

Meng Xu

List of Publications by Year in Descending Order

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Version: 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66 papers	953 citations	18 h-index	28 g-index
71 ext. papers	1,372 ext. citations	4.7 avg, IF	4.58 L-index

#	Paper	IF	Citations
66	Study on the mechanism of enhanced gel strength of heat-induced egg white by shikimic acid braising.. <i>Poultry Science</i> , 2022 , 101, 101774	3.9	0
65	Transcriptome and metabolome analyses reveal a key role of the anthocyanin biosynthetic pathway cascade in the pigmentation of a Cinnamomum camphora red bark mutant (Guantong 1). <i>Industrial Crops and Products</i> , 2022 , 175, 114236	5.9	3
64	Heterologous overexpression of StERF3 triggers cell death in Nicotiana benthamiana.. <i>Plant Science</i> , 2022 , 315, 111149	5.3	0
63	In-situ constructing nanostructured magnesium ferrite on steel slag for Cr(VI) photoreduction. <i>Journal of Hazardous Materials</i> , 2022 , 422, 126951	12.8	2
62	Stable reference gene selection for quantitative real-time PCR normalization in passion fruit (Passiflora edulis Sims.).. <i>Molecular Biology Reports</i> , 2022 , 1	2.8	1
61	High Performance of Patterned Solution-Processed WZnSnO Thin Film Transistor Using Fiber-Coupler Semiconductor Laser Annealing. <i>IEEE Transactions on Electron Devices</i> , 2022 , 69, 1858-1863	3.9	1
60	Integrated Degradome and Srna Sequencing Revealed miRNA-mRNA Regulatory Networks between the Phloem and Developing Xylem of Poplar.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1
59	Integrated SMRT and Illumina Sequencing Provide New Insights into Crocin Biosynthesis of Gardenia jasminoides. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 6321	6.3	0
58	Protoplast isolation and transcriptome analysis of developing xylem in Pinus massoniana (Pinaceae). <i>Molecular Biology Reports</i> , 2021 , 49, 1857	2.8	0
57	The chromosome-level genome sequence of the camphor tree provides insights into Lauraceae evolution and terpene biosynthesis. <i>Plant Biotechnology Journal</i> , 2021 ,	11.6	2
56	Activation of the Host Immune Response in (Drury) (Lepidoptera: Noctuidae) Induced by Bizio. <i>Insects</i> , 2021 , 12,	2.8	1
55	Interactions between Escherichia coli survival and manganese and iron oxides in water under freeze-thaw. <i>Environmental Pollution</i> , 2021 , 268, 115237	9.3	
54	Parent-offspring variation transmission in full-sib families revealed predominantly paternal inheritance of chloroplast DNA in Pinus massoniana (Pinaceae). <i>Tree Genetics and Genomes</i> , 2021 , 17, 1	2.1	1
53	Effects of stewing with tea polyphenol on the gel properties, microstructure, and secondary structure of boiled egg white. <i>Journal of Food Science</i> , 2021 , 86, 4262-4274	3.4	0
52	Uncovering miRNA-mRNA Regulatory Modules in Developing Xylem of via Small RNA and Degradome Sequencing. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
51	Full-length sequencing of Ginkgo biloba L. reveals the synthesis of terpenoids during seed development. <i>Industrial Crops and Products</i> , 2021 , 170, 113714	5.9	1
50	Integrating GC-MS and ssRNA-Seq analysis to identify long non-coding RNAs related to terpenoid biosynthesis in Cinnamomum camphora. <i>Industrial Crops and Products</i> , 2021 , 171, 113875	5.9	1

