

# Qingpo Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

1,418  
citations

331670

21  
h-index

377865

34  
g-index

35  
all docs

35  
docs citations

35  
times ranked

2257  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | The miR528-D3 Module Regulates Plant Height in Rice by Modulating the Gibberellin and Abscisic Acid Metabolisms. <i>Rice</i> , 2022, 15, .   | 4.0 | 13        |
| 2  | The miR528- <i>AO</i> Module Confers Enhanced Salt Tolerance in Rice by Modulating the Ascorbic Acid and Abscisic Acid Metabolism and ROS Scavenging. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 8634-8648. | 5.2 | 23        |
| 3  | Evolutionary divergence of function and expression of laccase genes in plants. <i>Journal of Genetics</i> , 2020, 99, 1.   | 0.7 | 21        |
| 4  | Evolutionary divergence of function and expression of laccase genes in plants. <i>Journal of Genetics</i> , 2020, 99, .  | 0.7 | 4         |
| 5  | The genome-wide dynamics of purging during selfing in maize. <i>Nature Plants</i> , 2019, 5, 980-990.  | 9.3 | 42        |
| 6  | Demography and its effects on genomic variation in crop domestication. <i>Nature Plants</i> , 2018, 4, 512-520.  | 9.3 | 173       |
| 7  | Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.   | 8.9 | 68        |
| 8  | Involvement of miR528 in the Regulation of Arsenite Tolerance in Rice ( <i>Oryza sativa</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 8849-8861.  | 5.2 | 43        |
| 9  | Mutational bias is the driving force for shaping the synonymous codon usage pattern of alternatively spliced genes in rice ( <i>Oryza sativa</i> L.). <i>Molecular Genetics and Genomics</i> , 2015, 290, 649-660.             | 2.1 | 18        |
| 10 | Genome-wide identification and evolutionary analysis of positively selected miRNA genes in domesticated rice. <i>Molecular Genetics and Genomics</i> , 2015, 290, 593-602.   | 2.1 | 13        |
| 11 | Genome-wide identification and analysis of miRNA-related single nucleotide polymorphisms (SNPs) in rice. <i>Rice</i> , 2013, 6, 10.  | 4.0 | 54        |
| 12 | Effect of silicate supplementation on the alleviation of arsenite toxicity in 93-11 ( <i>Oryza sativa</i> L.) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 3  | 5.3 | 26        |
| 13 | Novel miRNAs in the control of arsenite levels in rice. <i>Functional and Integrative Genomics</i> , 2012, 12, 649-658.  | 3.5 | 21        |
| 14 | Molecular Identification and Analysis of Arsenite Stress-Responsive miRNAs in Rice. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 6524-6536.   | 5.2 | 90        |
| 15 | Mutational Bias and Translational Selection Shaping the Codon Usage Pattern of Tissue-Specific Genes in Rice. <i>PLoS ONE</i> , 2012, 7, e48295.   | 2.5 | 26        |
| 16 | Functional divergence of the NIP III subgroup proteins involved altered selective constraints and positive selection. <i>BMC Plant Biology</i> , 2010, 10, 256.  | 3.6 | 23        |
| 17 | Divergence in function and expression of the NOD26-like intrinsic proteins in plants. <i>BMC Genomics</i> , 2009, 10, 313.   | 2.8 | 76        |
| 18 | Dicer-like (DCL) proteins in plants. <i>Functional and Integrative Genomics</i> , 2009, 9, 277-286.  | 3.5 | 136       |

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|----|--|-----|-----------|
| 19 | Gene Conversion and Positive Selection Driving the Evolution of the Caenorhabditis ssp. ZIM/HIM-8 Protein Family. <i>Journal of Molecular Evolution</i> , 2009, 68, 217-226.       | 1.8 | 2         |
| 20 | Identification of rice TUBBY-like genes and their evolution. <i>FEBS Journal</i> , 2008, 275, 163-171.   | 4.7 | 30        |
| 21 | Molecular evolution of the MLO gene family in <i>Oryza sativa</i> and their functional divergence. <i>Gene</i> , 2008, 409, 1-10.  | 2.2 | 62        |
| 22 | Evolution and functional divergence of monocarboxylate transporter genes in vertebrates. <i>Gene</i> , 2008, 423, 14-22.   | 2.2 | 11        |
| 23 | Computational identification and phylogenetic analysis of the MAPK gene family in <i>Oryza sativa</i> . <i>Plant Physiology and Biochemistry</i> , 2007, 45, 6-14.                 | 5.8 | 47        |
| 24 | Molecular Phylogeny, Evolution, and Functional Divergence of the LSD1-Like Gene Family: Inference from the Rice Genome. <i>Journal of Molecular Evolution</i> , 2007, 64, 354-363. | 1.8 | 14        |
| 25 | Computational identification of novel PR-1-type genes in <i>Oryza sativa</i> . <i>Journal of Genetics</i> , 2006, 85, 193-198.   | 0.7 | 42        |
| 26 | Computational identification and systematic analysis of the ACR gene family in <i>Oryza sativa</i> . <i>Journal of Plant Physiology</i> , 2006, 163, 445-451.                      | 3.5 | 10        |
| 27 | Analysis of codon usage pattern in the radioresistant bacterium <i>Deinococcus radiodurans</i> . <i>BioSystems</i> , 2006, 85, 99-106.   | 2.0 | 43        |
| 28 | Synonymous codon usage and gene function are strongly related in <i>Oryza sativa</i> . <i>BioSystems</i> , 2005, 80, 123-131.  | 2.0 | 47        |
| 29 | Comparative analysis of base biases around the stop codons in six eukaryotes. <i>BioSystems</i> , 2005, 81, 281-289.   | 2.0 | 18        |
| 30 | Comparative studies on sequence characteristics around translation initiation codon in four eukaryotes. <i>Journal of Genetics</i> , 2005, 84, 317-322.                            | 0.7 | 3         |
| 31 | Comparative studies on codon usage pattern of chloroplasts and their host nuclear genes in four plant species. <i>Journal of Genetics</i> , 2005, 84, 55-62.                       | 0.7 | 127       |
| 32 | Computational identification and sequence analysis of stop codon readthrough genes in <i>Oryza sativa</i> . <i>BioSystems</i> , 2004, 77, 33-39.                                   | 2.0 | 7         |
| 33 | Synonymous codon usage bias in <i>Oryza sativa</i> . <i>Plant Science</i> , 2004, 167, 101-105.  | 3.6 | 51        |
| 34 | Analysis of factors shaping codon usage in the mitochondrion genome of. <i>Mitochondrion</i> , 2004, 4, 313-320.   | 3.4 | 34        |