

David M Stelly

List of Publications by Year in descending order

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148
papers

9,519
citations

50276

46
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40979

93
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152
all docs

152
docs citations

152
times ranked

5133
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation and genome-wide association study of resistance to bacterial blight race 18 in U.S. Upland cotton germplasm. <i>Molecular Genetics and Genomics</i> , 2021, 296, 719-729.	2.1	7
2	Effects of Interspecific Chromosome Substitution in Upland Cotton on Cottonseed Macronutrients. <i>Plants</i> , 2021, 10, 1158.	3.5	2
3	Alteration of root and shoot morphologies by interspecific replacement of individual Upland cotton chromosome or chromosome segment pairs. <i>Euphytica</i> , 2021, 217, 1.	1.2	3
4	Genome-wide association study for tolerance to drought and salt tolerance and resistance to thrips at the seedling growth stage in US Upland cotton. <i>Industrial Crops and Products</i> , 2021, 169, 113645.	5.2	11
5	Assessing the Weed-Suppressing Potential of Cotton Chromosome Substitution Lines Using the Stair-Step Assay. <i>Plants</i> , 2021, 10, 2450.	3.5	3
6	Enhancing Upland cotton for drought resilience, productivity, and fiber quality: comparative evaluation and genetic dissection. <i>Molecular Genetics and Genomics</i> , 2020, 295, 155-176.	2.1	18
7	A genome-wide association study uncovers consistent quantitative trait loci for resistance to <i>Verticillium</i> wilt and <i>Fusarium</i> wilt race 4 in the US Upland cotton. <i>Theoretical and Applied Genetics</i> , 2020, 133, 563-577.	3.6	57
8	Effects of Interspecific Chromosome Substitution in Upland Cotton on Cottonseed Micronutrients. <i>Plants</i> , 2020, 9, 1081.	3.5	3
9	High-Temperature and Drought-Resilience Traits among Interspecific Chromosome Substitution Lines for Genetic Improvement of Upland Cotton. <i>Plants</i> , 2020, 9, 1747.	3.5	12
10	The <i>Gossypium longicalyx</i> Genome as a Resource for Cotton Breeding and Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1457-1467.	1.8	32
11	Effect of chromosome substitutions from <i>Gossypium barbadense</i> L., <i>G. tomentosum</i> Nutt. Ex Seem and <i>G. mustelinum</i> Watt into <i>G. hirsutum</i> L. on cottonseed protein and oil content. <i>Euphytica</i> , 2020, 216, 1.	1.2	4
12	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
13	First Report of <i>Cotton leafroll dwarf virus</i> Infecting Upland Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 5	1.4	21
14	Genome Editing, Gene Drives, and Synthetic Biology: Will They Contribute to Disease-Resistant Crops, and Who Will Benefit?. <i>Annual Review of Phytopathology</i> , 2019, 57, 165-188.	7.8	64
15	Registration of RMBHMTUPâ€C4, a Randomâ€Mated Cotton Population Containing Alleles from Four <i>Gossypium</i> Species. <i>Journal of Plant Registrations</i> , 2019, 13, 411-415.	0.5	2
16	Identification of microRNAs and their targets in four <i>Gossypium</i> species using RNA sequencing. <i>Current Plant Biology</i> , 2018, 14, 30-40.	4.7	8
17	Registration of Two CSâ€B17â€derived Upland Cotton Recombinant Inbred Lines with Improved Fiber Micronaire. <i>Journal of Plant Registrations</i> , 2018, 12, 97-100.	0.5	2
18	Morph-physiological responses of cotton interspecific chromosome substitution lines to low temperature and drought stresses. <i>Euphytica</i> , 2018, 214, 1.	1.2	6

