Xianlong Zhang

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172 papers	8,135 citations	51 h-index	85 g-index
187 ext. papers	11,523 ext. citations	7.4 avg, IF	6.16 L-index

#	Paper	IF	Citations
172	Genome sequence of cultivated Upland cotton (Gossypium hirsutum TM-1) provides insights into genome evolution. *Nature Biotechnology*, **2015**, 33, 524-30	44.5	683
171	Lignin metabolism has a central role in the resistance of cotton to the wilt fungus Verticillium dahliae as revealed by RNA-Seq-dependent transcriptional analysis and histochemistry. *Journal of Experimental Botany*, **2011**, 62, 5607-21	7	284
170	Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense. *Nature Genetics*, **2019**, 51, 224-229	36.3	266
169	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. *Nature Genetics*, **2017**, 49, 579-587	36.3	229
168	Expression of an Arabidopsis vacuolar H+-pyrophosphatase gene (AVP1) in cotton improves drought- and salt tolerance and increases fibre yield in the field conditions. *Plant Biotechnology Journal*, **2011**, 9, 88-99	11.6	209
167	Regulation of Somatic Embryogenesis in Higher Plants. *Critical Reviews in Plant Sciences*, **2010**, 29, 36-57	5.6	202
166	The genome sequence of Sea-Island cotton (Gossypium barbadense) provides insights into the allopolyploidization and development of superior spinnable fibres. *Scientific Reports*, **2015**, 5, 17662	4.9	181
165	A comprehensive meta QTL analysis for fiber quality, yield, yield related and morphological traits, drought tolerance, and disease resistance in tetraploid cotton. *BMC Genomics*, **2013**, 14, 776	4.5	154
164	Small RNA and degradome sequencing reveal complex miRNA regulation during cotton somatic embryogenesis. *Journal of Experimental Botany*, **2013**, 64, 1521-36	7	146
163	Drought coping strategies in cotton: increased crop per drop. *Plant Biotechnology Journal*, **2017**, 15, 271-284	11.6	142
162	Overexpression of rice NAC gene SNAC1 improves drought and salt tolerance by enhancing root development and reducing transpiration rate in transgenic cotton. *PLoS ONE*, **2014**, 9, e86895	3.7	139
161	CRISPR/Cas System: Recent Advances and Future Prospects for Genome Editing. *Trends in Plant Science*, **2019**, 24, 1102-1125	13.1	135
160	Sugar and auxin signaling pathways respond to high-temperature stress during anther development as revealed by transcript profiling analysis in cotton. *Plant Physiology*, **2014**, 164, 1293-308	6.6	129
159	High efficient multisites genome editing in allotetraploid cotton (Gossypium hirsutum) using CRISPR/Cas9 system. *Plant Biotechnology Journal*, **2018**, 16, 137-150	11.6	127
158	A comparative meta-analysis of QTL between intraspecific Gossypium hirsutum and interspecific G. hirsutum G. barbadense populations. *Molecular Genetics and Genomics*, **2015**, 290, 1003-25	3.1	124
157	Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC1 population between gossypium hirsutum and G. barbadense. *BMC Genomics*, **2011**, 12, 15	4.5	124
156	Long noncoding RNAs and their proposed functions in fibre development of cotton (Gossypium spp.). *New Phytologist*, **2015**, 207, 1181-97	9.8	112

155	GbTCP, a cotton TCP transcription factor, confers fibre elongation and root hair development by a complex regulating system. *Journal of Experimental Botany*, **2012**, 63, 6267-81	7	106
154	Population structure and genetic basis of the agronomic traits of upland cotton in China revealed by a genome-wide association study using high-density SNPs. *Plant Biotechnology Journal*, **2017**, 15, 1374-1386	11.6	99
153	Engineered chloroplast dsRNA silences cytochrome p450 monooxygenase, V-ATPase and chitin synthase genes in the insect gut and disrupts Helicoverpa zea larval development and pupation. *Plant Biotechnology Journal*, **2015**, 13, 435-46	11.6	96
152	Whole genome sequencing reveals rare off-target mutations and considerable inherent genetic or/and somaclonal variations in CRISPR/Cas9-edited cotton plants. *Plant Biotechnology Journal*, **2019**, 17, 858-868	11.6	96
