

Andrew H Paterson

List of Publications by Year in descending order

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341
papers

47,847
citations

2795

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g-index

348
all docs

348
docs citations

348
times ranked

26742
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation underlying kernel size, shape, and color in two interspecific <i>S. bicolor</i> – <i>S. halepense</i> subpopulations. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1261-1281.	0.8	1
2	GC content of plant genes is linked to past gene duplications. <i>PLoS ONE</i> , 2022, 17, e0261748.	1.1	6
3	Pyramiding novel EMS-generated mutant alleles to improve fiber quality components of elite upland cotton germplasm. <i>Industrial Crops and Products</i> , 2022, 178, 114594.	2.5	4
4	High-density genetic map and genome-wide association studies of aesthetic traits in <i>Phalaenopsis</i> orchids. <i>Scientific Reports</i> , 2022, 12, 3346.	1.6	6
5	Unraveling the genetic components of perenniality: Toward breeding for perennial grains. <i>Plants People Planet</i> , 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. <i>Frontiers in Plant Science</i> , 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. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3248-3256.	1.9	10
8	Exploiting genetic variation from unadapted germplasm—An example from improvement of sorghum in Ethiopia. <i>Plants People Planet</i> , 2022, 4, 523-536.	1.6	1
9	The celery genome sequence reveals sequential paleopolyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	4.1	62
10	Detection of quantitative trait loci regulating seed yield potential in two interspecific <i>S. bicolor</i> – <i>S. halepense</i> subpopulations. <i>Euphytica</i> , 2021, 217, 1.	0.6	3
11	Genome sequence and evolution of <i>Betula platyphylla</i> . <i>Horticulture Research</i> , 2021, 8, 37.	2.9	53
12	Loquat (<i>Eriobotrya japonica</i> (Thunb.) Lindl) population genomics suggests a two-staged domestication and identifies genes showing convergence/parallel selective sweeps with apple or peach. <i>Plant Journal</i> , 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. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
14	Chromosome number is key to longevity of polyploid lineages. <i>New Phytologist</i> , 2021, 231, 19-28.	3.5	14
15	Comparative evolution of vegetative branching in sorghum. <i>PLoS ONE</i> , 2021, 16, e0255922.	1.1	1
16	High resolution 3D terrestrial LiDAR for cotton plant main stalk and node detection. <i>Computers and Electronics in Agriculture</i> , 2021, 187, 106276.	3.7	18
17	Quantitative trait mapping of plant architecture in two BC1F2 populations of Sorghum Bicolor – <i>S. halepense</i> and comparisons to two other sorghum populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1185-1200.	1.8	6
18	Evaluation and Genetic Analysis of a Segregating Sorghum Population under Moisture Stress Conditions. <i>Journal of Crop Science and Biotechnology</i> , 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. <i>ISPRS Journal of Photogrammetry and Remote Sensing</i> , 2020, 160, 195-207.	4.9	62
20	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 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. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 333-340.	3.0	16
23	Transmission Genetics of a Sorghum bicolor × S. halepense Backcross Populations. <i>Frontiers in Plant Science</i> , 2020, 11, 467.	1.7	10
24	Reply to: Evaluating two different models of peanut's origin. <i>Nature Genetics</i> , 2020, 52, 560-563.	9.4	8
25	The Evolution of an Invasive Plant, Sorghum halepense L. (Johnsongrass). <i>Frontiers in Genetics</i> , 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 <i>Gossypium arboreum</i> SMA-4 mutant, promotes trichome and fiber initiation by cellular H ₂ O ₂ and Ca ²⁺ signals. <i>Plant Molecular Biology</i> , 2020, 103, 409-423.	2.0	15
28	Registration of eight upland cotton (<i>Gossypium hirsutum</i> L.) germplasm lines with qFL _{chr25} , a fiber length QTL introgressed from <i>Gossypium barbadense</i> . <i>Journal of Plant Registrations</i> , 2020, 14, 57-63.	0.4	1
29	Agro-morphological diversity of Ethiopian sorghum [<i>Sorghum bicolor</i> (L.) Moench] landraces under water limited environments. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 2149-2160.	0.8	10
30	Ground Based Hyperspectral Imaging to Characterize Canopy-Level Photosynthetic Activities. <i>Remote Sensing</i> , 2020, 12, 315.	1.8	8
31	Preferential gene retention increases the robustness of cold regulation in Brassicaceae and other plants after polyploidization. <i>Horticulture Research</i> , 2020, 7, 20.	2.9	47
32	The <i>Ligon lintless-2</i> Short Fiber Mutation Is Located within a Terminal Deletion of Chromosome 18 in Cotton. <i>Plant Physiology</i> , 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. <i>Computers and Electronics in Agriculture</i> , 2019, 166, 104976.	3.7	38
35	Joint QTL mapping and transcriptome sequencing analysis reveal candidate flowering time genes in <i>Brassica napus</i> L. <i>BMC Genomics</i> , 2019, 20, 21.	1.2	44
36	Polyploidy Index and Its Implications for the Evolution of Polyploids. <i>Frontiers in Genetics</i> , 2019, 10, 807.	1.1	29

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37	Molecular Dissection of Quantitative Variation in Bermudagrass Hybrids (<i>Cynodon</i>) 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. <i>Crop Science</i> , 2019, 59, 1073-1084.	0.8	8
39	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. <i>Molecular Plant</i> , 2019, 12, 920-934.	3.9	185
40	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
41	Whole-genome resequencing reveals <i>Brassica napus</i> origin and genetic loci involved in its improvement. <i>Nature Communications</i> , 2019, 10, 1154.	5.8	249
42	Multispectral imaging and unmanned aerial systems for cotton plant phenotyping. <i>PLoS ONE</i> , 2019, 14, e0205083.	1.1	55
43	Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 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. <i>GigaScience</i> , 2019, 8, .	3.3	106
45	Evaluation of a Chromosome Segment from <i>Gossypium barbadense</i> Harboring the Fiber Length QTL <i>qFL</i> – <i>Chr.25</i> in Four Diverse Upland Cotton Genetic Backgrounds. <i>Crop Science</i> , 2019, 59, 2621-2633.	0.8	4
46	Registration of GA R01–40–08, a <i>Gossypium hirsutum</i> Upland Cotton Germplasm Line with <i>qFL</i> – <i>Chr.1</i> Introgressed from <i>Gossypium barbadense</i> Conferring Improved Fiber Length. <i>Journal of Plant Registrations</i> , 2019, 13, 406-410.	0.4	1
47	Gene duplication and genetic innovation in cereal genomes. <i>Genome Research</i> , 2019, 29, 261-269.	2.4	29
48	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	4.1	136
49	High proportion of diploid hybrids produced by interspecific diploid–tetraploid Sorghum hybridization. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 387-390.	0.8	13
50	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
51	Genetic Analysis of <i>Gossypium</i> Fiber Quality Traits in Reciprocal Advanced Backcross Populations. <i>Plant Genome</i> , 2018, 11, 170057.	1.6	15
52	Development of Perennial Grain Sorghum. <i>Sustainability</i> , 2018, 10, 172.	1.6	50
53	The Rise of Cotton Genomics. <i>Trends in Plant Science</i> , 2018, 23, 953-955.	4.3	16
54	In-field High Throughput Phenotyping and Cotton Plant Growth Analysis Using LiDAR. <i>Frontiers in Plant Science</i> , 2018, 9, 16.	1.7	108

