

Shuangxia Jin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3111646/publications.pdf>

Version: 2024-02-01

70
papers

5,606
citations

76196

40
h-index

88477

70
g-index

71
all docs

71
docs citations

71
times ranked

5666
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	9.4	468
2	Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017, 49, 579-587.	9.4	367
3	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> , 2016, 5, 17662.	1.6	294
4	CRISPR/Cas System: Recent Advances and Future Prospects for Genome Editing. <i>Trends in Plant Science</i> , 2019, 24, 1102-1125.	4.3	292
5	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.	1.1	204
6	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.	4.1	202
7	Laccase GhLac1 Modulates Broad-Spectrum Biotic Stress Tolerance via Manipulating Phenylpropanoid Pathway and Jasmonic Acid Synthesis. <i>Plant Physiology</i> , 2018, 176, 1808-1823.	2.3	186
8	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.	5.6	162
9	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.	4.1	159
10	Engineered chloroplast dsRNA silences cytochrome p450 monooxygenase, <i>VvATPase</i> and <i>chitin synthase</i> genes in the insect gut and disrupts <i>Helicoverpa armigera</i> larval development and pupation. <i>Plant Biotechnology Journal</i> , 2015, 13, 435-446.	4.1	144
11	The Engineered Chloroplast Genome Just Got Smarter. <i>Trends in Plant Science</i> , 2015, 20, 622-640.	4.3	142
12	GhABF2, a bZIP transcription factor, confers drought and salinity tolerance in cotton (<i>Gossypium</i>) <i>Trends in Plant Science</i> , 2015, 20, 622-640.	1.6	124
13	Chloroplast-derived enzyme cocktails hydrolyse lignocellulosic biomass and release fermentable sugars. <i>Plant Biotechnology Journal</i> , 2010, 8, 332-350.	4.1	122
14	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. <i>Nature Communications</i> , 2019, 10, 4702.	5.8	115
15	Highly efficient and precise base editing of C to A in the allotetraploid cotton (<i>Gossypium</i>) <i>Plant Biotechnology Journal</i> , 2020, 18, 45-56.	4.1	114
16	Expression and characterization of antimicrobial peptides Retrocyclin101 and Protegrin1 in chloroplasts to control viral and bacterial infections. <i>Plant Biotechnology Journal</i> , 2011, 9, 100-115.	4.1	112
17	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, 1956-1975.	4.1	109
18	Genome editing with the CRISPR-Cas system: an art, ethics and global regulatory perspective. <i>Plant Biotechnology Journal</i> , 2020, 18, 1651-1669.	4.1	97

