

J Chris Pires

List of Publications by Year in descending order

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Version: 2024-02-01

167
papers

25,725
citations

13068

68
h-index

7333

152
g-index

190
all docs

190
docs citations

190
times ranked

19806
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent evolution of polyploid genomes from across the eukaryotic tree of life. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	16
2	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	9.4	55
3	Prospects of Feral Crop De Novo Redomestication. <i>Plant and Cell Physiology</i> , 2022, 63, 1641-1653.	1.5	8
4	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
5	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
6	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
7	Feralization: Confronting the Complexity of Domestication and Evolution. <i>Trends in Genetics</i> , 2021, 37, 302-305.	2.9	14
8	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
9	<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
10	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
11	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
12	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
13	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
14	Chromosome inheritance and meiotic stability in allopolyploid <i>Brassica napus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	27
15	Distinct C ₄ subtypes and C ₃ bundle sheath isolation in the Paniceae grasses. <i>Plant Direct</i> , 2021, 5, e373.	0.8	4
16	Current status of the multinational <i>Arabidopsis</i> community. <i>Plant Direct</i> , 2020, 4, e00248.	0.8	13
17	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	32
18	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10

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19	Evolutionary insights into plant breeding. <i>Current Opinion in Plant Biology</i> , 2020, 54, 93-100.	3.5	29
20	Evolution of Lomandroideae: Multiple origins of polyploidy and biome occupancy in Australia. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106836.	1.2	7
21	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
22	Affordable remote monitoring of plant growth in facilities using Raspberry Pi computers. <i>Applications in Plant Sciences</i> , 2019, 7, e11280.	0.8	26
23	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
24	Functional characterization of SMN evolution in mouse models of SMA. <i>Scientific Reports</i> , 2019, 9, 9472.	1.6	8
25	The renaissance of comparative biochemistry. <i>American Journal of Botany</i> , 2019, 106, 3-13.	0.8	5
26	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
27	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	0.8	14
28	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	13.7	1,162
29	Genome-wide nucleotide diversity and associations with geography, ploidy level and glucosinolate profiles in <i>Aethionema arabicum</i> (<i>Brassicaceae</i>). <i>Plant Systematics and Evolution</i> , 2018, 304, 619-630.	0.3	13
30	Phylotranscriptomic analysis and genome evolution of the Cyripedioideae (<i>Orchidaceae</i>). <i>American Journal of Botany</i> , 2018, 105, 631-640.	0.8	25
31	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
32	Transcriptome-wide comparison of selenium hyperaccumulator and nonaccumulator <i>Stanleya</i> species provides new insight into key processes mediating the hyperaccumulation syndrome. <i>Plant Biotechnology Journal</i> , 2018, 16, 1582-1594.	4.1	67
33	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
34	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
35	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
36	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

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37	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
38	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
39	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.	4.1	217
40	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <i>Plant Physiology</i> , 2017, 174, 904-921.	2.3	62
41	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
42	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	5.8	240
43	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27
44	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.	3.1	260
45	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
46	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
47	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
48	Molecular Resources from Transcriptomes in the Brassicaceae Family. <i>Frontiers in Plant Science</i> , 2017, 8, 1488.	1.7	11
49	Evolutionary relationships in Panicoid grasses based on plastome phylogenomics (Panicoideae; Tj ETQq1 1 0.784314 rgBT / Overlock 1.6 72	1.6	72
50	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
51	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
52	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.	3.5	181
53	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.	0.8	81
54	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

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55	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
56	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	5.8	375
57	Timing of rapid diversification and convergent origins of active pollination within Agavoideae (<i>Asparagaceae</i>). <i>American Journal of Botany</i> , 2016, 103, 1717-1729.	0.8	65
58	The Evolution of HD2 Proteins in Green Plants. <i>Trends in Plant Science</i> , 2016, 21, 1008-1016.	4.3	40
59	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
60	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. <i>Genome Biology and Evolution</i> , 2016, 8, evw060.	1.1	117
61	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.	3.5	259
62	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	1.1	93
63	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
64	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
65	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
66	Unreduced gametes: meiotic mishap or evolutionary mechanism?. <i>Trends in Genetics</i> , 2015, 31, 5-10.	2.9	177
67	Plastid phylogenomics of the cool-season grass subfamily: clarification of relationships among early-diverging tribes. <i>AoB PLANTS</i> , 2015, 7, plv046.	1.2	68
68	Evolution of <i>Asparagus</i> L. (<i>Asparagaceae</i>): Out-of-South-Africa and multiple origins of sexual dimorphism. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 25-44.	1.2	35
69	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
70	Resolving deep relationships of PACMAD grasses: a phylogenomic approach. <i>BMC Plant Biology</i> , 2015, 15, 178.	1.6	55
71	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
72	Biodiversity comparison among phylogenetic diversity metrics and between three North American prairies. <i>Applications in Plant Sciences</i> , 2015, 3, 1400108.	0.8	21

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73	Phylogeny and photosynthesis of the grass tribe Paniceae. <i>American Journal of Botany</i> , 2015, 102, 1493-1505.	0.8	58
74	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
75	Systematics and Evolution of Inflorescence Structure in the <i>Tradescantia</i> Alliance (Commelinaceae). <i>Systematic Botany</i> , 2014, 39, 105-116.	0.2	24
76	Comparative Phylogenomics Uncovers the Impact of Symbiotic Associations on Host Genome Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004487.	1.5	229
77	A multi-step comparison of short-read full plastome sequence assembly methods in grasses. <i>Taxon</i> , 2014, 63, 899-910.	0.4	28
78	Nonadditive Gene Expression in Polyploids. <i>Annual Review of Genetics</i> , 2014, 48, 485-517.	3.2	207
79	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
80	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
81	Phylogenomics of the plant family Araceae. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 91-102.	1.2	96
82	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
83	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
84	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
85	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
86	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
87	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
88	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.	3.5	261
89	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
90	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

