Yuan Liu

List of Publications by Year in descending order

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567281 526287 1,765 27 15 27 citations h-index g-index papers 28 28 28 2044 docs citations all docs times ranked citing authors

#	Article	IF	CITATIONS
1	The Tea Tree Genome Provides Insights into Tea Flavor and Independent Evolution of Caffeine Biosynthesis. Molecular Plant, 2017, 10, 866-877.	8.3	563
2	Thirteen Camelliachloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships. BMC Evolutionary Biology, 2014, 14, 151.	3.2	336
3	Rapid diversification of five <i>Oryza</i> AA genomes associated with rice adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4954-62.	7.1	145
4	Autotetraploid rice methylome analysis reveals methylation variation of transposable elements and their effects on gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E7022-9.	7.1	137
5	The Medicinal Herb Panax notoginseng Genome Provides Insights into Ginsenoside Biosynthesis and Genome Evolution. Molecular Plant, 2017, 10, 903-907.	8.3	95
6	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. Molecular Plant, 2020, 13, 336-350.	8.3	73
7	Evolution of Oryza chloroplast genomes promoted adaptation to diverse ecological habitats. Communications Biology, 2019, 2, 278.	4.4	62
8	Contradiction between Plastid Gene Transcription and Function Due to Complex Posttranscriptional Splicing: An Exemplary Study of ycf15 Function and Evolution in Angiosperms. PLoS ONE, 2013, 8, e59620.	2.5	55
9	The chromosome-level reference genome assembly for Panax notoginseng and insights into ginsenoside biosynthesis. Plant Communications, 2021, 2, 100113.	7.7	54
10	Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. Molecular Biology and Evolution, 2018, 35, 2272-2283.	8.9	27
11	Myo-inositol mediates reactive oxygen species-induced programmed cell death via salicylic acid-dependent and ethylene-dependent pathways in apple. Horticulture Research, 2020, 7, 138.	6.3	23
12	The Complete Plastid Genome Sequence of the Wild Rice Zizania latifolia and Comparative Chloroplast Genomics of the Rice Tribe Oryzeae, Poaceae. Frontiers in Ecology and Evolution, 2016, 4, .	2.2	22
13	Overexpression of MdMIPS1 enhances salt tolerance by improving osmosis, ion balance, and antioxidant activity in transgenic apple. Plant Science, 2020, 301, 110654.	3.6	20
14	SMRT sequencing of the Oryza rufipogon genome reveals the genomic basis of rice adaptation. Communications Biology, 2020, 3, 167.	4.4	20
15	The complete chloroplast genome of North American ginseng, <i>Panax quinquefolius</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3496-3497.	0.7	19
16	The complete plastid genome sequence of Panax notoginseng, a famous traditional Chinese medicinal plant of the family Araliaceae. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3438-3439.	0.7	15
17	Exogenous dopamine and overexpression of the dopamine synthase gene <i>MdTYDC</i> alleviated apple replant disease. Tree Physiology, 2021, 41, 1524-1541.	3.1	15
18	Improved hybrid <i>de novo</i> genome assembly and annotation of African wild rice, <i>Oryza longistaminata</i> , from Illumina and PacBio sequencing reads. Plant Genome, 2020, 13, e20001.	2.8	15

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19	Overexpression of $\langle i \rangle$ MdASMT9 $\langle i \rangle$, an $\langle i \rangle$ N $\langle i \rangle$ -acetylserotonin methyltransferase gene, increases melatonin biosynthesis and improves water-use efficiency in transgenic apple. Tree Physiology, 2022, 42, 1114-1126.	3.1	13
20	MdINT1 enhances apple salinity tolerance by regulating the antioxidant system, homeostasis of ions, and osmosis. Plant Physiology and Biochemistry, 2020, 154, 689-698.	5.8	9
21	Draft genomes of two outcrossing wild rice, Oryza rufipogon and O. longistaminata , reveal genomic features associated with matingâ€system evolution. Plant Direct, 2020, 4, e00232.	1.9	9
22	Cytological and RAPD data revealed genetic relationships among nine selected populations of the wild bramble species, Rubus parvifolius and R. coreanus (Rosaceae). Genetic Resources and Crop Evolution, 2010, 57, 431-441.	1.6	8
23	Karyotypic, palynological, and RAPD study on 12 taxa from two subsections of section Idaeobatus in RubusÂL. and taxonomic treatment of R.Âellipticus, R.Âpinfaensis, and R.Âellipticus var. obcordatus. Plant Systematics and Evolution, 2009, 283, 9-18.	0.9	6
24	The complete chloroplast genome sequence of Phyllostachys heterocycla, a fast-growing non-timber bamboo (Poaceae: Bambusoideae). Conservation Genetics Resources, 2017, 9, 217-219.	0.8	3
25	The complete chloroplast genome of the endangered wild Musa itinerans (Zingiberales: Musaceae). Conservation Genetics Resources, 2017, 9, 667-669.	0.8	3
26	The complete chloroplast genome sequence of Camellias (Camellia fangchengensis). Mitochondrial DNA Part B: Resources, 2018, 3, 34-35.	0.4	3
27	The complete chloroplast genome sequence of endangered camellias (Camellia pubifurfuracea). Conservation Genetics Resources, 2018, 10, 843-845.	0.8	3