

Jonathan F Wendel

List of Publications by Year in descending order

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184
papers

22,894
citations

10986

71
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9345

143
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201
all docs

201
docs citations

201
times ranked

12607
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome evolution in polyploids. <i>Plant Molecular Biology</i> , 2000, 42, 225-249.	3.9	1,439
2	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
3	Polyploidy and genome evolution in plants. <i>Current Opinion in Plant Biology</i> , 2005, 8, 135-141.	7.1	1,160
4	Genes duplicated by polyploidy show unequal contributions to the transcriptome and organ-specific reciprocal silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4649-4654.	7.1	793
5	Gene duplication and evolutionary novelty in plants. <i>New Phytologist</i> , 2009, 183, 557-564.	7.3	725
6	Polyploidy and the evolutionary history of cotton. <i>Advances in Agronomy</i> , 2003, 78, 139-186.	5.2	694
7	Evolutionary Genetics of Genome Merger and Doubling in Plants. <i>Annual Review of Genetics</i> , 2008, 42, 443-461.	7.6	618
8	The tortoise and the hare: choosing between noncoding plastome and nuclear <i>Adh</i> sequences for phylogeny reconstruction in a recently diverged plant group. <i>American Journal of Botany</i> , 1998, 85, 1301-1315.	1.7	423
9	Genetic and epigenetic consequences of recent hybridization and polyploidy in <i>Spartina</i> (Poaceae). <i>Molecular Ecology</i> , 2005, 14, 1163-1175.	3.9	399
10	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.	4.8	390
11	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in <i>Gossypium</i> . <i>Genome Research</i> , 2006, 16, 1252-1261.	5.5	378
12	The wondrous cycles of polyploidy in plants. <i>American Journal of Botany</i> , 2015, 102, 1753-1756.	1.7	363
13	Epigenetics and plant evolution. <i>New Phytologist</i> , 2005, 168, 81-91.	7.3	361
14	Divergent Evolution of Plant NBS-LRR Resistance Gene Homologues in Dicot and Cereal Genomes. <i>Journal of Molecular Evolution</i> , 2000, 50, 203-213.	1.8	352
15	Doubling down on genomes: Polyploidy and crop plants. <i>American Journal of Botany</i> , 2014, 101, 1711-1725.	1.7	336
16	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	8.8	331
17	A Bountiful Harvest: Genomic Insights into Crop Domestication Phenotypes. <i>Annual Review of Plant Biology</i> , 2013, 64, 47-70.	18.7	326
18	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	8.9	325

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19	Novel patterns of gene expression in polyploid plants. <i>Trends in Genetics</i> , 2005, 21, 539-543.	6.7	316
20	Phylogenetics of the Cotton Genus (<i>Gossypium</i>): Character-State Weighted Parsimony Analysis of Chloroplast-DNA Restriction Site Data and Its Systematic and Biogeographic Implications. <i>Systematic Botany</i> , 1992, 17, 115.	0.5	279
21	Rapid diversification of the cotton genus (<i>Gossypium</i> ; Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes. <i>American Journal of Botany</i> , 2002, 89, 707-725.	1.7	249
22	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
23	Organ-Specific Silencing of Duplicated Genes in a Newly Synthesized Cotton Allotetraploid. <i>Genetics</i> , 2004, 168, 2217-2226.	2.9	242
24	Meta-analysis of Polyploid Cotton QTL Shows Unequal Contributions of Subgenomes to a Complex Network of Genes and Gene Clusters Implicated in Lint Fiber Development. <i>Genetics</i> , 2007, 176, 2577-2588.	2.9	240
25	Duplicate gene expression in allopolyploid <i>Gossypium</i> reveals two temporally distinct phases of expression evolution. <i>BMC Biology</i> , 2008, 6, 16.	3.8	235
26	Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation in Cotton. <i>Genome Research</i> , 1998, 8, 479-492.	5.5	234
27	Genomic expression dominance in allopolyploids. <i>BMC Biology</i> , 2009, 7, 18.	3.8	232
28	Evolutionary rate variation, genomic dominance and duplicate gene expression evolution during allotetraploid cotton speciation. <i>New Phytologist</i> , 2010, 186, 184-193.	7.3	223
29	GENETIC DIVERSITY IN <i>GOSSYPIUM HIRSUTUM</i> AND THE ORIGIN OF UPLAND COTTON. <i>American Journal of Botany</i> , 1992, 79, 1291-1310.	1.7	216
30	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2009, 182, 503-517.	2.9	212
31	Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. <i>Nature Communications</i> , 2014, 5, 5519.	12.8	205
32	Toward a unified genetic map of higher plants, transcending the monocot-dicot divergence. <i>Nature Genetics</i> , 1996, 14, 380-382.	21.4	200
33	The long and short of doubling down: polyploidy, epigenetics, and the temporal dynamics of genome fractionation. <i>Current Opinion in Genetics and Development</i> , 2018, 49, 1-7.	3.3	186
34	Polyploidy and Crop Improvement. <i>Crop Science</i> , 2006, 46, S-3.	1.8	178
35	Evolution and Natural History of the Cotton Genus. , 2009, , 3-22.		169
36	Rapid DNA loss as a counterbalance to genome expansion through retrotransposon proliferation in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17811-17816.	7.1	164

