

Xianlong Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Genomic interrogation of a MAGIC population highlights genetic factors controlling fiber quality traits in cotton.. <i>Communications Biology</i> , 2022 , 5, 60	6.7	0
171	RNA-Seq with a novel glabrous-ZM24fl reveals some key lncRNAs and the associated targets in fiber initiation of cotton.. <i>BMC Plant Biology</i> , 2022 , 22, 61	5.3	1
170	Dynamic 3D genome architecture of cotton fiber reveals subgenome-coordinated chromatin topology for 4-staged single-cell differentiation.. <i>Genome Biology</i> , 2022 , 23, 45	18.3	0
169	Identification and Functional Analysis of lncRNA by CRISPR/Cas9 During the Cotton Response to Sap-Sucking Insect Infestation.. <i>Frontiers in Plant Science</i> , 2022 , 13, 784511	6.2	0
168	Development of an efficient and precise adenine base editor (ABE) with expanded target range in allotetraploid cotton (<i>Gossypium hirsutum</i>).. <i>BMC Biology</i> , 2022 , 20, 45	7.3	0
167	Fast anther dehiscence status recognition system established by deep learning to screen heat tolerant cotton.. <i>Plant Methods</i> , 2022 , 18, 53	5.8	
166	A super PPR cluster for restoring fertility revealed by genetic mapping, homocap-seq and de novo assembly in cotton. <i>Theoretical and Applied Genetics</i> , 2021 , 1	6	0
165	Plant Single Cell Transcriptome Hub (PsctH): an integrated online tool to explore the plant single-cell transcriptome landscape. <i>Plant Biotechnology Journal</i> , 2021 ,	11.6	1
164	Multi-Omics-Based Identification and Functional Characterization of Proves Its Potential Role in Drought Stress Tolerance in. <i>Frontiers in Plant Science</i> , 2021 , 12, 746771	6.2	2
163	Genome-wide identification of cotton GRAM family proteins reveals that GRAM31 regulates fiber length. <i>Journal of Experimental Botany</i> , 2021 , 72, 2477-2490	7	2
162	Herbicide Resistance: Another Hot Agronomic Trait for Plant Genome Editing. <i>Plants</i> , 2021 , 10,	4.5	6
161	Plant 3D genomics: the exploration and application of chromatin organization. <i>New Phytologist</i> , 2021 , 230, 1772-1786	9.8	7
160	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021 , 22, 119	18.3	10
159	GhWRKY1-like enhances cotton resistance to <i>Verticillium dahliae</i> via an increase in defense-induced lignification and S monolignol content. <i>Plant Science</i> , 2021 , 305, 110833	5.3	7
158	Orchestration of plant development and defense by indirect crosstalk of salicylic acid and brassinosteroid signaling via transcription factor GhTINY2. <i>Journal of Experimental Botany</i> , 2021 , 72, 4721-4743	7	4
157	Structural insights into homotrimeric assembly of cellulose synthase CesA7 from <i>Gossypium hirsutum</i> . <i>Plant Biotechnology Journal</i> , 2021 , 19, 1579-1587	11.6	8
156	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	8.3	10

155	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021 , 21, 229	5.3	1
154	A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. <i>New Phytologist</i> , 2021 , 231, 165-181	9.8	4
153	Gossypium tomentosum genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. <i>Genomics</i> , 2021 , 113, 1999-2004	4.3	2
152	Phosphate deficiency enhances cotton resistance to <i>Verticillium dahliae</i> through activating jasmonic acid biosynthesis and phenylpropanoid pathway. <i>Plant Science</i> , 2021 , 302, 110724	5.3	5
151	High-oleic acid content, nontransgenic allotetraploid cotton (<i>Gossypium hirsutum</i> L.) generated by knockout of GhFAD2 genes with CRISPR/Cas9 system. <i>Plant Biotechnology Journal</i> , 2021 , 19, 424-426	11.6	19
150	The application of temperature sensitivity CRISPR/LbCpf1 (LbCas12a) mediated genome editing in allotetraploid cotton (<i>G.hirsutum</i>) and creation of nontransgenic, gossypol-free cotton. <i>Plant Biotechnology Journal</i> , 2021 , 19, 221-223	11.6	11