#	ARTICLE	IF	CITATIONS
19	Factors affecting transformation efficiency of embryogenic callus of Upland cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	95
20	Release of Hormones from Conjugates: Chloroplast Expression of Î ² -Glucosidase Results in Elevated Phytohormone Levels Associated with Significant Increase in Biomass and Protection from Aphids or Whiteflies Conferred by Sucrose Esters. <i>Plant Physiology</i> , 2011, 155, 222-235.	2.3	94
21	Detection of somaclonal variation of cotton (<i>Gossypium hirsutum</i>) using cytogenetics, flow cytometry and molecular markers. <i>Plant Cell Reports</i> , 2008, 27, 1303-1316.	2.8	93
22	Multi-omics analyses reveal epigenomics basis for cotton somatic embryogenesis through successive regeneration acclimation process. <i>Plant Biotechnology Journal</i> , 2019, 17, 435-450.	4.1	88
23	Osmotin: A plant defense tool against biotic and abiotic stresses. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 149-159.	2.8	86
24	Green giantâ€”a tiny chloroplast genome with mighty power to produce high-value proteins: history and phylogeny. <i>Plant Biotechnology Journal</i> , 2021, 19, 430-447.	4.1	86
25	Suitable internal control genes for qRT-PCR normalization in cotton fiber development and somatic embryogenesis. <i>Science Bulletin</i> , 2007, 52, 3110-3117.	1.7	85
26	Robust CRISPR/Cpf1 (Cas12a)-mediated genome editing in allotetraploid cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	4.1	77
27	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021, 22, 119.	3.8	76
28	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.	3.8	69
29	<i>Pinellia ternata</i> agglutinin expression in chloroplasts confers broad spectrum resistance against aphid, whitefly, <i>Lepidopteran</i> insects, bacterial and viral pathogens. <i>Plant Biotechnology Journal</i> , 2012, 10, 313-327.	4.1	68
30	Expression of Î ³ -tocopherol methyltransferase in chloroplasts results in massive proliferation of the inner envelope membrane and decreases susceptibility to salt and metal-induced oxidative stresses by reducing reactive oxygen species. <i>Plant Biotechnology Journal</i> , 2014, 12, 1274-1285.	4.1	68
31	Factors affecting somatic embryogenesis and plant regeneration from a range of recalcitrant genotypes of Chinese cottons (<i>Gossypium hirsutum</i> L.). <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2004, 40, 371-375.	0.9	61
32	Vitrificationâ€”cryopreservation, an efficient method for eliminating <i>Candidatus Liberobacter asiaticus</i> , the citrus Huanglongbing pathogen, from in vitro adult shoot tips. <i>Plant Cell Reports</i> , 2008, 27, 241-250.	2.8	61
33	Transgenic Cotton Plants Expressing Double-stranded RNAs Target <i>HMG-CoA Reductase</i> (<i>HMGR</i>) Gene Inhibits the Growth, Development and Survival of Cotton Bollworms. <i>International Journal of Biological Sciences</i> , 2015, 11, 1296-1305.	2.6	59
34	Overexpression of <i>Rosa rugosa</i> anthocyanidin reductase enhances tobacco tolerance to abiotic stress through increased ROS scavenging and modulation of ABA signaling. <i>Plant Science</i> , 2016, 245, 35-49.	1.7	59
35	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.	4.1	58
36	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.	3.5	53

#	ARTICLE	IF	CITATIONS
37	The <i>Acer truncatum</i> genome provides insights into nervonic acid biosynthesis. <i>Plant Journal</i> , 2020, 104, 662-678.	2.8	52
38	High oleic acid content, nontransgenic allotetraploid cotton (<i>Gossypium hirsutum</i> L.) generated by knockout of <i>GhFAD2</i> genes with CRISPR/Cas9 system. <i>Plant Biotechnology Journal</i> , 2021, 19, 424-426.	4.1	50
39	Transcriptome, cytological and biochemical analysis of cytoplasmic male sterility and maintainer line in CMS-D8 cotton. <i>Plant Molecular Biology</i> , 2018, 97, 537-551.	2.0	49
40	An efficient grafting system for transgenic plant recovery in cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Cell, Tissue and Organ Culture</i> , 2006, 85, 181-185.	1.2	43
41	Production and characterization of somatic hybrids between upland cotton (<i>Gossypium hirsutum</i>) and wild cotton (<i>G. klotzschianum</i> Anderss) via electrofusion. <i>Theoretical and Applied Genetics</i> , 2004, 109, 472-479.	1.8	41
42	Release of Proteins from Intact Chloroplasts Induced by Reactive Oxygen Species during Biotic and Abiotic Stress. <i>PLoS ONE</i> , 2013, 8, e67106.	1.1	41
43	Analysis of genes differentially expressed during initial cellular dedifferentiation in cotton. <i>Science Bulletin</i> , 2008, 53, 3666-3676.	1.7	39
44	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.	4.1	39
45	Expression of Fungal Cutinase and Swollenin in Tobacco Chloroplasts Reveals Novel Enzyme Functions and/or Substrates. <i>PLoS ONE</i> , 2013, 8, e57187.	1.1	36
46	Structural insights into homotrimeric assembly of cellulose synthase CesA7 from <i>Gossypium hirsutum</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 1579-1587.	4.1	36
47	The chromosome-scale high-quality genome assembly of <i>Panax notoginseng</i> provides insight into dencichine biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 869-871.	4.1	34
48	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.	1.7	33
49	Metabolic engineering of cottonseed oil biosynthesis pathway via RNA interference. <i>Scientific Reports</i> , 2016, 6, 33342.	1.6	31
50	Chromosome-level genome of <i>Camellia lanceoleosa</i> provides a valuable resource for understanding genome evolution and self-incompatibility. <i>Plant Journal</i> , 2022, 110, 881-898.	2.8	29
51	Chromatin reorganization and endogenous auxin/cytokinin dynamic activity during somatic embryogenesis of cultured cotton cell. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 90, 63-70.	1.2	28
52	Plant Single Cell Transcriptome Hub (PsctH): an integrated online tool to explore the plant single-cell transcriptome landscape. <i>Plant Biotechnology Journal</i> , 2022, 20, 10-12.	4.1	27
53	Efficient CRISPR/Cas9 mediated Pooled-sgRNAs assembly accelerates targeting multiple genes related to male sterility in cotton. <i>Plant Methods</i> , 2021, 17, 16.	1.9	26
54	Herbicide Resistance: Another Hot Agronomic Trait for Plant Genome Editing. <i>Plants</i> , 2021, 10, 621.	1.6	26

#	ARTICLE	IF	CITATIONS
55	Red fluorescent protein (DsRed2), an ideal reporter for cotton genetic transformation and molecular breeding. <i>Crop Journal</i> , 2018, 6, 366-376.	2.3	22
56	Somatic embryogenesis and plant regeneration in wild cotton (<i>Gossypium klotzschianum</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 2003, 75, 247-253.	1.2	21
57	Pyramiding Bt genes for increasing resistance of cotton to two major lepidopteran pests: <i>Spodoptera litura</i> and <i>Heliothis armigera</i> . <i>Acta Physiologiae Plantarum</i> , 2014, 36, 2717-2727.	1.0	21
58	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.	2.1	19
59	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, 172-182.	2.3	18
60	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.	2.3	16
61	Overexpression of <i>Arabidopsis cyclin D2;1</i> in cotton results in leaf curling and other plant architectural modifications. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 110, 261-273.	1.2	13
62	Ectopic expression of <i>GhSAMDC1</i> improved plant vegetative growth and early flowering through conversion of spermidine to spermine in tobacco. <i>Scientific Reports</i> , 2020, 10, 14418.	1.6	13
63	Genome-Wide Analysis of Cotton miRNAs During Whitefly Infestation Offers New Insights into Plant-Herbivore Interaction. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5357.	1.8	12
64	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.	1.7	12
65	Silencing of a <i>LIM</i> gene in cotton exhibits enhanced resistance against <i>Apolygus lucorum</i> . <i>Journal of Cellular Physiology</i> , 2021, 236, 5921-5936.	2.0	8
66	Genetic manipulation of <i>Soc1</i> like genes promotes photosynthesis in flowers and leaves and enhances plant tolerance to high temperature. <i>Plant Biotechnology Journal</i> , 2021, 19, 8-10.	4.1	6
67	Overexpression of <i>KcNHX1</i> gene confers tolerance to multiple abiotic stresses in <i>Arabidopsis thaliana</i> . <i>Journal of Plant Research</i> , 2021, 134, 613-623.	1.2	4
68	Ectopic Expression of <i>GhSAMDC3</i> Enhanced Salt Tolerance Due to Accumulated Spd Content and Activation of Salt Tolerance-Related Genes in <i>Arabidopsis thaliana</i> . <i>DNA and Cell Biology</i> , 2021, 40, 1144-1157.	0.9	4
69	Isolation and Characterization of a Conserved Domain in the Eremophyte H ⁺ -PPase Family. <i>PLoS ONE</i> , 2013, 8, e70099.	1.1	3
70	The <i>Sophora alopecuroid</i> H ⁺ -PPase Gene <i>SaVP1</i> Confers Multiple Abiotic Stress Tolerance in <i>Arabidopsis</i> . <i>Plant Molecular Biology Reporter</i> , 2015, 33, 923-930.	1.0	3