

J Chris Pires

List of Publications by Year in descending order

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167
papers

25,725
citations

13865

67
h-index

7518

151
g-index

190
all docs

190
docs citations

190
times ranked

19806
citing authors

#	ARTICLE	IF	CITATIONS
1	An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG II. <i>Botanical Journal of the Linnean Society</i> , 2003, 141, 399-436.	1.6	2,573
2	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
4	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	27.8	1,162
5	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
6	Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147.	6.7	812
7	Current perspectives and the future of domestication studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6139-6146.	7.1	594
8	Genomic Changes in Resynthesized <i>Brassica napus</i> and Their Effect on Gene Expression and Phenotype. <i>Plant Cell</i> , 2007, 19, 3403-3417.	6.6	564
9	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	7.1	458
10	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	9.6	456
11	Homoeologous shuffling and chromosome compensation maintain genome balance in resynthesized allopolyploid <i>Brassica napus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7908-7913.	7.1	407
12	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	9.6	389
13	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
14	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	21.4	350
15	Gene and genome duplications: the impact of dosage-sensitivity on the fate of nuclear genes. <i>Chromosome Research</i> , 2009, 17, 699-717.	2.2	340
16	Recent and recurrent polyploidy in <i>Tragopogon</i> (Asteraceae): cytogenetic, genomic and genetic comparisons. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 485-501.	1.6	328
17	Flowering time divergence and genomic rearrangements in resynthesized <i>Brassica</i> polyploids (<i>Brassicaceae</i>). <i>Biological Journal of the Linnean Society</i> , 0, 82, 675-688.	1.6	313
18	Are all sex chromosomes created equal?. <i>Trends in Genetics</i> , 2011, 27, 350-357.	6.7	307

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19	Identification of shared single copy nuclear genes in <i>Arabidopsis</i> , <i>Populus</i> , <i>Vitis</i> and <i>Oryza</i> and their phylogenetic utility across various taxonomic levels. <i>BMC Evolutionary Biology</i> , 2010, 10, 61.	3.2	304
20	Homoeologous recombination in allopolyploids: the polyploid ratchet. <i>New Phytologist</i> , 2010, 186, 18-28.	7.3	285
21	Family-level relationships of Onagraceae based on chloroplast <i>rbcL</i> and <i>ndhF</i> data. <i>American Journal of Botany</i> , 2003, 90, 107-115.	1.7	264
22	Dosage, duplication, and diploidization: clarifying the interplay of multiple models for duplicate gene evolution over time. <i>Current Opinion in Plant Biology</i> , 2014, 19, 91-98.	7.1	261
23	Subgenome Dominance in an Interspecific Hybrid, Synthetic Allopolyploid, and a 140-Year-Old Naturally Established Neo-Allopolyploid Monkeyflower. <i>Plant Cell</i> , 2017, 29, 2150-2167.	6.6	260
24	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 394-412.	8.9	259
25	Patterns of Sequence Loss and Cytosine Methylation within a Population of Newly Resynthesized <i>Brassica napus</i> Allopolyploids. <i>Plant Physiology</i> , 2006, 140, 336-348.	4.8	250
26	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	12.8	240
27	Comparative Phylogenomics Uncovers the Impact of Symbiotic Associations on Host Genome Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004487.	3.5	229
28	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1265-1274.	8.3	217
29	Rapid Concerted Evolution of Nuclear Ribosomal DNA in Two <i>Tragopogon</i> Allopolyploids of Recent and Recurrent Origin. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY458586, AY458588, AY458589, and AY458587. <i>Genetics</i> , 2005, 169, 931-944.	2.9	209
30	Nonadditive Gene Expression in Polyploids. <i>Annual Review of Genetics</i> , 2014, 48, 485-517.	7.6	207
31	Assembling the Tree of the Monocotyledons: Plastome Sequence Phylogeny and Evolution of Poales. <i>Annals of the Missouri Botanical Garden</i> , 2010, 97, 584-616.	1.3	202
32	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	7.1	196
33	Comparative Analysis between Homoeologous Genome Segments of <i>Brassica napus</i> and Its Progenitor Species Reveals Extensive Sequence-Level Divergence. <i>Plant Cell</i> , 2009, 21, 1912-1928.	6.6	194
34	Ancient Vicariance or Recent Long-Distance Dispersal? Inferences about Phylogeny and South American-African Disjunctions in Rapateaceae and Bromeliaceae Based on <i>ndhF</i> Sequence Data. <i>International Journal of Plant Sciences</i> , 2004, 165, S35-S54.	1.3	187
35	Urticalean rosids: circumscription, rosid ancestry, and phylogenetics based on <i>rbcL</i> , <i>trnL</i> , <i>trnK</i> , and <i>ndhF</i> sequences. <i>American Journal of Botany</i> , 2002, 89, 1531-1546.	1.7	183
36	Plastid genomes reveal support for deep phylogenetic relationships and extensive rate variation among palms and other commelinid monocots. <i>New Phytologist</i> , 2016, 209, 855-870.	7.3	181

