

Zhichao Xu

List of Publications by Year in descending order

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72
papers

2,574
citations

249298

26
h-index

252626

46
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80
all docs

80
docs citations

80
times ranked

2340
citing authors

#	ARTICLE	IF	CITATIONS
1	Effective prediction of biosynthetic pathway genes involved in bioactive polyphyllins in <i>Paris polyphylla</i> . <i>Communications Biology</i> , 2022, 5, 50.	2.0	13
2	Discovery of Aryl Benzoyl Hydrazide Derivatives as Novel Potent Broad-Spectrum Inhibitors of Influenza A Virus RNA-Dependent RNA Polymerase (RdRp). <i>Journal of Medicinal Chemistry</i> , 2022, 65, 3814-3832.	2.9	10
3	Discovery of aminothiazole derivatives as novel human enterovirus A71 capsid protein inhibitors. <i>Bioorganic Chemistry</i> , 2022, 122, 105683.	2.0	4
4	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.	2.8	12
5	Genome sequencing of <i>Inonotus obliquus</i> reveals insights into candidate genes involved in secondary metabolite biosynthesis. <i>BMC Genomics</i> , 2022, 23, 314.	1.2	20
6	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in <i>Aralia elata</i> . <i>Nature Communications</i> , 2022, 13, 2224.	5.8	34
7	The genome of <i>Corydalis</i> reveals the evolution of benzylisoquinoline alkaloid biosynthesis in Ranunculales. <i>Plant Journal</i> , 2022, 111, 217-230.	2.8	19
8	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.	0.8	18
9	Identification and phylogenetic analysis of five <i>Crataegus</i> species (Rosaceae) based on complete chloroplast genomes. <i>Planta</i> , 2021, 254, 14.	1.6	27
10	Experimental Study of H-Shaped Honeycombed Stub Columns with Rectangular Concrete-Filled Steel Tube Flanges Subjected to Axial Load. <i>Advances in Civil Engineering</i> , 2021, 2021, 1-18.	0.4	4
11	Comparative and phylogenetic analyses of the chloroplast genomes of species of Paeoniaceae. <i>Scientific Reports</i> , 2021, 11, 14643.	1.6	19
12	Genome-Wide Analysis of Light-Regulated Alternative Splicing in <i>Artemisia annua</i> L.. <i>Frontiers in Plant Science</i> , 2021, 12, 733505.	1.7	4
13	Integrative analysis of metabolome and transcriptome reveals the mechanism of color formation in white root (<i>Salvia miltiorrhiza</i>). <i>Industrial Crops and Products</i> , 2021, 170, 113784.	2.5	20
14	Research progress on biosynthesis and synthetic biology of crocin. <i>Chinese Science Bulletin</i> , 2021, 66, 219-232.	0.4	1
15	Genome-wide identification of protein phosphatase 2C family members in <i>Glycyrrhiza uralensis</i> Fisch. and their response to abscisic acid and polyethylene glycol stress. <i>Journal of Taibah University for Science</i> , 2021, 15, 1260-1268.	1.1	2
16	Complete chloroplast genome sequence of the medicinal plant <i>Arctium lappa</i> . <i>Genome</i> , 2020, 63, 53-60.	0.9	10
17	Genomic-wide identification and expression analysis of AP2/ERF transcription factors related to andrographolide biosynthesis in <i>Andrographis paniculata</i> . <i>Industrial Crops and Products</i> , 2020, 157, 112878.	2.5	17
18	Geological methane emissions and wildfire risk in the degraded permafrost area of the Xiao Xing'an Mountains, China. <i>Scientific Reports</i> , 2020, 10, 21297.	1.6	25

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19	Genome-wide identification and analysis of AP2/ERF transcription factors related to camptothecin biosynthesis in <i>Camptotheca acuminata</i> . <i>Chinese Journal of Natural Medicines</i> , 2020, 18, 582-593.	0.7	9
20	Genome-wide identification of abscisic acid (ABA) receptor pyrabactin resistance 1-like protein (PYL) family members and expression analysis of PYL genes in response to different concentrations of ABA stress in <i>Glycyrrhiza uralensis</i> . <i>Chinese Journal of Natural Medicines</i> , 2020, 18, 606-611.	0.7	7
21	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.	1.1	32
22	Prospects and progress on crocin biosynthetic pathway and metabolic engineering. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3278-3286.	1.9	18
23	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.	3.0	49
24	The genome sequence of star fruit (<i>Averrhoa carambola</i>). <i>Horticulture Research</i> , 2020, 7, 95.	2.9	18
25	Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. <i>BMC Biology</i> , 2020, 18, 63.	1.7	94
26	The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. <i>New Phytologist</i> , 2020, 227, 930-943.	3.5	68
27	<i>In Vivo</i> Production of Five Crocins in the Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2020, 9, 1160-1168.	1.9	17
28	Mining genes associated with furanocoumarin biosynthesis in an endangered medicinal plant, <i>Glehnia littoralis</i> . <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	10
29	Structural design of a broadband spiral nanoantenna for solar energy collection. <i>International Journal of Modern Physics B</i> , 2020, 34, 2050122.	1.0	3
30	Genome-Wide Characterization and Analysis of bHLH Transcription Factors Related to Crocin Biosynthesis in <i>Gardenia jasminoides</i> Ellis (Rubiaceae). <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	13
31	Genomic Characterization of WRKY Transcription Factors Related to Andrographolide Biosynthesis in <i>Andrographis paniculata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 601689.	1.1	20
32	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.	3.0	11
33	Trends in herbgenomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308.	2.3	46
34	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.	0.4	17
35	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.	1.6	50
36	Hybrid Sequencing of Full-Length cDNA Transcripts of the Medicinal Plant <i>Scutellaria baicalensis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4426.	1.8	9

