

Jian-Feng Mao

List of Publications by Year in descending order

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75
papers

1,625
citations

304743

22
h-index

361022

35
g-index

77
all docs

77
docs citations

77
times ranked

1708
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	12.8	90
2	Distinct Niche Divergence Characterizes the Homoploid Hybrid Speciation of <i>Pinus densata</i> on the Tibetan Plateau. <i>American Naturalist</i> , 2011, 177, 424-439.	2.1	87
3	Demography and speciation history of the homoploid hybrid pine <i>Pinus densata</i> on the Tibetan Plateau. <i>Molecular Ecology</i> , 2012, 21, 4811-4827.	3.9	82
4	Transcriptome Analysis Reveals that Red and Blue Light Regulate Growth and Phytohormone Metabolism in Norway Spruce [<i>Picea abies</i> (L.) Karst.]. <i>PLoS ONE</i> , 2015, 10, e0127896.	2.5	77
5	Colonization of the Tibetan Plateau by the homoploid hybrid pine <i>Pinus densata</i> . <i>Molecular Ecology</i> , 2011, 20, 3796-3811.	3.9	71
6	Predicting Impacts of Future Climate Change on the Distribution of the Widespread Conifer <i>Platycladus orientalis</i> . <i>PLoS ONE</i> , 2015, 10, e0132326.	2.5	67
7	Impact of Geography and Climate on the Genetic Differentiation of the Subtropical Pine <i>Pinus yunnanensis</i> . <i>PLoS ONE</i> , 2013, 8, e67345.	2.5	55
8	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020, 104, 662-678.	5.7	52
9	High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, .	6.4	49
10	Landscape genomics predicts climate change-related genetic offset for the widespread <i>Platycladus orientalis</i> (Cupressaceae). <i>Evolutionary Applications</i> , 2020, 13, 665-676.	3.1	47
11	De Novo Transcriptome Assembly and Characterization for the Widespread and Stress-Tolerant Conifer <i>Platycladus orientalis</i> . <i>PLoS ONE</i> , 2016, 11, e0148985.	2.5	39
12	Wider geographic distribution and higher diversity of hexaploids than tetraploids in <i>Carassius</i> species complex reveal recurrent polyploidy effects on adaptive evolution. <i>Scientific Reports</i> , 2017, 7, 5395.	3.3	37
13	Development of high transferability cp<sc>SSR</sc> markers for individual identification and genetic investigation in Cupressaceae species. <i>Ecology and Evolution</i> , 2018, 8, 4967-4977.	1.9	36
14	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	6.4	36
15	Empirical assessment of the reproductive fitness components of the hybrid pine <i>Pinus densata</i> on the Tibetan Plateau. <i>Evolutionary Ecology</i> , 2009, 23, 447-462.	1.2	34
16	WEAK CROSSABILITY BARRIER BUT STRONG JUVENILE SELECTION SUPPORTS ECOLOGICAL SPECIATION OF THE HYBRID PINE <i>PINUS DENSATA</i> ON THE TIBETAN PLATEAU. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3120-3133.	2.3	33
17	S<sc>ub</sc>P<sc>haser</sc>: a robust allopolyploid subgenome phasing method based on subgenome-specific <i>k</i> -mers. <i>New Phytologist</i> , 2022, 235, 801-809.	7.3	33
18	Optimization of the genotyping-by-sequencing strategy for population genomic analysis in conifers. <i>Molecular Ecology Resources</i> , 2015, 15, 711-722.	4.8	32