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37	Clades, Clocks, and Continents: Historical and Biogeographical Analysis of Myrtaceae, Vochysiaceae, and Relatives in the Southern Hemisphere. <i>International Journal of Plant Sciences</i> , 2004, 165, S85-S105.	1.3	178
38	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. <i>New Phytologist</i> , 2012, 196, 596-605.	7.3	178
39	Unreduced gametes: meiotic mishap or evolutionary mechanism?. <i>Trends in Genetics</i> , 2015, 31, 5-10.	6.7	177
40	Rapid Chromosome Evolution in Recently Formed Polyploids in <i>Tragopogon</i> (Asteraceae). <i>PLoS ONE</i> , 2008, 3, e3353.	2.5	173
41	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. <i>PLoS ONE</i> , 2012, 7, e50226.	2.5	172
42	Origin, inheritance, and gene regulatory consequences of genome dominance in polyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5283-5288.	7.1	172
43	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	2.9	163
44	Monocot plastid phylogenomics, timeline, net rates of species diversification, the power of multi-gene analyses, and a functional model for the origin of monocots. <i>American Journal of Botany</i> , 2018, 105, 1888-1910.	1.7	161
45	Investigating the Path of Plastid Genome Degradation in an Early-Transitional Clade of Heterotrophic Orchids, and Implications for Heterotrophic Angiosperms. <i>Molecular Biology and Evolution</i> , 2014, 31, 3095-3112.	8.9	156
46	Two-Phase Resolution of Polyploidy in the <i>Arabidopsis</i> Metabolic Network Gives Rise to Relative and Absolute Dosage Constraints. <i>Plant Cell</i> , 2011, 23, 1719-1728.	6.6	137
47	Karyotype and Identification of All Homoeologous Chromosomes of Allopolyploid <i>Brassica napus</i> and Its Diploid Progenitors. <i>Genetics</i> , 2011, 187, 37-49.	2.9	121
48	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. <i>Genome Biology and Evolution</i> , 2016, 8, evw060.	2.5	117
49	Quality and quantity of data recovered from massively parallel sequencing: Examples in Asparagales and Poaceae. <i>American Journal of Botany</i> , 2012, 99, 330-348.	1.7	115
50	Genome redundancy and plasticity within ancient and recent Brassica crop species. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 665-674.	1.6	106
51	Dragnet Ecology—Just the Facts, Ma'am: The Privilege of Science in a Postmodern World. <i>BioScience</i> , 2001, 51, 475.	4.9	101
52	Polyphyly and Convergent Morphological Evolution in Commelinales and Commelinidae: Evidence from rbcL Sequence Data. <i>Molecular Phylogenetics and Evolution</i> , 1999, 12, 360-385.	2.7	100
53	Repeated evolution of net venation and fleshy fruits among monocots in shaded habitats confirms a priori predictions: evidence from an ndhF phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1481-1490.	2.6	100
54	Molecular cytogenetic analysis of recently evolved <i>Tragopogon</i> (Asteraceae) allopolyploids reveal a karyotype that is additive of the diploid progenitors. <i>American Journal of Botany</i> , 2004, 91, 1022-1035.	1.7	99