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37	DNA barcoding of <i>Corydalis</i> , the most taxonomically complicated genus of Papaveraceae. Ecology and Evolution, 2019, 9, 1934-1945.	0.8	23
38	Genome-wide analysis of methyl jasmonate-regulated isoform expression in the medicinal plant <i>Andrographis paniculata</i> . Industrial Crops and Products, 2019, 135, 39-48.	2.5	14
39	Identification and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three <i>Ephedra</i> Herbs Containing Ephedrine. BioMed Research International, 2019, 2019, 1-10.	0.9	18
40	The AP2/ERF transcription factor SmERF128 positively regulates diterpenoid biosynthesis in <i>Salvia miltiorrhiza</i> . Plant Molecular Biology, 2019, 100, 83-93.	2.0	55
41	Genome-Wide Identification and Characterization of <i>Salvia miltiorrhiza</i> Laccases Reveal Potential Targets for Salvianolic Acid B Biosynthesis. Frontiers in Plant Science, 2019, 10, 435.	1.7	20
42	Gene Losses and Variations in Chloroplast Genome of Parasitic Plant <i>Macrosolen</i> and Phylogenetic Relationships within Santalales. International Journal of Molecular Sciences, 2019, 20, 5812.	1.8	15
43	The genome of the medicinal plant <i>Andrographis paniculata</i> provides insight into the biosynthesis of the bioactive diterpenoid neoandrographolide. Plant Journal, 2019, 97, 841-857.	2.8	75
44	Large-scale analysis of small RNAs derived from traditional Chinese herbs in human tissues. Science China Life Sciences, 2019, 62, 321-332.	2.3	34
45	The Genome of <i>Salvia miltiorrhiza</i> . Compendium of Plant Genomes, 2019, , 45-53.	0.3	0
46	Traditional Chinese medicine containing aristolochic acids and their detection. Scientia Sinica Vitae, 2019, 49, 238-249.	0.1	1
47	Precise species detection of traditional Chinese patent medicine by shotgun metagenomic sequencing. Phytomedicine, 2018, 47, 40-47.	2.3	33
48	IDP-denovo: <i>de novo</i> transcriptome assembly and isoform annotation by hybrid sequencing. Bioinformatics, 2018, 34, 2168-2176.	1.8	41
49	Genomic survey of bZIP transcription factor genes related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . Acta Pharmaceutica Sinica B, 2018, 8, 295-305.	5.7	44
50	Biomonitoring for traditional herbal medicinal products using DNA metabarcoding and single molecule, real-time sequencing. Acta Pharmaceutica Sinica B, 2018, 8, 488-497.	5.7	55
51	Synthesis and structure-activity relationship study of arylsulfonamides as novel potent H5N1 inhibitors. European Journal of Medicinal Chemistry, 2018, 159, 206-216.	2.6	12
52	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.	3.9	122
53	Complete Chloroplast Genomes of <i>Papaver rhoeas</i> and <i>Papaver orientale</i> : Molecular Structures, Comparative Analysis, and Phylogenetic Analysis. Molecules, 2018, 23, 437.	1.7	73
54	Cloning and functional identification of novel <i>CYP71D375</i> related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . Scientia Sinica Vitae, 2018, 48, 390-398.	0.1	0

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55	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.	2.4	40
56	Gene losses and partial deletion of small single-copy regions of the chloroplast genomes of two hemiparasitic <i>Taxillus</i> species. <i>Scientific Reports</i> , 2017, 7, 12834.	1.6	67
57	Transcriptome-Guided Mining of Genes Involved in Crocin Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 518.	1.7	30
58	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.	1.7	36
59	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in <i>Dendrobium officinale</i> . <i>Genes</i> , 2017, 8, 257.	1.0	20
60	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.	1.7	64
61	Genome-Wide Identification of the AP2/ERF Gene Family Involved in Active Constituent Biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Plant Genome</i> , 2016, 9, plantgenome2015.08.0077.	1.6	38
62	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.	0.6	28
63	Selection and validation of reference genes for normalization of quantitative real-time reverse transcription PCR analysis in <i>Poria cocos</i> (Schw.) Wolf (Fuling). <i>Chinese Medicine</i> , 2016, 11, 8.	1.6	19
64	Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>Molecular Plant</i> , 2016, 9, 949-952.	3.9	255
65	Biosynthesis and Regulation of Active Compounds in Medicinal Model Plant <i>Salvia miltiorrhiza</i> . <i>Chinese Herbal Medicines</i> , 2016, 8, 3-11.	1.2	28
66	Chromosome-level genome map provides insights into diverse defense mechanisms in the medicinal fungus <i>Ganoderma sinense</i> . <i>Scientific Reports</i> , 2015, 5, 11087.	1.6	76
67	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.	1.6	97
68	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.	2.8	337
69	Genome-wide selection of superior reference genes for expression studies in <i>Ganoderma lucidum</i> . <i>Gene</i> , 2015, 574, 352-358.	1.0	12
70	Research and perspectives on AP2/ERF transcription factors in medicinal plants. <i>Chinese Science Bulletin</i> , 2015, 60, 1272-1284.	0.4	1
71	Identification and Evaluation of Reference Genes for qRT-PCR Normalization in <i>Ganoderma lucidum</i> . <i>Current Microbiology</i> , 2014, 68, 120-126.	1.0	35
72	Research strategy for model medicinal species. <i>Chinese Science Bulletin</i> , 2014, 59, 733-742.	0.4	2