151	A global survey of alternative splicing in allopolyploid cotton: landscape, complexity and regulation. *New Phytologist*, **2018**, 217, 163-178	9.8	95
150	Cotton WRKY1 mediates the plant defense-to-development transition during infection of cotton by Verticillium dahliae by activating JASMONATE ZIM-DOMAIN1 expression. *Plant Physiology*, **2014**, 166, 2179-94	6.6	94
149	Transcript profiling reveals complex auxin signalling pathway and transcription regulation involved in dedifferentiation and redifferentiation during somatic embryogenesis in cotton. *BMC Plant Biology*, **2012**, 12, 110	5.3	94
148	Laccase GhLac1 Modulates Broad-Spectrum Biotic Stress Tolerance via Manipulating Phenylpropanoid Pathway and Jasmonic Acid Synthesis. *Plant Physiology*, **2018**, 176, 1808-1823	6.6	94
147	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. *Nature Plants*, **2018**, 4, 90-97	11.5	82
146	Factors affecting transformation efficiency of embryogenic callus of Upland cotton (Gossypium hirsutum) with Agrobacterium tumefaciens. *Plant Cell, Tissue and Organ Culture*, **2005**, 81, 229-237	2.7	82
145	A genetic and metabolic analysis revealed that cotton fiber cell development was retarded by flavonoid naringenin. *Plant Physiology*, **2013**, 162, 86-95	6.6	81
144	The calcium sensor GhCaM7 promotes cotton fiber elongation by modulating reactive oxygen species (ROS) production. *New Phytologist*, **2014**, 202, 509-520	9.8	81
143	GbPDF1 is involved in cotton fiber initiation via the core cis-element HDZIP2ATATHB2. *Plant Physiology*, **2012**, 158, 890-904	6.6	81
142	CRISPR/Cas Systems in Genome Editing: Methodologies and Tools for sgRNA Design, Off-Target Evaluation, and Strategies to Mitigate Off-Target Effects. *Advanced Science*, **2020**, 7, 1902312	13.6	79
141	Long noncoding RNAs involve in resistance to Verticillium dahliae, a fungal disease in cotton. *Plant Biotechnology Journal*, **2018**, 16, 1172-1185	11.6	77
140	GhJAZ2 negatively regulates cotton fiber initiation by interacting with the R2R3-MYB transcription factor GhMYB25-like. *Plant Journal*, **2016**, 88, 921-935	6.9	76
139	Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway. *Nature Communications*, **2014**, 5, 5372	17.4	75
138	Comparative transcriptome analysis between somatic embryos (SEs) and zygotic embryos in cotton: evidence for stress response functions in SE development. *Plant Biotechnology Journal*, **2014**, 12, 161-73	11.6	72

137	Transcriptome analysis reveals a comprehensive insect resistance response mechanism in cotton to infestation by the phloem feeding insect Bemisia tabaci (whitefly). *Plant Biotechnology Journal*, **2016**, 14, 1956-75	11.6	72
136	Detection of somaclonal variation of cotton (Gossypium hirsutum) using cytogenetics, flow cytometry and molecular markers. *Plant Cell Reports*, **2008**, 27, 1303-16	5.1	71
135	An ethylene response-related factor, GbERF1-like, from Gossypium barbadense improves resistance to Verticillium dahliae via activating lignin synthesis. *Plant Molecular Biology*, **2016**, 91, 305-18	4.6	65
134	Suitable internal control genes for qRT-PCR normalization in cotton fiber development and somatic embryogenesis. *Science Bulletin*, **2007**, 52, 3110-3117		64
133	microRNAs involved in auxin signalling modulate male sterility under high-temperature stress in cotton (Gossypium hirsutum). *Plant Journal*, **2017**, 91, 977-994	6.9	63
132	A novel cotton WRKY gene, GhWRKY6-like, improves salt tolerance by activating the ABA signaling pathway and scavenging of reactive oxygen species. *Physiologia Plantarum*, **2018**, 162, 439-454	4.6	63
131	Small RNA and degradome profiling reveals a role for miRNAs and their targets in the developing fibers of Gossypium barbadense. *Plant Journal*, **2014**, 80, 331-44	6.9	63
