Dezhu Li

List of Publications by Year in descending order

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395 papers	15,837 citations	34100 52 h-index	30081 103 g-index
407 all docs	407 docs citations	407 times ranked	10883 citing authors

#	Article	IF	Citations
1	GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biology, 2020, 21, 241.	8.8	1,538
2	Comparative analysis of a large dataset indicates that internal transcribed spacer (ITS) should be incorporated into the core barcode for seed plants. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19641-19646.	7.1	738
3	PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. Plant Methods, 2019, 15, 50.	4.3	660
4	Origin of angiosperms and the puzzle of the Jurassic gap. Nature Plants, 2019, 5, 461-470.	9.3	467
5	The science and economics of ex situ plant conservation. Trends in Plant Science, 2009, 14, 614-621.	8.8	371
6	High-Throughput Sequencing of Six Bamboo Chloroplast Genomes: Phylogenetic Implications for Temperate Woody Bamboos (Poaceae: Bambusoideae). PLoS ONE, 2011, 6, e20596.	2.5	278
7	Diversification of Rosaceae since the Late Cretaceous based on plastid phylogenomics. New Phytologist, 2017, 214, 1355-1367.	7.3	278
8	Complete chloroplast genome of the genus Cymbidium: lights into the species identification, phylogenetic implications and population genetic analyses. BMC Evolutionary Biology, 2013, 13, 84.	3.2	262
9	Chloroplast Phylogenomic Analyses Resolve Deep-Level Relationships of an Intractable Bamboo Tribe Arundinarieae (Poaceae). Systematic Biology, 2014, 63, 933-950.	5.6	254
10	Highly effective sequencing whole chloroplast genomes of angiosperms by nine novel universal primer pairs. Molecular Ecology Resources, 2014, 14, 1024-1031.	4.8	239
11	Geological and ecological factors drive cryptic speciation of yews in a biodiversity hotspot. New Phytologist, 2013, 199, 1093-1108.	7.3	236
12	Telling plant species apart with DNA: from barcodes to genomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150338.	4.0	234
13	Genome assembly of a tropical maize inbred line provides insights into structural variation and crop improvement. Nature Genetics, 2019, 51, 1052-1059.	21.4	202
14	High variation and strong phylogeographic pattern among cpDNA haplotypes in Taxus wallichiana (Taxaceae) in China and North Vietnam. Molecular Ecology, 2007, 16, 4684-4698.	3.9	198
15	DNA barcoding for the discrimination of Eurasian yews (Taxus L., Taxaceae) and the discovery of cryptic species. Molecular Ecology Resources, 2011, 11, 89-100.	4.8	154
16	Higher level phylogenetic relationships within the bamboos (Poaceae: Bambusoideae) based on five plastid markers. Molecular Phylogenetics and Evolution, 2013, 67, 404-413.	2.7	148
17	Comparative Chloroplast Genomes of Camellia Species. PLoS ONE, 2013, 8, e73053.	2.5	141
18	Genome skimming herbarium specimens for DNA barcoding and phylogenomics. Plant Methods, 2018, 14, 43.	4.3	132

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19	Exploration of Plastid Phylogenomic Conflict Yields New Insights into the Deep Relationships of Leguminosae. Systematic Biology, 2020, 69, 613-622.	5.6	131
20	Insights into the historical assembly of East Asian subtropical evergreen broadleaved forests revealed by the temporal history of the tea family. New Phytologist, 2017, 215, 1235-1248.	7.3	119
21	Genome Sequences Provide Insights into the Reticulate Origin and Unique Traits of Woody Bamboos. Molecular Plant, 2019, 12, 1353-1365.	8.3	116
22	Extensive Pyrosequencing Reveals Frequent Intra-Genomic Variations of Internal Transcribed Spacer Regions of Nuclear Ribosomal DNA. PLoS ONE, 2012, 7, e43971.	2.5	112
23	De Novo Sequencing and Characterization of the Floral Transcriptome of Dendrocalamus latiflorus (Poaceae: Bambusoideae). PLoS ONE, 2012, 7, e42082.	2.5	111
