

Li-An Xu

List of Publications by Year in descending order

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57
papers

1,045
citations

471371

17
h-index

501076

28
g-index

60
all docs

60
docs citations

60
times ranked

976
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome analysis and identification of genes related to terpenoid biosynthesis in <i>Cinnamomum camphora</i> . <i>BMC Genomics</i> , 2018, 19, 550.	1.2	88
2	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.	1.6	75
3	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.	2.5	65
4	The complete chloroplast genome of <i>Cinnamomum camphora</i> and its comparison with related <i>Lauraceae</i> species. <i>PeerJ</i> , 2017, 5, e3820.	0.9	54
5	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.	1.6	49
6	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.	1.4	44
7	Analysis of genetic diversity of ancient <i>Ginkgo</i> populations using SSR markers. <i>Industrial Crops and Products</i> , 2020, 145, 111942.	2.5	37
8	Identifying secreted proteins of <i>Marssonina brunnea</i> by degenerate PCR. <i>Proteomics</i> , 2010, 10, 2406-2417.	1.3	33
9	Deep sequencing of the <i>Camellia chekiangoleosa</i> transcriptome revealed candidate genes for anthocyanin biosynthesis. <i>Gene</i> , 2014, 538, 1-7.	1.0	33
10	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, 1528.	1.7	33
11	Overexpression of the <i>GbF3</i> Gene Enhanced the Epigallocatechin, Galocatechin, and Catechin Contents in Transgenic <i>Populus</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 998-1006.	2.4	32
12	Transcriptome analysis of <i>Ginkgo biloba</i> kernels. <i>Frontiers in Plant Science</i> , 2015, 6, 819.	1.7	30
13	The reference genome of <i>Camellia chekiangoleosa</i> provides insights into <i>Camellia</i> evolution and tea oil biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	30
14	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.	2.8	27
15	Variation in the Concentrations of Major Secondary Metabolites in <i>Ginkgo</i> Leaves from Different Geographical Populations. <i>Forests</i> , 2017, 8, 266.	0.9	25
16	Genetic Diversity and Structure of Natural <i>Quercus variabilis</i> Population in China as Revealed by Microsatellites Markers. <i>Forests</i> , 2017, 8, 495.	0.9	22
17	A genetic linkage map of <i>Populus adenopoda</i> Maxim. × <i>P. alba</i> L. hybrid based on SSR and SRAP markers. <i>Euphytica</i> , 2010, 173, 193-205.	0.6	21
18	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.	2.5	17

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19	ARF family identification in <i>Tamarix chinensis</i> reveals the salt responsive expression of <i>TcARF6</i> targeted by miR167. <i>PeerJ</i> , 2020, 8, e8829.	0.9	17
20	Overexpression of GbF3H1 Provides a Potential to Improve the Content of Epicatechin and Galocatechin. <i>Molecules</i> , 2020, 25, 4836.	1.7	16
21	Molecular cloning, expression analysis and subcellular localization of four DELLA genes from hybrid poplar. <i>SpringerPlus</i> , 2016, 5, 1129.	1.2	15
22	Phenotypic variation in <i>Phoebe bournei</i> populations preserved in the primary distribution area. <i>Journal of Forestry Research</i> , 2018, 29, 35-44.	1.7	15
23	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.	3.6	15
24	Genome-wide identification and characterization of the MADS-box gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2019, 7, e8019.	0.9	15
25	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.	0.6	14
26	SNP development and diversity analysis for <i>Ginkgo biloba</i> based on transcriptome sequencing. <i>Trees - Structure and Function</i> , 2019, 33, 587-597.	0.9	14
27	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.	0.9	13
28	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, 257-268.	0.2	12
29	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.	1.7	12
30	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.	0.8	11
31	<i>Tamarix</i> microRNA Profiling Reveals New Insight into Salt Tolerance. <i>Forests</i> , 2018, 9, 180.	0.9	11
32	Genetic Mapping of Developmental Instability: Design, Model and Algorithm. <i>Genetics</i> , 2007, 176, 1187-1196.	1.2	10
33	Development and characterization of chloroplast microsatellite markers for <i>Pinus massoniana</i> and their application in <i>Pinus</i> (Pinaceae) species. <i>Journal of Genetics</i> , 2018, 97, 53-59.	0.4	10
34	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.	2.5	10
35	Identification and functional analysis of LysM effectors from <i>Marssonina brunnea</i> . <i>Australasian Plant Pathology</i> , 2014, 43, 615-622.	0.5	9
36	Identification and characterization of nine PAT1 branch genes in poplar. <i>Plant Growth Regulation</i> , 2017, 81, 355-364.	1.8	9

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37	Genome-Wide Identification of PLATZ Transcription Factors in <i>Ginkgo biloba</i> L. and Their Expression Characteristics During Seed Development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
38	Overexpression of <i>Ginkgo</i> BBX25 enhances salt tolerance in Transgenic <i>Populus</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 167, 946-954.	2.8	8
39	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.	2.5	8
40	Identification and Expression Analysis of the <i>Populus trichocarpa</i> GASA-Gene Family. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1507.	1.8	8
41	Development of novel chloroplast microsatellite markers for <i>Ginkgo biloba</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 7715-7720.	0.3	7
42	Transcriptome sequencing and SNP detection in <i>Phoebe chekiangensis</i> . <i>PeerJ</i> , 2017, 5, e3193.	0.9	7
43	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.	0.9	7
44	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.	2.5	5
45	Parent-offspring variation transmission in full-sib families revealed predominantly paternal inheritance of chloroplast DNA in <i>Pinus massoniana</i> (Pinaceae). <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	5
46	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.	2.5	5
47	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.	0.4	4
48	Exogenous GbHMGS1 Overexpression Improves the Contents of Three Terpenoids in Transgenic <i>Populus</i> . <i>Forests</i> , 2021, 12, 595.	0.9	4
49	Study on the Genetic Structure Based on Geographic Populations of the Endangered Tree Species: <i>Liriodendron chinense</i> . <i>Forests</i> , 2021, 12, 917.	0.9	4
50	Deciphering alternative splicing patterns in multiple tissues of <i>Ginkgo biloba</i> important secondary metabolites. <i>Industrial Crops and Products</i> , 2022, 181, 114812.	2.5	4
51	Cloning and expression analysis of Chitinase genes from <i>Populus canadensis</i> . <i>Russian Journal of Plant Physiology</i> , 2013, 60, 396-403.	0.5	3
52	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.	0.6	3
53	Development and characterization of genomic SSR markers for <i>Tamarix chinensis</i> (Tamaricaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e01219.	0.8	2
54	Comparison among three methods for obtaining chloroplast genome sequences from the conifer <i>Pinus massoniana</i> . <i>Genomics</i> , 2020, 112, 2459-2466.	1.3	2

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55	The complete chloroplast genome of <i>Camellia brevistyla</i> (Hayata) Coh. St. (Theaceae: Ericales) from China based on PacBio and Illumina data. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2246-2248.	0.2	1
56	Development and characterization of chloroplast microsatellite markers for and their application in (Pinaceae) species. <i>Journal of Genetics</i> , 2018, 97, e53-e59.	0.4	1
57	Effect of the PmARF6 Gene from Masson Pine (<i>Pinus massoniana</i>) on the Development of Arabidopsis. <i>Genes</i> , 2022, 13, 469.	1.0	0