

J Chris Pires

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2242231/publications.pdf>

Version: 2024-02-01

167
papers

25,725
citations

13087

68
h-index

7340

152
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.	0.8	2,573
2	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
4	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	13.7	1,162
5	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
6	Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147.	2.9	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.	3.3	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.	3.1	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.	3.3	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.	13.9	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.	3.3	407
12	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	13.9	389
13	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	5.8	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.	9.4	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.	1.0	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.	0.7	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> , 2004, 82, 675-688.	0.7	313
18	Are all sex chromosomes created equal?. <i>Trends in Genetics</i> , 2011, 27, 350-357.	2.9	307

#	ARTICLE	IF	CITATIONS
19	Identification of shared single copy nuclear genes in Arabidopsis, Populus, Vitis and Oryza and their phylogenetic utility across various taxonomic levels. BMC Evolutionary Biology, 2010, 10, 61.	3.2	304
20	Homoeologous recombination in allopolyploids: the polyploid ratchet. New Phytologist, 2010, 186, 18-28.	3.5	285
21	Family-level relationships of Onagraceae based on chloroplast <i>rbcL</i> and <i>ndhF</i> data. American Journal of Botany, 2003, 90, 107-115.	0.8	264
22	Dosage, duplication, and diploidization: clarifying the interplay of multiple models for duplicate gene evolution over time. Current Opinion in Plant Biology, 2014, 19, 91-98.	3.5	261
23	Subgenome Dominance in an Interspecific Hybrid, Synthetic Allopolyploid, and a 140-Year-Old Naturally Established Neo-Allopolyploid Monkeyflower. Plant Cell, 2017, 29, 2150-2167.	3.1	260
24	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. Molecular Biology and Evolution, 2016, 33, 394-412.	3.5	259
25	Patterns of Sequence Loss and Cytosine Methylation within a Population of Newly Resynthesized Brassica napus Allopolyploids. Plant Physiology, 2006, 140, 336-348.	2.3	250
26	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. Nature Communications, 2017, 8, 1279.	5.8	240
27	Comparative Phylogenomics Uncovers the Impact of Symbiotic Associations on Host Genome Evolution. PLoS Genetics, 2014, 10, e1004487.	1.5	229
28	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . Plant Biotechnology Journal, 2018, 16, 1265-1274.	4.1	217
29	Rapid Concerted Evolution of Nuclear Ribosomal DNA in Two Tragopogon 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. Genetics, 2005, 169, 931-944.	1.2	209
30	Nonadditive Gene Expression in Polyploids. Annual Review of Genetics, 2014, 48, 485-517.	3.2	207
31	Assembling the Tree of the Monocotyledons: Plastome Sequence Phylogeny and Evolution of Poales. Annals of the Missouri Botanical Garden, 2010, 97, 584-616.	1.3	202
32	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	3.3	196
33	Comparative Analysis between Homoeologous Genome Segments of <i>Brassica napus</i> and Its Progenitor Species Reveals Extensive Sequence-Level Divergence. Plant Cell, 2009, 21, 1912-1928.	3.1	194
34	Ancient Vicariance or Recent Long-Distance Dispersal? Inferences about Phylogeny and South American-African Disjunctions in Rapateaceae and Bromeliaceae Based on ndhF Sequence Data. International Journal of Plant Sciences, 2004, 165, S35-S54.	0.6	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. American Journal of Botany, 2002, 89, 1531-1546.	0.8	183
36	Plastid genomes reveal support for deep phylogenetic relationships and extensive rate variation among palms and other commelinid monocots. New Phytologist, 2016, 209, 855-870.	3.5	181

#	ARTICLE	IF	CITATIONS
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.	0.6	178
38	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. <i>New Phytologist</i> , 2012, 196, 596-605.	3.5	178
39	Unreduced gametes: meiotic mishap or evolutionary mechanism?. <i>Trends in Genetics</i> , 2015, 31, 5-10.	2.9	177
40	Rapid Chromosome Evolution in Recently Formed Polyploids in <i>Tragopogon</i> (Asteraceae). <i>PLoS ONE</i> , 2008, 3, e3353.	1.1	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.	1.1	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.	3.3	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.	1.2	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.	0.8	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.	3.5	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.	3.1	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.	1.2	121
48	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. <i>Genome Biology and Evolution</i> , 2016, 8, evw060.	1.1	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.	0.8	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.	0.7	106
51	Dragnet Ecology—Just the Facts, Ma'am! The Privilege of Science in a Postmodern World. <i>BioScience</i> , 2001, 51, 475.	2.2	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.	1.2	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.	1.2	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.	0.8	99

