

Li-An Xu

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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.

54
papers

553
citations

12
h-index

21
g-index

60
ext. papers

849
ext. citations

3.7
avg, IF

4.1
L-index

#	Paper	IF	Citations
54	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
53	Analysis of codon usage patterns in <i>Ginkgo biloba</i> reveals codon usage tendency from A/U-ending to G/C-ending. <i>Scientific Reports</i> , 2016 , 6, 35927	4.9	49
52	De novo transcriptome analysis revealed genes involved in flavonoid biosynthesis, transport and regulation in <i>Ginkgo biloba</i> . <i>Industrial Crops and Products</i> , 2018 , 124, 226-235	5.9	44
51	The complete chloroplast genome of and its comparison with related species. <i>PeerJ</i> , 2017 , 5, e3820	3.1	33
50	Deep sequencing of the <i>Camellia chekiangoleosa</i> transcriptome revealed candidate genes for anthocyanin biosynthesis. <i>Gene</i> , 2014 , 538, 1-7	3.8	27
49	Transcriptome analysis of <i>Ginkgo biloba</i> kernels. <i>Frontiers in Plant Science</i> , 2015 , 6, 819	6.2	25
48	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
47	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
46	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
45	Variation in the Concentrations of Major Secondary Metabolites in <i>Ginkgo</i> Leaves from Different Geographical Populations. <i>Forests</i> , 2017 , 8, 266	2.8	18
44	A genetic linkage map of <i>Populus adenopoda</i> Maxim. [P. <i>alba</i> L. hybrid based on SSR and SRAP markers. <i>Euphytica</i> , 2010 , 173, 193-205	2.1	18
43	Identifying secreted proteins of <i>Marssonina brunnea</i> by degenerate PCR. <i>Proteomics</i> , 2010 , 10, 2406-17	4.8	14
42	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
41	Genetic Diversity and Structure of Natural <i>Quercus variabilis</i> Population in China as Revealed by Microsatellites Markers. <i>Forests</i> , 2017 , 8, 495	2.8	11
40	Molecular cloning, expression analysis and subcellular localization of four DELLA genes from hybrid poplar. <i>SpringerPlus</i> , 2016 , 5, 1129		10
39	Comparative genome mapping among <i>Populus adenopoda</i> , <i>P. alba</i> , <i>P. deltoides</i> , <i>P. euramericana</i> and <i>P. trichocarpa</i> . <i>Genes and Genetic Systems</i> , 2011 , 86, 257-68	1.4	10
38	Analysis of genetic diversity of ancient <i>Ginkgo</i> populations using SSR markers. <i>Industrial Crops and Products</i> , 2020 , 145, 111942	5.9	10

37	SNP development and diversity analysis for Ginkgo biloba based on transcriptome sequencing. <i>Trees - Structure and Function</i> , 2019 , 33, 587-597	2.6	10
36	ARF family identification in reveals the salt responsive expression of targeted by miR167. <i>PeerJ</i> , 2020 , 8, e8829	3.1	9
35	Characterization of masson pine (<i>Pinus massoniana</i> Lamb.) microsatellite DNA by 454 genome shotgun sequencing. <i>Tree Genetics and Genomes</i> , 2014 , 10, 429-437	2.1	9
34	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
33	Genetic mapping of developmental instability: design, model and algorithm. <i>Genetics</i> , 2007 , 176, 1187-96		8
32	Relationship between first-season free growth components and later field height growth in maritime pine (<i>Pinus pinaster</i>). <i>Canadian Journal of Forest Research</i> , 1989 , 19, 690-699	1.9	8
31	Overexpression of Provides a Potential to Improve the Content of Epicatechin and Gallocatechin. <i>Molecules</i> , 2020 , 25,	4.8	8
30	Phenotypic variation in <i>Phoebe bournei</i> populations preserved in the primary distribution area. <i>Journal of Forestry Research</i> , 2018 , 29, 35-44	2	7
29	Overexpression of the VGene Enhanced the Epigallocatechin, Gallocatechin, and Catechin Contents in Transgenic. <i>Journal of Agricultural and Food Chemistry</i> , 2020 , 68, 998-1006	5.7	7
28	Small RNA and degradome sequencing reveal roles of miRNAs in strobilus development in masson pine (<i>Pinus massoniana</i>). <i>Industrial Crops and Products</i> , 2020 , 154, 112724	5.9	7
27	Development and characterization of chloroplast microsatellite markers for <i>Pinus massoniana</i> and their application in <i>Pinus</i> (<i>Pinaceae</i>) species. <i>Journal of Genetics</i> , 2018 , 97, 53-59	1.2	7
26	<i>Tamarix</i> microRNA Profiling Reveals New Insight into Salt Tolerance. <i>Forests</i> , 2018 , 9, 180	2.8	6
25	Identification and functional analysis of LysM effectors from <i>Marssonina brunnea</i> . <i>Australasian Plant Pathology</i> , 2014 , 43, 615-622	1.4	6
24	Transcriptome sequencing and SNP detection in. <i>PeerJ</i> , 2017 , 5, e3193	3.1	6
23	Genome-wide identification and characterization of the MADS-box gene family in. <i>PeerJ</i> , 2019 , 7, e8019	3.1	6
22	Development of novel chloroplast microsatellite markers for <i>Ginkgo biloba</i> . <i>Genetics and Molecular Research</i> , 2015 , 14, 7715-20	1.2	5
21	1. A genetic linkage map of <i>Pinus massoniana</i> based on SRAP, SSR and ESTP markers. <i>Silvae Genetica</i> , 2014 , 63, 1-8	1.1	4
20	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