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19	Effects of landscapes and range expansion on population structure and local adaptation. <i>New Phytologist</i> , 2020, 228, 330-343.	7.3	32
20	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	6.3	31
21	Combining mitochondrial and nuclear genome analyses to dissect the effects of colonization, environment, and geography on population structure in <i>Pinus tabulaeformis</i> . <i>Evolutionary Applications</i> , 2018, 11, 1931-1945.	3.1	28
22	Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> , 2021, 21, 1966-1982.	4.8	28
23	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	6.3	27
24	Recent Fragmentation May Not Alter Genetic Patterns in Endangered Long-Lived Species: Evidence From <i>Taxus cuspidata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1571.	3.6	24
25	Needle morphological evidence of the homoploid hybrid origin of <i>P. inus densata</i> based on analysis of artificial hybrids and the putative parents, <i>P. inus tabulaeformis</i> and <i>P. inus yunnanensis</i> . <i>Ecology and Evolution</i> , 2014, 4, 1890-1902.	1.9	23
26	Phase Partition and Phase-Based Process Monitoring Methods for Multiphase Batch Processes with Uneven Durations. <i>Industrial & Engineering Chemistry Research</i> , 2016, 55, 2035-2048.	3.7	23
27	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. <i>Genome Biology</i> , 2020, 21, 291.	8.8	23
28	Duplication and Divergence of Leucine-Rich Repeat Receptor-Like Protein Kinase (LRR-RLK) Genes in Basal Angiosperm <i>Amborella trichopoda</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1952.	3.6	21
29	Modelling environmentally suitable areas for the potential introduction and cultivation of the emerging oil crop <i>Paeonia ostii</i> in China. <i>Scientific Reports</i> , 2019, 9, 3213.	3.3	21
30	Genetic evaluation of the breeding population of a valuable reforestation conifer <i>Platycladus orientalis</i> (Cupressaceae). <i>Scientific Reports</i> , 2016, 6, 34821.	3.3	20
31	Chromosome-Scale Genome Assembly for Chinese Sour Jujube and Insights Into Its Genome Evolution and Domestication Signature. <i>Frontiers in Plant Science</i> , 2021, 12, 773090.	3.6	20
32	Genetic analyses reveal independent domestication origins of the emerging oil crop <i>Paeonia ostii</i> , a tree peony with a long-term cultivation history. <i>Scientific Reports</i> , 2017, 7, 5340.	3.3	19
33	Late Pleistocene speciation of three closely related tree peonies endemic to the Qinling–Daba Mountains, a major glacial refugium in Central China. <i>Ecology and Evolution</i> , 2019, 9, 7528-7548.	1.9	19
34	High quality haplotype-resolved genome assemblies of <i>Populus tomentosa</i> Carr., a stabilized interspecific hybrid species widespread in Asia. <i>Molecular Ecology Resources</i> , 2022, 22, 786-802.	4.8	19
35	Genetic structure of needle morphological and anatomical traits of <i>Pinus yunnanensis</i> . <i>Journal of Forestry Research</i> , 2016, 27, 13-25.	3.6	17
36	Genetic Variation Related to High Elevation Adaptation Revealed by Common Garden Experiments in <i>Pinus yunnanensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1405.	2.3	17

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37	Germination and early seedling growth of <i>Pinus densata</i> Mast. provenances. <i>Journal of Forestry Research</i> , 2016, 27, 283-294.	3.6	15
38	Predicting Future Seed Sourcing of <i>Platycladus orientalis</i> (L.) for Future Climates Using Climate Niche Models. <i>Forests</i> , 2017, 8, 471.	2.1	15
39	Local Adaptation and Response of <i>Platycladus orientalis</i> (L.) Franco Populations to Climate Change. <i>Forests</i> , 2019, 10, 622.	2.1	15
40	A strategy for characterization of persistent heteroduplex <scp>DNA</scp> in higher plants. <i>Plant Journal</i> , 2014, 80, 282-291.	5.7	14
41	A comprehensive annotation dataset of intact LTR retrotransposons of 300 plant genomes. <i>Scientific Data</i> , 2021, 8, 174.	5.3	14
42	Lilac (<i>Syringa oblata</i>) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	4.4	13
43	In-depth transcriptome characterization uncovers distinct gene family expansions for <i>Cupressus gigantea</i> important to this long-lived speciesâ€™ adaptability to environmental cues. <i>BMC Genomics</i> , 2019, 20, 213.	2.8	12
44	UV-B-induced molecular mechanisms of stress physiology responses in the major northern Chinese conifer<i>Pinus tabuliformis</i> Carr.. <i>Tree Physiology</i> , 2021, 41, 1247-1263.	3.1	12
45	Floral development and the formation of functionally unisexual flowers in <i>Xanthoceras sorbifolium</i> (Sapindaceae), a morphologically andromonoecious tree endemic to northern China. <i>Trees - Structure and Function</i> , 2019, 33, 1571-1582.	1.9	10
46	The complete chloroplast genome sequence annotation for <i>Malania oleifera</i> , a critically endangered and important bioresource tree. <i>Conservation Genetics Resources</i> , 2019, 11, 271-274.	0.8	10
47	A Variable-Correlation-Based Sparse Modeling Method for Industrial Process Monitoring. <i>Industrial & Engineering Chemistry Research</i> , 2017, 56, 6981-6992.	3.7	9
48	Novel polymorphic EST-derived microsatellite markers for the red-listed five needle pine, <i>Pinus dabeshanensis</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 191-192.	0.8	8
49	Low genetic diversity and population connectivity fuel vulnerability to climate change for the Tertiary relict pine <i>Pinus bungeana</i>. <i>Journal of Systematics and Evolution</i> , 2023, 61, 143-156.	3.1	8
50	Pollination dynamics in a<i>Platycladus orientalis</i> seed orchard as revealed by partial pedigree reconstruction. <i>Canadian Journal of Forest Research</i> , 2018, 48, 952-957.	1.7	7
51	Experimental and theoretical research on creep&fatigue behaviors of 316L steel with and without 650Â°C thermal aging. <i>Fatigue and Fracture of Engineering Materials and Structures</i> , 2022, 45, 1179-1198.	3.4	7
52	Global transcriptome analysis of <i>Sabina chinensis</i> (Cupressaceae), a valuable reforestation conifer. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	6
53	Concept for gene conservation strategy for the endangered Chinese yellowhorn, <i>Xanthoceras sorbifolium</i> , based on simulation of pairwise kinship coefficients. <i>Forest Ecology and Management</i> , 2019, 432, 976-982.	3.2	6
54	The complete mitochondrial and plastid genomes of <i>Rhododendron simsii</i>, an important parent of widely cultivated azaleas. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1197-1199.	0.4	6