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55	Genotyping by Sequencing of 393 <i>Sorghum bicolor</i> BTx623 × IS3620C Recombinant Inbred Lines Improves Sensitivity and Resolution of QTL Detection. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2563-2572.	0.8	28
56	Cross-taxon application of sugarcane EST-SSR to genetic diversity analysis of bermudagrass (<i>Cynodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	9
57	Keen insights from quinoa. <i>Nature</i> , 2017, 542, 300-302.	13.7	3
58	Targeted identification of association between cotton fiber quality traits and microsatellite markers. <i>Euphytica</i> , 2017, 213, 1.	0.6	6
59	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.	1.8	64
60	Fine mapping and candidate gene analysis of qFL- <i>chr1</i> , a fiber length QTL in cotton. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1309-1319.	1.8	33
61	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017, 174, 284-300.	2.3	112
62	QTL analysis of cotton fiber length in advanced backcross populations derived from a cross between <i>Gossypium hirsutum</i> and <i>G. mustelinum</i> . <i>Theoretical and Applied Genetics</i> , 2017, 130, 1297-1308.	1.8	36
63	Comparative genetic variation of fiber quality traits in reciprocal advanced backcross populations. <i>Euphytica</i> , 2017, 213, 1.	0.6	9
64	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
65	Segregation distortion and genome-wide digenic interactions affect transmission of introgressed chromatin from wild cotton species. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2219-2230.	1.8	10
66	SSR-enriched genetic linkage maps of bermudagrass (<i>Cynodon dactylon</i> × <i>transvaalensis</i>), and their comparison with allied plant genomes. <i>Theoretical and Applied Genetics</i> , 2017, 130, 819-839.	1.8	12
67	Identification and Characterization of miRNA Transcriptome in Asiatic Cotton (<i>Gossypium arboreum</i>) Using High Throughput Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 969.	1.7	15
68	Advanced Backcross QTL Analysis of Fiber Strength and Fineness in a Cross between <i>Gossypium hirsutum</i> and <i>G. mustelinum</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1848.	1.7	20
69	In-Field High-Throughput Phenotyping of Cotton Plant Height Using LiDAR. <i>Remote Sensing</i> , 2017, 9, 377.	1.8	70
70	Aerial Images and Convolutional Neural Network for Cotton Bloom Detection. <i>Frontiers in Plant Science</i> , 2017, 8, 2235.	1.7	77
71	Plant Genome Duplication Database. <i>Methods in Molecular Biology</i> , 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. <i>Methods in Molecular Biology</i> , 2017, 1533, 257-266.	0.4	0
74	Comparative genomic deconvolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. <i>New Phytologist</i> , 2016, 209, 1252-1263.	3.5	65
75	Reconstructing changes in the genotype, phenotype, and climatic niche of an introduced species. <i>Ecography</i> , 2016, 39, 894-903.	2.1	14
76	Evidence for fine-scale habitat specialisation in an invasive weed. <i>Journal of Plant Ecology</i> , 2016, , rtw124.	1.2	3
77	Comparative transmission genetics of introgressed chromatin in <i>Gossypium</i> (cotton) polyploids. <i>American Journal of Botany</i> , 2016, 103, 719-729.	0.8	14
78	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 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. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1673-1685.	0.8	19
80	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016, 172, 272-283.	2.3	88
81	Two Paleo-Hexaploidies Underlie Formation of Modern Solanaceae Genome Structure. <i>Compendium of Plant Genomes</i> , 2016, , 201-216.	0.3	0
82	The Evolution of Photoperiod-Insensitive Flowering in Sorghum, A Genomic Model for Panicoid Grasses. <i>Molecular Biology and Evolution</i> , 2016, 33, 2417-2428.	3.5	42
83	High throughput phenotyping of cotton plant height using depth images under field conditions. <i>Computers and Electronics in Agriculture</i> , 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> . <i>Crop Science</i> , 2016, 56, 1760-1768.	0.8	12
85	EMS-mutated cotton populations suggest overlapping genetic control of trichome and lint fiber variation. <i>Euphytica</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6785-6790.	3.3	235
87	An integrated approach to maintaining cereal productivity under climate change. <i>Global Food Security</i> , 2016, 8, 9-18.	4.0	110
88	Application of genotyping by sequencing technology to a variety of crop breeding programs. <i>Plant Science</i> , 2016, 242, 14-22.	1.7	183
89	Large-Scale Gene Relocations following an Ancient Genome Triplication Associated with the Diversification of Core Eudicots. <i>PLoS ONE</i> , 2016, 11, e0155637.	1.1	19
90	Multi-Phase US Spread and Habitat Switching of a Post-Columbian Invasive, <i>Sorghum halepense</i> . <i>PLoS ONE</i> , 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. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
92	Estimating genetic diversity among selected cotton genotypes and the identification of DNA markers associated with resistance to cotton leaf curl disease. <i>Turkish Journal of Botany</i> , 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). <i>G3: Genes, Genomes, Genetics</i> , 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). <i>BMC Plant Biology</i> , 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> × <i>S. propinquum</i> . <i>American Journal of Botany</i> , 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. <i>Molecular Plant</i> , 2015, 8, 885-898.	3.9	131
97	Unraveling the fabric of polyploidy. <i>Nature Biotechnology</i> , 2015, 33, 491-493.	9.4	17
98	Genetic map and QTL controlling fiber quality traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2015, 203, 615-628.	0.6	82
99	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
100	Comparative Analysis of Gene Conversion Between Duplicated Regions in <i>Brassica rapa</i> and <i>B. oleracea</i> Genomes. <i>Compendium of Plant Genomes</i> , 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>). <i>Genetics</i> , 2015, 201, 143-154.	1.2	33
102	Telomere-centric genome repatterning determines recurring chromosome number reductions during the evolution of eukaryotes. <i>New Phytologist</i> , 2015, 205, 378-389.	3.5	64
103	Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBTJ/Overl 0.6 99	0.6	99
104	Genetic analysis of vegetative branching in sorghum. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2387-2403.	1.8	35
105	Insights into the Common Ancestor of Eudicots. <i>Advances in Botanical Research</i> , 2014, 69, 137-174.	0.5	1
106	Synthetic Haplotypes, Species, Karyotypes, and Protoorganisms?. <i>Advances in Botanical Research</i> , 2014, 69, 363-376.	0.5	0
107	A Backdrop. <i>Advances in Botanical Research</i> , 2014, 69, 1-11.	0.5	2
108	Comparative and Evolutionary Analysis of Major Peanut Allergen Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 2468-2488.	1.1	15

