Andrew H Paterson

List of Publications by Year
in descending order

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341 papers	47,847 citations	3264 94 h-index	2289 206 g-index
348 all docs	348 docs citations	348 times ranked	29593 citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation underlying kernel size, shape, and color in two interspecific S. bicolor2â€‰Ã—â€‰S. halepense subpopulations. Genetic Resources and Crop Evolution, 2022, 69, 1261-1281.	0.8	1
2	GC content of plant genes is linked to past gene duplications. PLoS ONE, 2022, 17, e0261748.	1.1	6
3	Pyramiding novel EMS-generated mutant alleles to improve fiber quality components of elite upland cotton germplasm. Industrial Crops and Products, 2022, 178, 114594.	2.5	4
4	High-density genetic map and genome-wide association studies of aesthetic traits in Phalaenopsis orchids. Scientific Reports, 2022, 12, 3346.	1.6	6
5	Unraveling the genetic components of perenniality: Toward breeding for perennial grains. Plants People Planet, 2022, 4, 367-381.	1.6	2
6	Improved Upland Cotton Germplasm for Multiple Fiber Traits Mediated by Transferring and Pyramiding Novel Alleles From Ethyl Methanesulfonate-Generated Mutant Lines Into Elite Genotypes. Frontiers in Plant Science, 2022, 13, 842741.	1.7	5
7	Pervasive genome duplications across the plant tree of life and their links to major evolutionary innovations and transitions. Computational and Structural Biotechnology Journal, 2022, 20, 3248-3256.	1.9	10
8	Exploiting genetic variation from unadapted germplasmâ€"An example from improvement of sorghum in Ethiopia. Plants People Planet, 2022, 4, 523-536.	1.6	1
9	The celery genome sequence reveals sequential paleoâ€polyploidizations, karyotype evolution and resistance gene reduction in apiales. Plant Biotechnology Journal, 2021, 19, 731-744.	4.1	62
10	Detection of quantitative trait loci regulating seed yield potential in two interspecific S. bicolor2â€‰Ã—â€‰S. halepense subpopulations. Euphytica, 2021, 217, 1.	0.6	3
11	Genome sequence and evolution of<i>Betula platyphylla</i>. Horticulture Research, 2021, 8, 37.	2.9	53
12	Loquat (Eriobotrya japonica (Thunb.) Lindl) population genomics suggests a twoâ€staged domestication and identifies genes showing convergence/parallel selective sweeps with apple or peach. Plant Journal, 2021, 106, 942-952.	2.8	2
13	Genetic diversity, population structure, and selection signature in Ethiopian sorghum [<i>Sorghum bicolor</i> L. (Moench)] germplasm. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	13
14	Chromosome number is key to longevity of polyploid lineages. New Phytologist, 2021, 231, 19-28.	3.5	14
15	Comparative evolution of vegetative branching in sorghum. PLoS ONE, 2021, 16, e0255922.	1.1	1
16	High resolution 3D terrestrial LiDAR for cotton plant main stalk and node detection. Computers and Electronics in Agriculture, 2021, 187, 106276.	3.7	18
17	Quantitative trait mapping of plant architecture in two BC1F2 populations of Sorghum Bicolor Ã— S. halepense and comparisons to two other sorghum populations. Theoretical and Applied Genetics, 2021, 134, 1185-1200.	1.8	6
18	Evaluation and Genetic Analysis of a Segregating Sorghum Population under Moisture Stress Conditions. Journal of Crop Science and Biotechnology, 2020, 23, 29-38.	0.7	4

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19	Three-dimensional photogrammetric mapping of cotton bolls in situ based on point cloud segmentation and clustering. ISPRS Journal of Photogrammetry and Remote Sensing, 2020, 160, 195-207.	4.9	62
20	Deciphering the highâ€quality genome sequence of coriander that causes controversial feelings. Plant Biotechnology Journal, 2020, 18, 1444-1456.	4.1	56
21	Genetic Analysis of Stem Diameter and Water Contents To Improve Sorghum Bioenergy Efficiency. G3: Genes, Genomes, Genetics, 2020, 10, 3991-4000.	0.8	10
22	Paleo-polyploidization in Lycophytes. Genomics, Proteomics and Bioinformatics, 2020, 18, 333-340.	3.0	16
23	Transmission Genetics of a Sorghum bicolor Ã— S. halepense Backcross Populations. Frontiers in Plant Science, 2020, 11, 467.	1.7	10
24	Reply to: Evaluating two different models of peanutâ€™s origin. Nature Genetics, 2020, 52, 560-563.	9.4	8
25	The Evolution of an Invasive Plant, Sorghum halepense L. (â€˜Johnsongrassâ€™). Frontiers in Genetics, 2020, 11, 317.	1.1	30
26	Validation of QTLs for Fiber Quality Introgressed from <i>Gossypium mustelinum</i> by Selective Genotyping. G3: Genes, Genomes, Genetics, 2020, 10, 2377-2384.	0.8	7
27	GaHD1, a candidate gene for the Gossypium arboreum SMA-4 mutant, promotes trichome and fiber initiation by cellular H2O2 and Ca2+ signals. Plant Molecular Biology, 2020, 103, 409-423.	2.0	15
28	Registration of eight upland cotton (Gossypium hirsutumL.) germplasm lines withqFLâ€Chr.25, a fiberâ€length QTL introgressed fromGossypium barbadense. Journal of Plant Registrations, 2020, 14, 57-63.	0.4	1
29	Agro-morphological diversity of Ethiopian sorghum [Sorghum bicolor (L.) Moench] landraces under water limited environments. Genetic Resources and Crop Evolution, 2020, 67, 2149-2160.	0.8	10
30	Ground Based Hyperspectral Imaging to Characterize Canopy-Level Photosynthetic Activities. Remote Sensing, 2020, 12, 315.	1.8	8
31	Preferential gene retention increases the robustness of cold regulation in Brassicaceae and other plants after polyploidization. Horticulture Research, 2020, 7, 20.	2.9	47
32	The <i>Ligon lintless</i><i>-2</i> Short Fiber Mutation Is Located within a Terminal Deletion of Chromosome 18 in Cotton. Plant Physiology, 2020, 183, 277-288.	2.3	17
33	Genetic Analysis of the Transition from Wild to Domesticated Cotton (<i>Gossypium hirsutum</i>L.). G3: Genes, Genomes, Genetics, 2020, 10, 731-754.	0.8	14
34	Image processing algorithms for infield single cotton boll counting and yield prediction. Computers and Electronics in Agriculture, 2019, 166, 104976.	3.7	38
35	Joint QTL mapping and transcriptome sequencing analysis reveal candidate flowering time genes in Brassica napus L. BMC Genomics, 2019, 20, 21.	1.2	44
36	Polyploidy Index and Its Implications for the Evolution of Polyploids. Frontiers in Genetics, 2019, 10, 807.	1.1	29

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37	Molecular Dissection of Quantitative Variation in Bermudagrass Hybrids (<i>Cynodon) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 74 2581-2596.	0.8	5
38	Genetic Evaluation of Exotic Chromatins from Two Obsolete Interspecific Introgression Lines of Upland Cotton for Fiber Quality Improvement. Crop Science, 2019, 59, 1073-1084.	0.8	8
39	Sequencing of Cultivated Peanut, Arachis hypogaea, Yields Insights into Genome Evolution and Oil Improvement. Molecular Plant, 2019, 12, 920-934.	3.9	185
40	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. Nature Genetics, 2019, 51, 865-876.	9.4	398
41	Whole-genome resequencing reveals Brassica napus origin and genetic loci involved in its improvement. Nature Communications, 2019, 10, 1154.	5.8	249
42	Multispectral imaging and unmanned aerial systems for cotton plant phenotyping. PLoS ONE, 2019, 14, e0205083.	1.1	55
43	Gene duplication and evolution in recurring polyploidizationâ€“diploidization cycles in plants. Genome Biology, 2019, 20, 38.	3.8	542
44	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 2019, 8, .	3.3	106
45	Evaluation of a Chromosome Segment from G<i>ossypium barbadense</i> Harboring the Fiber Length QTL <i>qFLâ€Chr.25</i> in Four Diverse Upland Cotton Genetic Backgrounds. Crop Science, 2019, 59, 2621-2633.	0.8	4
46	Registration of GA R01â€40â€08, a <i>Gossypium hirsutum</i> Upland Cotton Germplasm Line with <i>qFLâ€Chr.1</i> Introgressed from <i>Gossypium barbadense</i> Conferring Improved Fiber Length. Journal of Plant Registrations, 2019, 13, 406-410.	0.4	1
47	Gene duplication and genetic innovation in cereal genomes. Genome Research, 2019, 29, 261-269.	2.4	29
48	Genome and evolution of the shadeâ€requiring medicinal herb <i>Panax ginseng</i>. Plant Biotechnology Journal, 2018, 16, 1904-1917.	4.1	136
49	High proportion of diploid hybrids produced by interspecific diploidÂÃ—Âtetraploid Sorghum hybridization. Genetic Resources and Crop Evolution, 2018, 65, 387-390.	0.8	13
50	Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L.. Nature Genetics, 2018, 50, 1565-1573.	9.4	463
51	Genetic Analysis of Gossypium Fiber Quality Traits in Reciprocal Advanced Backcross Populations. Plant Genome, 2018, 11, 170057.	1.6	15
52	Development of Perennial Grain Sorghum. Sustainability, 2018, 10, 172.	1.6	50
53	The Rise of Cotton Genomics. Trends in Plant Science, 2018, 23, 953-955.	4.3	16
54	In-field High Throughput Phenotyping and Cotton Plant Growth Analysis Using LiDAR. Frontiers in Plant Science, 2018, 9, 16.	1.7	108

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55	Genotyping by Sequencing of 393 <i>Sorghum bicolor</i> BTx623 Ã— IS3620C Recombinant Inbred Lines Improves Sensitivity and Resolution of QTL Detection. G3: Genes, Genomes, Genetics, 2018, 8, 2563-2572.	0.8	28
56	Cross-taxon application of sugarcane EST-SSR to genetic diversity analysis of bermudagrass (Cynodon) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	9
57	Keen insights from quinoa. Nature, 2017, 542, 300-302.	13.7	3
58	Targeted identification of association between cotton fiber quality traits and microsatellite markers. Euphytica, 2017, 213, 1.	0.6	6
59	Genetic and transcriptomic analyses of lignin- and lodging-related traits in Brassica napus. Theoretical and Applied Genetics, 2017, 130, 1961-1973.	1.8	64
60	Fine mapping and candidate gene analysis of qFL-chr1, a fiber length QTL in cotton. Theoretical and Applied Genetics, 2017, 130, 1309-1319.	1.8	33
61	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. Plant Physiology, 2017, 174, 284-300.	2.3	112
62	QTL analysis of cotton fiber length in advanced backcross populations derived from a cross between Gossypium hirsutum and G. mustelinum. Theoretical and Applied Genetics, 2017, 130, 1297-1308.	1.8	36
63	Comparative genetic variation of fiber quality traits in reciprocal advanced backcross populations. Euphytica, 2017, 213, 1.	0.6	9
64	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotechnology, 2017, 35, 969-976.	9.4	356
65	Segregation distortion and genome-wide digenic interactions affect transmission of introgressed chromatin from wild cotton species. Theoretical and Applied Genetics, 2017, 130, 2219-2230.	1.8	10
66	SSR-enriched genetic linkage maps of bermudagrass (Cynodon dactylonÂÃ—Âtransvaalensis), and their comparison with allied plant genomes. Theoretical and Applied Genetics, 2017, 130, 819-839.	1.8	12
67	Identification and Characterization of miRNA Transcriptome in Asiatic Cotton (Gossypium arboreum) Using High Throughput Sequencing. Frontiers in Plant Science, 2017, 8, 969.	1.7	15