130	Genome-wide SSR-based association mapping for fiber quality in nation-wide upland cotton inbreed cultivars in China. *BMC Genomics*, **2016**, 17, 352	4.5	63
129	High-efficient and precise base editing of C□G to T□A in the allotetraploid cotton (Gossypium hirsutum) genome using a modified CRISPR/Cas9 system. *Plant Biotechnology Journal*, **2020**, 18, 45-56	11.6	63
128	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. *Nature Communications*, **2019**, 10, 4702	17.4	62
127	Molecular cloning and functional characterization of a novel cotton CBL-interacting protein kinase gene (GhCIPK6) reveals its involvement in multiple abiotic stress tolerance in transgenic plants. *Biochemical and Biophysical Research Communications*, **2013**, 435, 209-15	3.4	62
126	Pinellia ternata agglutinin expression in chloroplasts confers broad spectrum resistance against aphid, whitefly, Lepidopteran insects, bacterial and viral pathogens. *Plant Biotechnology Journal*, **2012**, 10, 313-27	11.6	58
125	Factors affecting somatic embryogenesis and plant regeneration from a range of recalcitrant genotypes of Chinese cottons (Gossypium hirsutum L.). *In Vitro Cellular and Developmental Biology - Plant*, **2004**, 40, 371-375	2.3	56
124	High-density Linkage Map of Cultivated Allotetraploid Cotton Based on SSR, TRAP, SRAP and AFLP Markers. *Journal of Integrative Plant Biology*, **2007**, 49, 716-724	8.3	54
123	A high-density integrative linkage map for Gossypium hirsutum. *Euphytica*, **2009**, 166, 35-45	2.1	53
122	GhATAF1, a NAC transcription factor, confers abiotic and biotic stress responses by regulating phytohormonal signaling networks. *Plant Cell Reports*, **2016**, 35, 2167-79	5.1	51
121	Expression of the Arabidopsis vacuolar H+-pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. *Plant Biotechnology Reports*, **2013**, 7, 345-355	2.5	51
120	Genome editing with the CRISPR-Cas system: an art, ethics and global regulatory perspective. *Plant Biotechnology Journal*, **2020**, 18, 1651-1669	11.6	50

119	GbEXPATR, a species-specific expansin, enhances cotton fibre elongation through cell wall restructuring. *Plant Biotechnology Journal*, **2016**, 14, 951-63	11.6	50
118	Suppression of GhAGP4 gene expression repressed the initiation and elongation of cotton fiber. *Plant Cell Reports*, **2010**, 29, 193-202	5.1	49
117	Down-regulating annexin gene GhAnn2 inhibits cotton fiber elongation and decreases Ca2+ influx at the cell apex. *Plant Molecular Biology*, **2014**, 85, 613-25	4.6	48
116	Cotton GhCKI disrupts normal male reproduction by delaying tapetum programmed cell death via inactivating starch synthase. *Plant Journal*, **2013**, 75, 823-35	6.9	47
115	Robust CRISPR/Cpf1 (Cas12a)-mediated genome editing in allotetraploid cotton (Gossypium hirsutum). *Plant Biotechnology Journal*, **2019**, 17, 1862-1864	11.6	46
114	Multi-omics analyses reveal epigenomics basis for cotton somatic embryogenesis through successive regeneration acclimation process. *Plant Biotechnology Journal*, **2019**, 17, 435-450	11.6	46
113	Small RNA-mediated responses to low- and high-temperature stresses in cotton. *Scientific Reports*, **2016**, 6, 35558	4.9	44
112	Disrupted Genome Methylation in Response to High Temperature Has Distinct Affects on Microspore Abortion and Anther Indehiscence. *Plant Cell*, **2018**, 30, 1387-1403	11.6	43
111	Suppression of the homeobox gene HDTF1 enhances resistance to Verticillium dahliae and Botrytis cinerea in cotton. *Journal of Integrative Plant Biology*, **2016**, 58, 503-13	8.3	43
110	Expression profile analysis of genes involved in cell wall regeneration during protoplast culture in cotton by suppression subtractive hybridization and macroarray. *Journal of Experimental Botany*, **2008**, 59, 3661-74	7	41
109	Fibre elongation requires normal redox homeostasis modulated by cytosolic ascorbate peroxidase in cotton (Gossypium hirsutum). *Journal of Experimental Botany*, **2016**, 67, 3289-301	7	40