24	Should genes with missing data be excluded from phylogenetic analyses?. Molecular Phylogenetics and Evolution, 2014, 80, 308-318.	2.7	109
25	Plastid phylogenomic insights into relationships of all flowering plant families. BMC Biology, 2021, 19, 232.	3.8	109
26	Complex evolution in Arundinarieae (Poaceae: Bambusoideae): Incongruence between plastid and nuclear GBSSI gene phylogenies. Molecular Phylogenetics and Evolution, 2012, 63, 777-797.	2.7	102
27	DNA barcoding of Rhododendron (Ericaceae), the largest Chinese plant genus in biodiversity hotspots of the Himalayaâ€“Hengduan Mountains. Molecular Ecology Resources, 2015, 15, 932-944.	4.8	101
28	Plastid phylogenomic insights into the evolution of Caryophyllales. Molecular Phylogenetics and Evolution, 2019, 134, 74-86.	2.7	101
29	Molecular phylogeny of the nettle family (Urticaceae) inferred from multiple loci of three genomes and extensive generic sampling. Molecular Phylogenetics and Evolution, 2013, 69, 814-827.	2.7	99
30	Plastid Genome Evolution in the Early-Diverging Legume Subfamily Cercidoideae (Fabaceae). Frontiers in Plant Science, 2018, 9, 138.	3.6	97
31	Molecular systematics of Dendrobium (Orchidaceae, Dendrobieae) from mainland Asia based on plastid and nuclear sequences. Molecular Phylogenetics and Evolution, 2013, 69, 950-960.	2.7	96
32	Multi-gene analysis provides a well-supported phylogeny of Rosales. Molecular Phylogenetics and Evolution, 2011, 60, 21-28.	2.7	90
33	Large-scale phylogenetic analyses reveal multiple gains of actinorhizal nitrogen-fixing symbioses in angiosperms associated with climate change. Scientific Reports, 2015, 5, 14023.	3.3	89
34	Tree of life for the genera of Chinese vascular plants. Journal of Systematics and Evolution, 2016, 54, 277-306.	3.1	88
35	Development of a universal and simplified ddRAD library preparation approach for SNP discovery and genotyping in angiosperm plants. Plant Methods, 2016, 12, 39.	4.3	86
36	Molecular phylogenetics and character evolution of Cannabaceae. Taxon, 2013, 62, 473-485.	0.7	85

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37	Multi-locus plastid phylogenetic biogeography supports the Asian hypothesis of the temperate woody bamboos (Poaceae: Bambusoideae). Molecular Phylogenetics and Evolution, 2016, 96, 118-129.	2.7	85
38	Large multi-locus plastid phylogeny of the tribe Arundinarieae (Poaceae: Bambusoideae) reveals ten major lineages and low rate of molecular divergence. Molecular Phylogenetics and Evolution, 2010, 56, 821-839.	2.7	83
39	Lineage-Specific Reductions of Plastid Genomes in an Orchid Tribe with Partially and Fully Mycoheterotrophic Species. Genome Biology and Evolution, 2016, 8, 2164-2175.	2.5	81
40	Warmingâ€induced upward migration of the alpine treeline in the Changbai Mountains, northeast China. Global Change Biology, 2018, 24, 1256-1266.	9.5	81
41	Carbon monoxide enhances the chilling tolerance of recalcitrant Baccaurea ramiflora seeds via nitric oxide-mediated glutathione homeostasis. Free Radical Biology and Medicine, 2012, 53, 710-720.	2.9	79
42	Protect Third Pole's fragile ecosystem. Science, 2018, 362, 1368-1368.	12.6	76
43	Domestication Origin and Breeding History of the Tea Plant (Camellia sinensis) in China and India Based on Nuclear Microsatellites and cpDNA Sequence Data. Frontiers in Plant Science, 2017, 8, 2270.	3.6	71
44	Complete Plastid Genome Sequencing of Four Tilia Species (Malvaceae): A Comparative Analysis and Phylogenetic Implications. PLoS ONE, 2015, 10, e0142705.	2.5	69
45	Gene duplications and phylogenomic conflict underlie major pulses of phenotypic evolution in gymnosperms. Nature Plants, 2021, 7, 1015-1025.	9.3	68
46	Evaluation of the DNA Barcodes in Dendrobium (Orchidaceae) from Mainland Asia. PLoS ONE, 2015, 10, e0115168.	2.5	64
47	Chloroplast phylogenomics resolves key relationships in ferns. Journal of Systematics and Evolution, 2015, 53, 448-457.	3.1	64