49	Transcriptomic analysis of flower color variation in the ornamental crabapple (<i>Malus</i> spp.) half-sib family through Illumina and PacBio Sequel sequencing. <i>Plant Physiology and Biochemistry</i> , 2020 , 149, 27-35	5.4	8
48	Comparison among three methods for obtaining chloroplast genome sequences from the conifer <i>Pinus massoniana</i> . <i>Genomics</i> , 2020 , 112, 2459-2466	4.3	1
47	Deep sequencing identifies miRNAs and their target genes involved in the biosynthesis of terpenoids in <i>Cinnamomum camphora</i> . <i>Industrial Crops and Products</i> , 2020 , 145, 111853	5.9	16
46	Integrative analysis of wood biomass and developing xylem transcriptome provide insights into mechanisms of lignin biosynthesis in wood formation of <i>Pinus massoniana</i> . <i>International Journal of Biological Macromolecules</i> , 2020 , 163, 1926-1937	7.9	4
45	The <i>peu-miR160a-PeARF17.1/PeARF17.2</i> module participates in the adventitious root development of poplar. <i>Plant Biotechnology Journal</i> , 2020 , 18, 457-469	11.6	18
44	Research Progress on Plant Long Non-Coding RNA. <i>Plants</i> , 2020 , 9,	4.5	25
43	Roles of the SPL gene family and miR156 in the salt stress responses of tamarisk (<i>Tamarix chinensis</i>). <i>BMC Plant Biology</i> , 2019 , 19, 370	5.3	20
42	MiRNA-target pairs regulate adventitious rooting in <i>Populus</i> : a functional role for miR167a and its target Auxin response factor 8. <i>Tree Physiology</i> , 2019 , 39, 1922-1936	4.2	21
41	Exploring the adaptive mechanism of <i>Passiflora edulis</i> in karst areas via an integrative analysis of nutrient elements and transcriptional profiles. <i>BMC Plant Biology</i> , 2019 , 19, 185	5.3	2
40	LncRNA/circRNA-miRNA-mRNA networks regulate the development of root and shoot meristems of <i>Populus</i> . <i>Industrial Crops and Products</i> , 2019 , 133, 333-347	5.9	20
39	Rutheniumethynyl-triarylamine mixed-valence conjugated system: syntheses, (spectro-)electrochemistry, and theoretical calculations. <i>Journal of Coordination Chemistry</i> , 2019 , 72, 3385-3400	1.6	2
38	Genetic Diversity and Population Genetic Structure of <i>Cinnamomum camphora</i> in South China Revealed by EST-SSR Markers. <i>Forests</i> , 2019 , 10, 1019	2.8	8
37	Microsatellites characteristics analysis and SSR marker development for <i>Paphiopedilum hirsutissimum</i> based on transcriptome sequencing. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018 , 16, 394-396	1	1
36	Identification and characterization of long non-coding RNAs involved in the formation and development of poplar adventitious roots. <i>Industrial Crops and Products</i> , 2018 , 118, 334-346	5.9	27
35	RNA sequencing and SSR marker development for genetic diversity research in <i>Woonyoungia septentrionalis</i> (Magnoliaceae). <i>Conservation Genetics Resources</i> , 2018 , 10, 867-872	0.8	3
34	Electron receptor addition enhances butanol synthesis in ABE fermentation by <i>Clostridium acetobutylicum</i> . <i>Bioresource Technology</i> , 2018 , 247, 1201-1205	11	18
33	Study of spontaneous mutations in the transmission of poplar chloroplast genomes from mother to offspring. <i>BMC Genomics</i> , 2018 , 19, 411	4.5	2
32	Transcriptome analysis and identification of genes related to terpenoid biosynthesis in <i>Cinnamomum camphora</i> . <i>BMC Genomics</i> , 2018 , 19, 550	4.5	56