108	Functional characterization of cotton genes responsive to Verticillium dahliae through bioinformatics and reverse genetics strategies. *Journal of Experimental Botany*, **2014**, 65, 6679-92	7	40
107	Characteristics and analysis of simple sequence repeats in the cotton genome based on a linkage map constructed from a BC1 population between Gossypium hirsutum and G. barbadense. *Genome*, **2008**, 51, 534-46	2.4	38
106	Production and characterization of somatic hybrids between upland cotton (Gossypium hirsutum) and wild cotton (G. klotzschianum Anderss) via electrofusion. *Theoretical and Applied Genetics*, **2004** , 109, 472-9	6	38
105	MicroRNA 157-targeted SPL genes regulate floral organ size and ovule production in cotton. *BMC Plant Biology*, **2017**, 17, 7	5.3	37
104	Transgenic Cotton Plants Expressing Double-stranded RNAs Target HMG-CoA Reductase (HMGR) Gene Inhibits the Growth, Development and Survival of Cotton Bollworms. *International Journal of Biological Sciences*, **2015**, 11, 1296-305	11.2	37
103	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. *BMC Plant Biology*, **2018**, 18, 150	5.3	36
102	ROS Homeostasis Regulates Somatic Embryogenesis via the Regulation of Auxin Signaling in Cotton. *Molecular and Cellular Proteomics*, **2016**, 15, 2108-24	7.6	36

101	GhJAZ2 attenuates cotton resistance to biotic stresses via the inhibition of the transcriptional activity of GhbHLH171. *Molecular Plant Pathology*, **2018**, 19, 896-908	5.7	35
100	GbMPK3, a mitogen-activated protein kinase from cotton, enhances drought and oxidative stress tolerance in tobacco. *Plant Cell, Tissue and Organ Culture*, **2014**, 116, 153-162	2.7	34
99	GhTZF1 regulates drought stress responses and delays leaf senescence by inhibiting reactive oxygen species accumulation in transgenic Arabidopsis. *Plant Molecular Biology*, **2014**, 85, 163-77	4.6	34
98	The JASMONATE ZIM-Domain Gene Family Mediates JA Signaling and Stress Response in Cotton. *Plant and Cell Physiology*, **2017**, 58, 2139-2154	4.9	34
97	Analysis of genes differentially expressed during initial cellular dedifferentiation in cotton. *Science Bulletin*, **2008**, 53, 3666-3676		34
96	Defective pollen wall contributes to male sterility in the male sterile line 1355A of cotton. *Scientific Reports*, **2015**, 5, 9608	4.9	33
95	Transcriptomic repertoires depict the initiation of lint and fuzz fibres in cotton (Gossypium hirsutum L.). *Plant Biotechnology Journal*, **2018**, 16, 1002-1012	11.6	33
94	Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation. *Nucleic Acids Research*, **2016**, 44, 4067-79	20.1	33
93	Exogenous Jasmonic Acid Inhibits Cotton Fiber Elongation. *Journal of Plant Growth Regulation*, **2012**, 31, 599-605	4.7	32
92	GhCPK33 Negatively Regulates Defense against by Phosphorylating GhOPR3. *Plant Physiology*, **2018**, 178, 876-889	6.6	32
91	The GhmiR157a-GhSPL10 regulatory module controls initial cellular dedifferentiation and callus proliferation in cotton by modulating ethylene-mediated flavonoid biosynthesis. *Journal of Experimental Botany*, **2018**, 69, 1081-1093	7	30
90	An efficient grafting system for transgenic plant recovery in cotton (Gossypium hirsutum L.). *Plant Cell, Tissue and Organ Culture*, **2006**, 85, 181-185	2.7	30
89	QTL Mapping for Fiber Quality and Yield Traits Based on Introgression Lines Derived from Gossypium hirsutum G. tomentosum. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	28
88	Linkage and association mapping reveals the genetic basis of brown fibre (Gossypium hirsutum). *Plant Biotechnology Journal*, **2018**, 16, 1654	11.6	27
87	A transgenic strategy for controlling plant bugs (Adelphocoris suturalis) through expression of double-stranded RNA homologous to fatty acyl-coenzyme A reductase in cotton. *New Phytologist*, **2017**, 215, 1173-1185	9.8	26
86	GhHmgB3 deficiency deregulates proliferation and differentiation of cells during somatic embryogenesis in cotton. *Plant Biotechnology Journal*, **2011**, 9, 1038-48	11.6	26