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37	Taxonomy and Evolution of the Cotton Genus, <i>Gossypium</i> . <i>Agronomy</i> , 0, , 25-44.	0.2	159
38	Comparative Evolutionary and Developmental Dynamics of the Cotton (<i>Gossypium hirsutum</i>) Fiber Transcriptome. <i>PLoS Genetics</i> , 2014, 10, e1004073.	3.5	149
39	GENETIC DIVERSITY AND ORIGIN OF THE HAWAIIAN ISLANDS COTTON, <i>GOSSYPIUM TOMENTOSUM</i> . <i>American Journal of Botany</i> , 1992, 79, 1311-1319.	1.7	147
40	MOLECULAR DIVERGENCE BETWEEN ASIAN AND NORTH AMERICAN SPECIES OF LIRIODENDRON (MAGNOLIACEAE) WITH IMPLICATIONS FOR INTERPRETATION OF FOSSIL FLORAS. <i>American Journal of Botany</i> , 1990, 77, 1243-1256.	1.7	146
41	Targeted sequence capture as a powerful tool for evolutionary analysis ¹ . <i>American Journal of Botany</i> , 2012, 99, 312-319.	1.7	146
42	Comparative development of fiber in wild and cultivated cotton. <i>Evolution & Development</i> , 2001, 3, 3-17.	2.0	145
43	Reevaluating the origin of domesticated cotton (<i>Gossypium hirsutum</i> ; Malvaceae) using nuclear restriction fragment length polymorphisms (RFLPs). <i>American Journal of Botany</i> , 1994, 81, 1309-1326.	1.7	144
44	Partitioned expression of duplicated genes during development and evolution of a single cell in a polyploid plant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6191-6195.	7.1	143
45	MOLECULAR EVIDENCE FOR HOMOPLOID RETICULATE EVOLUTION AMONG AUSTRALIAN SPECIES OF <i>GOSSYPIUM</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 694-711.	2.3	139
46	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	5.5	138
47	Homoeologous nonreciprocal recombination in polyploid cotton. <i>New Phytologist</i> , 2010, 186, 123-134.	7.3	136
48	Feast and famine in plant genomes. <i>Genetica</i> , 2002, 115, 37-47.	1.1	135
49	Genetic Diversity in <i>Gossypium hirsutum</i> and the Origin of Upland Cotton. <i>American Journal of Botany</i> , 1992, 79, 1291.	1.7	129
50	Cryptic trysts, genomic mergers, and plant speciation. <i>New Phytologist</i> , 2004, 161, 133-142.	7.3	124
51	Homoeologous Exchanges, Segmental Allopolyploidy, and Polyploid Genome Evolution. <i>Frontiers in Genetics</i> , 2020, 11, 1014.	2.3	124
52	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	12.8	115
53	The legacy of diploid progenitors in allopolyploid gene expression patterns. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130354.	4.0	111
54	Re-evaluating the phylogeny of allopolyploid <i>Gossypium</i> L.. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 45-52.	2.7	110