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109	Ancient Gene Duplicates in <i>Gossypium</i> (Cotton) Exhibit Near-Complete Expression Divergence. <i>Genome Biology and Evolution</i> , 2014, 6, 559-571.	1.1	72
110	Introgression of homeologous quantitative trait loci (QTLs) for resistance to the root-knot nematode [<i>Meloidogyne arenaria</i> (Neal) Chitwood] in an advanced backcross-QTL population of peanut (<i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2014, 34, 393-406.	1.0	39
111	Extensive and Biased Intergenomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, <i>Gossypium</i> (Cotton). <i>Genetics</i> , 2014, 197, 1153-1163.	1.2	51
112	Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. <i>Plant Cell</i> , 2014, 26, 2792-2802.	3.1	220
113	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	1.2	136
114	Polyploidy-associated genome modifications during land plant evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130355.	1.8	90
115	Alleles conferring improved fiber quality from EMS mutagenesis of elite cotton genotypes. <i>Theoretical and Applied Genetics</i> , 2014, 127, 821-830.	1.8	21
116	Identifying QTL for fiber quality traits with three upland cotton (<i>Gossypium hirsutum</i> L.) populations. <i>Euphytica</i> , 2014, 198, 43-58.	0.6	67
117	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. <i>BMC Genomics</i> , 2014, 15, 162.	1.2	410
118	Sequencing of transcriptomes from two <i>Miscanthus</i> species reveals functional specificity in rhizomes, and clarifies evolutionary relationships. <i>BMC Plant Biology</i> , 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. <i>Plant Cell</i> , 2014, 26, 2420-2429.	3.1	88
120	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
121	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
122	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
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). <i>New Phytologist</i> , 2013, 198, 274-283.	3.5	57
124	Quantitative models of hydrolysis conversion efficiency and biomass crystallinity index for plant breeding. <i>Plant Breeding</i> , 2013, 132, 252-258.	1.0	6
125	The repetitive component of the A genome of peanut (<i>Arachis hypogaea</i>) and its role in remodelling intergenic sequence space since its evolutionary divergence from the B genome. <i>Annals of Botany</i> , 2013, 112, 545-559.	1.4	30
126	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 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 bicolor—Sorghum propinquum. Theoretical and Applied Genetics, 2013, 126, 2367-2380.	1.8	13
139	<i>MCSanX-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</i> — <i>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 <i>Morus notabilis</i> . Nature Communications, 2013, 4, 2445.	5.8	277
144	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants. Plant Physiology, 2013, 162, 769-778.	2.3	44

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

#	ARTICLE	IF	CITATIONS
163	Use of diversity arrays technology markers for integration into a cotton reference map and anchoring to a recombinant inbred line map. <i>Genome</i> , 2011, 54, 349-359.	0.9	5
164	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
165	Attenuated live vaccine usage affects accurate measures of virus diversity and mutation rates in avian coronavirus infectious bronchitis virus. <i>Virus Research</i> , 2011, 158, 225-234.	1.1	48
166	Comparative analysis of <i>Gossypium</i> and <i>Vitis</i> genomes indicates genome duplication specific to the <i>Gossypium</i> lineage. <i>Genomics</i> , 2011, 97, 313-320.	1.3	20
167	<i>Azospirillum</i> Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. <i>PLoS Genetics</i> , 2011, 7, e1002430.	1.5	191
168	Efficacy of <i>qFL1</i> , a Quantitative Trait Locus for Fiber Length in Cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	21
169	Gene Conversion in Angiosperm Genomes with an Emphasis on Genes Duplicated by Polyploidization. <i>Genes</i> , 2011, 2, 1-20.	1.0	47
170	Dissecting Genetic Networks Underlying Complex Phenotypes: The Theoretical Framework. <i>PLoS ONE</i> , 2011, 6, e14541.	1.1	29
171	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. <i>PLoS ONE</i> , 2011, 6, e28150.	1.1	139
172	Microcollinearity and genome evolution in the vicinity of an ethylene receptor gene of cultivated diploid and allotetraploid coffee species (<i>Coffea</i>). <i>Plant Journal</i> , 2011, 67, 305-317.	2.8	55
173	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.	3.5	63
174	Metabolite and mineral analyses of cotton near-isogenic lines introgressed with QTLs for productivity and drought-related traits. <i>Physiologia Plantarum</i> , 2011, 141, 265-275.	2.6	59
175	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
176	QTL alleles for improved fiber quality from a wild Hawaiian cotton, <i>Gossypium tomentosum</i> . <i>Theoretical and Applied Genetics</i> , 2011, 123, 1075-1088.	1.8	54
177	Genetic diversity analysis of maintainer and restorer accessions in upland cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.9	12
178	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.0	91
179	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.	1.2	142
180	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

#	ARTICLE	IF	CITATIONS
181	Size variation in homologous segments across divergent plant genomes. <i>Mobile Genetic Elements</i> , 2011, 1, 92-96.	1.8	3
182	Recombination in Avian Gamma-Coronavirus Infectious Bronchitis Virus. <i>Viruses</i> , 2011, 3, 1777-1799.	1.5	87
183	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.	3.1	80
184	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.	3.3	61
185	Paleo-Green Revolution for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10931-10932.	3.3	17
186	Genetic Improvement of C4 Grasses as Cellulosic Biofuel Feedstocks. , 2011, , 113-138.		5
187	Marker-Assisted Breeding in Higher Plants. , 2011, , 39-76.		6
188	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.	1.1	69
189	Sequencing and Utilization of the <i>Gossypium</i> Genomes. <i>Tropical Plant Biology</i> , 2010, 3, 71-74.	1.0	6
190	A comparative assessment of the utility of PCR-based marker systems in pearl millet. <i>Euphytica</i> , 2010, 174, 253-260.	0.6	13
191	Domestication and plant genomes. <i>Current Opinion in Plant Biology</i> , 2010, 13, 160-166.	3.5	89
192	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.	1.2	175
193	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). <i>BMC Genomics</i> , 2010, 11, 395.	1.2	48
194	Comparative Genomics in Crop Plants. , 2010, , 23-61.		5
195	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.	3.3	267
196	Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372.	8.6	202
197	Identification and Mapping of Nucleotide Binding Site–Leucine-rich Repeat Resistance Gene Analogs in Bermudagrass. <i>Journal of the American Society for Horticultural Science</i> , 2010, 135, 74-82.	0.5	6
198	Roadmap of Genomics Research in the 21st Century. , 2010, , 571-582.		0

#	ARTICLE	IF	CITATIONS
199	Molecular biogeographic study of recently described B- and A-genome <i>Arachis</i> species, also providing new insights into the origins of cultivated peanut. <i>Genome</i> , 2009, 52, 107-119.	0.9	51
200	A Recommendation for Naming Transcription Factor Proteins in the Grasses. <i>Plant Physiology</i> , 2009, 149, 4-6.	2.3	45
201	Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization. <i>Genome Research</i> , 2009, 19, 1026-1032.	2.4	83
202	Sixty Million Years in Evolution of Soft Grain Trait in Grasses: Emergence of the Softness Locus in the Common Ancestor of Pooideae and Ehrhartoideae, after their Divergence from Panicoideae. <i>Molecular Biology and Evolution</i> , 2009, 26, 1651-1661.	3.5	46
203	Comparative Genomics of Cotton and Arabidopsis. , 2009, , 431-449.		2
204	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.	3.1	194
205	Comparative Genomics of Grasses Promises a Bountiful Harvest. <i>Plant Physiology</i> , 2009, 149, 125-131.	2.3	42
206	QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. <i>Nucleic Acids Research</i> , 2009, 37, e101-e101.	6.5	222
207	Patterns of tandem repetition in plant whole genome assemblies. <i>Molecular Genetics and Genomics</i> , 2009, 281, 579-590.	1.0	16
208	Field evaluation of cotton near-isogenic lines introgressed with QTLs for productivity and drought related traits. <i>Molecular Breeding</i> , 2009, 23, 179-195.	1.0	55
209	Functional dissection of drought-responsive gene expression patterns in <i>Cynodon dactylon</i> L.. <i>Plant Molecular Biology</i> , 2009, 70, 1-16.	2.0	17
210	Duplication and Divergence of Grass Genomes: Integrating the Chloridoids. <i>Tropical Plant Biology</i> , 2009, 2, 51-62.	1.0	23
211	Genetic improvement of C4 grasses as cellulosic biofuel feedstocks. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2009, 45, 291-305.	0.9	102
212	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
213	Photosynthesis of cotton near-isogenic lines introgressed with QTLs for productivity and drought related traits. <i>Plant Science</i> , 2009, 177, 88-96.	1.7	41
214	Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.	0.8	1,031
215	Comparative genomic analysis of C4 photosynthetic pathway evolution in grasses. <i>Genome Biology</i> , 2009, 10, R68.	13.9	144
216	Bridging Classical and Molecular Genetics of Abiotic Stress Resistance in Cotton. , 2009, , 337-352.		9

#	ARTICLE	IF	CITATIONS
217	Gossypium DNA Markers: Types, Numbers, and Uses. , 2009, , 101-139.		14
218	Physical Composition and Organization of the Gossypium Genomes. , 2009, , 141-155.		1
219	Toward Characterizing the Spectrum of Diversity in the Gossypium Genus. , 2009, , 483-491.		0
220	The Fruits of Tropical Plant Genomics. Tropical Plant Biology, 2008, 1, 3-19.	1.0	10
221	Recent Origin of Dioecious and Gynodioecious Y Chromosomes in Papaya. Tropical Plant Biology, 2008, 1, 49-57.	1.0	62
222	Genome-Wide Analysis of Repetitive Elements in Papaya. Tropical Plant Biology, 2008, 1, 191-201.	1.0	24
223	Inheritance and alteration of genome methylation in F1 hybrid rice. Electrophoresis, 2008, 29, 4088-4095.	1.3	15
224	The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). Nature, 2008, 452, 991-996.	13.7	964
225	Novel nuclear intronâ€spanning primers for Arecaceae evolutionary biology. Molecular Ecology Resources, 2008, 8, 211-214.	2.2	20
226	Low X/Y divergence in four pairs of papaya sexâ€linked genes. Plant Journal, 2008, 53, 124-132.	2.8	78
227	Evolutionary Genetics of Genome Merger and Doubling in Plants. Annual Review of Genetics, 2008, 42, 443-461.	3.2	618
228	Synteny and Collinearity in Plant Genomes. Science, 2008, 320, 486-488.	6.0	1,156
229	Correspondence of Trichome Mutations in Diploid and Tetraploid Cottons. Journal of Heredity, 2008, 99, 182-186.	1.0	22
230	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. Genome Research, 2008, 18, 1944-1954.	2.4	515
231	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. Molecular Biology and Evolution, 2008, 25, 1415-1428.	3.5	57
232	Finding and Comparing Syntenic Regions among Arabidopsis and the Outgroups Papaya, Poplar, and Grape: CoGe with Rosids. Plant Physiology, 2008, 148, 1772-1781.	2.3	376
233	Transcriptome analysis of leaf tissue from Bermudagrass (Cynodon dactylon) using a normalised cDNA library. Functional Plant Biology, 2008, 35, 585.	1.1	20
234	Genomics of Sorghum. International Journal of Plant Genomics, 2008, 2008, 1-6.	2.2	101

