

Andrew H Paterson

List of Publications by Year in descending order

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341
papers

47,847
citations

2802

94
h-index

1980

206
g-index

348
all docs

348
docs citations

348
times ranked

26742
citing authors

#	ARTICLE	IF	CITATIONS
1	MCSanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. <i>Nucleic Acids Research</i> , 2012, 40, e49-e49.	14.5	4,252
2	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
3	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
4	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
5	Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. <i>Nature</i> , 1988, 335, 721-726.	27.8	1,532
6	Unravelling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events. <i>Nature</i> , 2003, 422, 433-438.	27.8	1,470
7	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
8	Synteny and Collinearity in Plant Genomes. <i>Science</i> , 2008, 320, 486-488.	12.6	1,156
9	Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.	1.7	1,031
10	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
11	Ancient polyploidization predating divergence of the cereals, and its consequences for comparative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9903-9908.	7.1	954
12	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
13	A rapid method for extraction of cotton (<i>Gossypium</i> spp.) genomic DNA suitable for RFLP or PCR analysis. <i>Plant Molecular Biology Reporter</i> , 1993, 11, 122-127.	1.8	768
14	Evolutionary Genetics of Genome Merger and Doubling in Plants. <i>Annual Review of Genetics</i> , 2008, 42, 443-461.	7.6	618
15	PGDD: a database of gene and genome duplication in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1152-D1158.	14.5	544
16	Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.	8.8	542
17	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. <i>Genome Research</i> , 2008, 18, 1944-1954.	5.5	515
18	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472

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19	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	21.4	463
20	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
21	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. <i>BMC Genomics</i> , 2014, 15, 162.	2.8	410
22	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	21.4	398
23	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.	4.8	390
24	Construction and characterization of bacterial artificial chromosome library of <i>Sorghum bicolor</i> . <i>Nucleic Acids Research</i> , 1994, 22, 4922-4931.	14.5	389
25	Finding and Comparing Syntenic Regions among <i>Arabidopsis</i> and the Outgroups <i>Papaya</i> , <i>Poplar</i> , and <i>Grape</i> : CoGe with Rosids. <i>Plant Physiology</i> , 2008, 148, 1772-1781.	4.8	376
26	Epistasis for Three Grain Yield Components in Rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 1997, 145, 453-465.	2.9	367
27	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
28	A primitive Y chromosome in papaya marks incipient sex chromosome evolution. <i>Nature</i> , 2004, 427, 348-352.	27.8	351
29	A 3347-Locus Genetic Recombination Map of Sequence-Tagged Sites Reveals Features of Genome Organization, Transmission and Evolution of Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2004, 166, 389-417.	2.9	331
30	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	9.6	329
31	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	8.9	325
32	An SNP Resource for Rice Genetics and Breeding Based on Subspecies <i>Indica</i> and <i>Japonica</i> Genome Alignments. <i>Genome Research</i> , 2004, 14, 1812-1819.	5.5	318
33	Comparative Genomics of Plant Chromosomes. <i>Plant Cell</i> , 2000, 12, 1523-1539.	6.6	301
34	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	5.7	287
35	Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . <i>Nature Communications</i> , 2013, 4, 2445.	12.8	277
36	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. <i>PLoS Genetics</i> , 2007, 3, e123.	3.5	270

