

Jingyuan Song

List of Publications by Year in descending order

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53
papers

4,963
citations

136950

32
h-index

168389

53
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54
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54
docs citations

54
times ranked

4536
citing authors

#	ARTICLE	IF	CITATIONS
1	O-methyltransferases catalyze the last step of geniposide biosynthesis in <i>Gardenia jasminoides</i> . <i>Industrial Crops and Products</i> , 2022, 177, 114438.	5.2	3
2	Comparative genomics reveal the convergent evolution of CYP82D and CYP706X members related to flavone biosynthesis in Lamiaceae and Asteraceae. <i>Plant Journal</i> , 2022, 109, 1305-1318.	5.7	12
3	TaqMan Probe-Based Quantitative Real-Time PCR to Detect <i>Panax notoginseng</i> in Traditional Chinese Patent Medicines. <i>Frontiers in Pharmacology</i> , 2022, 13, .	3.5	3
4	Identification and characterization of apocarotenoid modifiers and carotenogenic enzymes for biosynthesis of crocins in <i>Buddleja davidii</i> flowers. <i>Journal of Experimental Botany</i> , 2021, 72, 3200-3218.	4.8	12
5	Highly variable chloroplast genome from two endangered Papaveraceae lithophytes <i>Corydalis tomentella</i> and <i>Corydalis saxicola</i> . <i>Ecology and Evolution</i> , 2021, 11, 4158-4171.	1.9	18
6	Identification and phylogenetic analysis of five <i>Crataegus</i> species (Rosaceae) based on complete chloroplast genomes. <i>Planta</i> , 2021, 254, 14.	3.2	27
7	Introduction of mutations in plants with prime editing. <i>Methods</i> , 2021, 194, 83-93.	3.8	8
8	Complete chloroplast genome sequence of the medicinal plant <i>Arctium lappa</i> . <i>Genome</i> , 2020, 63, 53-60.	2.0	10
9	Comparative and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three <i>Paeonia</i> Section Moutan Species (Paeoniaceae). <i>Frontiers in Genetics</i> , 2020, 11, 980.	2.3	32
10	Comparative Genome Analysis of <i>Scutellaria baicalensis</i> and <i>Scutellaria barbata</i> Reveals the Evolution of Active Flavonoid Biosynthesis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 230-240.	6.9	49
11	Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. <i>BMC Biology</i> , 2020, 18, 63.	3.8	94
12	The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. <i>New Phytologist</i> , 2020, 227, 930-943.	7.3	68
13	<i>In Vivo</i> Production of Five Crocins in the Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2020, 9, 1160-1168.	3.8	17
14	The <i>Wolfiporia cocos</i> Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotium. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 455-467.	6.9	11
15	Trends in herbgenomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308.	4.9	46
16	Comparison and Phylogenetic Analysis of Chloroplast Genomes of Three Medicinal and Edible <i>Amomum</i> Species. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4040.	4.1	67
17	Complete chloroplast genome and comparative analysis of three <i>Lycium</i> (Solanaceae) species with medicinal and edible properties. <i>Gene Reports</i> , 2019, 17, 100464.	0.8	17
18	Development of Plastid Genomic Resources for Discrimination and Classification of <i>Epimedium wushanense</i> (Berberidaceae). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4003.	4.1	8