#	ARTICLE	IF	CITATIONS
235	Genomics of Sorghum, a Semi-Arid Cereal and Emerging Model for Tropical Grass Genomics. , 2008, , 469-482.		9
236	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. PLoS Genetics, 2007, 3, e123.	1.5	270
237	Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. Genetics, 2007, 177, 1753-1763.	1.2	85
238	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. Genetics, 2007, 176, 2577-2588.	1.2	240
239	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. Plant Physiology, 2007, 145, 1303-1310.	2.3	390
240	Sex chromosomes in flowering plants. American Journal of Botany, 2007, 94, 141-150.	0.8	111
241	Integrative Mapping of <i>Gossypium hirsutum</i> L. by Meiotic Fluorescent in Situ Hybridization of a Tandemly Repetitive Sequence (B77). Genetics, 2007, 176, 115-123.	1.2	10
242	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (<i>Gossypium</i>). Plant Journal, 2007, 50, 995-1006.	2.8	89
243	Characterization of terminal-repeat retrotransposon in miniature (TRIM) in Brassica relatives. Theoretical and Applied Genetics, 2007, 114, 627-636.	1.8	30
244	Leveraging the rice genome sequence for monocot comparative and translational genomics. Theoretical and Applied Genetics, 2007, 115, 237-243.	1.8	24
245	Recent Advances And Future Prospective in Molecular Breeding of Cotton For Drought and Salinity Stress Tolerance. , 2007, , 775-796.		11
246	Evidence for a Selective Sweep on Chromosome 1 of Cultivated Sorghum. Crop Science, 2006, 46, S-27.	0.8	11
247	An Integrated Web Resource for Cotton. Crop Science, 2006, 46, 1998-2007.	0.8	26
248	Chromosome structural changes in diploid and tetraploid A genomes of <i>Gossypium</i> . Genome, 2006, 49, 336-345.	0.9	71
249	Forage Potential of Opuntia Clones Maintained by the USDA, National Plant Germplasm System (NPGS) Collection. Crop Science, 2006, 46, 2161-2168.	0.8	25
250	Leafing through the genomes of our major crop plants: strategies for capturing unique information. Nature Reviews Genetics, 2006, 7, 174-184.	7.7	82
251	Molecular Markers for the Classification of Switchgrass (<i>Panicum virgatum</i> L.) Germplasm and to Assess Genetic Diversity in Three Synthetic Switchgrass Populations. Genetic Resources and Crop Evolution, 2006, 53, 1291-1302.	0.8	71
252	Many gene and domain families have convergent fates following independent whole-genome duplication events in Arabidopsis, Oryza, Saccharomyces and Tetraodon. Trends in Genetics, 2006, 22, 597-602.	2.9	181

#	ARTICLE	IF	CITATIONS
253	Restriction landmark genome scanning method using isoschizomers (MspI/HpaII) for DNA methylation analysis. <i>Electrophoresis</i> , 2006, 27, 2846-2856.	1.3	22
254	Challenges of Detecting Directional Selection After a Bottleneck: Lessons From <i>Sorghum bicolor</i> . <i>Genetics</i> , 2006, 173, 953-964.	1.2	86
255	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	2.4	138
256	Functional Classification, Genomic Organization, Putatively cis-Acting Regulatory Elements, and Relationship to Quantitative Trait Loci, of <i>Sorghum</i> Genes with Rhizome-Enriched Expression. <i>Plant Physiology</i> , 2006, 142, 1148-1159.	2.3	62
257	SyMAP: A system for discovering and viewing syntenic regions of FPC maps. <i>Genome Research</i> , 2006, 16, 1159-1168.	2.4	176
258	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.	3.3	168
259	Ancient duplication of cereal genomes. <i>New Phytologist</i> , 2005, 165, 658-661.	3.5	43
260	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.	2.0	111
261	Chromosome evolution in eukaryotes: a multi-kingdom perspective. <i>Trends in Genetics</i> , 2005, 21, 673-682.	2.9	238
262	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.	1.8	94
263	Construction and characterization of a peanut HindIII BAC library. <i>Theoretical and Applied Genetics</i> , 2005, 111, 630-639.	1.8	38
264	Exploratory integration of peanut genetic and physical maps and possible contributions from <i>Arabidopsis</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 87-94.	1.8	10
265	Genetic mapping of a cross between <i>Gossypium hirsutum</i> (cotton) and the Hawaiian endemic, <i>Gossypium tomentosum</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 665-676.	1.8	37
266	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.	1.8	72
267	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.	1.8	83
268	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.	1.8	94
269	Organization and evolution of resistance gene analogs in peanut. <i>Molecular Genetics and Genomics</i> , 2005, 274, 248-263.	1.0	37
270	Polyploidy, evolutionary opportunity, and crop adaptation. <i>Genetica</i> , 2005, 123, 191-196.	0.5	73