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55	The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity. <i>Nucleic Acids Research</i> , 2015, 43, gkv973.	14.5	98
56	Phylogenomics of the plant family Araceae. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 91-102.	2.7	96
57	Storytelling and story testing in domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6159-6164.	7.1	96
58	Phylogenomic analysis of transcriptome data elucidates co-occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	1.7	94
59	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	2.5	93
60	Genetic and physical maps around the sex-determining M-locus of the dioecious plant asparagus. <i>Molecular Genetics and Genomics</i> , 2007, 278, 221-234.	2.1	91
61	Diversification times among <i>Brassica</i> (Brassicaceae) crops suggest hybrid formation after 20 million years of divergence. <i>American Journal of Botany</i> , 2014, 101, 86-91.	1.7	91
62	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	3.3	91
63	Whole Genome and Tandem Duplicate Retention Facilitated Glucosinolate Pathway Diversification in the Mustard Family. <i>Genome Biology and Evolution</i> , 2013, 5, 2155-2173.	2.5	85
64	Phylogeny of the Asparagales based on three plastid and two mitochondrial genes. <i>American Journal of Botany</i> , 2012, 99, 875-889.	1.7	84
65	Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of <i>Brassica oleracea</i> . <i>Mitochondrion</i> , 2014, 19, 135-143.	3.4	81
66	Phylogenetics, divergence times and diversification from three genomic partitions in monocots. <i>Botanical Journal of the Linnean Society</i> , 2015, 178, 375-393.	1.6	81
67	Spreading Winge and flying high: The evolutionary importance of polyploidy after a century of study. <i>American Journal of Botany</i> , 2016, 103, 1139-1145.	1.7	81
68	<i>De novo</i> genetic variation associated with retrotransposon activation, genomic rearrangements and trait variation in a recombinant inbred line population of <i>Brassica napus</i> derived from interspecific hybridization with <i>Brassica rapa</i> . <i>Plant Journal</i> , 2011, 68, 212-224.	5.7	78
69	Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. <i>PLoS Genetics</i> , 2018, 14, e1007267.	3.5	78
70	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019, 10, 2878.	12.8	78
71	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 231-237.	2.0	76
72	Brassicales phylogeny inferred from 72 plastid genes: A reanalysis of the phylogenetic localization of two paleopolyploid events and origin of novel chemical defenses. <i>American Journal of Botany</i> , 2018, 105, 463-469.	1.7	76

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73	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	3.6	73
74	Evolutionary relationships in Panicoid grasses based on plastome phylogenomics (Panicaceae). <i>Journal of Biotechnology</i> , 2019, 10, 50-70.	3.6	72
75	A fully resolved chloroplast phylogeny of the brassica crops and wild relatives (Brassicaceae). <i>Journal of Biotechnology</i> , 2019, 10, 71-100.	0.7	71
76	The development of an Arabidopsis model system for genome-wide analysis of polyploidy effects. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 689-700.	1.6	69
77	Plastid phylogenomics of the cool-season grass subfamily: clarification of relationships among early-diverging tribes. <i>American Journal of Botany</i> , 2015, 7, 046.	2.3	68
78	Transcriptome-wide comparison of selenium hyperaccumulator and nonaccumulator <i>Stanleya pinnata</i> species provides new insight into key processes mediating the hyperaccumulation syndrome. <i>Plant Biotechnology Journal</i> , 2018, 16, 1582-1594.	8.3	67
79	Biodiversity assessment: State-of-the-art techniques in phylogenomics and species identification. <i>American Journal of Botany</i> , 2011, 98, 415-425.	1.7	66
80	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . <i>Molecular Ecology</i> , 2017, 26, 3373-3388.	3.9	66
81	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	21.4	66
82	Timing of rapid diversification and convergent origins of active pollination within Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2016, 103, 1717-1729.	1.7	65
83	Positionally-conserved but sequence-diverged: identification of long non-coding RNAs in the Brassicaceae and Cleomaceae. <i>BMC Plant Biology</i> , 2015, 15, 217.	3.6	64
84	Analysis of Gene Expression in Resynthesized Brassica napus Allopolyploids Using Arabidopsis 70mer Oligo Microarrays. <i>PLoS ONE</i> , 2009, 4, e4760.	2.5	64
85	Elucidating steroid alkaloid biosynthesis in <i>Veratrum californicum</i> : production of verazine in Sf9 cells. <i>Plant Journal</i> , 2015, 82, 991-1003.	5.7	62
86	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	4.8	62
87	Topological Data Analysis as a Morphometric Method: Using Persistent Homology to Demarcate a Leaf Morphospace. <i>Frontiers in Plant Science</i> , 2018, 9, 553.	3.6	62
88	Phylogeny and photosynthesis of the grass tribe Paniceae. <i>American Journal of Botany</i> , 2015, 102, 1493-1505.	1.7	58
89	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 230, 354-371.	7.3	57
90	Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in Arabidopsis and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57.	8.3	55