31	Tamarix microRNA Profiling Reveals New Insight into Salt Tolerance. <i>Forests</i> , 2018 , 9, 180	2.8	6
30	Novel SSR marker development and genetic diversity analysis of <i>Cinnamomum camphora</i> based on transcriptome sequencing. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018 , 16, 568-571	1	7
29	Overexpression of Improves Salt Tolerance in. <i>Genes</i> , 2018 , 9,	4.2	18
28	Transcriptome sequencing and development of novel genic SSR markers for <i>Dendrobium officinale</i> . <i>Molecular Breeding</i> , 2017 , 37, 1	3.4	22
27	Land use alters arbuscular mycorrhizal fungal communities and their potential role in carbon sequestration on the Tibetan Plateau. <i>Scientific Reports</i> , 2017 , 7, 3067	4.9	25
26	Physicochemical properties, antioxidant and antibacterial activities of dialdehyde microcrystalline cellulose. <i>Cellulose</i> , 2017 , 24, 2287-2298	5.5	29
25	Identification and characterization of nine PAT1 branch genes in poplar. <i>Plant Growth Regulation</i> , 2017 , 81, 355-364	3.2	2
24	Differentially expressed gene analysis of <i>Tamarix chinensis</i> provides insights into NaCl-stress response. <i>Trees - Structure and Function</i> , 2017 , 31, 645-658	2.6	12
23	Complete Chloroplast Genome of <i>Pinus massoniana</i> (Pinaceae): Gene Rearrangements, Loss of <i>ndh</i> Genes, and Short Inverted Repeats Contraction, Expansion. <i>Molecules</i> , 2017 , 22,	4.8	20
22	Variation in the Concentrations of Major Secondary Metabolites in Ginkgo Leaves from Different Geographical Populations. <i>Forests</i> , 2017 , 8, 266	2.8	18
21	De Novo Transcriptome Sequencing in <i>Passiflora edulis</i> Sims to Identify Genes and Signaling Pathways Involved in Cold Tolerance. <i>Forests</i> , 2017 , 8, 435	2.8	16
20	The complete chloroplast genome of and its comparison with related species. <i>PeerJ</i> , 2017 , 5, e3820	3.1	33
19	Molecular cloning, expression analysis and subcellular localization of four DELLA genes from hybrid poplar. <i>SpringerPlus</i> , 2016 , 5, 1129		10
18	Isolation and characterization of a poplar d-type cyclin gene associated with the SHORT-ROOT/SCARECROW network. <i>Trees - Structure and Function</i> , 2016 , 30, 255-263	2.6	7
17	Computational identification of genes modulating stem height-diameter allometry. <i>Plant Biotechnology Journal</i> , 2016 , 14, 2254-2264	11.6	9
16	A computational framework for mapping the timing of vegetative phase change. <i>New Phytologist</i> , 2016 , 211, 750-60	9.8	12
15	Diruthenium Complexes with Bridging Diethynyl Polyaromatic Ligands: Synthesis, Spectroelectrochemistry, and Theoretical Calculations. <i>Organometallics</i> , 2015 , 34, 3967-3978	3.8	37
14	Two WUSCHEL-related HOMEBOX genes, PeWOX11a and PeWOX11b, are involved in adventitious root formation of poplar. <i>Physiologia Plantarum</i> , 2015 , 155, 446-56	4.6	39

13	Transcriptome analysis of Ginkgo biloba kernels. <i>Frontiers in Plant Science</i> , 2015 , 6, 819	6.2	25
12	De novo transcriptome analysis of Liriodendron chinense petals and leaves by Illumina sequencing. <i>Gene</i> , 2014 , 534, 155-62	3.8	50
11	Characterization of masson pine (Pinus massoniana Lamb.) microsatellite DNA by 454 genome shotgun sequencing. <i>Tree Genetics and Genomes</i> , 2014 , 10, 429-437	2.1	9
10	High genetic diversity but limited gene flow among remnant and fragmented natural populations of Liriodendron chinense Sarg. <i>Biochemical Systematics and Ecology</i> , 2014 , 54, 230-236	1.4	17
9	Identification and characterization of three PeSHRs and one PeSCR involved in adventitious root development of Populus. <i>Plant Cell, Tissue and Organ Culture</i> , 2014 , 117, 253-264	2.7	11
8	Identification and expression analysis of twenty ARF genes in Populus. <i>Gene</i> , 2014 , 544, 134-44	3.8	16
7	Synthesis and Characterization of Dibenzoheterocycle-Bridged Dinuclear Ruthenium Alkynyl and Vinyl Complexes. <i>European Journal of Inorganic Chemistry</i> , 2014 , 2014, 2941-2951	2.3	24
6	Transient expression for functional gene analysis using Populus protoplasts. <i>Plant Cell, Tissue and Organ Culture</i> , 2013 , 114, 11-18	2.7	45
5	Overexpression of PeRHD3 alters the root architecture in Populus. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 424, 239-44	3.4	17
4	Reference gene selection for quantitative real-time polymerase chain reaction in Populus. <i>Analytical Biochemistry</i> , 2011 , 408, 337-9	3.1	99
3	Functional mapping of genotype-environment interactions for soybean growth by a semiparametric approach. <i>Plant Methods</i> , 2010 , 6, 13	5.8	16
2	EST-SSRs development and paternity analysis for Liriodendron spp. <i>New Forests</i> , 2010 , 40, 361-382	2.6	17
1	Fifteen polymorphic simple sequence repeat markers from expressed sequence tags of Liriodendron tulipifera. <i>Molecular Ecology Notes</i> , 2006 , 6, 728-730		11