85	Structure, evolution, and comparative genomics of tetraploid cotton based on a high-density genetic linkage map. *DNA Research*, **2016**, 23, 283-93	4.5	25
84	Generation, annotation and analysis of first large-scale expressed sequence tags from developing fiber of Gossypium barbadense L. *PLoS ONE*, **2011**, 6, e22758	3.7	25

83	LEAFY COTYLEDON1-CASEIN KINASE I-TCP15-PHYTOCHROME INTERACTING FACTOR4 Network Regulates Somatic Embryogenesis by Regulating Auxin Homeostasis. *Plant Physiology*, **2015**, 169, 2805-21	6.6	24
82	A peptide hormone gene, GhPSK promotes fibre elongation and contributes to longer and finer cotton fibre. *Plant Biotechnology Journal*, **2014**, 12, 861-71	11.6	24
81	Development of EST-based SNP and InDel markers and their utilization in tetraploid cotton genetic mapping. *BMC Genomics*, **2014**, 15, 1046	4.5	24
80	Identification of Multiple Stress Responsive Genes by Sequencing a Normalized cDNA Library from Sea-Land Cotton (Gossypium barbadense L.). *PLoS ONE*, **2016**, 11, e0152927	3.7	23
79	The chromosome-level wintersweet (Chimonanthus praecox) genome provides insights into floral scent biosynthesis and flowering in winter. *Genome Biology*, **2020**, 21, 200	18.3	23
78	Transfer of tomato immune receptor Ve1 confers Ave1-dependent Verticillium resistance in tobacco and cotton. *Plant Biotechnology Journal*, **2018**, 16, 638-648	11.6	23
77	Metabolic engineering of cottonseed oil biosynthesis pathway via RNA interference. *Scientific Reports*, **2016**, 6, 33342	4.9	22
76	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. *New Phytologist*, **2020**, 226, 1738-1752	9.8	22
75	Suppression of tryptophan synthase activates cotton immunity by triggering cell death via promoting SA synthesis. *Plant Journal*, **2019**, 98, 329-345	6.9	22
74	The Calcium Sensor CBL2 and Its Interacting Kinase CIPK6 Are Involved in Plant Sugar Homeostasis via Interacting with Tonoplast Sugar Transporter TST2. *Plant Physiology*, **2020**, 183, 236-249	6.6	21
73	Population genomics reveals a fine-scale recombination landscape for genetic improvement of cotton. *Plant Journal*, **2019**, 99, 494-505	6.9	20
72	The application of a heat-inducible CRISPR/Cas12b (C2c1) genome editing system in tetraploid cotton (G.hirsutum) plants. *Plant Biotechnology Journal*, **2020**, 18, 2436-2443	11.6	20
71	GbSOBIR1 confers Verticillium wilt resistance by phosphorylating the transcriptional factor GbbHLH171 in Gossypium barbadense. *Plant Biotechnology Journal*, **2019**, 17, 152-163	11.6	20
70	Genome-wide identification and characterization of TALE superfamily genes in cotton reveals their functions in regulating secondary cell wall biosynthesis. *BMC Plant Biology*, **2019**, 19, 432	5.3	20
69	Crosstalk between cytokinin and ethylene signaling pathways regulates leaf abscission in cotton in response to chemical defoliants. *Journal of Experimental Botany*, **2019**, 70, 1525-1538	7	20
68	High-oleic acid content, nontransgenic allotetraploid cotton (Gossypium hirsutum L.) generated by knockout of GhFAD2 genes with CRISPR/Cas9 system. *Plant Biotechnology Journal*, **2021**, 19, 424-426	11.6	19
67	Genetic mapping and characteristics of genes specifically or preferentially expressed during fiber development in cotton. *PLoS ONE*, **2013**, 8, e54444	3.7	18
66	ABA signaling is negatively regulated by GbWRKY1 through JAZ1 and ABI1 to affect salt and drought tolerance. *Plant Cell Reports*, **2020**, 39, 181-194	5.1	18

65	Interaction between calcium and potassium modulates elongation rate in cotton fiber cells. *Journal of Experimental Botany*, **2017**, 68, 5161-5175	7	16
64	Studies of new EST-SSRs derived from Gossypium barbadense. *Science Bulletin*, **2007**, 52, 2522-2531		16
63	Linkage mapping and expression analysis of miRNAs and their target genes during fiber development in cotton. *BMC Genomics*, **2013**, 14, 706	4.5	15