48	Plastome Phylogenetics: 30 Years of Inferences Into Plant Evolution. Advances in Botanical Research, 2018, , 293-313.	1.1	64
49	Biogeographical diversification of mainland Asian Dendrobium (Orchidaceae) and its implications for the historical dynamics of evergreen broadâ€leaved forests. Journal of Biogeography, 2016, 43, 1310-1323.	3.0	63
50	A comprehensive genericâ€level phylogeny of the sunflower family: Implications for the systematics of Chinese Asteraceae. Journal of Systematics and Evolution, 2016, 54, 416-437.	3.1	63
51	The monophyly of Chimonocalamus and conflicting gene trees in Arundinarieae (Poaceae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Evolution, 2013, 68, 340-356.	2.7	62
52	Evidence for horizontal transfer of mitochondrial DNA to the plastid genome in a bamboo genus. Scientific Reports, 2015, 5, 11608.	3.3	62
53	A worldwide phylogenetic classification of the Poaceae (Gramineae) III: An update. Journal of Systematics and Evolution, 2022, 60, 476-521.	3.1	61
54	Genetic Diversity and Population Structure: Implications for Conservation of Wild Soybean (Glycine) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 of Molecular Sciences, 2012, 13, 12608-12628.	4.1	60

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55	Phylogenetics of the Thamnocalamus group and its allies (Gramineae: Bambusoideae): inference from the sequences of GBSSI gene and ITS spacer. Molecular Phylogenetics and Evolution, 2004, 30, 1-12.	2.7	58
56	A molecular phylogenetic and fruit evolutionary analysis of the major groups of the paleotropical woody bamboos (Gramineae: Bambusoideae) based on nuclear ITS, GBSSI gene and plastid trnL-F DNA sequences. Molecular Phylogenetics and Evolution, 2008, 48, 809-824.	2.7	57
57	Plastomes of Mimosoideae: structural and size variation, sequence divergence, and phylogenetic implication. Tree Genetics and Genomes, 2017, 13, 1.	1.6	56
58	Prevalence of isomeric plastomes and effectiveness of plastome super-barcodes in yews (Taxus) worldwide. Scientific Reports, 2019, 9, 2773.	3.3	54
59	Identification of SNP markers for inferring phylogeny in temperate bamboos (P oaceae: B ambusoideae) using RAD sequencing. Molecular Ecology Resources, 2013, 13, 938-945.	4.8	53
60	Detection of Low Genetic Variation in a Critically Endangered Chinese Pine, Pinus squamata, Using RAPD and ISSR Markers. Biochemical Genetics, 2005, 43, 239-249.	1.7	52
61	Rapid diversification of alpine bamboos associated with the uplift of the Hengduan Mountains. Journal of Biogeography, 2019, 46, 2678-2689.	3.0	52
62	Upward elevation and northwest range shifts for alpine Meconopsis species in the Himalayaâ€“Hengduan Mountains region. Ecology and Evolution, 2019, 9, 4055-4064.	1.9	52
63	Flowers ofCypripedium fargesii(Orchidaceae) fool flat-footed flies (Platypezidae) by faking fungus-infected foliage. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7478-7480.	7.1	51
64	Biogeographic history of Pistacia (Anacardiaceae), emphasizing the evolution of the Madrean-Tethyan and the eastern Asian-Tethyan disjunctions. Molecular Phylogenetics and Evolution, 2014, 77, 136-146.	2.7	51
65	Towards a comprehensive phylogeny of the large temperate genus Pedicularis (Orobanchaceae), with an emphasis on species from the Himalaya-Hengduan Mountains. BMC Plant Biology, 2015, 15, 176.	3.6	51
66	Genome-wide RAD sequencing data provide unprecedented resolution of the phylogeny of temperate bamboos (Poaceae: Bambusoideae). Scientific Reports, 2017, 7, 11546.	3.3	51
67	Greater than the sum of the parts: how the species composition in different forest strata influence ecosystem function. Ecology Letters, 2019, 22, 1449-1461.	6.4	51
68	Indications for Three Independent Domestication Events for the Tea Plant (Camellia sinensis (L.) O.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Microsatellites. PLoS ONE, 2016, 11, e0155369.	2.5	51