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91	Resolving deep relationships of PACMAD grasses: a phylogenomic approach. <i>BMC Plant Biology</i> , 2015, 15, 178.	3.6	55
92	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	21.4	55
93	Exploring the complexity of tree thinking expertise in an undergraduate systematics course. <i>Science Education</i> , 2011, 95, 794-823.	3.0	53
94	Population Structure and Phylogenetic Relationships in a Diverse Panel of <i>Brassica rapa</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 321.	3.6	53
95	Independent evolution of ancestral and novel defenses in a genus of toxic plants (<i>Erysimum</i>), Tj ETQq1 1 0.784314,rgBT /Overlock 10	6.8	52
96	The Evolutionary History of Wild, Domesticated, and Feral <i>Brassica oleracea</i> (Brassicaceae). <i>Molecular Biology and Evolution</i> , 2021, 38, 4419-4434.	8.9	49
97	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of <i>Brassica napus</i> – <i>B. carinata</i> . <i>Genetics</i> , 2011, 187, 659-673.	2.9	48
98	G α and regulator of G α protein signaling (RGS) protein pairs maintain functional compatibility and conserved interaction interfaces throughout evolution despite frequent loss of RGS proteins in plants. <i>New Phytologist</i> , 2017, 216, 562-575.	7.3	46
99	Allopolyploidization Lays the Foundation for Evolution of Distinct Populations: Evidence From Analysis of Synthetic <i>Arabidopsis</i> Allohexaploids. <i>Genetics</i> , 2012, 191, 535-547.	2.9	44
100	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.3	44
101	Long identical multispecies elements in plant and animal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1183-91.	7.1	43
102	A phylogenetic evaluation of a biosystematic framework: <i>Brodiaea</i> and related petaloid monocots (Themidaceae). <i>American Journal of Botany</i> , 2002, 89, 1342-1359.	1.7	42
103	Introgression of B-genome chromosomes in a doubled haploid population of <i>Brassica napus</i> – <i>B. carinata</i> . <i>Genome</i> , 2010, 53, 619-629.	2.0	42
104	Integrating Networks, Phylogenomics, and Population Genomics for the Study of Polyploidy. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 253-278.	8.3	42
105	Epigenetic regulation of flowering time in polyploids. <i>Current Opinion in Plant Biology</i> , 2011, 14, 174-178.	7.1	40
106	Molecular systematics of <i>Allium</i> subgenus <i>Amerallium</i> (Amaryllidaceae) in North America. <i>American Journal of Botany</i> , 2013, 100, 701-711.	1.7	40
107	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	8.8	40
108	Anatolian origins and diversification of <i>Aethionema</i> , the sister lineage of the core Brassicaceae. <i>American Journal of Botany</i> , 2017, 104, 1042-1054.	1.7	40

