

Jingyuan Song

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

4,963
citations

136950

32
h-index

168389

53
g-index

54
all docs

54
docs citations

54
times ranked

4536
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Validation of the ITS2 Region as a Novel DNA Barcode for Identifying Medicinal Plant Species. PLoS ONE, 2010, 5, e8613. | 2.5 | 1,152 |
| 2 | Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . Nature Communications, 2012, 3, 913. | 12.8 | 458 |
| 3 | 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. Plant Journal, 2015, 82, 951-961. | 5.7 | 337 |
| 4 | The Complete Chloroplast Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . PLoS ONE, 2013, 8, e57607. | 2.5 | 297 |
| 5 | Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . Molecular Plant, 2016, 9, 949-952. | 8.3 | 255 |
| 6 | A renaissance in herbal medicine identification: From morphology to DNA. Biotechnology Advances, 2014, 32, 1237-1244. | 11.7 | 252 |
| 7 | An authenticity survey of herbal medicines from markets in China using DNA barcoding. Scientific Reports, 2016, 6, 18723. | 3.3 | 137 |
| 8 | Genome Analysis of the Ancient Tracheophyte <i>Selaginella tamariscina</i> Reveals Evolutionary Features Relevant to the Acquisition of Desiccation Tolerance. Molecular Plant, 2018, 11, 983-994. | 8.3 | 122 |
| 9 | Functional divergence of diterpene syntheses in the medicinal plant <i>Salvia miltiorrhiza</i> Bunge. Plant Physiology, 2015, 169, pp.00695.2015. | 4.8 | 118 |
| 10 | Genome-wide characterisation and analysis of bHLH transcription factors related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . Scientific Reports, 2015, 5, 11244. | 3.3 | 97 |
| 11 | Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. BMC Biology, 2020, 18, 63. | 3.8 | 94 |
| 12 | Transcriptional data mining of <i>Salvia miltiorrhiza</i> in response to methyl jasmonate to examine the mechanism of bioactive compound biosynthesis and regulation. Physiologia Plantarum, 2014, 152, 241-255. | 5.2 | 86 |
| 13 | High-accuracy <i>de novo</i> assembly and SNP detection of chloroplast genomes using a SMRT circular consensus sequencing strategy. New Phytologist, 2014, 204, 1041-1049. | 7.3 | 86 |
| 14 | Survey of commercial <i>Rhodiola</i> products revealed species diversity and potential safety issues. Scientific Reports, 2015, 5, 8337. | 3.3 | 85 |
| 15 | Molecular Structure and Phylogenetic Analyses of Complete Chloroplast Genomes of Two <i>Aristolochia</i> Medicinal Species. International Journal of Molecular Sciences, 2017, 18, 1839. | 4.1 | 79 |
| 16 | Genome-wide identification of phenolic acid biosynthetic genes in <i>Salvia miltiorrhiza</i> . Planta, 2015, 241, 711-725. | 3.2 | 77 |
| 17 | Complete Chloroplast Genomes of <i>Papaver rhoeas</i> and <i>Papaver orientale</i> : Molecular Structures, Comparative Analysis, and Phylogenetic Analysis. Molecules, 2018, 23, 437. | 3.8 | 73 |
| 18 | The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. New Phytologist, 2020, 227, 930-943. | 7.3 | 68 |

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|----|--|------|-----------|
| 19 | Comparison and Phylogenetic Analysis of Chloroplast Genomes of Three Medicinal and Edible Amomum Species. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4040. | 4.1 | 67 |
| 20 | Application of the ITS2 Region for Barcoding Medicinal Plants of Selaginellaceae in Pteridophyta. <i>PLoS ONE</i> , 2013, 8, e67818. | 2.5 | 65 |
| 21 | 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 |
| 22 | An integrated system for identifying the hidden assassins in traditional medicines containing aristolochic acids. <i>Scientific Reports</i> , 2015, 5, 11318. | 3.3 | 63 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | Trends in herbgenomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308. | 4.9 | 46 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | Precise species detection of traditional Chinese patent medicine by shotgun metagenomic sequencing. <i>Phytomedicine</i> , 2018, 47, 40-47. | 5.3 | 33 |
| 35 | Comparative and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three <i>Paeonia</i> Section Moutan Species (<i>Paeoniaceae</i>). <i>Frontiers in Genetics</i> , 2020, 11, 980. | 2.3 | 32 |
| 36 | Transcriptome-Guided Mining of Genes Involved in Crocin Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 518. | 3.6 | 30 |

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|----|---|------|-----------|
| 37 | Abundant and Selective RNA-Editing Events in the Medicinal Mushroom <i>Ganoderma lucidum</i> . <i>Genetics</i> , 2014, 196, 1047-1057. | 2.9 | 28 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | <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 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | Complete chloroplast genome sequence of the medicinal plant <i>Arctium lappa</i> . <i>Genome</i> , 2020, 63, 53-60. | 2.0 | 10 |
| 48 | 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 |
| 49 | Introduction of mutations in plants with prime editing. <i>Methods</i> , 2021, 194, 83-93. | 3.8 | 8 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |