Qingxin Song

List of Publications by Year
in descending order

36	4,622	218677	345221
papers	citations	26 h-index	36 g-index

37	37	37	4927
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
2	Soybean NAC transcription factors promote abiotic stress tolerance and lateral root formation in transgenic plants. Plant Journal, 2011, 68, 302-313.	5.7	471
3	Identification of miRNAs and their target genes in developing soybean seeds by deep sequencing. BMC Plant Biology, 2011, 11, 5.	3.6	287
4	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249
5	Epigenetic and developmental regulation in plant polyploids. Current Opinion in Plant Biology, 2015, 24, 101-109.	7.1	173
6	Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. Genome Biology, 2017, 18, 99.	8.8	153
7	Genome-Wide Analysis of DNA Methylation in Soybean. Molecular Plant, 2013, 6, 1961-1974.	8.3	143
8	Plant NAC-type transcription factor proteins contain a NARD domain for repression of transcriptional activation. Planta, 2010, 232, 1033-1043.	3.2	135
9	Identification of Rice Ethylene-Response Mutants and Characterization of MHZ7/OsEIN2 in Distinct Ethylene Response and Yield Trait Regulation. Molecular Plant, 2013, 6, 1830-1848.	8.3	117
10	The Rice Circadian Clock Regulates Tiller Growth and Panicle Development Through Strigolactone Signaling and Sugar Sensing. Plant Cell, 2020, 32, 3124-3138.	6.6	112
11	Natural variation in timing of stress-responsive gene expression predicts heterosis in intraspecific hybrids of Arabidopsis. Nature Communications, 2015, 6, 7453.	12.8	109
12	Temporal Shift of Circadian-Mediated Gene Expression and Carbon Fixation Contributes to Biomass Heterosis in Maize Hybrids. PLoS Genetics, 2016, 12, e1006197.	3.5	100
13	Soybean GmMYB73 promotes lipid accumulation in transgenic plants. BMC Plant Biology, 2014, 14, 73.	3.6	83
14	Soybean GmbZIP123 gene enhances lipid content in the seeds of transgenic Arabidopsis plants. Journal of Experimental Botany, 2013, 64, 4329-4341.	4.8	81
15	Selection for a Zinc-Finger Protein Contributes to Seed Oil Increase during Soybean Domestication. Plant Physiology, 2017, 173, 2208-2224.	4.8	73
16	Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall synthesis, represses lignification, and prolongs elongation. BMC Genomics, 2015, 16, 477.	2.8	72
17	Polyploidy and small RNA regulation of cotton fiber development. Trends in Plant Science, 2014, 19, 516-528.	8.8	68
18	Single-cell RNA-seq analysis reveals ploidy-dependent and cell-specific transcriptome changes in Arabidopsis female gametophytes. Genome Biology, 2020, 21, 178.	8.8	63

#	Article	IF	Citations
19	Dynamic Roles for Small RNAs and DNA Methylation during Ovule and Fiber Development in Allotetraploid Cotton. PLoS Genetics, 2015, 11, e1005724.	3.5	57
20	Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. Plant Cell, 2021, 33, 1430-1446.	6.6	55
21	Diurnal down-regulation of ethylene biosynthesis mediates biomass heterosis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5606-5611.	7.1	49
22	The transcription factor AtDOF4.2 regulates shoot branching and seed coat formation in Arabidopsis. Biochemical Journal, 2013, 449, 373-388.	3.7	48
23	Temporal Regulation of the Metabolome and Proteome in Photosynthetic and Photorespiratory Pathways Contributes to Maize Heterosis. Plant Cell, 2020, 32, 3706-3722.	6.6	45
24	DNA hypomethylation in tetraploid rice potentiates stress-responsive gene expression for salt tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	44
25	Comparison of Arachis monticola with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced Science, 2020, 7, 1901672.	11.2	43
26	Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. Nature Ecology and Evolution, 2021, 5, 1382-1393.	7.8	41
27	Histone Modifications Define Expression Bias of Homoeologous Genomes in Allotetraploid Cotton. Plant Physiology, 2016, 172, 1760-1771.	4.8	30
28	Dynamic and reversible DNA methylation changes induced by genome separation and merger of polyploid wheat. BMC Biology, 2020, 18, 171.	3.8	26
29	Histone H3K27 dimethylation landscapes contribute to genome stability and genetic recombination during wheat polyploidization. Plant Journal, 2021, 105, 678-690.	5.7	24
30	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (Gossypium hirsutum) Tj ETQq0 0 0 rgBT /Overlock 10 T 7, 15274.	3.3	23
31	Diurnal regulation of SDG2 and JMJ14 by circadian clock oscillators orchestrates histone modification rhythms in Arabidopsis. Genome Biology, 2019, 20, 170.	8.8	22
32	Open chromatin interaction maps reveal functional regulatory elements and chromatin architecture variations during wheat evolution. Genome Biology, 2022, 23, 34.	8.8	22
33	Small RNAs mediate transgenerational inheritance of genome-wide trans-acting epialleles in maize. Genome Biology, 2022, 23, 53.	8.8	19
34	An epigenetic basis of inbreeding depression in maize. Science Advances, 2021, 7, .	10.3	10
35	Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. BMC Research Notes, 2014, 7, 493.	1.4	9
36	<scp>iSoybean</scp> : a database for the mutational fingerprints of soybean. Plant Biotechnology Journal, 2022, , .	8.3	6