#	ARTICLE	IF	CITATIONS
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.	6.5	98
56	Phylogenomics of the plant family Araceae. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 91-102.	1.2	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.	3.3	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.	0.8	94
59	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	1.1	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.	1.0	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.	0.8	91
62	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	1.7	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.	1.1	85
64	Phylogeny of the Asparagales based on three plastid and two mitochondrial genes. <i>American Journal of Botany</i> , 2012, 99, 875-889.	0.8	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.	1.6	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.	0.8	81
67	Spreading Wings and flying high: The evolutionary importance of polyploidy after a century of study. <i>American Journal of Botany</i> , 2016, 103, 1139-1145.	0.8	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.	2.8	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.	1.5	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.	5.8	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.	1.0	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.	0.8	76

#	ARTICLE	IF	CITATIONS
73	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	1.7	73
74	Evolutionary relationships in Panicoid grasses based on plastome phylogenomics (Panicaceae). <i>Journal of Biotechnology</i> , 2019, 10, 1-10.	1.6	72
75	A fully resolved chloroplast phylogeny of the brassica crops and wild relatives (Brassicaceae). <i>Journal of Biotechnology</i> , 2019, 10, 1-10.	1.6	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.	0.7	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, 1046.	1.2	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.	4.1	67
79	Biodiversity assessment: State-of-the-art techniques in phylogenomics and species identification. <i>American Journal of Botany</i> , 2011, 98, 415-425.	0.8	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.	2.0	66
81	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	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.	0.8	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.	1.6	64
84	Analysis of Gene Expression in Resynthesized Brassica napus Allopolyploids Using Arabidopsis 70mer Oligo Microarrays. <i>PLoS ONE</i> , 2009, 4, e4760.	1.1	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.	2.8	62
86	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	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.	1.7	62
88	Phylogeny and photosynthesis of the grass tribe Paniceae. <i>American Journal of Botany</i> , 2015, 102, 1493-1505.	0.8	58
89	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 230, 354-371.	3.5	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.	4.1	55

#	ARTICLE	IF	CITATIONS
91	Resolving deep relationships of PACMAD grasses: a phylogenomic approach. <i>BMC Plant Biology</i> , 2015, 15, 178.	1.6	55
92	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	9.4	55
93	Exploring the complexity of tree thinking expertise in an undergraduate systematics course. <i>Science Education</i> , 2011, 95, 794-823.	1.8	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.	1.7	53
95	Independent evolution of ancestral and novel defenses in a genus of toxic plants (<i>Erysimum</i>). <i>Tj ETQq1 1 0.784314,rgBT /Overlock 10</i>	2.8	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.	3.5	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.	1.2	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.	3.5	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.	1.2	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.	4.1	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.	3.3	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.	0.8	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.	0.9	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.	3.8	42
105	Epigenetic regulation of flowering time in polyploids. <i>Current Opinion in Plant Biology</i> , 2011, 14, 174-178.	3.5	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.	0.8	40
107	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	4.3	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.	0.8	40

#	ARTICLE	IF	CITATIONS
109	Taking the Next Step: Building an Arabidopsis Information Portal. <i>Plant Cell</i> , 2012, 24, 2248-2256.	3.1	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.	2.3	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.	1.2	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.	1.2	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.	0.6	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.	0.8	32
115	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	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.	3.5	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.	1.4	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.	3.2	29
119	Evolutionary insights into plant breeding. <i>Current Opinion in Plant Biology</i> , 2020, 54, 93-100.	3.5	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.	1.8	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.	0.4	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.	13.9	28
123	A multi-step comparison of short-read full plastome sequence assembly methods in grasses. <i>Taxon</i> , 2014, 63, 899-910.	0.4	28
124	Plant systematics in the next 50 years: remapping the new frontier. <i>Taxon</i> , 2001, 50, 713-732.	0.4	27
125	Molecular and Morphological Phylogenetic Analyses of Themidaceae (Asparagales). <i>Kew Bulletin</i> , 2001, 56, 601.	0.4	27
126	Introduction to special issue on biodiversity. <i>American Journal of Botany</i> , 2011, 98, 333-335.	0.8	27