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37	Angiosperm genome comparisons reveal early polyploidy in the monocot lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 472-477.	7.1	267
38	Sequencing papaya X and Y chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	7.1	264
39	QTL analysis of genotype × environment interactions affecting cotton fiber quality. <i>Theoretical and Applied Genetics</i> , 2003, 106, 384-396.	3.6	251
40	Whole-genome resequencing reveals <i>Brassica napus</i> origin and genetic loci involved in its improvement. <i>Nature Communications</i> , 2019, 10, 1154.	12.8	249
41	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	3.6	243
42	Meta-analysis of Polyploid Cotton QTL Shows Unequal Contributions of Subgenomes to a Complex Network of Genes and Gene Clusters Implicated in Lint Fiber Development. <i>Genetics</i> , 2007, 176, 2577-2588.	2.9	240
43	Chromosome evolution in eukaryotes: a multi-kingdom perspective. <i>Trends in Genetics</i> , 2005, 21, 673-682.	6.7	238
44	Draft genome of the peanut A-genome progenitor (<i>Arachis duranensis</i>) provides insights into geocarpy, oil biosynthesis, and allergens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6785-6790.	7.1	235
45	Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation in Cotton. <i>Genome Research</i> , 1998, 8, 479-492.	5.5	234
46	QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. <i>Nucleic Acids Research</i> , 2009, 37, e101-e101.	14.5	222
47	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	8.3	221
48	Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. <i>Plant Cell</i> , 2014, 26, 2792-2802.	6.6	220
49	Polymorphism and concerted evolution in a tandemly repeated gene family: 5S ribosomal DNA in diploid and allopolyploid cottons. <i>Journal of Molecular Evolution</i> , 1996, 42, 685-705.	1.8	217
50	Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372.	18.7	202
51	Toward a unified genetic map of higher plants, transcending the monocot–dicot divergence. <i>Nature Genetics</i> , 1996, 14, 380-382.	21.4	200
52	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
53	Genome and gene duplications and gene expression divergence: a view from plants. <i>Annals of the New York Academy of Sciences</i> , 2012, 1256, 1-14.	3.8	194
54	Azospirillum Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. <i>PLoS Genetics</i> , 2011, 7, e1002430.	3.5	191

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55	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. <i>Molecular Plant</i> , 2019, 12, 920-934.	8.3	185
56	A High-Density Genetic Recombination Map of Sequence-Tagged Sites for <i>Sorghum</i> , as a Framework for Comparative Structural and Evolutionary Genomics of Tropical Grains and Grasses. <i>Genetics</i> , 2003, 165, 367-386.	2.9	185
57	Application of genotyping by sequencing technology to a variety of crop breeding programs. <i>Plant Science</i> , 2016, 242, 14-22.	3.6	183
58	Many gene and domain families have convergent fates following independent whole-genome duplication events in <i>Arabidopsis</i> , <i>Oryza</i> , <i>Saccharomyces</i> and <i>Tetraodon</i> . <i>Trends in Genetics</i> , 2006, 22, 597-602.	6.7	181
59	SyMAP: A system for discovering and viewing syntenic regions of FPC maps. <i>Genome Research</i> , 2006, 16, 1159-1168.	5.5	176
60	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.	2.8	175
61	Integration of Cot Analysis, DNA Cloning, and High-Throughput Sequencing Facilitates Genome Characterization and Gene Discovery. <i>Genome Research</i> , 2002, 12, 795-807.	5.5	172
62	Buffering of crucial functions by paleologous duplicated genes may contribute cyclicity to angiosperm genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2730-2735.	7.1	168
63	Genomic Dissection of Genotype x Environment Interactions Conferring Adaptation of Cotton to Arid Conditions. <i>Genome Research</i> , 2001, 11, 1988-1995.	5.5	160
64	An EST-enriched Comparative Map of <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2000, 10, 776-788.	5.5	149
65	Transmission Genetics of Chromatin From a Synthetic Amphidiploid to Cultivated Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 823-837.	2.9	148
66	Comparative genomic analysis of C4 photosynthetic pathway evolution in grasses. <i>Genome Biology</i> , 2009, 10, R68.	9.6	144
67	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.	2.6	142
68	Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13206-13211.	7.1	141
69	Genetics of Hybrid Sterility and Hybrid Breakdown in an Interspecific Rice (<i>Oryza sativa</i> L.) Population. <i>Genetics</i> , 1997, 145, 1139-1148.	2.9	141
70	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. <i>PLoS ONE</i> , 2011, 6, e28150.	2.5	139
71	QTL Analysis in a Complex Autopolyploid: Genetic Control of Sugar Content in Sugarcane. <i>Genome Research</i> , 2001, 11, 2075-2084.	5.5	138
72	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	5.5	138