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19	Elevating the conversation about GE crops. <i>Nature Biotechnology</i> , 2017, 35, 302-304.	17.5	6
20	Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 99.	8.8	153
21	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Ov 7, 15274.	3.3	23
22	Diversity analysis of cotton (<i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. <i>BMC Plant Biology</i> , 2017, 17, 37.	3.6	56
23	Genotypic comparisons of chromosomes 01, 04, and 18 from three tetraploid species of <i>Gossypium</i> in topcrosses with five elite cultivars of <i>G. hirsutum</i> L. <i>Euphytica</i> , 2017, 213, 1.	1.2	6
24	Insights Into Upland Cotton (<i>Gossypium hirsutum</i> L.) Genetic Recombination Based on 3 High-Density Single-Nucleotide Polymorphism and a Consensus Map Developed Independently With Common Parents. <i>Genomics Insights</i> , 2017, 10, 117863101773510.	3.0	12
25	Species Shuffling of Chromosomes to Study the Effects on Fiber Traits Using Chromosome Substitution Lines. <i>Crop Science</i> , 2017, 57, 1211-1226.	1.8	8
26	Four Chromosome-Specific (<i>Gossypium barbadense</i> Chromosome 5sh) Upland Cotton RILs with Improved Elongation. <i>Journal of Plant Registrations</i> , 2017, 11, 165-167.	0.5	2
27	SNP-Based MAS in Cotton under Depressed Recombination for Renlon Flanking Recombinants: Results and Inferences on Wide Cross Breeding Strategies. <i>Crop Science</i> , 2016, 56, 1526-1539.	1.8	7
28	Jones hybrid™ hickory: a case study in <i>Carya</i> curation. <i>SpringerPlus</i> , 2016, 5, 1860.	1.2	1
29	DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. <i>PLoS Genetics</i> , 2016, 12, e1006012.	3.5	27
30	Estimating Broad Sense Heritability and Investigating the Mechanism of Genetic Transmission of Cold Tolerance Using Mannitol as a Measure of Post-freeze Juice Degradation in Sugarcane and Energycane (<i>Saccharum</i> spp.). <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 1657-1663.	5.2	9
31	Registration of BARBREN-713 Germplasm Line of Upland Cotton Resistant to Reniform and Root-Knot Nematodes. <i>Journal of Plant Registrations</i> , 2015, 9, 89-93.	0.5	29
32	Non-destructive high-throughput DNA extraction and genotyping methods for cotton seeds and seedlings. <i>BioTechniques</i> , 2015, 58, 234-243.	1.8	10
33	A Long-Read Transcriptome Assembly of Cotton (<i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	2.8	12
34	Phytohormonal Networks Promote Differentiation of Fiber Initials on Pre-Anthesis Cotton Ovules Grown In Vitro and In Planta. <i>PLoS ONE</i> , 2015, 10, e0125046.	2.5	24
35	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton (<i>Gossypium</i>) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1095-1105.	1.8	20
36	Molecular confirmation of <i>Gossypium hirsutum</i> chromosome substitution lines. <i>Euphytica</i> , 2015, 205, 459-473.	1.2	17