149	Efficient CRISPR/Cas9 mediated Pooled-sgRNAs assembly accelerates targeting multiple genes related to male sterility in cotton. <i>Plant Methods</i> , 2021 , 17, 16	5.8	8
148	GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to <i>Verticillium dahliae</i> . <i>Plant Cell Reports</i> , 2021 , 40, 735-751	5.1	6
147	A Single-Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in. <i>Advanced Science</i> , 2021 , 8, 2002723	13.6	8
146	Disruption of topologically associating domains by structural variations in tetraploid cottons. <i>Genomics</i> , 2021 , 113, 3405-3414	4.3	0
145	Silencing of aLLIM gene in cotton exhibits enhanced resistance against <i>Apolygus lucorum</i> . <i>Journal of Cellular Physiology</i> , 2021 , 236, 5921-5936	7	0
144	Phenylpropanoid metabolism and pigmentation show divergent patterns between brown color and green color cottons as revealed by metabolic and gene expression analyses. <i>Journal of Cotton Research</i> , 2020 , 3,	2.3	7
143	The application of a heat-inducible CRISPR/Cas12b (C2c1) genome editing system in tetraploid cotton (<i>G.hirsutum</i>) plants. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2436-2443	11.6	20
142	Phenomix-based GWAS analysis reveals the genetic architecture for drought resistance in cotton. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2533-2544	11.6	13
141	Genome-wide identification of MAPK cascade genes reveals the GhMAP3K14-GhMKK11-GhMPK31 pathway is involved in the drought response in cotton. <i>Plant Molecular Biology</i> , 2020 , 103, 211-223	4.6	12
140	Transcriptome and metabolome analysis reveal that oral secretions from <i>Helicoverpa armigera</i> and <i>Spodoptera litura</i> influence wound-induced host response in cotton. <i>Crop Journal</i> , 2020 , 8, 929-942	4.6	6
139	Phenotypic plasticity and genetic variation of cotton yield and its related traits under water-limited conditions. <i>Crop Journal</i> , 2020 , 8, 966-976	4.6	5
138	The Calcium Sensor CBL2 and Its Interacting Kinase CIPK6 Are Involved in Plant Sugar Homeostasis via Interacting with Tonoplast Sugar Transporter TST2. <i>Plant Physiology</i> , 2020 , 183, 236-249	6.6	21

137	Genetic dissection of an allotetraploid interspecific CSSLs guides interspecific genetics and breeding in cotton. <i>BMC Genomics</i> , 2020 , 21, 431	4.5	9
136	Repression of microRNA 160 results in retarded seed integument growth and smaller final seed size in cotton. <i>Crop Journal</i> , 2020 , 8, 602-612	4.6	7
135	CRISPR/Cas Systems in Genome Editing: Methodologies and Tools for sgRNA Design, Off-Target Evaluation, and Strategies to Mitigate Off-Target Effects. <i>Advanced Science</i> , 2020 , 7, 1902312	13.6	79
134	The laccase gene GhLac1 modulates fiber initiation and elongation by coordinating jasmonic acid and flavonoid metabolism. <i>Crop Journal</i> , 2020 , 8, 522-533	4.6	5
133	Genome editing with the CRISPR-Cas system: an art, ethics and global regulatory perspective. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1651-1669	11.6	50
132	ABA signaling is negatively regulated by GbWRKY1 through JAZ1 and ABI1 to affect salt and drought tolerance. <i>Plant Cell Reports</i> , 2020 , 39, 181-194	5.1	18
131	Combined GWAS and eQTL analysis uncovers a genetic regulatory network orchestrating the initiation of secondary cell wall development in cotton. <i>New Phytologist</i> , 2020 , 226, 1738-1752	9.8	22
130	High day and night temperatures distinctively disrupt fatty acid and jasmonic acid metabolism, inducing male sterility in cotton. <i>Journal of Experimental Botany</i> , 2020 , 71, 6128-6141	7	5
129	Transcriptomic profiles of non-embryogenic and embryogenic callus cells in a highly regenerative upland cotton line (<i>Gossypium hirsutum</i> L.). <i>BMC Developmental Biology</i> , 2020 , 20, 25	3.1	9
128	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020 , 104, 662-678	6.9	14
127	The chromosome-level wintersweet (<i>Chimonanthus praecox</i>) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020 , 21, 200	18.3	23
126	A cotton germin-like protein GbGLP2 controls fiber length via regulating genes involved in secondary cell wall synthesis. <i>Molecular Breeding</i> , 2020 , 40, 1	3.4	1
125	High-efficient and precise base editing of C to T in the allotetraploid cotton (<i>Gossypium hirsutum</i>) genome using a modified CRISPR/Cas9 system. <i>Plant Biotechnology Journal</i> , 2020 , 18, 45-56	11.6	63
124	Robust CRISPR/Cpf1 (Cas12a)-mediated genome editing in allotetraploid cotton (<i>Gossypium hirsutum</i>). <i>Plant Biotechnology Journal</i> , 2019 , 17, 1862-1864	11.6	46
123	Population genomics reveals a fine-scale recombination landscape for genetic improvement of cotton. <i>Plant Journal</i> , 2019 , 99, 494-505	6.9	20
122	Proteomic analysis reveals that sugar and fatty acid metabolisms play a central role in sterility of the male-sterile line 1355A of cotton. <i>Journal of Biological Chemistry</i> , 2019 , 294, 7057-7067	5.4	7
121	GbSOBIR1 confers Verticillium wilt resistance by phosphorylating the transcriptional factor GbbHLH171 in <i>Gossypium barbadense</i> . <i>Plant Biotechnology Journal</i> , 2019 , 17, 152-163	11.6	20
120	GhL1L1 affects cell fate specification by regulating GhPIN1-mediated auxin distribution. <i>Plant Biotechnology Journal</i> , 2019 , 17, 63-74	11.6	13

119	Multi-omics analyses reveal epigenomics basis for cotton somatic embryogenesis through successive regeneration acclimation process. <i>Plant Biotechnology Journal</i> , 2019 , 17, 435-450	11.6	46
118	Genome-wide identification and characterization of TALE superfamily genes in cotton reveals their functions in regulating secondary cell wall biosynthesis. <i>BMC Plant Biology</i> , 2019 , 19, 432	5.3	20
117	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019 , 10, 4702	17.4	62
116	CRISPR/Cas System: Recent Advances and Future Prospects for Genome Editing. <i>Trends in Plant Science</i> , 2019 , 24, 1102-1125	13.1	135
115	Down regulation of cotton GbTRP1 leads to accumulation of anthranilates and confers resistance to <i>Verticillium dahliae</i> . <i>Journal of Cotton Research</i> , 2019 , 2,	2.3	1
114	Crosstalk between cytokinin and ethylene signaling pathways regulates leaf abscission in cotton in response to chemical defoliant. <i>Journal of Experimental Botany</i> , 2019 , 70, 1525-1538	7	20
113	Suppression of tryptophan synthase activates cotton immunity by triggering cell death via promoting SA synthesis. <i>Plant Journal</i> , 2019 , 98, 329-345	6.9	22
112	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019 , 51, 224-229	36.3	266
111	Whole genome sequencing reveals rare off-target mutations and considerable inherent genetic or/and somaclonal variations in CRISPR/Cas9-edited cotton plants. <i>Plant Biotechnology Journal</i> , 2019 , 17, 858-868	11.6	96
110	Linkage and association mapping reveals the genetic basis of brown fibre (<i>Gossypium hirsutum</i>). <i>Plant Biotechnology Journal</i> , 2018 , 16, 1654	11.6	27
109	Evolutionary dynamics of 3D genome architecture following polyploidization in cotton. <i>Nature Plants</i> , 2018 , 4, 90-97	11.5	82
108	The GhmiR157a-GhSPL10 regulatory module controls initial cellular dedifferentiation and callus proliferation in cotton by modulating ethylene-mediated flavonoid biosynthesis. <i>Journal of Experimental Botany</i> , 2018 , 69, 1081-1093	7	30
107	High efficient multisites genome editing in allotetraploid cotton (<i>Gossypium hirsutum</i>) using CRISPR/Cas9 system. <i>Plant Biotechnology Journal</i> , 2018 , 16, 137-150	11.6	127
106	GhJAZ2 attenuates cotton resistance to biotic stresses via the inhibition of the transcriptional activity of GhbHLH171. <i>Molecular Plant Pathology</i> , 2018 , 19, 896-908	5.7	35
105	A novel cotton WRKY gene, GhWRKY6-like, improves salt tolerance by activating the ABA signaling pathway and scavenging of reactive oxygen species. <i>Physiologia Plantarum</i> , 2018 , 162, 439-454	4.6	63
104	Transcriptomic repertoires depict the initiation of lint and fuzz fibres in cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2018 , 16, 1002-1012	11.6	33
103	A global survey of alternative splicing in allopolyploid cotton: landscape, complexity and regulation. <i>New Phytologist</i> , 2018 , 217, 163-178	9.8	95
102	Red fluorescent protein (DsRed2), an ideal reporter for cotton genetic transformation and molecular breeding. <i>Crop Journal</i> , 2018 , 6, 366-376	4.6	7

101	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. <i>BMC Plant Biology</i> , 2018 , 18, 150	5.3	36
100	QTL Mapping for Fiber Quality and Yield Traits Based on Introgression Lines Derived from <i>Gossypium hirsutum</i> [G. tomentosum]. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	28
99	Promoters of Arabidopsis Casein kinase I-like 2 and 7 confer specific high-temperature response in anther. <i>Plant Molecular Biology</i> , 2018 , 98, 33-49	4.6	5
98	Disrupted Genome Methylation in Response to High Temperature Has Distinct Affects on Microspore Abortion and Anther Indehiscence. <i>Plant Cell</i> , 2018 , 30, 1387-1403	11.6	43
97	Laccase GhLac1 Modulates Broad-Spectrum Biotic Stress Tolerance via Manipulating Phenylpropanoid Pathway and Jasmonic Acid Synthesis. <i>Plant Physiology</i> , 2018 , 176, 1808-1823	6.6	94
96	Long noncoding RNAs involve in resistance to <i>Verticillium dahliae</i> , a fungal disease in cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 1172-1185	11.6	77
95	Transfer of tomato immune receptor Ve1 confers Ave1-dependent <i>Verticillium</i> resistance in tobacco and cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 638-648	11.6	23
94	The cotton HD-Zip transcription factor GhHB12 regulates flowering time and plant architecture via the GhmiR157-GhSPL pathway. <i>Communications Biology</i> , 2018 , 1, 229	6.7	8
93	GhCPK33 Negatively Regulates Defense against by Phosphorylating GhOPR3. <i>Plant Physiology</i> , 2018 , 178, 876-889	6.6	32
92	Drought coping strategies in cotton: increased crop per drop. <i>Plant Biotechnology Journal</i> , 2017 , 15, 271-284	11.6	142
91	MicroRNA 157-targeted SPL genes regulate floral organ size and ovule production in cotton. <i>BMC Plant Biology</i> , 2017 , 17, 7	5.3	37
90	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017 , 49, 579-587	36.3	229
89	microRNAs involved in auxin signalling modulate male sterility under high-temperature stress in cotton (<i>Gossypium hirsutum</i>). <i>Plant Journal</i> , 2017 , 91, 977-994	6.9	63
88	A transgenic strategy for controlling plant bugs (<i>Adelphocoris suturalis</i>) through expression of double-stranded RNA homologous to fatty acyl-coenzyme A reductase in cotton. <i>New Phytologist</i> , 2017 , 215, 1173-1185	9.8	26
87	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. <i>Plant Biotechnology Journal</i> , 2017 , 15, 1374-1386	11.6	99
86	Interaction between calcium and potassium modulates elongation rate in cotton fiber cells. <i>Journal of Experimental Botany</i> , 2017 , 68, 5161-5175	7	16
85	The JASMONATE ZIM-Domain Gene Family Mediates JA Signaling and Stress Response in Cotton. <i>Plant and Cell Physiology</i> , 2017 , 58, 2139-2154	4.9	34
84	GhATAF1, a NAC transcription factor, confers abiotic and biotic stress responses by regulating phytohormonal signaling networks. <i>Plant Cell Reports</i> , 2016 , 35, 2167-79	5.1	51

83	GhJAZ2 negatively regulates cotton fiber initiation by interacting with the R2R3-MYB transcription factor GhMYB25-like. <i>Plant Journal</i> , 2016 , 88, 921-935	6.9	76
82	Metabolic engineering of cottonseed oil biosynthesis pathway via RNA interference. <i>Scientific Reports</i> , 2016 , 6, 33342	4.9	22
81	Genomic heterozygosity and hybrid breakdown in cotton (<i>Gossypium</i>): different traits, different effects. <i>BMC Genetics</i> , 2016 , 17, 58	2.6	6
80	Fibre elongation requires normal redox homeostasis modulated by cytosolic ascorbate peroxidase in cotton (<i>Gossypium hirsutum</i>). <i>Journal of Experimental Botany</i> , 2016 , 67, 3289-301	7	40
79	Structure, evolution, and comparative genomics of tetraploid cotton based on a high-density genetic linkage map. <i>DNA Research</i> , 2016 , 23, 283-93	4.5	25
78	An ethylene response-related factor, GbERF1-like, from <i>Gossypium barbadense</i> improves resistance to <i>Verticillium dahliae</i> via activating lignin synthesis. <i>Plant Molecular Biology</i> , 2016 , 91, 305-18	4.6	65
77	Transgenic Bt cotton driven by the green tissue-specific promoter shows strong toxicity to lepidopteran pests and lower Bt toxin accumulation in seeds. <i>Science China Life Sciences</i> , 2016 , 59, 172-82	8.5	12
76	Ascorbate Alleviates Fe Deficiency-Induced Stress in Cotton () by Modulating ABA Levels. <i>Frontiers in Plant Science</i> , 2016 , 7, 1997	6.2	7
75	Identification of Multiple Stress Responsive Genes by Sequencing a Normalized cDNA Library from Sea-Land Cotton (<i>Gossypium barbadense</i> L.). <i>PLoS ONE</i> , 2016 , 11, e0152927	3.7	23
74	Genome-wide SSR-based association mapping for fiber quality in nation-wide upland cotton inbred cultivars in China. <i>BMC Genomics</i> , 2016 , 17, 352	4.5	63
73	Suppression of the homeobox gene HDTF1 enhances resistance to <i>Verticillium dahliae</i> and <i>Botrytis cinerea</i> in cotton. <i>Journal of Integrative Plant Biology</i> , 2016 , 58, 503-13	8.3	43
72	ROS Homeostasis Regulates Somatic Embryogenesis via the Regulation of Auxin Signaling in Cotton. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2108-24	7.6	36
71	Small RNA-mediated responses to low- and high-temperature stresses in cotton. <i>Scientific Reports</i> , 2016 , 6, 35558	4.9	44
70	Transcriptome analysis reveals a comprehensive insect resistance response mechanism in cotton to infestation by the phloem feeding insect <i>Bemisia tabaci</i> (whitefly). <i>Plant Biotechnology Journal</i> , 2016 , 14, 1956-75	11.6	72
69	GbEXPATR, a species-specific expansin, enhances cotton fibre elongation through cell wall restructuring. <i>Plant Biotechnology Journal</i> , 2016 , 14, 951-63	11.6	50
68	Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation. <i>Nucleic Acids Research</i> , 2016 , 44, 4067-79	20.1	33
67	The Sophora Alopecuroid H + -PPase Gene SaVP1 Confers Multiple Abiotic Stress Tolerance in Arabidopsis. <i>Plant Molecular Biology Reporter</i> , 2015 , 33, 923-930	1.7	3
66	A comparative meta-analysis of QTL between intraspecific <i>Gossypium hirsutum</i> and interspecific <i>G. hirsutum</i> × <i>G. barbadense</i> populations. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 1003-25	3.1	124

65	Defective pollen wall contributes to male sterility in the male sterile line 1355A of cotton. <i>Scientific Reports</i> , 2015 , 5, 9608	4.9	33
64	Long noncoding RNAs and their proposed functions in fibre development of cotton (<i>Gossypium</i> spp.). <i>New Phytologist</i> , 2015 , 207, 1181-97	9.8	112
63	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015 , 33, 524-30	44.5	683
62	Engineered chloroplast dsRNA silences cytochrome p450 monooxygenase, V-ATPase and chitin synthase genes in the insect gut and disrupts <i>Helicoverpa zea</i> larval development and pupation. <i>Plant Biotechnology Journal</i> , 2015 , 13, 435-46	11.6	96
61	LEAFY COTYLEDON1-CASEIN KINASE I-TCP15-PHYTOCHROME INTERACTING FACTOR4 Network Regulates Somatic Embryogenesis by Regulating Auxin Homeostasis. <i>Plant Physiology</i> , 2015 , 169, 2805-21	6.6	24
60	Transgenic Cotton Plants Expressing Double-stranded RNAs Target HMG-CoA Reductase (HMGR) Gene Inhibits the Growth, Development and Survival of Cotton Bollworms. <i>International Journal of Biological Sciences</i> , 2015 , 11, 1296-305	11.2	37
59	Genome Sequencing. <i>Agronomy</i> , 2015 , 289-302	0.8	3
58	A cotton fiber-preferential promoter, PGbEXPA2, is regulated by GA and ABA in Arabidopsis. <i>Plant Cell Reports</i> , 2015 , 34, 1539-49	5.1	14
57	The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2015 , 5, 17662	4.9	181
56	A peptide hormone gene, GhPSK promotes fibre elongation and contributes to longer and finer cotton fibre. <i>Plant Biotechnology Journal</i> , 2014 , 12, 861-71	11.6	24
55	Comparative transcriptome analysis between somatic embryos (SEs) and zygotic embryos in cotton: evidence for stress response functions in SE development. <i>Plant Biotechnology Journal</i> , 2014 , 12, 161-73	11.6	72
54	GbMPK3, a mitogen-activated protein kinase from cotton, enhances drought and oxidative stress tolerance in tobacco. <i>Plant Cell, Tissue and Organ Culture</i> , 2014 , 116, 153-162	2.7	34
53	GhTZF1 regulates drought stress responses and delays leaf senescence by inhibiting reactive oxygen species accumulation in transgenic Arabidopsis. <i>Plant Molecular Biology</i> , 2014 , 85, 163-77	4.6	34
52	Sugar and auxin signaling pathways respond to high-temperature stress during anther development as revealed by transcript profiling analysis in cotton. <i>Plant Physiology</i> , 2014 , 164, 1293-308	6.6	129
51	GhH2A12, a replication-dependent histone H2A gene from <i>Gossypium hirsutum</i> , is negatively involved in the development of cotton fiber cells. <i>Plant Cell Reports</i> , 2014 , 33, 1711-21	5.1	5
50	Small RNA and degradome profiling reveals a role for miRNAs and their targets in the developing fibers of <i>Gossypium barbadense</i> . <i>Plant Journal</i> , 2014 , 80, 331-44	6.9	63
49	Comparison and development of ESTBSRs from two 454 sequencing libraries of <i>Gossypium barbadense</i> . <i>Euphytica</i> , 2014 , 198, 277-288	2.1	4
48	Down-regulating annexin gene GhAnn2 inhibits cotton fiber elongation and decreases Ca ²⁺ influx at the cell apex. <i>Plant Molecular Biology</i> , 2014 , 85, 613-25	4.6	48

47	Functional characterization of cotton genes responsive to <i>Verticillium dahliae</i> through bioinformatics and reverse genetics strategies. <i>Journal of Experimental Botany</i> , 2014 , 65, 6679-92	7	40
46	The calcium sensor GhCaM7 promotes cotton fiber elongation by modulating reactive oxygen species (ROS) production. <i>New Phytologist</i> , 2014 , 202, 509-520	9.8	81
45	Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway. <i>Nature Communications</i> , 2014 , 5, 5372	17.4	75
44	Cotton WRKY1 mediates the plant defense-to-development transition during infection of cotton by <i>Verticillium dahliae</i> by activating JASMONATE ZIM-DOMAIN1 expression. <i>Plant Physiology</i> , 2014 , 166, 2179-94	6.6	94
43	Development of EST-based SNP and InDel markers and their utilization in tetraploid cotton genetic mapping. <i>BMC Genomics</i> , 2014 , 15, 1046	4.5	24
42	Flavonoid Pathway in Cotton Fiber Development. <i>Scientia Sinica Vitae</i> , 2014 , 44, 758-765	1.4	3
41	Overexpression of rice NAC gene SNAC1 improves drought and salt tolerance by enhancing root development and reducing transpiration rate in transgenic cotton. <i>PLoS ONE</i> , 2014 , 9, e86895	3.7	139