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55	Plant Mitochondrial Genome Evolution and Cytoplasmic Male Sterility. <i>Critical Reviews in Plant Sciences</i> , 2017, 36, 55-69.	5.7	105
56	Genomics of Evolutionary Novelty in Hybrids and Polyploids. <i>Frontiers in Genetics</i> , 2020, 11, 792.	2.3	103
57	Molecular Divergence Between Asian and North American Species of <i>Liriodendron</i> (Magnoliaceae) with Implications for Interpretation of Fossil Floras. <i>American Journal of Botany</i> , 1990, 77, 1243.	1.7	103
58	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. <i>BMC Genomics</i> , 2012, 13, 302.	2.8	102
59	Reevaluating the Origin of Domesticated Cotton (<i>Gossypium hirsutum</i> ; Malvaceae) Using Nuclear Restriction Fragment Length Polymorphisms (RFLPs). <i>American Journal of Botany</i> , 1994, 81, 1309.	1.7	98
60	GENETIC DIVERSITY IN A CLONAL NARROW ENDEMIC, <i>ERYTHRONIUM PROPELLANS</i> , AND IN ITS WIDESPREAD PROGENITOR, <i>ERYTHRONIUM ALBIDUM</i> . <i>American Journal of Botany</i> , 1989, 76, 1136-1151.	1.7	97
61	A majority of cotton genes are expressed in single-celled fiber. <i>Planta</i> , 2007, 227, 319-329.	3.2	97
62	A New Species of Cotton from Wake Atoll, <i>Gossypium stephensii</i> (Malvaceae). <i>Systematic Botany</i> , 2017, 42, 115-123.	0.5	94
63	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. <i>PLoS Genetics</i> , 2008, 4, e25.	3.5	93
64	The Origin and Evolution of <i>Gossypium</i> . , 2010, , 1-18.		92
65	Cladistic biogeography of <i>Gleditsia</i> (Leguminosae) based on <i>ndh F</i> and <i>rpl16</i> chloroplast gene sequences. <i>American Journal of Botany</i> , 1998, 85, 1753-1765.	1.7	91
66	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.	5.7	89
67	Trade-offs among anti-herbivore resistance traits: insights from <i>Gossypieae</i> (Malvaceae). <i>American Journal of Botany</i> , 2004, 91, 871-880.	1.7	87
68	Parallel expression evolution of oxidative stress-related genes in fiber from wild and domesticated diploid and polyploid cotton (<i>Gossypium</i>). <i>BMC Genomics</i> , 2009, 10, 378.	2.8	87
69	Gene expression in developing fibres of Upland cotton (<i>Gossypium hirsutum</i> L.) was massively altered by domestication. <i>BMC Biology</i> , 2010, 8, 139.	3.8	87
70	Recent Insights into Mechanisms of Genome Size Change in Plants. <i>Journal of Botany</i> , 2010, 2010, 1-8.	1.2	86
71	Persistence of Subgenomes in Paleopolyploid Cotton after 60 My of Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 1063-1071.	8.9	85
72	Phylogenetically Distinct Cellulose Synthase Genes Support Secondary Wall Thickening in <i>Arabidopsis</i> Shoot Trichomes and Cotton Fiber. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 205-220.	8.5	84