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37	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209.	1.8	226
38	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
39	Phylogenetic analysis of <i>Gossypium</i> L. using restriction fragment length polymorphism of repeated sequences. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1859-1872.	2.1	1
40	Development and bin mapping of gene-associated interspecific SNPs for cotton (<i>Gossypium hirsutum</i> L.) introgression breeding efforts. <i>BMC Genomics</i> , 2014, 15, 945.	2.8	25
41	miR828 and miR858 regulate homoeologous MYB2 gene functions in <i>Arabidopsis trichome</i> and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050.	12.8	215
42	Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. <i>BMC Research Notes</i> , 2014, 7, 493.	1.4	9
43	Detection of DNA and Ploidy Variation within Vegetatively Propagated Zoysiagrass Cultivars. <i>Journal of the American Society for Horticultural Science</i> , 2014, 139, 547-552.	1.0	6
44	Registration of LONREN-1 and LONREN-2 Germplasm Lines of Upland Cotton Resistant to Reniform Nematode. <i>Journal of Plant Registrations</i> , 2014, 8, 187-190.	0.5	21
45	Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2013, 14, 208.	2.8	15
46	Interspecific chromosomal effects on agronomic traits in <i>Gossypium hirsutum</i> by AD analysis using intermated <i>G. barbadense</i> chromosome substitution lines. <i>Theoretical and Applied Genetics</i> , 2013, 126, 109-117.	3.6	27
47	Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1809-1818.	1.8	73
48	U niqueness of the <i>Gossypium mustelinum</i> Genome Revealed by GISH and 45 S rDNA FISH. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 654-662.	8.5	8
49	A Cotton-Fiber-Associated Cyclin-Dependent Kinase A Gene: Characterization and Chromosomal Location. <i>International Journal of Plant Genomics</i> , 2012, 2012, 1-10.	2.2	6
50	Genetic effects of nine <i>Gossypium barbadense</i> L. chromosome substitution lines in top crosses with five elite Upland cotton <i>G. hirsutum</i> L. cultivars. <i>Euphytica</i> , 2012, 187, 161-173.	1.2	17
51	A High-Density Simple Sequence Repeat and Single Nucleotide Polymorphism Genetic Map of the Tetraploid Cotton Genome. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 43-58.	1.8	97
52	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
53	Genome Physical Mapping of Polyploids: A BIBAC Physical Map of Cultivated Tetraploid Cotton, <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2012, 7, e33644.	2.5	11
54	Pollen Tube Growth After Intergeneric Pollinations of <i>Homozygous Sorghum</i> . <i>Crop Science</i> , 2012, 52, 1553-1560.	1.8	9

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55	Delineation of interspecific epistasis on fiber quality traits in <i>Gossypium hirsutum</i> by ADAA analysis of intermated <i>G. barbadense</i> chromosome substitution lines. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1351-1361.	3.6	17
56	Molecular evolution of the clustered MIC-3 multigene family of <i>Gossypium</i> species. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1359-1373.	3.6	4
57	Activation of Arabidopsis Seed Hair Development by Cotton Fiber-Related Genes. <i>PLoS ONE</i> , 2011, 6, e21301.	2.5	53
58	Clustering, haplotype diversity and locations of MIC-3: a unique root-specific defense-related gene family in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2010, 120, 587-606.	3.6	10
59	Genetic dissection of chromosome substitution lines of cotton to discover novel <i>Gossypium barbadense</i> L. alleles for improvement of agronomic traits. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1193-1205.	3.6	31
60	Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. <i>Chromosoma</i> , 2010, 119, 255-266.	2.2	32
61	Elimination of a Reproductive Barrier Facilitates Intergeneric Hybridization of <i>Sorghum bicolor</i> and <i>Saccharum</i> . <i>Crop Science</i> , 2010, 50, 1188-1195.	1.8	23
62	Early-generation germplasm introgression from <i>Sorghum macrospermum</i> into sorghum (<i>S.</i>) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	2.8	16
63	Linkage Mapping of Resistance to Reniform Nematode in Cotton following Introgression from <i>Gossypium longicalyx</i> (Hutch. & Lee). <i>Crop Science</i> , 2009, 49, 1151-1164.	1.8	53
64	Citrus asymmetric somatic hybrids produced via fusion of gamma-irradiated and iodoacetamide-treated protoplasts. <i>Pesquisa Agropecuaria Brasileira</i> , 2009, 44, 454-462.	0.9	7
65	Ploidy manipulation of the gametophyte, endosperm and sporophyte in nature and for crop improvement: a tribute to Professor Stanley J. Peloquin (1921-2008). <i>Annals of Botany</i> , 2009, 104, 795-807.	2.9	51
66	Sampling nucleotide diversity in cotton. <i>BMC Plant Biology</i> , 2009, 9, 125.	3.6	72
67	Integrative placement and orientation of non-redundant SSR loci in cotton linkage groups by deficiency analysis. <i>Molecular Breeding</i> , 2009, 23, 693-707.	2.1	18
68	Status of the USA cotton germplasm collection and crop vulnerability. <i>Genetic Resources and Crop Evolution</i> , 2009, 56, 507-532.	1.6	28
69	Wild Brazilian Mustard (<i>Brassica juncea</i> L.) Seed Oil Methyl Esters as Biodiesel Fuel. <i>JAACS, Journal of the American Oil Chemists' Society</i> , 2009, 86, 917-926.	1.9	86
70	Genome-wide analysis reveals rapid and dynamic changes in miRNA and siRNA sequence and expression during ovule and fiber development in allotetraploid cotton (<i>Gossypium hirsutum</i> L.). <i>Genome Biology</i> , 2009, 10, R122.	9.6	128
71	Fusion of protoplasts with irradiated microprotoplasts as a tool for radiation hybrid panel in citrus. <i>Pesquisa Agropecuaria Brasileira</i> , 2009, 44, 1616-1623.	0.9	2
72	BAC-derived SSR markers chromosome locations in cotton. <i>Euphytica</i> , 2008, 161, 361-370.	1.2	23