19	Effects of parental genetic distance on offspring growth performance in <i>Pinus massoniana</i> : significance of parental-selection in a clonal seed orchard. <i>Euphytica</i> , 2019 , 215, 1	2.1	3
18	Multi-omics analysis of <i>Ginkgo biloba</i> preliminarily reveals the co-regulatory mechanism between stilbenes and flavonoids. <i>Industrial Crops and Products</i> , 2021 , 167, 113434	5.9	3
17	Cloning and expression analysis of Chitinase genes from <i>Populus canadensis</i> . <i>Russian Journal of Plant Physiology</i> , 2013 , 60, 396-403	1.6	2
16	Identification and characterization of nine PAT1 branch genes in poplar. <i>Plant Growth Regulation</i> , 2017 , 81, 355-364	3.2	2
15	Overexpression of the <i>Ginkgo biloba</i> WD40 gene GbLWD1-like improves salt tolerance in transgenic <i>Populus</i> . <i>Plant Science</i> , 2021 , 313, 111092	5.3	2
14	Development and characterization of genomic SSR markers for (<i>Tamaricaceae</i>). <i>Applications in Plant Sciences</i> , 2019 , 7, e01219	2.3	1
13	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
12	Population Genetic Structure Analysis Reveals Significant Genetic Differentiation of the Endemic Species <i>Camellia chekiangoleosa</i> Hu. with a Narrow Geographic Range. <i>Forests</i> , 2022 , 13, 234	2.8	1
11	Selection of crown type provides a potential to improve the content of isorhamnetin in <i>Ginkgo biloba</i> . <i>Industrial Crops and Products</i> , 2020 , 143, 111943	5.9	1
10	Study on the Genetic Structure Based on Geographic Populations of the Endangered Tree Species: <i>Liriodendron chinense</i> . <i>Forests</i> , 2021 , 12, 917	2.8	1
9	Parent-offspring variation transmission in full-sib families revealed predominantly paternal inheritance of chloroplast DNA in <i>Pinus massoniana</i> (<i>Pinaceae</i>). <i>Tree Genetics and Genomes</i> , 2021 , 17, 1	2.1	1
8	Full-length sequencing of <i>Ginkgo biloba</i> L. reveals the synthesis of terpenoids during seed development. <i>Industrial Crops and Products</i> , 2021 , 170, 113714	5.9	1
7	Integrating GC-MS and ssRNA-Seq analysis to identify long non-coding RNAs related to terpenoid biosynthesis in <i>Cinnamomum camphora</i> . <i>Industrial Crops and Products</i> , 2021 , 171, 113875	5.9	1
6	Development and characterization of chloroplast microsatellite markers for and their application in (<i>Pinaceae</i>) species. <i>Journal of Genetics</i> , 2018 , 97, e53-e59	1.2	1
5	Exogenous GbHMGS1 Overexpression Improves the Contents of Three Terpenoids in Transgenic <i>Populus</i> . <i>Forests</i> , 2021 , 12, 595	2.8	0
4	Overexpression of <i>Ginkgo</i> BBX25 enhances salt tolerance in Transgenic <i>Populus</i> . <i>Plant Physiology and Biochemistry</i> , 2021 , 167, 946-954	5.4	0
3	Deciphering alternative splicing patterns in multiple tissues of <i>Ginkgo biloba</i> important secondary metabolites. <i>Industrial Crops and Products</i> , 2022 , 181, 114812	5.9	0
2	Genetic, age, and ontogenetic variation of phyllotactic arrangements in pine species. <i>Canadian Journal of Botany</i> , 1989 , 67, 1254-1261		

- 1 The complete chloroplast genome of (Hayata) Coh. St. (Theaceae: Ericales) from China based on PacBio and Illumina data. *Mitochondrial DNA Part B: Resources*, **2021**, 6, 2246-2248 0.5