#	ARTICLE	IF	CITATIONS
271	Pedigree vs. DNA Marker-Based Genetic Similarity Estimates in Cotton. <i>Crop Science</i> , 2005, 45, 2281-2287.	0.8	64
272	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.	2.3	66
273	Grains of knowledge: Genomics of model cereals. <i>Genome Research</i> , 2005, 15, 1643-1650.	2.4	103
274	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.	3.3	141
275	Comparative genomics of <i>Gossypium</i> and <i>Arabidopsis</i> : Unraveling the consequences of both ancient and recent polyploidy. <i>Genome Research</i> , 2005, 15, 1198-1210.	2.4	54
276	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.	1.2	71
277	Polyploidy, evolutionary opportunity, and crop adaptation. , 2005, , 191-196.		5
278	Reducing the Genetic Vulnerability of Cotton. <i>Crop Science</i> , 2004, 44, 1900-1901.	0.8	47
279	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.	1.2	106
280	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.	1.2	331
281	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	2.4	80
282	High-Density Linkage Mapping Revealed Suppression of Recombination at the Sex Determination Locus in Papaya. <i>Genetics</i> , 2004, 166, 419-436.	1.2	132
283	A comparative phylogenetic approach for dating whole genome duplication events. <i>Bioinformatics</i> , 2004, 20, 180-185.	1.8	38
284	A detailed look at 7 million years of genome evolution in a 439 kb contiguous sequence at the barley Hv-eIF4E locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	2.8	91
285	A primitive Y chromosome in papaya marks incipient sex chromosome evolution. <i>Nature</i> , 2004, 427, 348-352.	13.7	351
286	An SNP Resource for Rice Genetics and Breeding Based on Subspecies Indica and Japonica Genome Alignments. <i>Genome Research</i> , 2004, 14, 1812-1819.	2.4	318
287	Comparative genome analysis of monocots and dicots, toward characterization of angiosperm diversity. <i>Current Opinion in Biotechnology</i> , 2004, 15, 120-125.	3.3	34
288	EST derived PCR-based markers for functional gene homologues in cotton. <i>Genome</i> , 2004, 47, 449-462.	0.9	44

#	ARTICLE	IF	CITATIONS
289	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.	3.3	954
290	Comparative Genomics in Cereals. , 2004, , 119-133.		0
291	QTL analysis of genotype \times environment interactions affecting cotton fiber quality. <i>Theoretical and Applied Genetics</i> , 2003, 106, 384-396.	1.8	251
292	Unravelling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events. <i>Nature</i> , 2003, 422, 433-438.	13.7	1,470
293	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	3.5	325
294	Structure and evolution of cereal genomes. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 644-650.	1.5	93
295	A Rapid and Direct Approach to Identify Promoters That Confer High Levels of Gene Expression in Monocots. <i>Crop Science</i> , 2003, 43, 1805-1813.	0.8	23
296	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.	1.2	185
297	Comparative analysis of QTLs affecting plant height and flowering among closely-related diploid and polyploid genomes. <i>Genome</i> , 2002, 45, 794-803.	0.9	64
298	Molecular Analysis of Sorghum Resistance to the Greenbug (Homoptera: Aphididae). <i>Journal of Economic Entomology</i> , 2002, 95, 448-457.	0.8	44
299	Genetic, Physical, and Informatics Resources for Maize. On the Road to an Integrated Map. <i>Plant Physiology</i> , 2002, 130, 1598-1605.	2.3	106
300	Integration of Cot Analysis, DNA Cloning, and High-Throughput Sequencing Facilitates Genome Characterization and Gene Discovery. <i>Genome Research</i> , 2002, 12, 795-807.	2.4	172
301	Construction of a <i>Saccharum</i> Consensus Genetic Map from Two Interspecific Crosses. <i>Crop Science</i> , 2002, 42, 570-583.	0.8	40
302	Efficient capture of unique sequences from eukaryotic genomes. <i>Trends in Genetics</i> , 2002, 18, 547-550.	2.9	78
303	Applied plant genomics: the secret is integration. <i>Current Opinion in Plant Biology</i> , 2002, 5, 141-145.	3.5	10
304	What has QTL mapping taught us about plant domestication?. <i>New Phytologist</i> , 2002, 154, 591-608.	3.5	123
305	Access to the maize genome: an integrated physical and genetic map. <i>Plant Physiology</i> , 2002, 128, 9-12.	2.3	57
306	Construction of a Consensus Genetic Map from Two Interspecific Crosses. <i>Crop Science</i> , 2002, 42, 570.	0.8	39