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73	<i>MCS-X</i> : detecting transposed gene duplications based on multiple colinearity scans. <i>Bioinformatics</i> , 2013, 29, 1458-1460.	4.1	137
74	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	2.8	136
75	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136
76	Title is missing!. <i>Molecular Breeding</i> , 1998, 4, 419-426.	2.1	134
77	MULTILOCUS INTERACTIONS RESTRICT GENE INTROGRESSION IN INTERSPECIFIC POPULATIONS OF POLYPLOID <i>GOSSYPIUM</i> (COTTON). <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 798-814.	2.3	133
78	High-Density Linkage Mapping Revealed Suppression of Recombination at the Sex Determination Locus in Papaya. <i>Genetics</i> , 2004, 166, 419-436.	2.9	132
79	Genome Alignment Spanning Major Poaceae Lineages Reveals Heterogeneous Evolutionary Rates and Alters Inferred Dates for Key Evolutionary Events. <i>Molecular Plant</i> , 2015, 8, 885-898.	8.3	131
80	What has QTL mapping taught us about plant domestication?. <i>New Phytologist</i> , 2002, 154, 591-608.	7.3	123
81	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017, 174, 284-300.	4.8	112
82	Crop-to-weed introgression has impacted allelic composition of johnsongrass populations with and without recent exposure to cultivated sorghum. <i>Molecular Ecology</i> , 2005, 14, 2143-2154.	3.9	111
83	Sex chromosomes in flowering plants. <i>American Journal of Botany</i> , 2007, 94, 141-150.	1.7	111
84	An integrated approach to maintaining cereal productivity under climate change. <i>Global Food Security</i> , 2016, 8, 9-18.	8.1	110
85	D-Subgenome Bias of Xcm Resistance Genes in Tetraploid <i>Gossypium</i> (Cotton) Suggests That Polyploid Formation Has Created Novel Avenues for Evolution. <i>Genetics</i> , 1998, 149, 1987-1996.	2.9	110
86	In-field High Throughput Phenotyping and Cotton Plant Growth Analysis Using LiDAR. <i>Frontiers in Plant Science</i> , 2018, 9, 16.	3.6	108
87	Genetic, Physical, and Informatics Resources for Maize. On the Road to an Integrated Map. <i>Plant Physiology</i> , 2002, 130, 1598-1605.	4.8	106
88	Comparative Population Genetics of the Panicoid Grasses: Sequence Polymorphism, Linkage Disequilibrium and Selection in a Diverse Sample of <i>Sorghum bicolor</i> . <i>Genetics</i> , 2004, 167, 471-483.	2.9	106
89	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	6.4	106
90	Grains of knowledge: Genomics of model cereals. <i>Genome Research</i> , 2005, 15, 1643-1650.	5.5	103