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73	Copy Number Lability and Evolutionary Dynamics of the <i>Adh</i> Gene Family in Diploid and Tetraploid Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2000, 155, 1913-1926.	2.9	83
74	Gene Expression Dominance in Allopolyploids: Hypotheses and Models. <i>Trends in Plant Science</i> , 2018, 23, 393-402.	8.8	81
75	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	5.5	80
76	Crop plants as models for understanding plant adaptation and diversification. <i>Frontiers in Plant Science</i> , 2013, 4, 290.	3.6	80
77	The miR319-Targeted GhTCP4 Promotes the Transition from Cell Elongation to Wall Thickening in Cotton Fiber. <i>Molecular Plant</i> , 2020, 13, 1063-1077.	8.3	79
78	Global analysis of gene expression in cotton fibers from wild and domesticated <i>Gossypium barbadense</i> . <i>Evolution & Development</i> , 2008, 10, 567-582.	2.0	77
79	Evolution of the BBAA Component of Bread Wheat during Its History at the Allohexaploid Level. <i>Plant Cell</i> , 2014, 26, 2761-2776.	6.6	77
80	A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. <i>Genetics</i> , 2006, 173, 1823-1827.	2.9	74
81	Genome-Wide Disruption of Gene Expression in Allopolyploids but Not Hybrids of Rice Subspecies. <i>Molecular Biology and Evolution</i> , 2014, 31, 1066-1076.	8.9	74
82	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
83	Proteomic profiling of developing cotton fibers from wild and domesticated <i>Gossypium barbadense</i> . <i>New Phytologist</i> , 2013, 200, 570-582.	7.3	72
84	Ancient Gene Duplicates in <i>Gossypium</i> (Cotton) Exhibit Near-Complete Expression Divergence. <i>Genome Biology and Evolution</i> , 2014, 6, 559-571.	2.5	72
85	<i>De Novo</i> Genome Sequence Assemblies of <i>Gossypium raimondii</i> and <i>Gossypium turneri</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3079-3085.	1.8	72
86	Intersimple sequence repeat (ISSR) polymorphisms as a genetic marker system in cotton. <i>Molecular Ecology Notes</i> , 2001, 1, 205-208.	1.7	69
87	GENETIC DIVERSITY, INTROGRESSION, AND INDEPENDENT DOMESTICATION OF OLD WORLD CULTIVATED COTTONS. <i>American Journal of Botany</i> , 1989, 76, 1795-1806.	1.7	68
88	<i>Cis</i> controls and regulatory novelty accompanying allopolyploidization. <i>New Phytologist</i> , 2019, 221, 1691-1700.	7.3	68
89	Designations for individual genomes and chromosomes in <i>Gossypium</i> . <i>Journal of Cotton Research</i> , 2018, 1, .	2.5	66
90	Cytoneuclear responses to genome doubling. <i>American Journal of Botany</i> , 2017, 104, 1277-1280.	1.7	62

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91	Parallel up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (<i>Gossypium</i>). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21152-21157.	7.1	61
92	The Cytonuclear Dimension of Allopolyploid Evolution: An Example from Cotton Using Rubisco. Molecular Biology and Evolution, 2012, 29, 3023-3036.	8.9	59
93	Chloroplast DNA Structural Variation, Phylogeny, and Age of Divergence among Diploid Cotton Species. PLoS ONE, 2016, 11, e0157183.	2.5	58
94	Unraveling cis and trans regulatory evolution during cotton domestication. Nature Communications, 2019, 10, 5399.	12.8	58
95	Parallel Domestication, Convergent Evolution and Duplicated Gene Recruitment in Allopolyploid Cotton. Genetics, 2008, 179, 1725-1733.	2.9	57
96	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. Molecular Biology and Evolution, 2008, 25, 1415-1428.	8.9	57
97	Cytonuclear Evolution of Rubisco in Four Allopolyploid Lineages. Molecular Biology and Evolution, 2014, 31, 2624-2636.	8.9	57
98	Diversity analysis of cotton (<i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. BMC Plant Biology, 2017, 17, 37.	3.6	56
99	Core cis-element variation confers subgenome-biased expression of a transcription factor that functions in cotton fiber elongation. New Phytologist, 2018, 218, 1061-1075.	7.3	56
100	DNA methylation repatterning accompanying hybridization, whole genome doubling and homoeolog exchange in nascent segmental rice allotetraploids. New Phytologist, 2019, 223, 979-992.	7.3	56
101	Ty1-copia-retrotransposon behavior in a polyploid cotton. Chromosome Research, 2000, 8, 73-76.	2.2	55
102	Genetic diversity in and phylogenetic relationships of the Brazilian endemic cotton, <i>Gossypium mustelinum</i> (Malvaceae). Plant Systematics and Evolution, 1994, 192, 49-59.	0.9	53
103	Genomically Biased Accumulation of Seed Storage Proteins in Allopolyploid Cotton. Genetics, 2011, 189, 1103-1115.	2.9	53
104	Plant speciation – rise of the poor cousins. New Phytologist, 2004, 161, 3-8.	7.3	52
105	Molecular evolution of the plastid genome during diversification of the cotton genus. Molecular Phylogenetics and Evolution, 2017, 112, 268-276.	2.7	52
106	Jeans, Genes, and Genomes: Cotton as a Model for Studying Polyploidy. , 2012, , 181-207.		50
107	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). BMC Genomics, 2010, 11, 395.	2.8	48
108	Targeted Capture of Homoeologous Coding and Noncoding Sequence in Polyploid Cotton. G3: Genes, Genomes, Genetics, 2012, 2, 921-930.	1.8	48

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109	Weedy Adaptation in <i>Setaria</i> spp. I. Isozyme Analysis of Genetic Diversity and Population Genetic Structure in <i>Setaria viridis</i> . <i>American Journal of Botany</i> , 1995, 82, 308.	1.7	47
110	WEEDY ADAPTATION IN <i>SETARIA</i> SPP. I. ISOZYME ANALYSIS OF GENETIC DIVERSITY AND POPULATION GENETIC STRUCTURE IN <i>SETARIA VIRIDIS</i> . <i>American Journal of Botany</i> , 1995, 82, 308-317.	1.7	45
111	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667 53-71.	2.5	45
112	Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. <i>Advanced Science</i> , 2021, 8, 2003634.	11.2	45
113	Bidirectional cytoplasmic and nuclear introgression in the New World cottons <i>Gossypium barbadense</i> and <i>G. Hirsutum</i> (Malvaceae). <i>American Journal of Botany</i> , 1993, 80, 1203-1208.	1.7	44
114	Genetic Diversity in a Clonal Narrow Endemic, <i>Erythronium propullans</i> , and in Its Widespread Progenitor, <i>Erythronium albidum</i> . <i>American Journal of Botany</i> , 1989, 76, 1136.	1.7	44
115	The history and disposition of transposable elements in polyploid <i>Gossypium</i> . <i>Genome</i> , 2010, 53, 599-607.	2.0	43
116	A reevaluation of the homoploid hybrid origin of <i>Aegilops tauschii</i> , the donor of the wheat D-subgenome. <i>New Phytologist</i> , 2015, 208, 4-8.	7.3	43
117	Rapid evolutionary divergence of <i>Gossypium barbadense</i> and <i>G. hirsutum</i> mitochondrial genomes. <i>BMC Genomics</i> , 2015, 16, 770.	2.8	42
118	Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids. <i>National Science Review</i> , 2021, 8, nwaa277.	9.5	42
119	The Genome Sequence of <i>Gossypoides kirkii</i> Illustrates a Descending Dysploidy in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1541.	3.6	41
120	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. <i>Molecular Biology and Evolution</i> , 2021, 38, 3621-3636.	8.9	41
121	Independent Domestication of Two Old World Cotton Species. <i>Genome Biology and Evolution</i> , 2016, 8, 1940-1947.	2.5	40
122	Evolutionary Conservation and Divergence of Gene Coexpression Networks in <i>Gossypium</i> (Cotton) Seeds. <i>Genome Biology and Evolution</i> , 2016, 8, evw280.	2.5	40
123	Genetic Diversity, Introgression, and Independent Domestication of Old World Cultivated Cottons. <i>American Journal of Botany</i> , 1989, 76, 1795.	1.7	38
124	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. <i>Genetics</i> , 2015, 200, 91-104.	2.9	37
125	Composition and Expression of Conserved MicroRNA Genes in Diploid Cotton (<i>Gossypium</i>) Species. <i>Genome Biology and Evolution</i> , 2013, 5, 2449-2459.	2.5	35
126	Insights into the Ecology and Evolution of Polyploid Plants through Network Analysis. <i>Molecular Ecology</i> , 2016, 25, 2644-2660.	3.9	35