68	Advanced Backcross QTL Analysis of Fiber Strength and Fineness in a Cross between Gossypium hirsutum and G. mustelinum. Frontiers in Plant Science, 2017, 8, 1848.	1.7	20
69	In-Field High-Throughput Phenotyping of Cotton Plant Height Using LiDAR. Remote Sensing, 2017, 9, 377.	1.8	70
70	Aerial Images and Convolutional Neural Network for Cotton Bloom Detection. Frontiers in Plant Science, 2017, 8, 2235.	1.7	77
71	Plant Genome Duplication Database. Methods in Molecular Biology, 2017, 1533, 267-277.	0.4	30
72	Segregation distortion and genome-wide digenic interactions affect transmission of introgressed chromatin from wild cotton species. , 2017, 130, 2219.		1

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73	CSGRqtl: A Comparative Quantitative Trait Locus Database for Saccharinae Grasses. Methods in Molecular Biology, 2017, 1533, 257-266.	0.4	0
74	Comparative genomic deâ€convolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. New Phytologist, 2016, 209, 1252-1263.	3.5	65
75	Reconstructing changes in the genotype, phenotype, and climatic niche of an introduced species. Ecography, 2016, 39, 894-903.	2.1	14
76	Evidence for fine-scale habitat specialisation in an invasive weed. Journal of Plant Ecology, 2016, , rtw124.	1.2	3
77	Comparative transmission genetics of introgressed chromatin in Gossypium (cotton) polyploids. American Journal of Botany, 2016, 103, 719-729.	0.8	14
78	Global agricultural intensification during climate change: a role for genomics. Plant Biotechnology Journal, 2016, 14, 1095-1098.	4.1	221
79	A Genetic Map Between<i>Gossypium hirsutum</i>and the Brazilian Endemic<i>G. mustelinum</i>and Its Application to QTL Mapping. G3: Genes, Genomes, Genetics, 2016, 6, 1673-1685.	0.8	19
80	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). Plant Physiology, 2016, 172, 272-283.	2.3	88
81	Two Paleo-Hexaploidies Underlie Formation of Modern Solanaceae Genome Structure. Compendium of Plant Genomes, 2016, , 201-216.	0.3	0
82	The Evolution of Photoperiod-Insensitive Flowering in Sorghum, A Genomic Model for Panicoid Grasses. Molecular Biology and Evolution, 2016, 33, 2417-2428.	3.5	42
83	High throughput phenotyping of cotton plant height using depth images under field conditions. Computers and Electronics in Agriculture, 2016, 130, 57-68.	3.7	97
84	Advanced Backcross Quantitative Trait Locus Analysis of Fiber Elongation in a Cross between <i>Gossypium hirsutum</i> and <i>G. mustelinum</i>. Crop Science, 2016, 56, 1760-1768.	0.8	12
85	EMS-mutated cotton populations suggest overlapping genetic control of trichome and lint fiber variation. Euphytica, 2016, 208, 597-608.	0.6	8
86	Draft genome of the peanut A-genome progenitor (<i>Arachis duranensis</i>) provides insights into geocarpy, oil biosynthesis, and allergens. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6785-6790.	3.3	235
87	An integrated approach to maintaining cereal productivity under climate change. Global Food Security, 2016, 8, 9-18.	4.0	110
88	Application of genotyping by sequencing technology to a variety of crop breeding programs. Plant Science, 2016, 242, 14-22.	1.7	183
89	Large-Scale Gene Relocations following an Ancient Genome Triplication Associated with the Diversification of Core Eudicots. PLoS ONE, 2016, 11, e0155637.	1.1	19
90	Multi-Phase US Spread and Habitat Switching of a Post-Columbian Invasive, Sorghum halepense. PLoS ONE, 2016, 11, e0164584.	1.1	28

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91	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	1.7	243
92	Estimating genetic diversity among selected cotton genotypes and the identificationof DNA markers associated with resistance to cotton leaf curl disease. Turkish Journal of Botany, 2015, 39, 1033-1041.	0.5	11