#	ARTICLE	IF	CITATIONS
127	Selection for Higher Gene Copy Number after Different Types of Plant Gene Duplications. <i>Genome Biology and Evolution</i> , 2011, 3, 1369-1380.	1.1	27
128	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27
129	Chromosome inheritance and meiotic stability in allopolyploid <i>Brassica napus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	27
130	Affordable remote monitoring of plant growth in facilities using Raspberry Pi computers. <i>Applications in Plant Sciences</i> , 2019, 7, e11280.	0.8	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.	3.5	26
132	Phylotranscriptomic analysis and genome evolution of the Cyripedioideae (Orchidaceae). <i>American Journal of Botany</i> , 2018, 105, 631-640.	0.8	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.	1.1	24
134	Systematics and Evolution of Inflorescence Structure in the <i>Tradescantia</i> Alliance (Commelinaceae). <i>Systematic Botany</i> , 2014, 39, 105-116.	0.2	24
135	Retrotransposon Proliferation Coincident with the Evolution of Dioecy in <i>Asparagus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2679-2685.	0.8	22
136	Biodiversity comparison among phylogenetic diversity metrics and between three North American prairies. <i>Applications in Plant Sciences</i> , 2015, 3, 1400108.	0.8	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.	1.1	21
138	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	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.	0.6	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.	1.2	18
141	A physical map of <i>Brassica oleracea</i> shows complexity of chromosomal changes following recursive paleopolyploidizations. <i>BMC Genomics</i> , 2011, 12, 470.	1.2	17
142	Convergent evolution of polyploid genomes from across the eukaryotic tree of life. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	16
143	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
144	Origin of a novel regulatory module by duplication and degeneration of an ancient plant transcription factor. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 159-173.	1.2	14

#	ARTICLE	IF	CITATIONS
145	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	0.8	14
146	Feralization: Confronting the Complexity of Domestication and Evolution. <i>Trends in Genetics</i> , 2021, 37, 302-305.	2.9	14
147	A Renaissance of Cytogenetics: Studies in Polyploidy and Chromosomal Evolution1. <i>Annals of the Missouri Botanical Garden</i> , 2008, 95, 275-281.	1.3	13
148	Genome-wide nucleotide diversity and associations with geography, ploidy level and glucosinolate profiles in <i>Aethionema arabicum</i> (Brassicaceae). <i>Plant Systematics and Evolution</i> , 2018, 304, 619-630.	0.3	13
149	Current status of the multinational <i>Arabidopsis</i> community. <i>Plant Direct</i> , 2020, 4, e00248.	0.8	13
150	The Molecular Basis of Kale Domestication: Transcriptional Profiling of Developing Leaves Provides New Insights Into the Evolution of a <i>Brassica oleracea</i> Vegetative Morphotype. <i>Frontiers in Plant Science</i> , 2021, 12, 637115.	1.7	12
151	Structural and Functional Evolution of Resynthesized Polyploids. , 2011, , 195-214.		12
152	Is DNA Alive? A Study of Conceptual Change Through Targeted Instruction. <i>Research in Science Education</i> , 2013, 43, 1361-1375.	1.4	11
153	Molecular Resources from Transcriptomes in the Brassicaceae Family. <i>Frontiers in Plant Science</i> , 2017, 8, 1488.	1.7	11
154	The Genomes of All Angiosperms: A Call for a Coordinated Global Census. <i>Journal of Botany</i> , 2011, 2011, 1-10.	1.2	10
155	Contrasting patterns of support among plastid genes and genomes for major clades of the monocotyledons. , 0, , 315-349.		10
156	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10
157	The Fate of <i>Arabidopsis thaliana</i> Homeologous CNSs and Their Motifs in the Paleohexaploid <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 646-660.	1.1	8
158	Functional characterization of SMN evolution in mouse models of SMA. <i>Scientific Reports</i> , 2019, 9, 9472.	1.6	8
159	Prospects of Feral Crop De Novo Redomestication. <i>Plant and Cell Physiology</i> , 2022, 63, 1641-1653.	1.5	8
160	Evolution of Lomandroideae: Multiple origins of polyploidy and biome occupancy in Australia. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106836.	1.2	7
161	The renaissance of comparative biochemistry. <i>American Journal of Botany</i> , 2019, 106, 3-13.	0.8	5
162	Distinct C ₄ subtypes and C ₃ bundle sheath isolation in the Paniceae grasses. <i>Plant Direct</i> , 2021, 5, e373.	0.8	4

#	ARTICLE	IF	CITATIONS
163	New infraspecific names in North American Liliales. <i>Taxon</i> , 2001, 50, 201-201.	0.4	1
164	Getting up to speed. <i>Current Opinion in Plant Biology</i> , 2012, 15, 111-114.	3.5	1
165	Editorial overview: Genome studies and molecular genetics: Of plant genes, genomes, and genomics. <i>Current Opinion in Plant Biology</i> , 2016, 30, iv-vi.	3.5	1
166	Preface. <i>Cytogenetic and Genome Research</i> , 2010, 129, 5-5.	0.6	0
167	Editorial overview: Genome studies and molecular genetics: Treasure troves of evolution. <i>Current Opinion in Plant Biology</i> , 2018, 42, iii-v.	3.5	0