

Yuan Liu

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,765
citations

567281

15
h-index

526287

27
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28
all docs

28
docs citations

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times ranked

2044
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Overexpression of <i>MdASMT9</i> , an <i>N</i> -acetylserotonin methyltransferase gene, increases melatonin biosynthesis and improves water-use efficiency in transgenic apple. <i>Tree Physiology</i> , 2022, 42, 1114-1126. | 3.1 | 13 |
| 2 | Exogenous dopamine and overexpression of the dopamine synthase gene <i>MdTYDC</i> alleviated apple replant disease. <i>Tree Physiology</i> , 2021, 41, 1524-1541. | 3.1 | 15 |
| 3 | The chromosome-level reference genome assembly for <i>Panax notoginseng</i> and insights into ginsenoside biosynthesis. <i>Plant Communications</i> , 2021, 2, 100113. | 7.7 | 54 |
| 4 | The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 336-350. | 8.3 | 73 |
| 5 | Overexpression of <i>MdMIPS1</i> enhances salt tolerance by improving osmosis, ion balance, and antioxidant activity in transgenic apple. <i>Plant Science</i> , 2020, 301, 110654. | 3.6 | 20 |
| 6 | <i>MdINT1</i> enhances apple salinity tolerance by regulating the antioxidant system, homeostasis of ions, and osmosis. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 689-698. | 5.8 | 9 |
| 7 | Myo-inositol mediates reactive oxygen species-induced programmed cell death via salicylic acid-dependent and ethylene-dependent pathways in apple. <i>Horticulture Research</i> , 2020, 7, 138. | 6.3 | 23 |
| 8 | Draft genomes of two outcrossing wild rice, <i>Oryza rufipogon</i> and <i>O. longistaminata</i> , reveal genomic features associated with mating system evolution. <i>Plant Direct</i> , 2020, 4, e00232. | 1.9 | 9 |
| 9 | Improved hybrid <i>de novo</i> genome assembly and annotation of African wild rice, <i>Oryza longistaminata</i> , from Illumina and PacBio sequencing reads. <i>Plant Genome</i> , 2020, 13, e20001. | 2.8 | 15 |
| 10 | SMRT sequencing of the <i>Oryza rufipogon</i> genome reveals the genomic basis of rice adaptation. <i>Communications Biology</i> , 2020, 3, 167. | 4.4 | 20 |
| 11 | Evolution of <i>Oryza</i> chloroplast genomes promoted adaptation to diverse ecological habitats. <i>Communications Biology</i> , 2019, 2, 278. | 4.4 | 62 |
| 12 | The complete chloroplast genome sequence of Camellias (<i>Camellia fangchengensis</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 34-35. | 0.4 | 3 |
| 13 | The complete chloroplast genome sequence of endangered camellias (<i>Camellia pubifurfuracea</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 843-845. | 0.8 | 3 |
| 14 | Darwinian Positive Selection on the Pleiotropic Effects of <i>KITLG</i> Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. <i>Molecular Biology and Evolution</i> , 2018, 35, 2272-2283. | 8.9 | 27 |
| 15 | The Tea Tree Genome Provides Insights into Tea Flavor and Independent Evolution of Caffeine Biosynthesis. <i>Molecular Plant</i> , 2017, 10, 866-877. | 8.3 | 563 |
| 16 | The complete chloroplast genome sequence of <i>Phyllostachys heterocycla</i> , a fast-growing non-timber bamboo (Poaceae: Bambusoideae). <i>Conservation Genetics Resources</i> , 2017, 9, 217-219. | 0.8 | 3 |
| 17 | The Medicinal Herb <i>Panax notoginseng</i> Genome Provides Insights into Ginsenoside Biosynthesis and Genome Evolution. <i>Molecular Plant</i> , 2017, 10, 903-907. | 8.3 | 95 |
| 18 | The complete chloroplast genome of the endangered wild <i>Musa itinerans</i> (Zingiberales: Musaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 667-669. | 0.8 | 3 |

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|----|--|-----|-----------|
| 19 | The Complete Plastid Genome Sequence of the Wild Rice <i>Zizania latifolia</i> and Comparative Chloroplast Genomics of the Rice Tribe Oryzaceae, Poaceae. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, . | 2.2 | 22 |
| 20 | The complete plastid genome sequence of <i>Panax notoginseng</i> , a famous traditional Chinese medicinal plant of the family Araliaceae. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3438-3439. | 0.7 | 15 |
| 21 | The complete chloroplast genome of North American ginseng, <i>Panax quinquefolius</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3496-3497. | 0.7 | 19 |
| 22 | Autotetraploid rice methylome analysis reveals methylation variation of transposable elements and their effects on gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E7022-9. | 7.1 | 137 |
| 23 | Thirteen <i>Camellia</i> chloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships. <i>BMC Evolutionary Biology</i> , 2014, 14, 151. | 3.2 | 336 |
| 24 | Rapid diversification of five <i>Oryza</i> AA genomes associated with rice adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4954-62. | 7.1 | 145 |
| 25 | Contradiction between Plastid Gene Transcription and Function Due to Complex Posttranscriptional Splicing: An Exemplary Study of <i>ycf15</i> Function and Evolution in Angiosperms. <i>PLoS ONE</i> , 2013, 8, e59620. | 2.5 | 55 |
| 26 | Cytological and RAPD data revealed genetic relationships among nine selected populations of the wild bramble species, <i>Rubus parvifolius</i> and <i>R. coreanus</i> (Rosaceae). <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 431-441. | 1.6 | 8 |
| 27 | Karyotypic, palynological, and RAPD study on 12 taxa from two subsections of section <i>Idaeobatus</i> in <i>Rubus</i> L. and taxonomic treatment of <i>R. ellipticus</i> , <i>R. pinfaensis</i> , and <i>R. ellipticus</i> var. <i>obcordatus</i> . <i>Plant Systematics and Evolution</i> , 2009, 283, 9-18. | 0.9 | 6 |