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127	Segmental allotetraploidy generates extensive homoeologous expression rewiring and phenotypic diversity at the population level in rice. <i>Molecular Ecology</i> , 2017, 26, 5451-5466.	3.9	35
128	W<sc>eedy adaptation in</sc><i>S<sc>etaria</sc></i><sc>spp</sc>. II. G<sc>enetec diversity and population genetic structure in</sc><i>S<sc>glauca</sc>, S</i>. <sc><i>geniculata</i></sc>, <sc>and</sc><i>S<sc>faberii</sc></i> (P<sc>oaceae</sc>). <i>American Journal of Botany</i> , 1995, 82, 1031-1039.	1.7	34
129	Coordinated and Fine-Scale Control of Homoeologous Gene Expression in Allotetraploid Cotton. <i>Journal of Heredity</i> , 2009, 100, 487-490.	2.4	34
130	Salt–tolerance diversity in diploid and polyploid cotton (<i>Gossypium</i>) species. <i>Plant Journal</i> , 2020, 101, 1135-1151.	5.7	34
131	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. <i>Plant Journal</i> , 2016, 88, 992-1005.	5.7	33
132	Genomic and GWAS analyses demonstrate phylogenomic relationships of <i>Gossypium barbadense</i> in China and selection for fibre length, lint percentage and <i>Fusarium wilt</i> resistance. <i>Plant Biotechnology Journal</i> , 2022, 20, 691-710.	8.3	33
133	Multiple patterns of rDNA evolution following polyploidy in <i>Oryza</i> . <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 136-142.	2.7	32
134	Reticulate Evolution Helps Explain Apparent Homoplasmy in Floral Biology and Pollination in Baobabs (<i>Adansonia</i> ; <i>Bombacoideae</i> ; <i>Malvaceae</i>). <i>Systematic Biology</i> , 2020, 69, 462-478.	5.6	32
135	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
136	A Transcriptome Profile for Developing Seed of Polyploid Cotton. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.08.0041.	2.8	30
137	Conservation and Divergence in Duplicated Fiber Coexpression Networks Accompanying Domestication of the Polyploid <i>Gossypium hirsutum</i> L. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2879-2892.	1.8	30
138	Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in <i>Panax</i> . <i>Nature Communications</i> , 2022, 13, 1902.	12.8	30
139	The Utility of Graph Clustering of 5S Ribosomal DNA Homoeologs in Plant Allopolyploids, Homoploid Hybrids, and Cryptic Introgressants. <i>Frontiers in Plant Science</i> , 2020, 11, 41.	3.6	28
140	Morphological Diversity and Relationships in the A–Genome Cottons, <i>Gossypium arboreum</i> and <i>G. herbaceum</i> . <i>Crop Science</i> , 1994, 34, 519-527.	1.8	26
141	Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (<i>Gossypieae</i>) Yields Insights into Genome Downsizing. <i>Genome Biology and Evolution</i> , 2017, 9, 3328-3344.	2.5	26
142	Proteomics profiling of fiber development and domestication in upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tff	3.2	25
143	Gene-body CG methylation and divergent expression of duplicate genes in rice. <i>Scientific Reports</i> , 2017, 7, 2675.	3.3	25
144	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 12-31.	8.5	25

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145	Genome-wide characterization of the GRF family and their roles in response to salt stress in <i>Gossypium</i> . <i>BMC Genomics</i> , 2020, 21, 575.	2.8	23
146	Homoeologous gene expression and co-expression network analyses and evolutionary inference in allopolyploids. <i>Briefings in Bioinformatics</i> , 2021, 22, 1819-1835.	6.5	23
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