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19	Comparative and Phylogenetic Analyses of Ginger (<i>Zingiber officinale</i>) in the Family Zingiberaceae Based on the Complete Chloroplast Genome. <i>Plants</i> , 2019, 8, 283.	3.5	50
20	The AP2/ERF transcription factor SmERF128 positively regulates diterpenoid biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Plant Molecular Biology</i> , 2019, 100, 83-93.	3.9	55
21	Precise species detection of traditional Chinese patent medicine by shotgun metagenomic sequencing. <i>Phytomedicine</i> , 2018, 47, 40-47.	5.3	33
22	Genomic survey of bZIP transcription factor genes related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 295-305.	12.0	44
23	Biomonitoring for traditional herbal medicinal products using DNA metabarcoding and single molecule, real-time sequencing. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 488-497.	12.0	55
24	Genome Analysis of the Ancient Tracheophyte <i>Selaginella tamariscina</i> Reveals Evolutionary Features Relevant to the Acquisition of Desiccation Tolerance. <i>Molecular Plant</i> , 2018, 11, 983-994.	8.3	122
25	Complete Chloroplast Genomes of <i>Papaver rhoeas</i> and <i>Papaver orientale</i> : Molecular Structures, Comparative Analysis, and Phylogenetic Analysis. <i>Molecules</i> , 2018, 23, 437.	3.8	73
26	The 2-oxoglutarate-dependent dioxygenase superfamily participates in tanshinone production in <i>Salvia miltiorrhiza</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 2299-2308.	4.8	40
27	Transcriptome-Guided Mining of Genes Involved in Crocin Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 518.	3.6	30
28	Quality Control of the Traditional Patent Medicine Yimu Wan Based on SMRT Sequencing and DNA Barcoding. <i>Frontiers in Plant Science</i> , 2017, 8, 926.	3.6	36
29	Molecular Structure and Phylogenetic Analyses of Complete Chloroplast Genomes of Two <i>Aristolochia</i> Medicinal Species. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1839.	4.1	79
30	Global Identification of the Full-Length Transcripts and Alternative Splicing Related to Phenolic Acid Biosynthetic Genes in <i>Salvia miltiorrhiza</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 100.	3.6	64
31	Genome-wide analysis of auxin response factor gene family members in medicinal model plant <i>Salvia miltiorrhiza</i> . <i>Biology Open</i> , 2016, 5, 848-857.	1.2	28
32	An authenticity survey of herbal medicines from markets in China using DNA barcoding. <i>Scientific Reports</i> , 2016, 6, 18723.	3.3	137
33	Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>Molecular Plant</i> , 2016, 9, 949-952.	8.3	255
34	An integrated system for identifying the hidden assassins in traditional medicines containing aristolochic acids. <i>Scientific Reports</i> , 2015, 5, 11318.	3.3	63
35	Cloning and analysis of 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate reductase genes HsHDR1 and HsHDR2 in <i>Huperzia serrate</i> . <i>Acta Pharmaceutica Sinica B</i> , 2015, 5, 583-589.	12.0	4
36	Survey of commercial <i>Rhodiola</i> products revealed species diversity and potential safety issues. <i>Scientific Reports</i> , 2015, 5, 8337.	3.3	85

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37	Genome-wide characterisation and analysis of bHLH transcription factors related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Scientific Reports</i> , 2015, 5, 11244.	3.3	97
38	Functional divergence of diterpene syntheses in the medicinal plant <i>Salvia miltiorrhiza</i> Bunge. <i>Plant Physiology</i> , 2015, 169, pp.00695.2015.	4.8	118
39	Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salvia miltiorrhiza</i> and tanshinone biosynthesis. <i>Plant Journal</i> , 2015, 82, 951-961.	5.7	337
40	Genome-wide selection of superior reference genes for expression studies in <i>Ganoderma lucidum</i> . <i>Gene</i> , 2015, 574, 352-358.	2.2	12
41	Genome-wide identification of phenolic acid biosynthetic genes in <i>Salvia miltiorrhiza</i> . <i>Planta</i> , 2015, 241, 711-725.	3.2	77
42	Natural Resource Monitoring of <i>Rheum tanguticum</i> by Multilevel Remote Sensing. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-9.	1.2	3
43	Identification and Evaluation of Reference Genes for qRT-PCR Normalization in <i>Ganoderma lucidum</i> . <i>Current Microbiology</i> , 2014, 68, 120-126.	2.2	35
44	Transcriptional data mining of <i>Salvia miltiorrhiza</i> in response to methyl jasmonate to examine the mechanism of bioactive compound biosynthesis and regulation. <i>Physiologia Plantarum</i> , 2014, 152, 241-255.	5.2	86
45	A renaissance in herbal medicine identification: From morphology to DNA. <i>Biotechnology Advances</i> , 2014, 32, 1237-1244.	11.7	252
46	High accuracy <i>de novo</i> assembly and SNP detection of chloroplast genomes using a SMRT circular consensus sequencing strategy. <i>New Phytologist</i> , 2014, 204, 1041-1049.	7.3	86
47	Abundant and Selective RNA-Editing Events in the Medicinal Mushroom <i>Ganoderma lucidum</i> . <i>Genetics</i> , 2014, 196, 1047-1057.	2.9	28
48	Complete chloroplast genome sequence of <i>Magnolia grandiflora</i> and comparative analysis with related species. <i>Science China Life Sciences</i> , 2013, 56, 189-198.	4.9	58
49	The Complete Chloroplast Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>PLoS ONE</i> , 2013, 8, e57607.	2.5	297
50	Transcriptome Analysis of Buds and Leaves Using 454 Pyrosequencing to Discover Genes Associated with the Biosynthesis of Active Ingredients in <i>Lonicera japonica</i> Thunb.. <i>PLoS ONE</i> , 2013, 8, e62922.	2.5	47
51	Application of the ITS2 Region for Barcoding Medicinal Plants of Selaginellaceae in Pteridophyta. <i>PLoS ONE</i> , 2013, 8, e67818.	2.5	65
52	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012, 3, 913.	12.8	458
53	Validation of the ITS2 Region as a Novel DNA Barcode for Identifying Medicinal Plant Species. <i>PLoS ONE</i> , 2010, 5, e8613.	2.5	1,152