40	Isolation, characterization and mapping of genes differentially expressed during fibre development between <i>Gossypium hirsutum</i> and <i>G. barbadense</i> by cDNA-SRAP. <i>Journal of Genetics</i> , 2013 , 92, 175-181	1.2	8
39	Expression of the Arabidopsis vacuolar H ⁺ -pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. <i>Plant Biotechnology Reports</i> , 2013 , 7, 345-355	2.5	51
38	A comprehensive meta QTL analysis for fiber quality, yield, yield related and morphological traits, drought tolerance, and disease resistance in tetraploid cotton. <i>BMC Genomics</i> , 2013 , 14, 776	4.5	154
37	Small RNA and degradome sequencing reveal complex miRNA regulation during cotton somatic embryogenesis. <i>Journal of Experimental Botany</i> , 2013 , 64, 1521-36	7	146
36	A genetic and metabolic analysis revealed that cotton fiber cell development was retarded by flavonoid naringenin. <i>Plant Physiology</i> , 2013 , 162, 86-95	6.6	81
35	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. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 435, 209-15	3.4	62
34	Cotton GhCKI disrupts normal male reproduction by delaying tapetum programmed cell death via inactivating starch synthase. <i>Plant Journal</i> , 2013 , 75, 823-35	6.9	47
33	Linkage mapping and expression analysis of miRNAs and their target genes during fiber development in cotton. <i>BMC Genomics</i> , 2013 , 14, 706	4.5	15
32	Genetic mapping and characteristics of genes specifically or preferentially expressed during fiber development in cotton. <i>PLoS ONE</i> , 2013 , 8, e54444	3.7	18
31	Isolation, characterization and mapping of genes differentially expressed during fibre development between <i>Gossypium hirsutum</i> and <i>G. barbadense</i> by cDNA-SRAP. <i>Journal of Genetics</i> , 2013 , 92, 175-81	1.2	5
30	Pinellia ternata agglutinin expression in chloroplasts confers broad spectrum resistance against aphid, whitefly, Lepidopteran insects, bacterial and viral pathogens. <i>Plant Biotechnology Journal</i> , 2012 , 10, 313-27	11.6	58

29	Unbiased genomic distribution of genes related to cell morphogenesis in cotton by chromosome mapping. <i>Plant Cell, Tissue and Organ Culture</i> , 2012 , 108, 529-534	2.7	7
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25	Transcript profiling reveals complex auxin signalling pathway and transcription regulation involved in dedifferentiation and redifferentiation during somatic embryogenesis in cotton. <i>BMC Plant Biology</i> , 2012 , 12, 110	5.3	94
24	Development and Evaluation of Intron and Insertion/Deletion Markers for <i>Gossypium barbadense</i> . <i>Plant Molecular Biology Reporter</i> , 2012 , 30, 605-613	1.7	11
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15	Regulation of Somatic Embryogenesis in Higher Plants. <i>Critical Reviews in Plant Sciences</i> , 2010 , 29, 36-57	5.6	202
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13	Mapped SSR markers unevenly distributed on the cotton chromosomes. <i>Frontiers of Agriculture in China</i> , 2010 , 4, 257-264		2
12	A high-density integrative linkage map for <i>Gossypium hirsutum</i> . <i>Euphytica</i> , 2009 , 166, 35-45	2.1	53

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10	Expression profile analysis of genes involved in cell wall regeneration during protoplast culture in cotton by suppression subtractive hybridization and macroarray. <i>Journal of Experimental Botany</i> , 2008 , 59, 3661-74	7	41
9	Detection of somaclonal variation of cotton (<i>Gossypium hirsutum</i>) using cytogenetics, flow cytometry and molecular markers. <i>Plant Cell Reports</i> , 2008 , 27, 1303-16	5.1	71
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