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91	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
92	Is DNA Alive? A Study of Conceptual Change Through Targeted Instruction. <i>Research in Science Education</i> , 2013, 43, 1361-1375.	1.4	11
93	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
94	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
95	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
96	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
97	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	1.7	73
98	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
99	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
100	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
101	Taking the Next Step: Building an <i>Arabidopsis</i> Information Portal. <i>Plant Cell</i> , 2012, 24, 2248-2256.	3.1	38
102	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. <i>New Phytologist</i> , 2012, 196, 596-605.	3.5	178
103	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	13.9	389
104	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
105	A fully resolved chloroplast phylogeny of the brassica crops and wild relatives (Brassicaceae:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.4	71
106	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
107	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
108	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

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109	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
110	Getting up to speed. <i>Current Opinion in Plant Biology</i> , 2012, 15, 111-114.	3.5	1
111	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
112	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
113	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
114	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
115	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
116	The Genomes of All Angiosperms: A Call for a Coordinated Global Census. <i>Journal of Botany</i> , 2011, 2011, 1-10.	1.2	10
117	<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
118	Are all sex chromosomes created equal?. <i>Trends in Genetics</i> , 2011, 27, 350-357.	2.9	307
119	Epigenetic regulation of flowering time in polyploids. <i>Current Opinion in Plant Biology</i> , 2011, 14, 174-178.	3.5	40
120	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
121	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
122	Exploring the complexity of tree thinking expertise in an undergraduate systematics course. <i>Science Education</i> , 2011, 95, 794-823.	1.8	53
123	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
124	Introduction to special issue on biodiversity ¹ . <i>American Journal of Botany</i> , 2011, 98, 333-335.	0.8	27
125	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
126	Structural and Functional Evolution of Resynthesized Polyploids. , 2011, , 195-214.		12

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127	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
128	Homoeologous recombination in allopolyploids: the polyploid ratchet. New Phytologist, 2010, 186, 18-28.	3.5	285
129	Preface. Cytogenetic and Genome Research, 2010, 129, 5-5.	0.6	0
130	Integration of Genetic, Physical, and Cytogenetic Maps for <i>Brassica rapa</i> Chromosome A7. Cytogenetic and Genome Research, 2010, 129, 190-198.	0.6	18
131	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
132	Introgression of B-genome chromosomes in a doubled haploid population of <i>Brassica napus</i>—<i>B. carinata</i>. Genome, 2010, 53, 619-629.	0.9	42
133	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
134	Mitotic instability in resynthesized and natural polyploids of the genus <i>Arabidopsis</i> (Brassicaceae). American Journal of Botany, 2009, 96, 1656-1664.	0.8	32
135	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
136	Complexity of genome evolution by segmental rearrangement in Brassica rapa revealed by sequence-level analysis. BMC Genomics, 2009, 10, 539.	1.2	33
137	Gene and genome duplications: the impact of dosage-sensitivity on the fate of nuclear genes. Chromosome Research, 2009, 17, 699-717.	1.0	340
138	Analysis of Gene Expression in Resynthesized Brassica napus Allopolyploids Using Arabidopsis 70mer Oligo Microarrays. PLoS ONE, 2009, 4, e4760.	1.1	64
139	A Renaissance of Cytogenetics: Studies in Polyploidy and Chromosomal Evolution. Annals of the Missouri Botanical Garden, 2008, 95, 275-281.	1.3	13
140	Rapid Chromosome Evolution in Recently Formed Polyploids in Tragopogon (Asteraceae). PLoS ONE, 2008, 3, e3353.	1.1	173
141	Genomic Changes in Resynthesized <i>Brassica napus</i> and Their Effect on Gene Expression and Phenotype. Plant Cell, 2007, 19, 3403-3417.	3.1	564
142	Genetic and physical maps around the sex-determining M-locus of the dioecious plant asparagus. Molecular Genetics and Genomics, 2007, 278, 221-234.	1.0	91
143	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
144	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). OMICS A Journal of Integrative Biology, 2006, 10, 231-237.	1.0	76

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145	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.	1.2	209
146	Repeated evolution of net venation and fleshy fruits among monocots in shaded habitats confirms a priori predictions: evidence from an <i>ndhF</i> phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1481-1490.	1.2	100
147	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
148	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
149	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
150	Flowering time divergence and genomic rearrangements in resynthesized Brassica polyploids (Brassicaceae). <i>Biological Journal of the Linnean Society</i> , 2004, 82, 675-688.	0.7	313
151	The development of an <i>Arabidopsis</i> model system for genome-wide analysis of polyploidy effects. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 689-700.	0.7	69
152	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
153	Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in <i>Arabidopsis</i> and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57.	4.1	55
154	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
155	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.	0.6	187
156	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
157	Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147.	2.9	812
158	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
159	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.	0.8	264
160	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
161	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.	0.8	183
162	Dragnet Ecology—Just the Facts, Ma'am! The Privilege of Science in a Postmodern World. <i>BioScience</i> , 2001, 51, 475.	2.2	101

#	ARTICLE	IF	CITATIONS
163	Plant systematics in the next 50 years—re-mapping the new frontier. <i>Taxon</i> , 2001, 50, 713-732.	0.4	27
164	New infraspecific names in North American Liliales. <i>Taxon</i> , 2001, 50, 201-201.	0.4	1
165	Molecular and Morphological Phylogenetic Analyses of Themidaceae (Asparagales). <i>Kew Bulletin</i> , 2001, 56, 601.	0.4	27
166	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
167	Contrasting patterns of support among plastid genes and genomes for major clades of the monocotyledons. , 0, , 315-349.		10