69	Molecular systematics of subtribe Orchidinae and Asian taxa of Habenariinae (Orchideae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 2014, 77, 41-53.	2.7	50
70	Genetic Variation and Evolution of the Alpine Bamboos (Poaceae: Bambusoideae) using DNA Sequence Data. Journal of Plant Research, 2001, 114, 315-322.	2.4	49
71	Phylogenetic Studies on the Thamnocalamus Group and Its Allies (Gramineae: Bambusoideae) Based on ITS Sequence Data. Molecular Phylogenetics and Evolution, 2002, 22, 20-30.	2.7	48
72	Fifteen novel universal primer pairs for sequencing whole chloroplast genomes and a primer pair for nuclear ribosomal DNAs. Journal of Systematics and Evolution, 2016, 54, 219-227.	3.1	48

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73	Ancestral State Reconstruction Reveals Rampant Homoplasy of Diagnostic Morphological Characters in Urticaceae, Conflicting with Current Classification Schemes. PLoS ONE, 2015, 10, e0141821.	2.5	47
74	A well-supported nuclear phylogeny of Poaceae and implications for the evolution of C4 photosynthesis. Molecular Plant, 2022, 15, 755-777.	8.3	47
75	Sampling Strategy and Potential Utility of Indels for DNA Barcoding of Closely Related Plant Species: A Case Study in Taxus. International Journal of Molecular Sciences, 2012, 13, 8740-8751.	4.1	46
76	Identification of the Medicinal Plants inAconitumL. by DNA Barcoding Technique. Planta Medica, 2010, 76, 1622-1628.	1.3	45
77	Using Morphological, Molecular and Climatic Data to Delimitate Yews along the Hindu Kush-Himalaya and Adjacent Regions. PLoS ONE, 2012, 7, e46873.	2.5	45
78	Reciprocal herkogamy promotes disassortative mating in a distylous species with intramorph compatibility. New Phytologist, 2015, 206, 1503-1512.	7.3	45
79	Multiple measures could alleviate long-branch attraction in phylogenomic reconstruction of Cupressoideae (Cupressaceae). Scientific Reports, 2017, 7, 41005.	3.3	45
80	Incongruence between Nuclear and Chloroplast DNA Phylogenies in Pedicularis Section Cyathophora (Orobanchaceae). PLoS ONE, 2013, 8, e74828.	2.5	43
81	Differential expression networks and inheritance patterns of long nonâ€coding <scp>RNA</scp>s in castor bean seeds. Plant Journal, 2018, 95, 324-340.	5.7	43
82	Morphometric analysis of the Taxus wallichiana complex (Taxaceae) based on herbarium material. Botanical Journal of the Linnean Society, 2007, 155, 307-335.	1.6	42
83	Genetic diversity within and among populations of the endangered species Taxus fuana (Taxaceae) from Pakistan and implications for its conservation. Biochemical Systematics and Ecology, 2008, 36, 183-193.	1.3	42
84	Trait-Based Community Assembly along an Elevational Gradient in Subalpine Forests: Quantifying the Roles of Environmental Factors in Inter- and Intraspecific Variability. PLoS ONE, 2016, 11, e0155749.	2.5	41
85	Comparative analyses of plastid genomes from fourteen Cornales species: inferences for phylogenetic relationships and genome evolution. BMC Genomics, 2017, 18, 956.	2.8	40
86	Testing Darwin's transoceanic dispersal hypothesis for the inland nettle family (Urticaceae). Ecology Letters, 2018, 21, 1515-1529.	6.4	40
87	Plant DNA barcoding in China. Journal of Systematics and Evolution, 2011, 49, 165-168.	3.1	39
88	Factors affecting stress tolerance in recalcitrant embryonic axes from seeds of four Quercus (Fagaceae) species native to the USA or China. Annals of Botany, 2014, 114, 1747-1759.	2.9	39
89	Insights into the Genetic Relationships and Breeding Patterns of the African Tea Germplasm Based on nSSR Markers and cpDNA Sequences. Frontiers in Plant Science, 2016, 7, 1244.	3.6	39
90	Phylogenomic analyses of large-scale nuclear genes provide new insights into the evolutionary relationships within the rosids. Molecular Phylogenetics and Evolution, 2016, 105, 166-176.	2.7	38

