <i>Pi-ta</i> susceptible alleles. Genetics, 2022, 220, .	2.9	2
22	In rice splice variants that restore the reading frame after frameshifting indel introduction are common, often induced by the indels and sometimes lead to organism-level rescue. PLoS Genetics, 2022, 18, e1010071.	3.5	2
23	Comparative population genomic analysis provides insights into breeding of modern indica rice in China. Gene, 2021, 768, 145303.	2.2	1
24	Identifying mutations in sd1, Pi54 and Pi-ta, and positively selected genes of TN1, the first semidwarf rice in Green Revolution. , 2022, 63, 9.		0