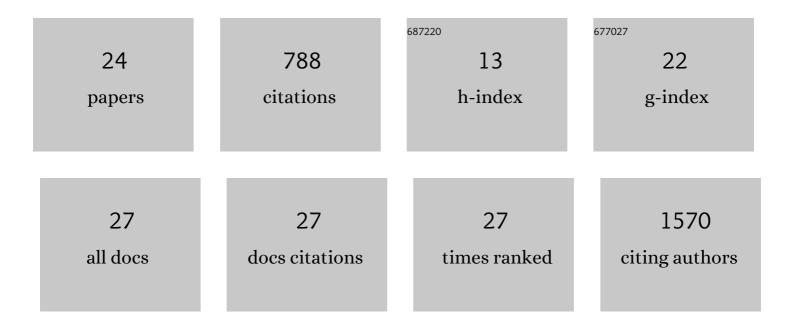
Long Wang

List of Publications by Year in descending order

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LONG WANG

| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Fitness benefits play a vital role in the retention of the <i>Pi-ta</i> susceptible alleles. Genetics, 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. PLoS Genetics, 2022, 18, e1010071. | 1.5 | 2 |
| 3 | 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 |
| 4 | 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. | 2.1 | 10 |
| 5 | Comparative population genomic analysis provides insights into breeding of modern indica rice in China. Gene, 2021, 768, 145303. | 1.0 | 1 |
| 6 | Chromosomal-level genome assembly of the semi-dwarf rice Taichung Native 1, an initiator of Green Revolution. Genomics, 2021, 113, 2656-2674. | 1.3 | 11 |
| 7 | Somatic mutation analysis in Salix suchowensis reveals early segregated cell lineages. Molecular Biology and Evolution, 2021, 38, 5292-5308. | 3.5 | 10 |
| 8 | 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. | 3.8 | 24 |
| 9 | 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. | 3.3 | 63 |
| 10 | The architecture of intra-organism mutation rate variation in plants. PLoS Biology, 2019, 17, e3000191. | 2.6 | 89 |
| 11 | Highâ€resolution insight into recombination events at the <i><scp>SD</scp>1</i> locus in rice. Plant Journal, 2019, 97, 683-692. | 2.8 | 8 |
| 12 | Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice ERECTA Genes. Frontiers in Plant Science, 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. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7559-E7567. | 3.3 | 50 |
| 14 | Contributions of Zea mays subspecies mexicana haplotypes to modern maize. Nature Communications, 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. BMC Genomics, 2017, 18, 307. | 1.2 | 25 |
| 16 | Impaired Spatial Learning is Associated with Disrupted Integrity of the White Matter in Akt3 Knockout Mice. CNS Neuroscience and Therapeutics, 2017, 23, 99-102. | 1.9 | 9 |
| 17 | Insertions/Deletions-Associated Nucleotide Polymorphism in Arabidopsis thaliana. Frontiers in Plant Science, 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. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161016. | 1.2 | 64 |

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|----|---|------|-----------|
| 19 | 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. | 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 | Parent–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 Arabidopsis thaliana 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 |