

# Shuxun Yu

## List of Publications by Year in descending order

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107  
papers

6,129  
citations

147801

31  
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76900

74  
g-index

121  
all docs

121  
docs citations

121  
times ranked

3646  
citing authors

#	ARTICLE	IF	CITATIONS
1	Overexpression of a Cotton Aquaporin Gene GhTIP1;1-like Confers Cold Tolerance in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1361.	4.1	9
2	The MADS transcription factor GhFYF is involved in abiotic stress responses in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Gene</i> , 2022, 815, 146138.	2.2	6
3	A Comprehensive Identification and Function Analysis of Serine/Arginine-Rich (SR) Proteins in Cotton ( <i>Gossypium</i> spp.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 4566.	4.1	4
4	Characterization and Functional Analysis of GhNAC82, A NAM Domain Gene, Coordinates the Leaf Senescence in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Plants</i> , 2022, 11, 1491.	3.5	3
5	The MADS transcription factor GhAP1.7 coordinates the flowering regulatory pathway in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Gene</i> , 2021, 769, 145235.	2.2	10
6	High-resolution temporal dynamic transcriptome landscape reveals a GhCAL-mediated flowering regulatory pathway in cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 153-166.	8.3	27
7	Genomic analyses reveal the genetic basis of early maturity and identification of loci and candidate genes in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2021, 19, 109-123.	8.3	42
8	GhGPAT12/25 Are Essential for the Formation of Anther Cuticle and Pollen Exine in Cotton ( <i>Gossypium</i> ) Tj ETQq0 0.0 rgBT /Overlock 10	3.6	7
9	QTL mapping and candidate gene identification of lint percentage based on a recombinant inbred line population of upland cotton. <i>Euphytica</i> , 2021, 217, 1.	1.2	2
10	Overexpression of GhMPK3 from Cotton Enhances Cold, Drought, and Salt Stress in Arabidopsis. <i>Agronomy</i> , 2021, 11, 1049.	3.0	15
11	Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	8
12	Comprehensive identification and expression analysis of B-Box genes in cotton. <i>BMC Genomics</i> , 2021, 22, 439.	2.8	12
13	Genome-Wide Identification of the Early Flowering 4 (ELF4) Gene Family in Cotton and Silent GhELF4-1 and GhELF3-6 Decreased Cotton Stress Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 686852.	2.3	1
14	Non-functional <i>GoFLA19s</i> are responsible for the male sterility caused by hybrid breakdown in cotton ( <i>Gossypium</i> spp.). <i>Plant Journal</i> , 2021, 107, 1198-1212.	5.7	8
15	Genetic variation in <i>MYB5_A12</i> is associated with fibre initiation and elongation in tetraploid cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 1892-1894.	8.3	14
16	GhLUX1 and GhELF3 Are Two Components of the Circadian Clock That Regulate Flowering Time of <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 691489.	3.6	4
17	A comprehensive identification and function analysis of the ATBS1 Interacting Factors (AIFs) gene family of <i>Gossypium</i> species in fiber development and under multiple stresses. <i>Industrial Crops and Products</i> , 2021, 171, 113853.	5.2	2
18	Phylogenetic Analysis of the Membrane Attack Complex/Perforin Domain-Containing Proteins in <i>Gossypium</i> and the Role of GhMACPF26 in Cotton Under Cold Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 684227.	3.6	6

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19	Uncovering Novel Genomic Regions and Candidate Genes for Senescence-Related Traits by Genome-Wide Association Studies in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 809522.	3.6	3
20	Evolution and Stress Responses of CLO Genes and Potential Function of the GhCLO06 Gene in Salt Resistance of Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 801239.	3.6	3
21	QTL and candidate gene identification of the node of the first fruiting branch (NFFB) by QTL-seq in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2021, 22, 882.	2.8	11
22	Pectate lyase-like Gene GhPEL76 regulates organ elongation in Arabidopsis and fiber elongation in cotton. <i>Plant Science</i> , 2020, 293, 110395.	3.6	23
23	Genome-wide identification of NF-YA gene family in cotton and the positive role of GhNF-YA10 and GhNF-YA23 in salt tolerance. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 2103-2115.	7.5	12
24	Deficiencies in the formation and regulation of anther cuticle and tryphine contribute to male sterility in cotton PGMS line. <i>BMC Genomics</i> , 2020, 21, 825.	2.8	7
25	A comprehensive analysis of cotton VQ gene superfamily reveals their potential and extensive roles in regulating cotton abiotic stress. <i>BMC Genomics</i> , 2020, 21, 795.	2.8	17
26	Transcriptomic Profiling of Young Cotyledons Response to Chilling Stress in Two Contrasting Cotton ( <i>Gossypium hirsutum</i> L.) Genotypes at the Seedling Stage. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5095.	4.1	24
27	Overexpression of CDSP32 (GhTRX134) Cotton Gene Enhances Drought, Salt, and Oxidative Stress Tolerance in Arabidopsis. <i>Plants</i> , 2020, 9, 1388.	3.5	20
28	Genome-wide identification and expression patterns analysis of the RPD3/HDA1 gene family in cotton. <i>BMC Genomics</i> , 2020, 21, 643.	2.8	11
29	Transcriptome Analysis Reveals a Gene Expression Pattern Associated with Fuzz Fiber Initiation Induced by High Temperature in <i>Gossypium barbadense</i> . <i>Genes</i> , 2020, 11, 1066.	2.4	9
30	Genome-Wide Identification and Expression Analysis of the NHX (Sodium/Hydrogen Antiporter) Gene Family in Cotton. <i>Frontiers in Genetics</i> , 2020, 11, 964.	2.3	19
31	Identification and profiling of microRNAs and differentially expressed genes during anther development between a genetic male-sterile mutant and its wildtype cotton via high-throughput RNA sequencing. <i>Molecular Genetics and Genomics</i> , 2020, 295, 645-660.	2.1	8
32	Genome-wide identification and characterization of multiple C2 domains and transmembrane region proteins in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2020, 21, 445.	2.8	6
33	The Cotton BEL1-Like Transcription Factor GhBLH7-D06 Negatively Regulates the Defense Response against <i>Verticillium dahliae</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7126.	4.1	18
34	A Comparative Genome-Wide Analysis of the R2R3-MYB Gene Family Among Four <i>Gossypium</i> Species and Their Sequence Variation and Association With Fiber Quality Traits in an Interspecific <i>G. hirsutum</i> × <i>G. barbadense</i> Population. <i>Frontiers in Genetics</i> , 2019, 10, 741.	2.3	16
35	Transcriptome analysis reveals differences in the mechanisms of fiber initiation and elongation between long- and short-fiber cotton ( <i>Gossypium hirsutum</i> L.) lines. <i>BMC Genomics</i> , 2019, 20, 633.	2.8	29
36	Genome-wide identification and expression analysis of the BURP domain-containing genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2019, 20, 558.	2.8	17

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37	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.	3.6	31
38	Analysis of the MIR160 gene family and the role of MIR160a_A05 in regulating fiber length in cotton. <i>Planta</i> , 2019, 250, 2147-2158.	3.2	17
39	Genome-Wide Identification and Characterization of Glycosyltransferase Family 47 in Cotton. <i>Frontiers in Genetics</i> , 2019, 10, 824.	2.3	26
40	Identification of Loci and Candidate Genes Responsible for Fiber Length in Upland Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	20
41	QTL analysis and candidate gene identification for plant height in cotton based on an interspecific backcross inbred line population of <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 2663-2676.	3.6	48
42	Genome-wide association study of the oil content in upland cotton ( <i>Gossypium hirsutum</i> L.) and identification of GhPRXR1, a candidate gene for a stable QTLqOC-Dt5-1. <i>Plant Science</i> , 2019, 286, 89-97.	3.6	35
43	A comparative analysis of small RNAs between two Upland cotton backcross inbred lines with different fiber length: Expression and distribution. <i>Crop Journal</i> , 2019, 7, 198-208.	5.2	7
44	The WRKY transcription factor GhWRKY27 coordinates the senescence regulatory pathway in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 116.	3.6	39
45	Fine mapping and molecular characterization of the virescent gene vsp in Upland cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0,784314 rgBT /Overlock 15	3.6	15
46	The Cotton GhWRKY91 Transcription Factor Mediates Leaf Senescence and Responses to Drought Stress in Transgenic <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1352.	3.6	35
47	Differentially expressed genes between two groups of backcross inbred lines differing in fiber length developed from Upland × Pima cotton. <i>Molecular Biology Reports</i> , 2019, 46, 1199-1212.	2.3	5
48	Genome-wide association study identified genetic variations and candidate genes for plant architecture component traits in Chinese upland cotton. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1299-1314.	3.6	62
49	QTL delineation for five fiber quality traits based on an intra-specific <i>Gossypium hirsutum</i> L. recombinant inbred line population. <i>Molecular Genetics and Genomics</i> , 2018, 293, 831-843.	2.1	10
50	Fine mapping and candidate gene analysis of the virescent gene v 1 in Upland cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.1	12
51	Genetic variation of dynamic fiber elongation and developmental quantitative trait locus mapping of fiber length in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2018, 19, 882.	2.8	33
52	Identification, Expression, and Functional Analysis of the Group IId WRKY Subfamily in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1684.	3.6	32
53	Genome-wide identification and expression analyses of the pectate lyase (PEL) gene family in cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2018, 19, 661.	2.8	32
54	Genome- Wide Analysis and Characterization of the TRX Gene Family in Upland Cotton. <i>Tropical Plant Biology</i> , 2018, 11, 119-130.	1.9	15

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55	Characterization and functional analysis of GhWRKY42, a group IId WRKY gene, in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Genetics</i> , 2018, 19, 48.	2.7	32
56	Functional analysis of nine cotton genes related to leaf senescence in <i>Gossypium hirsutum</i> L. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 729-739.	3.1	4
57	Transcriptome analysis of nitric oxide-responsive genes in upland cotton ( <i>Gossypium hirsutum</i> ). <i>PLoS ONE</i> , 2018, 13, e0192367.	2.5	23
58	Identification of the group IIa WRKY subfamily and the functional analysis of GhWRKY17 in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>PLoS ONE</i> , 2018, 13, e0191681.	2.5	33
59	Identification of GT Factors in Response to Stresses and Leaf Senescence in <i>Gossypium hirsutum</i> L. <i>Journal of Plant Growth Regulation</i> , 2017, 36, 22-42.	5.1	2
60	A genome-wide analysis of the lysophosphatidate acyltransferase (LPAAT) gene family in cotton: organization, expression, sequence variation, and association with seed oil content and fiber quality. <i>BMC Genomics</i> , 2017, 18, 218.	2.8	32
61	Proteomic Analysis of Differences in Fiber Development between Wild and Cultivated <i>Gossypium hirsutum</i> L.. <i>Journal of Proteome Research</i> , 2017, 16, 2811-2824.	3.7	11
62	Identification of candidate genes for fiber length quantitative trait loci through RNA-Seq and linkage and physical mapping in cotton. <i>BMC Genomics</i> , 2017, 18, 427.	2.8	32
63	An NAM Domain Gene, GhNAC79, Improves Resistance to Drought Stress in Upland Cotton. <i>Frontiers in Plant Science</i> , 2017, 8, 1657.	3.6	32
64	iTRAQ-Based Quantitative Proteomic Analysis Reveals Cold Responsive Proteins Involved in Leaf Senescence in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1984.	4.1	16
65	Global analysis of DNA methylation in young (J1) and senescent (J2) <i>Gossypium hirsutum</i> L. cotyledons by MeDIP-Seq. <i>PLoS ONE</i> , 2017, 12, e0179141.	2.5	12
66	A genome-wide analysis of the small auxin-up RNA (SAUR) gene family in cotton. <i>BMC Genomics</i> , 2017, 18, 815.	2.8	47
67	Dissecting Genetic Network of Fruit Branch Traits in Upland Cotton by Association Mapping Using SSR Markers. <i>PLoS ONE</i> , 2017, 12, e0162815.	2.5	8
68	High-density genetic linkage map construction by F2 populations and QTL analysis of early-maturity traits in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>PLoS ONE</i> , 2017, 12, e0182918.	2.5	40
69	Characterization and Functional Analysis of PEBP Family Genes in Upland Cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 1,0,784314,rgBT /Ove	2.5	26
70	High-density linkage map construction and QTL analysis for earliness-related traits in <i>Gossypium hirsutum</i> L. <i>BMC Genomics</i> , 2016, 17, 909.	2.8	51
71	RNA-Seq-Mediated Transcriptome Analysis of a Fiberless Mutant Cotton and Its Possible Origin Based on SNP Markers. <i>PLoS ONE</i> , 2016, 11, e0151994.	2.5	28
72	Detection of Favorable QTL Alleles and Candidate Genes for Lint Percentage by GWAS in Chinese Upland Cotton. <i>Frontiers in Plant Science</i> , 2016, 7, 1576.	3.6	119