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109	Taking the Next Step: Building an Arabidopsis Information Portal. <i>Plant Cell</i> , 2012, 24, 2248-2256.	6.6	38
110	Watching the grin fade: Tracing the effects of polyploidy on different evolutionary time scales. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 320-331.	5.0	37
111	Evolution of <i>Asparagus L.</i> (Asparagaceae): Out-of-South-Africa and multiple origins of sexual dimorphism. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 25-44.	2.7	35
112	Complexity of genome evolution by segmental rearrangement in <i>Brassica rapa</i> revealed by sequence-level analysis. <i>BMC Genomics</i> , 2009, 10, 539.	2.8	33
113	Convergent Evolution and the Origin of Complex Phenotypes in the Age of Systems Biology. <i>International Journal of Plant Sciences</i> , 2016, 177, 305-318.	1.3	33
114	Mitotic instability in resynthesized and natural polyploids of the genus <i>Arabidopsis</i> (Brassicaceae). <i>American Journal of Botany</i> , 2009, 96, 1656-1664.	1.7	32
115	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	1.7	32
116	<i>Brassica rapa</i> Domestication: Untangling Wild and Feral Forms and Convergence of Crop Morphotypes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3358-3372.	8.9	30
117	Seed colour loci, homoeology and linkage groups of the C genome chromosomes revealed in <i>Brassica rapa</i> - <i>B. oleracea</i> monosomic alien addition lines. <i>Annals of Botany</i> , 2012, 109, 1227-1242.	2.9	29
118	Robust Yet Fragile: Expression Noise, Protein Misfolding, and Gene Dosage in the Evolution of Genomes. <i>Annual Review of Genetics</i> , 2016, 50, 113-131.	7.6	29
119	Evolutionary insights into plant breeding. <i>Current Opinion in Plant Biology</i> , 2020, 54, 93-100.	7.1	29
120	Comparative genetics at the gene and chromosome levels between rice (<i>Oryza sativa</i>) and wildrice (<i>Zizania palustris</i>). <i>Theoretical and Applied Genetics</i> , 2003, 107, 773-782.	3.6	28
121	Preparation of Samples for Comparative Studies of Plant Chromosomes Using In Situ Hybridization Methods. <i>Methods in Enzymology</i> , 2005, 395, 443-460.	1.0	28
122	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. <i>Genome Biology</i> , 2011, 12, R48.	9.6	28
123	A multi-step comparison of short-read full plastome sequence assembly methods in grasses. <i>Taxon</i> , 2014, 63, 899-910.	0.7	28
124	Plant systematics in the next 50 years—re-mapping the new frontier. <i>Taxon</i> , 2001, 50, 713-732.	0.7	27
125	Molecular and Morphological Phylogenetic Analyses of Themidaceae (Asparagales). <i>Kew Bulletin</i> , 2001, 56, 601.	0.9	27
126	Introduction to special issue on biodiversity. <i>American Journal of Botany</i> , 2011, 98, 333-335.	1.7	27

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127	Selection for Higher Gene Copy Number after Different Types of Plant Gene Duplications. <i>Genome Biology and Evolution</i> , 2011, 3, 1369-1380.	2.5	27
128	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	3.3	27
129	Chromosome inheritance and meiotic stability in allopolyploid <i>Brassica napus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	27
130	Affordable remote monitoring of plant growth in facilities using Raspberry Pi computers. <i>Applications in Plant Sciences</i> , 2019, 7, e11280.	2.1	26
131	Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2021, 230, 372-386.	7.3	26
132	Phylotranscriptomic analysis and genome evolution of the Cyripedioideae (Orchidaceae). <i>American Journal of Botany</i> , 2018, 105, 631-640.	1.7	25
133	Secondary Structure Analyses of the Nuclear rRNA Internal Transcribed Spacers and Assessment of Its Phylogenetic Utility across the Brassicaceae (Mustards). <i>PLoS ONE</i> , 2014, 9, e101341.	2.5	24
134	Systematics and Evolution of Inflorescence Structure in the <i>Tradescantia</i> Alliance (Commelinaceae). <i>Systematic Botany</i> , 2014, 39, 105-116.	0.5	24
135	Retrotransposon Proliferation Coincident with the Evolution of Dioecy in <i>Asparagus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2679-2685.	1.8	22
136	Biodiversity comparison among phylogenetic diversity metrics and between three North American prairies. <i>Applications in Plant Sciences</i> , 2015, 3, 1400108.	2.1	21
137	Patterns of Population Variation in Two Paleopolyploid Eudicot Lineages Suggest That Dosage-Based Selection on Homeologs Is Long-Lived. <i>Genome Biology and Evolution</i> , 2018, 10, 999-1011.	2.5	21
138	The contributions from the progenitor genomes of the mesopolyploid Brassicaceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	5.5	21
139	Integration of Genetic, Physical, and Cytogenetic Maps for <i>Brassica rapa</i> ; Chromosome A7. <i>Cytogenetic and Genome Research</i> , 2010, 129, 190-198.	1.1	18
140	Usability of reference-free transcriptome assemblies for detection of differential expression: a case study on <i>Aethionema arabicum</i> dimorphic seeds. <i>BMC Genomics</i> , 2019, 20, 95.	2.8	18
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