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55	Centromere-Specific Retrotransposons and Very-Long-Chain Fatty Acid Biosynthesis in the Genome of Yellowhorn (<i>Xanthoceras sorbifolium</i> , Sapindaceae), an Oil-Producing Tree With Significant Drought Resistance. <i>Frontiers in Plant Science</i> , 2021, 12, 766389.	3.6	6
56	Efficiently developing a large set of polymorphic EST-SSR markers for <i>Xanthoceras sorbifolium</i> by mining raw reads from high-throughput sequencing. <i>Conservation Genetics Resources</i> , 2015, 7, 423-425.	0.8	5
57	Development of 36 novel polymorphic microsatellites for the critically endangered tree <i>Pinus squamata</i> , by transcriptome database mining. <i>Conservation Genetics Resources</i> , 2015, 7, 93-94.	0.8	5
58	Complete plastome sequences of <i>Picea asperata</i> and <i>P. crassifolia</i> and comparative analyses with <i>P. abies</i> and <i>P. morrissonicola</i> . <i>Genome</i> , 2019, 62, 317-328.	2.0	5
59	Genome-Wide Variant Identification and High-Density Genetic Map Construction Using RADseq for <i>Platycladus orientalis</i> (Cupressaceae). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3663-3672.	1.8	5
60	Development of novel EST-SSR markers for <i>Ephedra sinica</i> (Ephedraceae) by transcriptome database mining. <i>Applications in Plant Sciences</i> , 2019, 7, e01212.	2.1	4
61	Development of a Large Gene-Associated SSR Marker Set and in-Depth Genetic Characterization in Scarlet Sage. <i>Frontiers in Genetics</i> , 2020, 11, 504.	2.3	4
62	Adaptive Differentiation in Seedling Traits in a Hybrid Pine Species Complex, <i>Pinus densata</i> and Its Parental Species, on the Tibetan Plateau. <i>PLoS ONE</i> , 2015, 10, e0118501.	2.5	4
63	UV-B and UV-C radiation trigger both common and distinctive signal perceptions and transmissions in <i>Pinus tabulaeformis</i> Carr.. <i>Tree Physiology</i> , 2022, 42, 1587-1600.	3.1	4
64	Characterisation of EST-based SSR loci in the endangered tree Manchurian fir <i>Abies holophylla</i> : a transcriptomic approach. <i>Conservation Genetics Resources</i> , 2015, 7, 415-418.	0.8	3
65	Development of 23 novel polymorphic EST-SSR markers for the endangered relict conifer <i>Metasequoia glyptostroboides</i> . <i>Applications in Plant Sciences</i> , 2015, 3, 1500038.	2.1	2
66	Isolation and characterization of thirty-eight microsatellite loci for the <i>Pinus wangii</i> , an endangered species. <i>Conservation Genetics Resources</i> , 2015, 7, 397-398.	0.8	2
67	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer <i>Sabina chinensis</i> . <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	2
68	Seedling performance of <i>Pinus densata</i> and its parental population in the habitat of <i>P. tabulaeformis</i> . <i>Chinese Journal of Plant Ecology</i> , 2013, 37, 150-163.	0.6	2
69	Variation in <i>Platycladus orientalis</i> (Cupressaceae) Reproductive Output and Its Effect on Seed Orchard Crops' Genetic Diversity. <i>Forests</i> , 2021, 12, 1429.	2.1	2
70	The Terpene Synthase Gene Family in Norway Spruce. <i>Compendium of Plant Genomes</i> , 2020, , 177-192.	0.5	2
71	The complete mitochondrial genome of an endangered tree: <i>Malania oleifera</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3829-3830.	0.4	2
72	Transcriptome-wide Identification and Characterization of microRNAs and Their Targets in a Highly Adaptable Conifer <i>Platycladus orientalis</i> . <i>Journal of the American Society for Horticultural Science</i> , 2022, 147, 7-17.	1.0	2

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73	Repetitive Elements, Sequence Turnover and Cyto-Nuclear Gene Transfer in Gymnosperm Mitogenomes. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
74	The Influence of Crust Layer on Reactor Pressure Vessel Failure Under Pressurized Core Meltdown Accident. <i>Journal of Nuclear Engineering and Radiation Science</i> , 2018, 4, .	0.4	1
75	Approaches used to detect and test hybridization: combining phylogenetic and population genetic analyses. <i>Biodiversity Science</i> , 2017, 25, 577-599.	0.6	1