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73	Cotton (<i>Gossypium</i> spp.) R2R3-MYB transcription factors SNP identification, phylogenomic characterization, chromosome localization, and linkage mapping. <i>Theoretical and Applied Genetics</i> , 2008, 116, 1015-1026.	3.6	42
74	Genetic analysis of agronomic and fibre traits using four interspecific chromosome substitution lines in cotton. <i>Plant Breeding</i> , 2008, 127, 612-618.	1.9	18
75	Genetic recombination in <i>Sorghum bicolor</i> – <i>S. macrosperrum</i> interspecific hybrids. <i>Genome</i> , 2008, 51, 749-756.	2.0	25
76	Fluorescent in situ hybridization of 18S and 5S rDNA in papaya (<i>Carica papaya</i> L.) and wild relatives. <i>Caryologia</i> , 2008, 61, 411-416.	0.3	15
77	Phytohormone Regulation of Cotton Fiber Development In Vitro. , 2007, , 153-156.		1
78	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.	4.8	390
79	Integrative Mapping of <i>Gossypium hirsutum</i> L. by Meiotic Fluorescent In Situ Hybridization of a Tandemly Repetitive Sequence (B77). <i>Genetics</i> , 2007, 176, 115-123.	2.9	10
80	Genetic Effects of Thirteen <i>Gossypium barbadense</i> L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: II. Fiber Quality Traits. <i>Crop Science</i> , 2007, 47, 561-570.	1.8	57
81	Introgression of Resistance to Nematode <i>Rotylenchulus reniformis</i> into Upland Cotton (<i>Gossypium hirsutum</i>) from <i>Gossypium longicalyx</i> . <i>Crop Science</i> , 2007, 47, 1865-1877.	1.8	68
82	Molecular and SNP characterization of two genome specific transcription factor genes GhMyb8 and GhMyb10 in cotton species. <i>Euphytica</i> , 2007, 159, 259-273.	1.2	14
83	Transcriptome profiling, sequence characterization, and SNP-based chromosomal assignment of the EXPANSIN genes in cotton. <i>Molecular Genetics and Genomics</i> , 2007, 278, 539-553.	2.1	50
84	Genetic Effects of Thirteen <i>Gossypium barbadense</i> L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: I. Yield and Yield Components. <i>Crop Science</i> , 2006, 46, 1169-1178.	1.8	63
85	Genotype Dependent Interspecific Hybridization of <i>Sorghum bicolor</i> . <i>Crop Science</i> , 2006, 46, 2617-2622.	1.8	37
86	Accumulation of genome-specific transcripts, transcription factors and phytohormonal regulators during early stages of fiber cell development in allotetraploid cotton. <i>Plant Journal</i> , 2006, 47, 761-775.	5.7	191
87	Developmental and gene expression analyses of a cotton naked seed mutant. <i>Planta</i> , 2006, 223, 418-432.	3.2	110
88	Wide-cross whole-genome radiation hybrid mapping of the cotton (<i>Gossypium barbadense</i> L.) genome. <i>Molecular Genetics and Genomics</i> , 2006, 275, 105-113.	2.1	18
89	Cotton genome mapping with new microsatellites from Acala [®] Maxxa [™] BAC-ends. <i>Molecular Genetics and Genomics</i> , 2006, 275, 479-491.	2.1	113
90	An additive-dominance model to determine chromosomal effects in chromosome substitution lines and other gemplasms. <i>Theoretical and Applied Genetics</i> , 2006, 112, 391-399.	3.6	28

