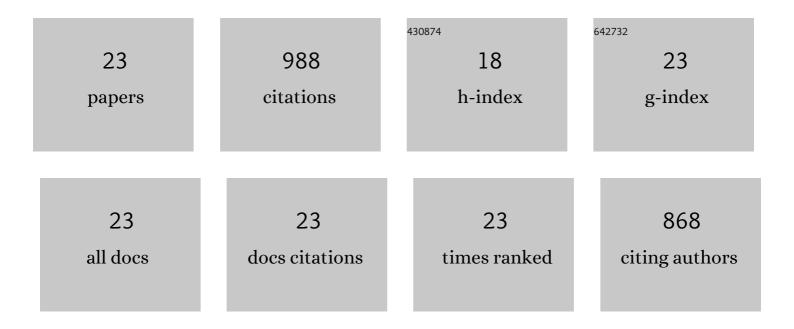
Jiangjie Lu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An innovative procedure of genome-wide association analysis fits studies on germplasm population and plant breeding. Theoretical and Applied Genetics, 2017, 130, 2327-2343.	3.6	121
2	Identification and analysis of genes associated with the synthesis of bioactive constituents in Dendrobium officinale using RNA-Seq. Scientific Reports, 2017, 7, 187.	3.3	84
3	Development of SSR Markers and Assessment of Genetic Diversity in Medicinal Chrysanthemum morifolium Cultivars. Frontiers in Genetics, 2016, 7, 113.	2.3	77
4	Detecting the QTL-allele system of seed isoflavone content in Chinese soybean landrace population for optimal cross design and gene system exploration. Theoretical and Applied Genetics, 2016, 129, 1557-1576.	3.6	70
5	The Mitochondrial Genome of Soybean Reveals Complex Genome Structures and Gene Evolution at Intercellular and Phylogenetic Levels. PLoS ONE, 2013, 8, e56502.	2.5	67
6	Advances in Dendrobium molecular research: Applications in genetic variation, identification and breeding. Molecular Phylogenetics and Evolution, 2016, 95, 196-216.	2.7	63
7	The linkage maps of Dendrobium species based on RAPD and SRAP markers. Journal of Genetics and Genomics, 2010, 37, 197-204.	3.9	59
8	Application of the Ribosomal DNA ITS2 Region of Physalis (Solanaceae): DNA Barcoding and Phylogenetic Study. Frontiers in Plant Science, 2016, 7, 1047.	3.6	49
9	Start codon targeted (SCoT) and target region amplification polymorphism (TRAP) for evaluating the genetic relationship of Dendrobium species. Gene, 2015, 567, 182-188.	2.2	46
10	A transcriptome-wide, organ-specific regulatory map of Dendrobium officinale, an important traditional Chinese orchid herb. Scientific Reports, 2016, 6, 18864.	3.3	44
11	Phytochemistry, pharmacology, and potential clinical applications of saffron: A review. Journal of Ethnopharmacology, 2021, 281, 114555.	4.1	42
12	Preliminary genetic linkage maps of Chinese herb Dendrobium nobile and D. moniliforme. Journal of Genetics, 2013, 92, 205-212.	0.7	36
13	High-Density Genetic Map Construction and Stem Total Polysaccharide Content-Related QTL Exploration for Chinese Endemic Dendrobium (Orchidaceae). Frontiers in Plant Science, 2018, 9, 398.	3.6	36
14	A Chromosome-Level Genome Assembly of <i>Dendrobium Huoshanense</i> Using Long Reads and Hi-C Data. Genome Biology and Evolution, 2020, 12, 2486-2490.	2.5	30
15	Development of Species-Specific SCAR Markers, Based on a SCoT Analysis, to Authenticate Physalis (Solanaceae) Species. Frontiers in Genetics, 2018, 9, 192.	2.3	29
16	Comparative Metabolomic and Proteomic Analyses Reveal the Regulation Mechanism Underlying MeJA-Induced Bioactive Compound Accumulation in Cutleaf Groundcherry (<i>Physalis angulata</i> L.) Hairy Roots. Journal of Agricultural and Food Chemistry, 2018, 66, 6336-6347.	5.2	28
17	Dendrobium SSR markers play a good role in genetic diversity and phylogenetic analysis of Orchidaceae species. Scientia Horticulturae, 2015, 183, 160-166.	3.6	24
18	Exploration of presence/absence variation and corresponding polymorphic markers in soybean genome. Journal of Integrative Plant Biology, 2014, 56, 1009-1019.	8.5	21

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#	Article	IF	CITATIONS
19	MepmiRDB: a medicinal plant microRNA database. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	19
20	Bioactive compounds induced in Physalis angulata L. by methyl-jasmonate: an investigation of compound accumulation patterns and biosynthesis-related candidate genes. Plant Molecular Biology, 2020, 103, 341-354.	3.9	15
21	The Physalis floridana genome provides insights into the biochemical and morphological evolution of Physalis fruits. Horticulture Research, 2021, 8, 244.	6.3	15
22	Ultraviolet-B Irradiation Increases Antioxidant Capacity of Pakchoi (Brassica rapa L.) by Inducing Flavonoid Biosynthesis. Plants, 2022, 11, 766.	3.5	11
23	Transcriptome-wide identification of microRNAs and functional insights inferred from microRNA—target pairs in Physalis angulata L. Plant Signaling and Behavior, 2019, 14, 1629267.	2.4	2