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91	Integrating a comprehensive <scp>DNA</scp> barcode reference library with a global map of yews (Taxus L.) for forensic identification. Molecular Ecology Resources, 2018, 18, 1115-1131.	4.8	38
92	The Hemiparasitic Plant Phtheirospermum (Orobanchaceae) Is Polyphyletic and Contains Cryptic Species in the Hengduan Mountains of Southwest China. Frontiers in Plant Science, 2018, 9, 142.	3.6	38
93	Parallel ddRAD and Genome Skimming Analyses Reveal a Radiative and Reticulate Evolutionary History of the Temperate Bamboos. Systematic Biology, 2021, 70, 756-773.	5.6	38
94	Simultaneous diversification of Polypodiales and angiosperms in the Mesozoic. Cladistics, 2021, 37, 518-539.	3.3	38
95	Spatiotemporal maintenance of flora in the Himalaya biodiversity hotspot: Current knowledge and future perspectives. Ecology and Evolution, 2021, 11, 10794-10812.	1.9	38
96	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. PLoS ONE, 2013, 8, e64642.	2.5	37
97	Plastid phylogenomics and biogeographic analysis support a trans-Tethyan origin and rapid early radiation of Cornales in the Mid-Cretaceous. Molecular Phylogenetics and Evolution, 2019, 140, 106601.	2.7	37
98	Evolution and biogeographic diversification of the witch-hazel genus (Hamamelis L., Hamamelidaceae) in the Northern Hemisphere. Molecular Phylogenetics and Evolution, 2010, 56, 675-689.	2.7	36
99	DNA barcoding ofâ€,Pedicularisâ€,L. (Orobanchaceae): Evaluating four universal barcode loci in a large and hemiparasitic genus. Journal of Systematics and Evolution, 2011, 49, 425-437.	3.1	36
100	Molecular phylogeography of Fagus engleriana (Fagaceae) in subtropical China: limited admixture among multiple refugia. Tree Genetics and Genomes, 2012, 8, 1203-1212.	1.6	36
101	Reassessing the relationships between Gordoniaand Polyspora (Theaceae) based on the combined analyses of molecular data from the nuclear, plastid and mitochondrial genomes. Plant Systematics and Evolution, 2004, 248, 45.	0.9	35
102	Paraphyly of Cyrtomium (Dryopteridaceae): evidence from rbcL and trnL-F sequence data. Journal of Plant Research, 2005, 118, 129-135.	2.4	35
103	Origin and differentiation of endemism in the flora of China. Frontiers of Biology in China: Selected Publications From Chinese Universities, 2007, 2, 125-143.	0.2	35
104	Reticulate evolution, cryptic species, and character convergence in the core East Asian clade of Gaultheria (Ericaceae). Molecular Phylogenetics and Evolution, 2010, 57, 364-379.	2.7	35
105	Phylogenomic analysis reveals multiple evolutionary origins of selfing from outcrossing in a lineage of heterostylous plants. New Phytologist, 2019, 224, 1290-1303.	7.3	35
106	Testing genome skimming for species discrimination in the large and taxonomically difficult genus Rhododendron. Molecular Ecology Resources, 2022, 22, 404-414.	4.8	35
107	Grasses through space and time: An overview of the biogeographical and macroevolutionary history of Poaceae. Journal of Systematics and Evolution, 2022, 60, 522-569.	3.1	35
108	Phylogenetic relationships of Chinese Adiantum based on five plastid markers. Journal of Plant Research, 2012, 125, 237-249.	2.4	34

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109	Comparative phylogeography of two sympatric beeches in subtropical China: Speciesâ€specific geographic mosaic of lineages. Ecology and Evolution, 2013, 3, 4461-4472.	1.9	34
110	Plastid Phylogenomic Analyses Resolve Tofieldiaceae as the Root of the Early Diverging Monocot Order Alismatales. Genome Biology and Evolution, 2016, 8, 932-945.	2.5	34
111	Comparative chloroplast genomes of eleven Schima (Theaceae) species: Insights into DNA barcoding and phylogeny. PLoS ONE, 2017, 12, e0178026.	2.5	34
112	Genetic Diversity and Geographic Differentiation in Tacca chantrieri (Taccaceae): an Autonomous Selfing Plant with Showy Floral Display. Annals of Botany, 2006, 98, 449-457.	2.9	33