62	Increasing cotton genome coverage with polymorphic SSRs as revealed by SSCP. *Genome*, **2012**, 55, 459-70	2.4	15
61	A cotton fiber-preferential promoter, PGbEXPA2, is regulated by GA and ABA in Arabidopsis. *Plant Cell Reports*, **2015**, 34, 1539-49	5.1	14
60	The Acer truncatum genome provides insights into nervonic acid biosynthesis. *Plant Journal*, **2020**, 104, 662-678	6.9	14
59	Phenomics-based GWAS analysis reveals the genetic architecture for drought resistance in cotton. *Plant Biotechnology Journal*, **2020**, 18, 2533-2544	11.6	13
58	GhL1L1 affects cell fate specification by regulating GhPIN1-mediated auxin distribution. *Plant Biotechnology Journal*, **2019**, 17, 63-74	11.6	13
57	Genome-wide identification of MAPK cascade genes reveals the GhMAP3K14-GhMKK11-GhMPK31 pathway is involved in the drought response in cotton. *Plant Molecular Biology*, **2020**, 103, 211-223	4.6	12
56	Transgenic Bt cotton driven by the green tissue-specific promoter shows strong toxicity to lepidopteran pests and lower Bt toxin accumulation in seeds. *Science China Life Sciences*, **2016**, 59, 172-82	8.5	12
55	Overexpression of Arabidopsis cyclin D2;1 in cotton results in leaf curling and other plant architectural modifications. *Plant Cell, Tissue and Organ Culture*, **2012**, 110, 261-273	2.7	12
54	Development and Evaluation of Intron and Insertion–Deletion Markers for Gossypium barbadense. *Plant Molecular Biology Reporter*, **2012**, 30, 605-613	1.7	11
53	The application of temperature sensitivity CRISPR/LbCpf1 (LbCas12a) mediated genome editing in allotetraploid cotton (G. hirsutum) and creation of nontransgenic, gossypol-free cotton. *Plant Biotechnology Journal*, **2021**, 19, 221-223	11.6	11
52	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. *Genome Biology*, **2021**, 22, 119	18.3	10
51	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. *Molecular Biology and Evolution*, **2021**, 38, 3621-3636	8.3	10
50	Genetic dissection of an allotetraploid interspecific CSSLs guides interspecific genetics and breeding in cotton. *BMC Genomics*, **2020**, 21, 431	4.5	9
49	Transcriptomic profiles of non-embryogenic and embryogenic callus cells in a highly regenerative upland cotton line (Gossypium hirsutum L.). *BMC Developmental Biology*, **2020**, 20, 25	3.1	9
48	Isolation, characterization and mapping of genes differentially expressed during fibre development between Gossypium hirsutum and G. barbadense by cDNA-SRAP. *Journal of Genetics*, **2013**, 92, 175-181	1.2	8

47	Functional Markers for Cellulose Synthase and Their Comparison to SSRs in Cotton. *Plant Molecular Biology Reporter*, **2012**, 30, 1270-1275	1.7	8
46	Structural insights into homotrimeric assembly of cellulose synthase CesA7 from Gossypium hirsutum. *Plant Biotechnology Journal*, **2021**, 19, 1579-1587	11.6	8
45	Efficient CRISPR/Cas9 mediated Pooled-sgRNAs assembly accelerates targeting multiple genes related to male sterility in cotton. *Plant Methods*, **2021**, 17, 16	5.8	8
44	A Single-Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in. *Advanced Science*, **2021**, 8, 2002723	13.6	8
43	The cotton HD-Zip transcription factor GhHB12 regulates flowering time and plant architecture via the GhmiR157-GhSPL pathway. *Communications Biology*, **2018**, 1, 229	6.7	8
42	Proteomic analysis reveals that sugar and fatty acid metabolisms play a central role in sterility of the male-sterile line 1355A of cotton. *Journal of Biological Chemistry*, **2019**, 294, 7057-7067	5.4	7
41	Phenylpropanoid metabolism and pigmentation show divergent patterns between brown color and green color cottons as revealed by metabolic and gene expression analyses. *Journal of Cotton Research*, **2020**, 3,	2.3	7
40	Repression of microRNA 160 results in retarded seed integument growth and smaller final seed size in cotton. *Crop Journal*, **2020**, 8, 602-612	4.6	7