93	Comparative Genetics of Seed Size Traits in Divergent Cereal Lineages Represented by Sorghum (Panicoidae) and Rice (Oryzoidae). G3: Genes, Genomes, Genetics, 2015, 5, 1117-1128.	0.8	45
94	Genetic analysis of inflorescence and plant height components in sorghum (Panicoidae) and comparative genetics with rice (Oryzoidae). BMC Plant Biology, 2015, 15, 107.	1.6	78
95	Genetic analysis of rhizomatousness and its relationship with vegetative branching of recombinant inbred lines of <i>Sorghum bicolor</i> Ã— <i>S. propinquum</i>. American Journal of Botany, 2015, 102, 718-724.	0.8	31
96	Genome Alignment Spanning Major Poaceae Lineages Reveals Heterogeneous Evolutionary Rates and Alters Inferred Dates for Key Evolutionary Events. Molecular Plant, 2015, 8, 885-898.	3.9	131
97	Unraveling the fabric of polyploidy. Nature Biotechnology, 2015, 33, 491-493.	9.4	17
98	Genetic map and QTL controlling fiber quality traits in upland cotton (Gossypium hirsutum L.). Euphytica, 2015, 203, 615-628.	0.6	82
99	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	9.4	472
100	Comparative Analysis of Gene Conversion Between Duplicated Regions in Brassica rapa and B. oleracea Genomes. Compendium of Plant Genomes, 2015, , 121-129.	0.3	3
101	The Hairless Stem Phenotype of Cotton (<i>Gossypium barbadense</i>) Is Linked to a <i>Copia</i>-Like Retrotransposon Insertion in a <i>Homeodomain-Leucine Zipper</i> Gene (<i>HD1</i>). Genetics, 2015, 201, 143-154.	1.2	33
102	Telomereâ€centric genome repatterning determines recurring chromosome number reductions during the evolution of eukaryotes. New Phytologist, 2015, 205, 378-389.	3.5	64
103	Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Overlo	0.6	99
104	Genetic analysis of vegetative branching in sorghum. Theoretical and Applied Genetics, 2014, 127, 2387-2403.	1.8	35
105	Insights into the Common Ancestor of Eudicots. Advances in Botanical Research, 2014, 69, 137-174.	0.5	1
106	Synthetic Haplotypes, Species, Karyotypes, and Protoorganisms?. Advances in Botanical Research, 2014, 69, 363-376.	0.5	0
107	A Backdrop. Advances in Botanical Research, 2014, 69, 1-11.	0.5	2
108	Comparative and Evolutionary Analysis of Major Peanut Allergen Gene Families. Genome Biology and Evolution, 2014, 6, 2468-2488.	1.1	15

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109	Ancient Gene Duplicates in Gossypium (Cotton) Exhibit Near-Complete Expression Divergence. Genome Biology and Evolution, 2014, 6, 559-571.	1.1	72
110	Introgression of homeologous quantitative trait loci (QTLs) for resistance to the root-knot nematode [Meloidogyne arenaria (Neal) Chitwood] in an advanced backcross-QTL population of peanut (Arachis hypogaea L.). Molecular Breeding, 2014, 34, 393-406.	1.0	39
111	Extensive and Biased Intergenomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, <i>Gossypium</i> (Cotton). Genetics, 2014, 197, 1153-1163.	1.2	51
112	Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. Plant Cell, 2014, 26, 2792-2802.	3.1	220
113	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	1.2	136
114	Polyploidy-associated genome modifications during land plant evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130355.	1.8	90
115	Alleles conferring improved fiber quality from EMS mutagenesis of elite cotton genotypes. Theoretical and Applied Genetics, 2014, 127, 821-830.	1.8	21
116	Identifying QTL for fiber quality traits with three upland cotton (Gossypium hirsutum L.) populations. Euphytica, 2014, 198, 43-58.	0.6	67
117	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. BMC Genomics, 2014, 15, 162.	1.2	410
