

# Andrew H Paterson

## List of Publications by Year in descending order

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341  
papers

47,847  
citations

2795

94  
h-index

1974

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.  | 6.5  | 4,252     |
| 2  | The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.   | 13.7 | 2,642     |
| 3  | Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.  | 6.0  | 2,089     |
| 4  | The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.   | 9.4  | 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.  | 13.7 | 1,532     |
| 6  | Unravelling angiosperm genome evolution by phylogenetic analysis of chromosomal duplication events. <i>Nature</i> , 2003, 422, 433-438.   | 13.7 | 1,470     |
| 7  | 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     |
| 8  | Synteny and Collinearity in Plant Genomes. <i>Science</i> , 2008, 320, 486-488.   | 6.0  | 1,156     |
| 9  | Polyploidy and angiosperm diversification. <i>American Journal of Botany</i> , 2009, 96, 336-348.   | 0.8  | 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.   | 13.7 | 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. | 3.3  | 954       |
| 12 | The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.  | 5.8  | 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.  | 1.0  | 768       |
| 14 | Evolutionary Genetics of Genome Merger and Doubling in Plants. <i>Annual Review of Genetics</i> , 2008, 42, 443-461.  | 3.2  | 618       |
| 15 | PGDD: a database of gene and genome duplication in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1152-D1158.   | 6.5  | 544       |
| 16 | Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.   | 3.8  | 542       |
| 17 | Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. <i>Genome Research</i> , 2008, 18, 1944-1954.  | 2.4  | 515       |
| 18 | The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.   | 9.4  | 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.  | 9.4  | 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.   | 13.9 | 456       |
| 21 | SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. <i>BMC Genomics</i> , 2014, 15, 162.   | 1.2  | 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.  | 9.4  | 398       |
| 23 | Toward Sequencing Cotton ( <i>Gossypium</i> ) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.   | 2.3  | 390       |
| 24 | 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       |
| 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.    | 2.3  | 376       |
| 26 | Epistasis for Three Grain Yield Components in Rice ( <i>Oryza sativa</i> L.). <i>Genetics</i> , 1997, 145, 453-465.   | 1.2  | 367       |
| 27 | 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       |
| 28 | A primitive Y chromosome in papaya marks incipient sex chromosome evolution. <i>Nature</i> , 2004, 427, 348-352.  | 13.7 | 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. | 1.2  | 331       |
| 30 | Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.   | 13.9 | 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.  | 3.5  | 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.                                     | 2.4  | 318       |
| 33 | Comparative Genomics of Plant Chromosomes. <i>Plant Cell</i> , 2000, 12, 1523-1539.   | 3.1  | 301       |
| 34 | Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.  | 2.8  | 287       |
| 35 | Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . <i>Nature Communications</i> , 2013, 4, 2445.   | 5.8  | 277       |
| 36 | Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. <i>PLoS Genetics</i> , 2007, 3, e123.   | 1.5  | 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.  | 3.3 | 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.   | 3.3 | 264       |
| 39 | QTL analysis of genotype × environment interactions affecting cotton fiber quality. <i>Theoretical and Applied Genetics</i> , 2003, 106, 384-396.   | 1.8 | 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.   | 5.8 | 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.  | 1.7 | 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.   | 1.2 | 240       |
| 43 | Chromosome evolution in eukaryotes: a multi-kingdom perspective. <i>Trends in Genetics</i> , 2005, 21, 673-682.   | 2.9 | 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. | 3.3 | 235       |
| 45 | Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation in Cotton. <i>Genome Research</i> , 1998, 8, 479-492.  | 2.4 | 234       |
| 46 | QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. <i>Nucleic Acids Research</i> , 2009, 37, e101-e101.  | 6.5 | 222       |
| 47 | Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.   | 4.1 | 221       |
| 48 | Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. <i>Plant Cell</i> , 2014, 26, 2792-2802.  | 3.1 | 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.  | 0.8 | 217       |
| 50 | Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372.  | 8.6 | 202       |
| 51 | Toward a unified genetic map of higher plants, transcending the monocot–dicot divergence. <i>Nature Genetics</i> , 1996, 14, 380-382.   | 9.4 | 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.   | 3.1 | 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.  | 1.8 | 194       |
| 54 | Azospirillum Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. <i>PLoS Genetics</i> , 2011, 7, e1002430.  | 1.5 | 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.   | 3.9  | 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.            | 1.2  | 185       |
| 57 | Application of genotyping by sequencing technology to a variety of crop breeding programs. <i>Plant Science</i> , 2016, 242, 14-22.   | 1.7  | 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. | 2.9  | 181       |
| 59 | SyMAP: A system for discovering and viewing syntenic regions of FPC maps. <i>Genome Research</i> , 2006, 16, 1159-1168.   | 2.4  | 176       |
| 60 | Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.   | 1.2  | 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.  | 2.4  | 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.    | 3.3  | 168       |
| 63 | 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       |
| 64 | 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       |
| 65 | Transmission Genetics of Chromatin From a Synthetic Amphidiploid to Cultivated Peanut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook<br>823-837.   | 1.2  | 148       |
| 66 | Comparative genomic analysis of C4 photosynthetic pathway evolution in grasses. <i>Genome Biology</i> , 2009, 10, R68.  | 13.9 | 144       |