113	Low genetic diversity and high genetic differentiation in the critically endangered Omphalogramma souliei (Primulaceae): implications for its conservation. Journal of Systematics and Evolution, 2009, 47, 103-109.	3.1	33
114	Phylogenetic analyses of the banana family (Musaceae) based on nuclear ribosomal (ITS) and chloroplast (trnLâ€F) evidence. Taxon, 2010, 59, 20-28.	0.7	33
115	High universality of matK primers for barcoding gymnosperms. Journal of Systematics and Evolution, 2011, 49, 169-175.	3.1	33
116	Evolution of Angiosperm Pollen. 1. Introduction1. Annals of the Missouri Botanical Garden, 2015, 100, 177-226.	1.3	33
117	Nuclear microsatellites reveal the genetic architecture and breeding history of tea germplasm of East Africa. Tree Genetics and Genomes, 2016, 12, 1.	1.6	33
118	Phylogeographic insights on the evolutionary breakdown of heterostyly. New Phytologist, 2017, 214, 1368-1380.	7.3	33
119	Ornithophilous and Chiropterophilous Pollination in Musa itinerans (Musaceae), a Pioneer Species in Tropical Rain Forests of Yunnan, Southwestern China1. Biotropica, 2002, 34, 254-260.	1.6	32
120	Yews (Taxus) along the Hindu Kush-Himalayan region: Exploring the ethnopharmacological relevance among communities of Mongol and Caucasian origins. Journal of Ethnopharmacology, 2013, 147, 190-203.	4.1	32
121	Forest community assembly is driven by different strataâ€dependent mechanisms along an elevational gradient. Journal of Biogeography, 2019, 46, 2174-2187.	3.0	32
122	ThePharus latifoliusgenome bridges the gap of early grass evolution. Plant Cell, 2021, 33, 846-864.	6.6	32
123	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. Genome Biology, 2021, 22, 113.	8.8	32
124	Molecular Authentication of the Traditional Tibetan Medicinal Plant Swertia mussotii. Planta Medica, 2006, 72, 1223-1226.	1.3	31
125	Molecular Phylogeny of the Polystichoid Ferns in Asia Based on <I>rbcL</I> Sequences. Systematic Botany, 2007, 32, 26-33.	0.5	31
126	Genomic DNA methylation analyses reveal the distinct profiles in castor bean seeds with persistent endosperms. Plant Physiology, 2016, 171, pp.00056.2016.	4.8	31

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127	Plastome characteristics of Cannabaceae. Plant Diversity, 2018, 40, 127-137.	3.7	31
128	Transcriptome analysis reveals crucial genes involved in the biosynthesis of nervonic acid in woody Malania oleifera oilseeds. BMC Plant Biology, 2018, 18, 247.	3.6	31
129	Pollen morphology of the tribe Rhinantheae (Orobanchaceae) and its systematic significances. Plant Systematics and Evolution, 2007, 268, 177-198.	0.9	30
130	Biogeographic disjunction between eastern Asia and North America in the Adiantum pedatum complex (Pteridaceae). American Journal of Botany, 2011, 98, 1680-1693.	1.7	30
131	Dark purple nectar as a foraging signal in a birdâ€pollinated Himalayan plant. New Phytologist, 2012, 193, 188-195.	7.3	30
132	Phylogenetic relationships in thePterygiellacomplex (Orobanchaceae) inferred from molecular and morphological evidence. Botanical Journal of the Linnean Society, 2013, 171, 491-507.	1.6	30
133	Fruit and seed morphology in some representative genera of tribe Rhinantheae sensu lato (Orobanchaceae) and related taxa. Plant Systematics and Evolution, 2015, 301, 479-500.	0.9	30
134	Trait variation and functional diversity maintenance of understory herbaceous species coexisting along an elevational gradient in Yulong Mountain, Southwest China. Plant Diversity, 2016, 38, 303-311.	3.7	30
135	Why is fruit colour so variable? Phylogenetic analyses reveal relationships between fruitâ€colour evolution, biogeography and diversification. Global Ecology and Biogeography, 2019, 28, 891-903.	5.8	30
136	Distributional responses to climate change for alpine species of Cyananthus and Primula endemic to the Himalaya-Hengduan Mountains. Plant Diversity, 2019, 41, 26-32.	3.7	30