118	Sequencing of transcriptomes from two Miscanthus species reveals functional specificity in rhizomes, and clarifies evolutionary relationships. BMC Plant Biology, 2014, 14, 134.	1.6	17
119	Comparative Analysis of <i>Miscanthus</i> and <i>Saccharum</i> Reveals a Shared Whole-Genome Duplication but Different Evolutionary Fates. Plant Cell, 2014, 26, 2420-2429.	3.1	88
120	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. Science, 2014, 345, 950-953.	6.0	2,089
121	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	5.8	918
122	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. Genome Biology, 2014, 15, R77.	13.9	456
123	Gene body methylation shows distinct patterns associated with different gene origins and duplication modes and has a heterogeneous relationship with gene expression in <i>Oryza sativa</i> (rice). New Phytologist, 2013, 198, 274-283.	3.5	57
124	Quantitative models of hydrolysis conversion efficiency and biomass crystallinity index for plant breeding. Plant Breeding, 2013, 132, 252-258.	1.0	6
125	The repetitive component of the A genome of peanut (Arachis hypogaea) and its role in remodelling intergenic sequence space since its evolutionary divergence from the B genome. Annals of Botany, 2013, 112, 545-559.	1.4	30
126	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	13.9	329

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127	Different patterns of gene structure divergence following gene duplication in Arabidopsis. BMC Genomics, 2013, 14, 652.	1.2	88
128	A proposal to use gamete cycling in vitro to improve crops and livestock. Nature Biotechnology, 2013, 31, 877-880.	9.4	5
129	The Sorghum Genome Sequence: A Core Resource for Saccharinae Genomics. , 2013, , 105-119.		1
130	A genome-wide BAC end-sequence survey of sugarcane elucidates genome composition, and identifies BACs covering much of the euchromatin. Plant Molecular Biology, 2013, 81, 139-147.	2.0	26
131	Tissue specific analysis of bioconversion traits in the bioenergy grass Sorghum bicolor. Industrial Crops and Products, 2013, 50, 118-130.	2.5	7
132	Comparative Genomics of Grasses: A Saccharinae-Centric View. , 2013, , 429-445.		1
133	Comparative Genomic Analysis of C4 Photosynthesis Pathway Evolution in Grasses. , 2013, , 447-477.		4
134	Synthesis: Fundamental Insights and Practical Applications from the Saccharinae Clade. , 2013, , 541-549.		0
135	Genome Sequencing and Comparative Genomics in Cereals. , 2013, , 101-126.		0
136	Biofuel and energy crops: high-yield Saccharinae take center stage in the post-genomics era. Genome Biology, 2013, 14, 210.	3.8	27
137	Cot-based sampling of genomes for polymorphic low-copy DNA. Molecular Breeding, 2013, 32, 977-980.	1.0	0
138	Identification of bioconversion quantitative trait loci in the interspecific cross Sorghum bicolorÂÃ—ÂSorghum propinquum. Theoretical and Applied Genetics, 2013, 126, 2367-2380.	1.8	13
139	<i>MCScanX-transposed</i>: detecting transposed gene duplications based on multiple colinearity scans. Bioinformatics, 2013, 29, 1458-1460.	1.8	137
140	A Whole-Genome DNA Marker Map for Cotton Based on the D-Genome Sequence of <i>Gossypium raimondii</i> L.. G3: Genes, Genomes, Genetics, 2013, 3, 1759-1767.	0.8	34
141	Genetic Analysis of Recombinant Inbred Lines for<i>Sorghum bicolor Ã— Sorghum propinquum</i>. G3: Genes, Genomes, Genetics, 2013, 3, 101-108.	0.8	43
142	Seed shattering in a wild sorghum is conferred by a locus unrelated to domestication. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15824-15829.	3.3	59
143	Draft genome sequence of the mulberry tree Morus notabilis. Nature Communications, 2013, 4, 2445.	5.8	277