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91	Genetic improvement of C4 grasses as cellulosic biofuel feedstocks. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2009, 45, 291-305.	2.1	102
92	Genomics of Sorghum. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-6.	2.2	101
93	Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT / Overl	1.2	99
94	Identification of peanut (<i>Arachis hypogaea</i> L.) RAPD markers diagnostic of root-knot nematode (<i>Meloidogyne arenaria</i> (Neal) Chitwood) resistance. <i>Molecular Breeding</i> , 1996, 2, 369-379.	2.1	98
95	High throughput phenotyping of cotton plant height using depth images under field conditions. <i>Computers and Electronics in Agriculture</i> , 2016, 130, 57-68.	7.7	97
96	Genetic mapping and comparative analysis of seven mutants related to seed fiber development in cotton. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1137-1146.	3.6	94
97	Molecular dissection of interspecific variation between <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> (cotton) by a backcross-self approach: I. Fiber elongation. <i>Theoretical and Applied Genetics</i> , 2005, 111, 757-763.	3.6	94
98	Structure and evolution of cereal genomes. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 644-650.	3.3	93
99	A detailed look at 7â€fmillion years of genome evolution in a 439â€fkb contiguous sequence at the barley Hv-eIF4E locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	5.7	91
100	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.9	91
101	Polyploidy-associated genome modifications during land plant evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130355.	4.0	90
102	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (<i>Gossypium</i>). <i>Plant Journal</i> , 2007, 50, 995-1006.	5.7	89
103	Domestication and plant genomes. <i>Current Opinion in Plant Biology</i> , 2010, 13, 160-166.	7.1	89
104	Different patterns of gene structure divergence following gene duplication in Arabidopsis. <i>BMC Genomics</i> , 2013, 14, 652.	2.8	88
105	Comparative Analysis of <i>Miscanthus</i> and <i>Saccharum</i> Reveals a Shared Whole-Genome Duplication but Different Evolutionary Fates. <i>Plant Cell</i> , 2014, 26, 2420-2429.	6.6	88
106	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016, 172, 272-283.	4.8	88
107	RFLP facilitated analysis of tiller and leaf angles in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 1999, 109, 79-84.	1.2	87
108	Recombination in Avian Gamma-Coronavirus Infectious Bronchitis Virus. <i>Viruses</i> , 2011, 3, 1777-1799.	3.3	87

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109	Challenges of Detecting Directional Selection After a Bottleneck: Lessons From <i>Sorghum bicolor</i> . <i>Genetics</i> , 2006, 173, 953-964.	2.9	86
110	Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. <i>Genetics</i> , 2007, 177, 1753-1763.	2.9	85
111	Comparative Mapping of Quantitative Trait Loci Sculpting the Curd of <i>Brassica oleracea</i> . <i>Genetics</i> , 2000, 155, 1927-1954.	2.9	84
112	Molecular dissection of phenotypic variation between <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> (cotton) by a backcross-self approach: III. Fiber length. <i>Theoretical and Applied Genetics</i> , 2005, 111, 772-781.	3.6	83
113	Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization. <i>Genome Research</i> , 2009, 19, 1026-1032.	5.5	83
114	Leafing through the genomes of our major crop plants: strategies for capturing unique information. <i>Nature Reviews Genetics</i> , 2006, 7, 174-184.	16.3	82
115	Genetic map and QTL controlling fiber quality traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2015, 203, 615-628.	1.2	82
116	Toward Integration of Comparative Genetic, Physical, Diversity, and Cytomolecular Maps for Grasses and Grains, Using the Sorghum Genome as a Foundation. <i>Plant Physiology</i> , 2001, 125, 1325-1341.	4.8	81
117	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	5.5	80
118	Seventy Million Years of Concerted Evolution of a Homoeologous Chromosome Pair, in Parallel, in Major Poaceae Lineages. <i>Plant Cell</i> , 2011, 23, 27-37.	6.6	80
119	Efficient capture of unique sequences from eukaryotic genomes. <i>Trends in Genetics</i> , 2002, 18, 547-550.	6.7	78
120	Low X/Y divergence in four pairs of papaya sex-linked genes. <i>Plant Journal</i> , 2008, 53, 124-132.	5.7	78
121	Genetic analysis of inflorescence and plant height components in sorghum (Panicoidae) and comparative genetics with rice (Oryzoidae). <i>BMC Plant Biology</i> , 2015, 15, 107.	3.6	78
122	Aerial Images and Convolutional Neural Network for Cotton Bloom Detection. <i>Frontiers in Plant Science</i> , 2017, 8, 2235.	3.6	77
123	Brassica genomics: a complement to, and early beneficiary of, the Arabidopsis sequence. <i>Genome Biology</i> , 2001, 2, reviews1011.1.	9.6	74
124	Ploidy, evolutionary opportunity, and crop adaptation. <i>Genetica</i> , 2005, 123, 191-196.	1.1	73
125	Molecular dissection of interspecific variation between <i>Gossypium hirsutum</i> and <i>G. barbadense</i> (cotton) by a backcross-self approach: II. Fiber fineness. <i>Theoretical and Applied Genetics</i> , 2005, 111, 764-771.	3.6	72
126	Ancient Gene Duplicates in <i>Gossypium</i> (Cotton) Exhibit Near-Complete Expression Divergence. <i>Genome Biology and Evolution</i> , 2014, 6, 559-571.	2.5	72