#	ARTICLE	IF	CITATIONS
307	Brassica genomics: a complement to, and early beneficiary of, the Arabidopsis sequence. <i>Genome Biology</i> , 2001, 2, reviews1011.1.	13.9	74
308	Genomic Dissection of Genotype x Environment Interactions Conferring Adaptation of Cotton to Arid Conditions. <i>Genome Research</i> , 2001, 11, 1988-1995.	2.4	160
309	QTL Analysis in a Complex Autopolyploid: Genetic Control of Sugar Content in Sugarcane. <i>Genome Research</i> , 2001, 11, 2075-2084.	2.4	138
310	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.	2.3	81
311	Transmission Genetics of Chromatin From a Synthetic Amphidiploid to Cultivated Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 823-837.	1.2	148
312	MULTILOCUS INTERACTIONS RESTRICT GENE INTROGRESSION IN INTERSPECIFIC POPULATIONS OF POLYPLOID GOSSYPIUM (COTTON). <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 798-814.	1.1	133
313	Use of RFLP markers for identification of individuals homozygous for resistance to <i>Meloidogyne arenaria</i> in peanut. <i>Nematology</i> , 2000, 2, 575-580.	0.2	39
314	MULTILOCUS INTERACTIONS RESTRICT GENE INTROGRESSION IN INTERSPECIFIC POPULATIONS OF POLYPLOID GOSSYPIUM (COTTON). <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 798.	1.1	20
315	An EST-enriched Comparative Map of <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2000, 10, 776-788.	2.4	149
316	Comparative Genomics of Plant Chromosomes. <i>Plant Cell</i> , 2000, 12, 1523-1539.	3.1	301
317	Comparative Mapping of Quantitative Trait Loci Sculpting the Curd of <i>Brassica oleracea</i> . <i>Genetics</i> , 2000, 155, 1927-1954.	1.2	84
318	RFLP facilitated analysis of tiller and leaf angles in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 1999, 109, 79-84.	0.6	87
319	Title is missing!. <i>Molecular Breeding</i> , 1999, 5, 511-520.	1.0	34
320	Carbon isotope ratio in cotton varies with growth stage and plant organ. <i>Plant Science</i> , 1999, 142, 47-56.	1.7	48
321	Title is missing!. <i>Molecular Breeding</i> , 1998, 4, 419-426.	1.0	134
322	The molecular basis of C4 photosynthesis in sorghum: isolation, characterization and RFLP mapping of mesophyll- and bundle-sheath-specific cDNAs obtained by differential screening. <i>Plant Molecular Biology</i> , 1998, 37, 319-335.	2.0	46
323	Macromolecular organization and genetic mapping of a rapidly evolving chromosome-specific tandem repeat family (B77) in cotton (<i>Gossypium</i>). <i>Plant Molecular Biology</i> , 1998, 38, 1031-1041.	2.0	16
324	Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation in Cotton. <i>Genome Research</i> , 1998, 8, 479-492.	2.4	234

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325	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.	1.2	110
326	Epistasis for Three Grain Yield Components in Rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 1997, 145, 453-465.	1.2	367
327	Genetics of Hybrid Sterility and Hybrid Breakdown in an Intersubspecific Rice (<i>Oryza sativa</i> L.) Population. <i>Genetics</i> , 1997, 145, 1139-1148.	1.2	141
328	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.	0.8	217
329	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.	1.0	98
330	Toward a unified genetic map of higher plants, transcending the monocot-dicot divergence. <i>Nature Genetics</i> , 1996, 14, 380-382.	9.4	200
331	Genome-Wide High-Resolution Mapping by Recurrent Interbreeding Using <i>Arabidopsis thaliana</i> as a Model. <i>Genetics</i> , 1996, 142, 247-258.	1.2	72
332	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	2.8	287
333	Isolation of megabase-size DNA from sorghum and applications for physical mapping and bacterial and yeast artificial chromosome library construction. <i>Plant Molecular Biology Reporter</i> , 1995, 13, 82-94.	1.0	15
334	Construction and characterization of bacterial artificial chromosome library of <i>Sorghum bicolor</i> . <i>Nucleic Acids Research</i> , 1994, 22, 4922-4931.	6.5	389
335	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
336	A simple method for isolation of megabase DNA from cotton. <i>Plant Molecular Biology Reporter</i> , 1994, 12, 110-115.	1.0	8
337	Genome mapping in plants. <i>Current Opinion in Biotechnology</i> , 1993, 4, 142-147.	3.3	41
338	An improved method of plant megabase DNA isolation in agarose microbeads suitable for physical mapping and YAC cloning. <i>Plant Journal</i> , 1993, 4, 893-898.	2.8	41
339	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.	1.0	768
340	PCR amplification from single seeds, facilitating DNA marker-assisted breeding. <i>Nucleic Acids Research</i> , 1993, 21, 2527-2527.	6.5	13
341	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.	13.7	1,532