144	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants Â Â. Plant Physiology, 2013, 162, 769-778.	2.3	44

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145	CSGRqtl, a Comparative Quantitative Trait Locus Database for Saccharinae Grasses. Plant Physiology, 2013, 161, 594-599.	2.3	37
146	Mapping and Validation of Fiber Strength Quantitative Trait Loci on Chromosome 24 in Upland Cotton. Crop Science, 2012, 52, 1115-1122.	0.8	23
147	The Cytonuclear Dimension of Allopolyploid Evolution: An Example from Cotton Using Rubisco. Molecular Biology and Evolution, 2012, 29, 3023-3036.	3.5	59
148	MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Research, 2012, 40, e49-e49.	6.5	4,252
149	PGDD: a database of gene and genome duplication in plants. Nucleic Acids Research, 2012, 41, D1152-D1158.	6.5	544
150	Rapid divergence and expansion of the X chromosome in papaya. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13716-13721.	3.3	52
151	Sequencing papaya X and Y ^h chromosomes reveals molecular basis of incipient sex chromosome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13710-13715.	3.3	264
152	Association analysis of photoperiodic flowering time genes in west and central African sorghum [Sorghum bicolor (L.) Moench]. BMC Plant Biology, 2012, 12, 32.	1.6	30
153	Genomes for jeans: cotton genomics for engineering superior fiber. Trends in Biotechnology, 2012, 30, 521-527.	4.9	30
154	Ancient and Recent Polyploidy in Monocots. , 2012, , 93-108.		18
155	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	13.7	1,204
156	Cotton genetic resources. A review. Agronomy for Sustainable Development, 2012, 32, 419-432.	2.2	69
157	SSR-based genetic maps of Miscanthus sinensis and M. sacchariflorus, and their comparison to sorghum. Theoretical and Applied Genetics, 2012, 124, 1325-1338.	1.8	57
158	Genome of papaya, a fast growing tropical fruit tree. Tree Genetics and Genomes, 2012, 8, 445-462.	0.6	21
159	Analysis of Crystallinity Index and Hydrolysis Rates in the Bioenergy Crop Sorghum bicolor. Bioenergy Research, 2012, 5, 387-397.	2.2	37
160	Genome and gene duplications and gene expression divergence: a view from plants. Annals of the New York Academy of Sciences, 2012, 1256, 1-14.	1.8	194
161	Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the Arachis Aâ€“B genome divergence. Molecular Genetics and Genomics, 2012, 287, 21-38.	1.0	43
162	Inference of subgenomic origin of BACs in an interspecific hybrid sugarcane cultivar by overlapping oligonucleotide hybridizations. Genome, 2011, 54, 727-737.	0.9	7

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163	Use of diversity arrays technology markers for integration into a cotton reference map and anchoring to a recombinant inbred line map. Genome, 2011, 54, 349-359.	0.9	5
164	A physical map for the Amborella trichopoda genome sheds light on the evolution of angiosperm genome structure. Genome Biology, 2011, 12, R48.	13.9	28
165	Attenuated live vaccine usage affects accurate measures of virus diversity and mutation rates in avian coronavirus infectious bronchitis virus. Virus Research, 2011, 158, 225-234.	1.1	48
166	Comparative analysis of Gossypium and Vitis genomes indicates genome duplication specific to the Gossypium lineage. Genomics, 2011, 97, 313-320.	1.3	20
167	Azospirillum Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. PLoS Genetics, 2011, 7, e1002430.	1.5	191
168	Efficacy of <i>qFLâ€chr1</i>, a Quantitative Trait Locus for Fiber Length in Cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	21
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