| 67 | Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.   | 1.2  | 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.      | 3.3  | 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.  | 1.2  | 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.   | 1.1  | 139       |
| 71 | QTL Analysis in a Complex Autopolyploid: Genetic Control of Sugar Content in Sugarcane. <i>Genome Research</i> , 2001, 11, 2075-2084.   | 2.4  | 138       |
| 72 | A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.   | 2.4  | 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.  | 1.8 | 137       |
| 74 | Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.  | 1.2 | 136       |
| 75 | 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       |
| 76 | Title is missing!. <i>Molecular Breeding</i> , 1998, 4, 419-426.   | 1.0 | 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. | 1.1 | 133       |
| 78 | 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       |
| 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.                | 3.9 | 131       |
| 80 | What has QTL mapping taught us about plant domestication?. <i>New Phytologist</i> , 2002, 154, 591-608.  | 3.5 | 123       |
| 81 | Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017, 174, 284-300.  | 2.3 | 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.            | 2.0 | 111       |
| 83 | Sex chromosomes in flowering plants. <i>American Journal of Botany</i> , 2007, 94, 141-150.  | 0.8 | 111       |
| 84 | An integrated approach to maintaining cereal productivity under climate change. <i>Global Food Security</i> , 2016, 8, 9-18.   | 4.0 | 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.        | 1.2 | 110       |
| 86 | In-field High Throughput Phenotyping and Cotton Plant Growth Analysis Using LiDAR. <i>Frontiers in Plant Science</i> , 2018, 9, 16.  | 1.7 | 108       |
| 87 | 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       |
| 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. | 1.2 | 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, .                          | 3.3 | 106       |
| 90 | Grains of knowledge: Genomics of model cereals. <i>Genome Research</i> , 2005, 15, 1643-1650.  | 2.4 | 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.   | 0.9 | 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  | 0.6 | 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.                               | 1.0 | 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.   | 3.7 | 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.  | 1.8 | 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. | 1.8 | 94        |
| 98  | Structure and evolution of cereal genomes. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 644-650.  | 1.5 | 93        |
| 99  | A detailed look at 7 million years of genome evolution in a 439 kb contiguous sequence at the barley <i>Hv-eIF4E</i> locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.                            | 2.8 | 91        |
| 100 | The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.  | 1.0 | 91        |
| 101 | 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        |
| 102 | Microcolinearity and genome evolution in the <i>AdhA</i> region of diploid and polyploid cotton ( <i>Gossypium</i> ). <i>Plant Journal</i> , 2007, 50, 995-1006.  | 2.8 | 89        |
| 103 | Domestication and plant genomes. <i>Current Opinion in Plant Biology</i> , 2010, 13, 160-166.   | 3.5 | 89        |
| 104 | Different patterns of gene structure divergence following gene duplication in <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2013, 14, 652.   | 1.2 | 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.   | 3.1 | 88        |
| 106 | The Genome of a Southern Hemisphere Seagrass Species ( <i>Zostera muelleri</i> ). <i>Plant Physiology</i> , 2016, 172, 272-283.   | 2.3 | 88        |
| 107 | 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        |
| 108 | Recombination in Avian Gamma-Coronavirus Infectious Bronchitis Virus. <i>Viruses</i> , 2011, 3, 1777-1799.  | 1.5 | 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.  | 1.2  | 86        |
| 110 | Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. <i>Genetics</i> , 2007, 177, 1753-1763.   | 1.2  | 85        |
| 111 | Comparative Mapping of Quantitative Trait Loci Sculpting the Curd of <i>Brassica oleracea</i> . <i>Genetics</i> , 2000, 155, 1927-1954.  | 1.2  | 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. | 1.8  | 83        |
| 113 | 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        |
| 114 | Leafing through the genomes of our major crop plants: strategies for capturing unique information. <i>Nature Reviews Genetics</i> , 2006, 7, 174-184.  | 7.7  | 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.  | 0.6  | 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.                               | 2.3  | 81        |
| 117 | Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.  | 2.4  | 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.   | 3.1  | 80        |
| 119 | Efficient capture of unique sequences from eukaryotic genomes. <i>Trends in Genetics</i> , 2002, 18, 547-550.  | 2.9  | 78        |
| 120 | Low X/Y divergence in four pairs of papaya sex-linked genes. <i>Plant Journal</i> , 2008, 53, 124-132.   | 2.8  | 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.  | 1.6  | 78        |
| 122 | Aerial Images and Convolutional Neural Network for Cotton Bloom Detection. <i>Frontiers in Plant Science</i> , 2017, 8, 2235.  | 1.7  | 77        |
| 123 | Brassica genomics: a complement to, and early beneficiary of, the Arabidopsis sequence. <i>Genome Biology</i> , 2001, 2, reviews1011.1.  | 13.9 | 74        |
| 124 | Ploidy, evolutionary opportunity, and crop adaptation. <i>Genetica</i> , 2005, 123, 191-196.   | 0.5  | 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.    | 1.8  | 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.  | 1.1  | 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.   | 1.2 | 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.  | 1.2 | 71        |
| 129 | Chromosome structural changes in diploid and tetraploid A genomes of <i>Gossypium</i> . <i>Genome</i> , 2006, 49, 336-345.   | 0.9 | 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. | 0.8 | 71        |
| 131 | In-Field High-Throughput Phenotyping of Cotton Plant Height Using LiDAR. <i>Remote Sensing</i> , 2017, 9, 377.   | 1.8 | 70        |
| 132 | Cotton genetic resources. A review. <i>Agronomy for Sustainable Development</i> , 2012, 32, 419-432.   | 2.2 | 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.   | 1.1 | 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.  | 0.6 | 67        |
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