137	Revisiting the phylogeny of Dipsacales: New insights from phylogenomic analyses of complete plastomic sequences. Journal of Systematics and Evolution, 2020, 58, 103-117.	3.1	30
138	Untangling the hybrid origin of the Chinese tea roses: evidence from DNA sequences of single-copy nuclear and chloroplast genes. Plant Systematics and Evolution, 2011, 297, 157-170.	0.9	28
139	Asymmetrical natural hybridization varies among hybrid swarms between two diploid Rhododendron species. Annals of Botany, 2017, 120, 51-61.	2.9	28
140	New Genes Interacted With Recent Whole-Genome Duplicates in the Fast Stem Growth of Bamboos. Molecular Biology and Evolution, 2021, 38, 5752-5768.	8.9	28
141	Phylogenetics of Tribe Collabieae (Orchidaceae, Epidendroideae) Based on Four Chloroplast Genes with Morphological Appraisal. PLoS ONE, 2014, 9, e87625.	2.5	28
142	Phylogenetic Analysis of the Wintergreen Group (Ericaceae) based on Six Genic Regions. Systematic Botany, 2011, 36, 990-1003.	0.5	27
143	Low genetic diversity and high inbreeding of the endangered yews in Central Himalaya: implications for conservation of their highly fragmented populations. Diversity and Distributions, 2014, 20, 1270-1284.	4.1	27
144	The evolution of floral deception in Epipactis veratrifolia (Orchidaceae): from indirect defense to pollination. BMC Plant Biology, 2014, 14, 63.	3.6	27

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145	Evolution of Angiosperm Pollen. 2. The Basal Angiosperms1. Annals of the Missouri Botanical Garden, 2015, 100, 227-269.	1.3	27
146	Floral traits influence pollen vectorsâ€™ choices in higher elevation communities in the Himalaya-Hengduan Mountains. BMC Ecology, 2016, 16, 26.	3.0	27
147	Negative correlation between rates of molecular evolution and flowering cycles in temperate woody bamboos revealed by plastid phylogenomics. BMC Plant Biology, 2017, 17, 260.	3.6	27
148	Evolutionary history of a relict conifer, Pseudotaxus chienii (Taxaceae), in south-east China during the late Neogene: old lineage, young populations. Annals of Botany, 2020, 125, 105-117.	2.9	27
149	A new subtribal classification of Arundinarieae (Poaceae, Bambusoideae) with the description of a new genus. Plant Diversity, 2020, 42, 127-134.	3.7	27
150	Highly heterogeneous generic delimitation within the temperate bamboo clade (Poaceae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td	0.7	26
151	Phylogeny of Bambusa and its allies (Poaceae: Bambusoideae) inferred from nuclear GBSSI gene and plastid psbA-trnH, rpl32-trnL and rps16 intron DNA sequences. Taxon, 2010, 59, 1102-1110.	0.7	26
152	Plastid phylogenomics and adaptive evolution of Gaultheria series Trichophyllae (Ericaceae), a clade from sky islands of the Himalaya-Hengduan Mountains. Molecular Phylogenetics and Evolution, 2017, 110, 7-18.	2.7	26
153	Phylogeny of Saururaceae based on mitochondrial matR gene sequence data. Journal of Plant Research, 2002, 115, 71-76.	2.4	25
154	Flower heliotropism of AnemoneÂrivularis (Ranunculaceae) in the Himalayas: effects on floral temperature and reproductive fitness. Plant Ecology, 2010, 209, 301-312.	1.6	25
155	DNA barcoding of East Asian Amentotaxus (Taxaceae): Potential new species and implications for conservation. Journal of Systematics and Evolution, 2017, 55, 16-24.	3.1	25
156	Plastid NDH Pseudogenization and Gene Loss in a Recently Derived Lineage from the Largest Hemiparasitic Plant Genus Pedicularis (Orobanchaceae). Plant and Cell Physiology, 2021, 62, 971-984.	3.1	25
157	Molecular phylogeny and biogeography of Holcoglossum (Orchidaceae: Aeridinae) based on nuclear ITS, and chloroplast trnL-F and matK. Taxon, 2009, 58, 849-861.	0.7	24
158	Genetic diversity, demographical history and conservation aspects of the endangered yew tree Taxus contorta (syn. Taxus fuana) in Pakistan. Tree Genetics and Genomes, 2014, 10, 653-665.	1.6	24
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