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73	Identification of favorable SNP alleles and candidate genes for traits related to early maturity via GWAS in upland cotton. <i>BMC Genomics</i> , 2016, 17, 687.	2.8	138
74	Two genomic regions associated with fiber quality traits in Chinese upland cotton under apparent breeding selection. <i>Scientific Reports</i> , 2016, 6, 38496.	3.3	68
75	A comparative transcriptome analysis of two sets of backcross inbred lines differing in lint-yield derived from a <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> population. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1749-1767.	2.1	14
76	Genome-wide characterization and comparative analysis of the MLO gene family in cotton. <i>Plant Physiology and Biochemistry</i> , 2016, 103, 106-119.	5.8	12
77	GhNAC12, a neutral candidate gene, leads to early aging in cotton ( <i>Gossypium hirsutum</i> L). <i>Gene</i> , 2016, 576, 268-274.	2.2	34
78	Functional characterization of GhSOC1 and GhMADS42 homologs from upland cotton ( <i>Gossypium</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	3.6	26
79	iTRAQ-facilitated proteomic profiling of anthers from a photosensitive male sterile mutant and wild-type cotton ( <i>Gossypium hirsutum</i> L). <i>Journal of Proteomics</i> , 2015, 126, 68-81.	2.4	57
80	Genome-wide analysis of the family 1 glycosyltransferases in cotton. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1805-1818.	2.1	47
81	Genome sequence of cultivated Upland cotton ( <i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	17.5	1,064
82	Global analysis of the <i>Gossypium hirsutum</i> L. Transcriptome during leaf senescence by RNA-Seq. <i>BMC Plant Biology</i> , 2015, 15, 43.	3.6	85
83	Data for proteomic profiling of Anthers from a photosensitive male sterile mutant and wild-type cotton ( <i>Gossypium hirsutum</i> L). <i>Data in Brief</i> , 2015, 4, 500-509.	1.0	6
84	Genomic organization, differential expression, and functional analysis of the SPL gene family in <i>Gossypium hirsutum</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 115-126.	2.1	43
85	Upland Cotton Gene GhFPF1 Confers Promotion of Flowering Time and Shade-Avoidance Responses in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2014, 9, e91869.	2.5	23
86	Proteomic analysis of anthers from wild-type and photosensitive genetic male sterile mutant cotton ( <i>Gossypium hirsutum</i> L). <i>BMC Plant Biology</i> , 2014, 14, 390.	3.6	19
87	Molecular cloning and functional analysis of NAC family genes associated with leaf senescence and stresses in <i>Gossypium hirsutum</i> L.. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 117, 167-186.	2.3	21
88	Identification and Profiling of Known and Novel Fiber MicroRNAs during the Secondary Wall Thickening Stage in Cotton ( <i>Gossypium hirsutum</i> ) via High-Throughput Sequencing. <i>Journal of Genetics and Genomics</i> , 2014, 41, 553-556.	3.9	3
89	Quantitative phosphoproteomic profiling of fiber differentiation and initiation in a fiberless mutant of cotton. <i>BMC Genomics</i> , 2014, 15, 466.	2.8	33
90	Genome-wide analysis of the WRKY gene family in cotton. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1103-1121.	2.1	118

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91	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	21.4	883
92	Quantitative Phosphoproteomics Analysis of Nitric Oxide-Responsive Phosphoproteins in Cotton Leaf. <i>PLoS ONE</i> , 2014, 9, e94261.	2.5	34
93	Transcriptomic analysis of differentially expressed genes during anther development in genetic male sterile and wild type cotton by digital gene-expression profiling. <i>BMC Genomics</i> , 2013, 14, 97.	2.8	66
94	Mapping quantitative trait loci for lint yield and fiber quality across environments in a <i>Gossypium hirsutum</i> – <i>Gossypium barbadense</i> backcross inbred line population. <i>Theoretical and Applied Genetics</i> , 2013, 126, 275-287.	3.6	164
95	Isolation and expression profiling of GhNAC transcription factor genes in cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314,rgBT /Overlock 10	2.2	60
96	Molecular Cloning and Function Analysis of Two <i>SQUAMOSA</i> -like <i>MADS</i> -Box Genes From <i>Gossypium hirsutum</i> L.. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 597-607.	8.5	17
97	Selection and Characterization of a Novel Photoperiod-Sensitive Male Sterile Line in Upland Cotton. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 608-618.	8.5	15
98	Comparative expression profiling of miRNA during anther development in genetic male sterile and wild type cotton. <i>BMC Plant Biology</i> , 2013, 13, 66.	3.6	65
99	Generation and Analysis of a Large-Scale Expressed Sequence Tag Database from a Full-Length Enriched cDNA Library of Developing Leaves of <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2013, 8, e76443.	2.5	10
100	Mapping quantitative trait loci for cottonseed oil, protein and gossypol content in a <i>Gossypium hirsutum</i> – <i>Gossypium barbadense</i> backcross inbred line population. <i>Euphytica</i> , 2012, 187, 191-201.	1.2	75
101	Cytological and genetic analysis of a virescent mutant in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2012, 187, 235-245.	1.2	15
102	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 2012, 44, 1098-1103.	21.4	935
103	Label-Free Quantitative Proteomics Analysis of Cotton Leaf Response to Nitric Oxide. <i>Journal of Proteome Research</i> , 2011, 10, 5416-5432.	3.7	35
104	Toward Sequencing Cotton ( <i>Gossypium</i> ) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.	4.8	390
105	AFLP-RGA Markers in Comparison with RGA and AFLP in Cultivated Tetraploid Cotton. <i>Crop Science</i> , 2007, 47, 180-187.	1.8	24
106	High-density Linkage Map of Cultivated Allotetraploid Cotton Based on SSR, TRAP, SRAP and AFLP Markers. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 716-724.	8.5	65
107	Detection of Stable Elite Haplotypes and Potential Candidate Genes of Boll Weight Across Multiple Environments via CWAS in Upland Cotton. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	6