

# Long Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

788  
citations

687220

13  
h-index

677027

22  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1570  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fitness benefits play a vital role in the retention of the <i>Pi-ta</i> susceptible alleles. <i>Genetics</i> , 2022, 220, .	1.2	2
2	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. <i>PLoS Genetics</i> , 2022, 18, e1010071.	1.5	2
3	Identifying mutations in <i>sd1</i> , <i>Pi54</i> and <i>Pi-ta</i> , and positively selected genes of <i>TN1</i> , the first semidwarf rice in Green Revolution. , 2022, 63, 9.		0
4	Deletion of <i>PDK1</i> in oligodendrocyte lineage cells causes white matter abnormality and myelination defect in the central nervous system. <i>Neurobiology of Disease</i> , 2021, 148, 105212.	2.1	10
5	Comparative population genomic analysis provides insights into breeding of modern indica rice in China. <i>Gene</i> , 2021, 768, 145303.	1.0	1
6	Chromosomal-level genome assembly of the semi-dwarf rice Taichung Native 1, an initiator of Green Revolution. <i>Genomics</i> , 2021, 113, 2656-2674.	1.3	11
7	Somatic mutation analysis in <i>Salix suchowensis</i> reveals early segregated cell lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 5292-5308.	3.5	10
8	Repeat-induced point mutation in <i>Neurospora crassa</i> causes the highest known mutation rate and mutational burden of any cellular life. <i>Genome Biology</i> , 2020, 21, 142.	3.8	24
9	Large-scale identification and functional analysis of <i>NLR</i> genes in blast resistance in the Tetep rice genome sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18479-18487.	3.3	63
10	The architecture of intra-organism mutation rate variation in plants. <i>PLoS Biology</i> , 2019, 17, e3000191.	2.6	89
11	High-resolution insight into recombination events at the <i>SD1</i> locus in rice. <i>Plant Journal</i> , 2019, 97, 683-692.	2.8	8
12	Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice <i>ERECTA</i> Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 473.	1.7	33
13	Identifying a large number of high-yield genes in rice by pedigree analysis, whole-genome sequencing, and CRISPR-Cas9 gene knockout. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7559-E7567.	3.3	50
14	Contributions of <i>Zea mays</i> subspecies <i>mexicana</i> haplotypes to modern maize. <i>Nature Communications</i> , 2017, 8, 1874.	5.8	102
15	Selective sweep with significant positive selection serves as the driving force for the differentiation of japonica and indica rice cultivars. <i>BMC Genomics</i> , 2017, 18, 307.	1.2	25
16	Impaired Spatial Learning is Associated with Disrupted Integrity of the White Matter in <i>Akt3</i> Knockout Mice. <i>CNS Neuroscience and Therapeutics</i> , 2017, 23, 99-102.	1.9	9
17	Insertions/Deletions-Associated Nucleotide Polymorphism in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1792.	1.7	4
18	Mutation rate analysis via parent-progeny sequencing of the perennial peach. I. A low rate in woody perennials and a higher mutagenicity in hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161016.	1.2	64

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19	Mutation rate analysis via parentâ€™ progeny sequencing of the perennial peach. II. No evidence for recombination-associated mutation. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161785.	1.2	17
20	Cloning of novel rice blast resistance genes from two rapidly evolving NBS-LRR gene families in rice. Plant Molecular Biology, 2016, 90, 95-105.	2.0	19
21	Parentâ€™ progeny sequencing indicates higher mutation rates in heterozygotes. Nature, 2015, 523, 463-467.	13.7	157
22	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.	3.3	69
23	Genome-Wide Survey of Pseudogenes in 80 Fully Re-sequenced <i>Arabidopsis thaliana</i> Accessions. PLoS ONE, 2012, 7, e51769.	1.1	14
24	Limited accumulation of high-frequency somatic mutations in a 1700-year-old <i>Osmanthus fragrans</i> tree. Tree Physiology, 0, , .	1.4	4