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91	Effects of Chromosome-Specific Introgression in Upland Cotton on Fiber and Agronomic Traits. <i>Genetics</i> , 2006, 172, 1927-1938.	2.9	84
92	Genetic mapping of new cotton fiber loci using EST-derived microsatellites in an interspecific recombinant inbred line cotton population. <i>Molecular Genetics and Genomics</i> , 2005, 274, 428-441.	2.1	168
93	Registration of 17 Upland (<i>Gossypium hirsutum</i>) Cotton Germplasm Lines Disomic for Different G. barbadense Chromosome or Arm Substitutions. <i>Crop Science</i> , 2005, 45, 2663-2665.	1.8	92
94	Toward Sequencing the Sorghum Genome. A U.S. National Science Foundation-Sponsored Workshop Report. <i>Plant Physiology</i> , 2005, 138, 1898-1902.	4.8	55
95	Comprehensive Molecular Cytogenetic Analysis of Sorghum Genome Architecture: Distribution of Euchromatin, Heterochromatin, Genes and Recombination in Comparison to Rice. <i>Genetics</i> , 2005, 171, 1963-1976.	2.9	94
96	Molecular Cytogenetic Maps of Sorghum Linkage Groups 2 and 8. <i>Genetics</i> , 2005, 169, 955-965.	2.9	38
97	Chromosomal Assignment of RFLP Linkage Groups Harboring Important QTLs on an Intraspecific Cotton (<i>Gossypium hirsutum</i> L.) Joinmap. <i>Journal of Heredity</i> , 2005, 96, 132-144.	2.4	127
98	Chromosome Identification and Nomenclature of Sorghum bicolor. <i>Genetics</i> , 2005, 169, 1169-1173.	2.9	117
99	Wide-Cross Whole-Genome Radiation Hybrid Mapping of Cotton (<i>Gossypium hirsutum</i> L.). <i>Genetics</i> , 2004, 167, 1317-1329.	2.9	35
100	Genetic mapping and QTL analysis of fiber-related traits in cotton (<i>Gossypium</i>). <i>Theoretical and Applied Genetics</i> , 2004, 108, 280-291.	3.6	219
101	Integrated karyotyping of sorghum by in situ hybridization of landed BACs. <i>Genome</i> , 2002, 45, 402-412.	2.0	84
102	Fluorescence in situ hybridization of single copy transgenes in rice chromosomes. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2001, 37, 1-5.	2.1	9
103	Bacterial Artificial Chromosome-Based Physical Map of the Rice Genome Constructed by Restriction Fingerprint Analysis. <i>Genetics</i> , 2001, 158, 1711-1724.	2.9	92
104	Ty1-copia-retrotransposon behavior in a polyploid cotton. <i>Chromosome Research</i> , 2000, 8, 73-76.	2.2	55
105	Cytogenetic alignment of the bovine chromosome 13 genome map by fluorescence in-situ hybridization of human chromosome 10 and 20 comparative markers. <i>Chromosome Research</i> , 1999, 7, 115-120.	2.2	7
106	New ribosomal RNA gene locations in <i>Gossypium hirsutum</i> mapped by meiotic FISH. <i>Chromosoma</i> , 1999, 108, 200-207.	2.2	21
107	Identification and distinction among segmental duplication-deficiencies by fluorescence in situ hybridization (FISH)-adorned multivalent analysis. <i>Genome</i> , 1999, 42, 763-771.	2.0	6
108	A Candidate Recombination Modifier Gene for <i>Zea mays</i> L. <i>Genetics</i> , 1999, 151, 821-830.	2.9	30