39	Red fluorescent protein (DsRed2), an ideal reporter for cotton genetic transformation and molecular breeding. *Crop Journal*, **2018**, 6, 366-376	4.6	7
38	Unbiased genomic distribution of genes related to cell morphogenesis in cotton by chromosome mapping. *Plant Cell, Tissue and Organ Culture*, **2012**, 108, 529-534	2.7	7
37	Ascorbate Alleviates Fe Deficiency-Induced Stress in Cotton () by Modulating ABA Levels. *Frontiers in Plant Science*, **2016**, 7, 1997	6.2	7
36	Plant 3D genomics: the exploration and application of chromatin organization. *New Phytologist*, **2021**, 230, 1772-1786	9.8	7
35	GhWRKY1-like enhances cotton resistance to Verticillium dahliae via an increase in defense-induced lignification and S monolignol content. *Plant Science*, **2021**, 305, 110833	5.3	7
34	Transcriptome and metabolome analysis reveal that oral secretions from Helicoverpa armigera and Spodoptera litura influence wound-induced host response in cotton. *Crop Journal*, **2020**, 8, 929-942	4.6	6
33	Genomic heterozygosity and hybrid breakdown in cotton (Gossypium): different traits, different effects. *BMC Genetics*, **2016**, 17, 58	2.6	6
32	Herbicide Resistance: Another Hot Agronomic Trait for Plant Genome Editing. *Plants*, **2021**, 10,	4.5	6
31	GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to Verticillium dahliae. *Plant Cell Reports*, **2021**, 40, 735-751	5.1	6
30	Phenotypic plasticity and genetic variation of cotton yield and its related traits under water-limited conditions. *Crop Journal*, **2020**, 8, 966-976	4.6	5

29	The laccase gene GhLac1 modulates fiber initiation and elongation by coordinating jasmonic acid and flavonoid metabolism. *Crop Journal*, **2020**, 8, 522-533	4.6	5
28	Promoters of Arabidopsis Casein kinase I-like 2 and 7 confer specific high-temperature response in anther. *Plant Molecular Biology*, **2018**, 98, 33-49	4.6	5
27	GhH2A12, a replication-dependent histone H2A gene from Gossypium hirsutum, is negatively involved in the development of cotton fiber cells. *Plant Cell Reports*, **2014**, 33, 1711-21	5.1	5
26	High day and night temperatures distinctively disrupt fatty acid and jasmonic acid metabolism, inducing male sterility in cotton. *Journal of Experimental Botany*, **2020**, 71, 6128-6141	7	5
25	Phosphate deficiency enhances cotton resistance to Verticillium dahliae through activating jasmonic acid biosynthesis and phenylpropanoid pathway. *Plant Science*, **2021**, 302, 110724	5.3	5
24	Isolation, characterization and mapping of genes differentially expressed during fibre development between Gossypium hirsutum and G. barbadense by cDNA-SRAP. *Journal of Genetics*, **2013**, 92, 175-81	1.2	5
23	Comparison and development of EST-SSRs from two 454 sequencing libraries of Gossypium barbadense. *Euphytica*, **2014**, 198, 277-288	2.1	4
22	Orchestration of plant development and defense by indirect crosstalk of salicylic acid and brassinosteorid signaling via transcription factor GhTINY2. *Journal of Experimental Botany*, **2021**, 72, 4721-4743	7	4
21	A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. *New Phytologist*, **2021**, 231, 165-181	9.8	4
20	The Sophora Alopecuroid H + -PPase Gene SaVP1 Confers Multiple Abiotic Stress Tolerance in Arabidopsis. *Plant Molecular Biology Reporter*, **2015**, 33, 923-930	1.7	3
19	Genome Sequencing. *Agronomy*, **2015**, 289-302	0.8	3
18	Flavonoid Pathway in Cotton Fiber Development. *Scientia Sinica Vitae*, **2014**, 44, 758-765	1.4	3
17	Mapped SSR markers unevenly distributed on the cotton chromosomes. *Frontiers of Agriculture in China*, **2010**, 4, 257-264		2
16	Multi-Omics-Based Identification and Functional Characterization of Proves Its Potential Role in Drought Stress Tolerance in. *Frontiers in Plant Science*, **2021**, 12, 746771	6.2	2
15	Genome-wide identification of cotton GRAM family proteins reveals that GRAM31 regulates fiber length. *Journal of Experimental Botany*, **2021**, 72, 2477-2490	7	2
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