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127	Genome-Wide High-Resolution Mapping by Recurrent Interbreeding Using <i>Arabidopsis thaliana</i> as a Model. <i>Genetics</i> , 1996, 142, 247-258.	2.9	72
128	Equilibrium Processes Cannot Explain High Levels of Short- and Medium-Range Linkage Disequilibrium in the Domesticated Grass <i>Sorghum bicolor</i> . <i>Genetics</i> , 2005, 171, 1247-1256.	2.9	71
129	Chromosome structural changes in diploid and tetraploid A genomes of <i>Gossypium</i> . <i>Genome</i> , 2006, 49, 336-345.	2.0	71
130	Molecular Markers for the Classification of Switchgrass (<i>Panicum virgatum</i> L.) Germplasm and to Assess Genetic Diversity in Three Synthetic Switchgrass Populations. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1291-1302.	1.6	71
131	In-Field High-Throughput Phenotyping of Cotton Plant Height Using LiDAR. <i>Remote Sensing</i> , 2017, 9, 377.	4.0	70
132	Cotton genetic resources. A review. <i>Agronomy for Sustainable Development</i> , 2012, 32, 419-432.	5.3	69
133	Comparative Analysis of Serine/Arginine-Rich Proteins across 27 Eukaryotes: Insights into Sub-Family Classification and Extent of Alternative Splicing. <i>PLoS ONE</i> , 2011, 6, e24542.	2.5	69
134	Identifying QTL for fiber quality traits with three upland cotton (<i>Gossypium hirsutum</i> L.) populations. <i>Euphytica</i> , 2014, 198, 43-58.	1.2	67
135	Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. <i>Plant Physiology</i> , 2005, 139, 869-884.	4.8	66
136	Comparative genomic deconvolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. <i>New Phytologist</i> , 2016, 209, 1252-1263.	7.3	65
137	Comparative analysis of QTLs affecting plant height and flowering among closely-related diploid and polyploid genomes. <i>Genome</i> , 2002, 45, 794-803.	2.0	64
138	Pedigree vs. DNA Marker-Based Genetic Similarity Estimates in Cotton. <i>Crop Science</i> , 2005, 45, 2281-2287.	1.8	64
139	Telomere-centric genome repatterning determines recurring chromosome number reductions during the evolution of eukaryotes. <i>New Phytologist</i> , 2015, 205, 378-389.	7.3	64
140	Genetic and transcriptomic analyses of lignin- and lodging-related traits in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 1961-1973.	3.6	64
141	QTL mapping of naturally-occurring variation in flowering time of <i>Arabidopsis thaliana</i> . <i>Molecular Genetics and Genomics</i> , 1994, 245, 548-555.	2.4	63
142	Comparative analysis of peanut NBS-LRR gene clusters suggests evolutionary innovation among duplicated domains and erosion of gene microsynteny. <i>New Phytologist</i> , 2011, 192, 164-178.	7.3	63
143	Functional Classification, Genomic Organization, Putatively cis-Acting Regulatory Elements, and Relationship to Quantitative Trait Loci, of Sorghum Genes with Rhizome-Enriched Expression. <i>Plant Physiology</i> , 2006, 142, 1148-1159.	4.8	62
144	Recent Origin of Dioecious and Gynodioecious Y Chromosomes in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 49-57.	1.9	62

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145	Three-dimensional photogrammetric mapping of cotton bolls in situ based on point cloud segmentation and clustering. <i>ISPRS Journal of Photogrammetry and Remote Sensing</i> , 2020, 160, 195-207.	11.1	62
146	The celery genome sequence reveals sequential paleo-polyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	8.3	62
147	Parallel up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (<i>Gossypium</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21152-21157.	7.1	61
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