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109	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.	3.9	16
110	Physical assignment of six type I anchor loci to bovine chromosome 19 by fluorescence in situ hybridization. <i>Animal Genetics</i> , 1998, 29, 130-134.	1.7	17
111	Comparative mapping of bovine chromosome 13 by fluorescence in situ hybridization. <i>Animal Genetics</i> , 1998, 29, 265-272.	1.7	11
112	Brief communication. Tetraploid nature of <i>Sorghum bicolor</i> (L.) Moench. <i>Journal of Heredity</i> , 1998, 89, 188-190.	2.4	36
113	Resistance Gene Candidates Identified by PCR with Degenerate Oligonucleotide Primers Map to Clusters of Resistance Genes in Lettuce. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 815-823.	2.6	213
114	Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation in <i>Cotton</i> . <i>Genome Research</i> , 1998, 8, 479-492.	5.5	234
115	Evolution of interspersed repetitive elements in <i>Gossypium</i> (Malvaceae). <i>American Journal of Botany</i> , 1998, 85, 1364-1368.	1.7	93
116	Physical Mapping of the liguleless Linkage Group in <i>Sorghum bicolor</i> Using Rice RFLP-Selected <i>Sorghum</i> BACs. <i>Genetics</i> , 1998, 148, 1983-1992.	2.9	51
117	Use of meiotic FISH for identification of a new monosome in <i>Gossypium hirsutum</i> L. <i>Genome</i> , 1997, 40, 34-40.	2.0	38
118	FISH of a maize sh2-selected sorghum BAC to chromosomes of <i>Sorghum bicolor</i> . <i>Genome</i> , 1997, 40, 475-478.	2.0	33
119	A Rapid Stain-Clearing Method for Video Based Cytological Analysis of Cotton Megagametophytes. <i>Biotechnic and Histochemistry</i> , 1997, 72, 16-21.	1.3	0
120	A rapid procedure for the isolation of C ₀ t ₁ -1 DNA from plants. <i>Genome</i> , 1997, 40, 138-142.	2.0	219
121	ISH-facilitated analysis of meiotic bivalent pairing. <i>Genome</i> , 1996, 39, 784-792.	2.0	11
122	Distribution of 5S and 18S-28S rDNA loci in a tetraploid cotton (<i>Gossypium hirsutum</i> L.) and its putative diploid ancestors. <i>Chromosoma</i> , 1996, 105, 55-61.	2.2	174
123	Distribution of 5S and 18S-28S rDNA loci in a tetraploid cotton (<i>Gossypium hirsutum</i> L.) and its putative diploid ancestors. <i>Chromosoma</i> , 1996, 105, 55-61.	2.2	23
124	A New Procedure to Prepare Slides of Metaphase Chromosomes of Roses. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 1996, 31, 855-857.	1.0	24
125	A maximum likelihood algorithm for genome mapping of cytogenetic loci from meiotic configuration data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 9824-9828.	7.1	9
126	Fluorescent in situ hybridization of a bacterial artificial chromosome. <i>Genome</i> , 1995, 38, 646-651.	2.0	107

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127	Identification of a homeologous chromosome pair by in situ DNA hybridization to ribosomal RNA loci in meiotic chromosomes of cotton (<i>Gossypium hirsutum</i>). <i>Genome</i> , 1993, 36, 1015-1022.	2.0	51
128	Quantitative trait variation in phenotypically normal regenerants of cotton. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 1991, 27, 132-138.	2.1	8
129	Identification of Four <i>Gossypium sturtianum</i> Monosomic Alien Addition Derivatives from a Backcrossing Program with <i>G. hirsutum</i> . <i>Crop Science</i> , 1991, 31, 337-341.	1.8	28
130	Genetic Effects on the Timing of Le dav 2 Induced Necrosis of Cotton. <i>Crop Science</i> , 1990, 30, 70-74.	1.8	5
131	Pollen Fertility of Some Simple and Compound Translocations of Cotton. <i>Crop Science</i> , 1990, 30, 952-955.	1.8	4
132	Method to Evaluate Pollen Viability of Upland Cotton: Tests with Chromosome Translocations. <i>Crop Science</i> , 1989, 29, 1165-1169.	1.8	12
133	Cytogenetic abnormalities of cotton somaclones from callus cultures. <i>Genome</i> , 1989, 32, 762-770.	2.0	56
134	In Situ Hybridization of Biotinylated Dna Probes to Cotton Meiotic Chromosomes. <i>Biotechnic & Histochemistry</i> , 1989, 64, 25-37.	0.4	18
135	Cytogenetic abnormalities in cotton (<i>Gossypium hirsutum</i> L.) cell cultures. <i>Genome</i> , 1989, 32, 1128-1134.	2.0	27
136	Allelic Composition of Cotton at the Le 1 and Le 2 Loci.. <i>Crop Science</i> , 1989, 29, 707-712.	1.8	1
137	Proposed Schemes for Massâ€Extraction of Doubled Haploids of Cotton. <i>Crop Science</i> , 1988, 28, 885-890.	1.8	12
138	Introgression of the Glandedâ€Plant and Glandlessâ€Seed Trait from <i>Gossypium sturtianum</i> Willis into Cultivated Upland Cotton Using Ovule Culture 1. <i>Crop Science</i> , 1987, 27, 880-884.	1.8	47
139	FORMATION OF 2N MEGAGAMETOPHYTES IN DIPLOID TUBERâ€BEARING SOLANUMS. <i>American Journal of Botany</i> , 1986, 73, 1351-1363.	1.7	19
140	Diploid female gametophyte formation in 24-chromosome potatoes: genetic evidence for the prevalence of the second meiotic division restitution mode. <i>Genome</i> , 1986, 28, 101-108.	0.7	33
141	Formation of 2N Megagametophytes in Diploid Tuber-Bearing Solanums. <i>American Journal of Botany</i> , 1986, 73, 1351.	1.7	15
142	Screening for 2n female gametophytes, female fertility, and 2x Ã— 4x crossability in potatoes (<i>Solanum</i>) Tj ETQq0 0,0 rgBT /Overlock 10	0.3	13
143	Relative Development of Basal, Medial, and Apical Ovules in Soybean 1. <i>Crop Science</i> , 1985, 25, 877-879.	1.8	7
144	Mayer'S Hemalum-Methyl Salicylate: A Stain-Clearing Technique for Observations Within Whole Ovules. <i>Biotechnic & Histochemistry</i> , 1984, 59, 155-161.	0.4	95

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145	Variable development in anthers of partially male-sterile soybeans. <i>Journal of Heredity</i> , 1982, 73, 101-108.	2.4	15
146	A partially male-sterile mutant line of soybeans, <i>Glycine max</i> (L.) Merr.: Characterization of the msp phenotype variation. <i>Euphytica</i> , 1980, 29, 539-546.	1.2	26
147	A partially male-sterile mutant line of soybeans, <i>Glycine max</i> (L.) Merr.: inheritance. <i>Euphytica</i> , 1980, 29, 295-303.	1.2	20
148	The Utilization of Translocation Lines and Microsatellite Markers for the Identification of Unknown Cotton Monosomic Lines. , 0, , .		1