Qingxin Song

List of Publications by Year
in descending order

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Version: 2024-02-01

36 papers	4,622 citations	218677 26 h-index	345221 36 g-index
37 all docs	37 docs citations	37 times ranked	4927 citing authors

#	Article	IF	Citations
1	Open chromatin interaction maps reveal functional regulatory elements and chromatin architecture variations during wheat evolution. Genome Biology, 2022, 23, 34.	8.8	22
2	Small RNAs mediate transgenerational inheritance of genome-wide trans-acting epialleles in maize. Genome Biology, 2022, 23, 53.	8.8	19
3	<scp>iSoybean</scp> : a database for the mutational fingerprints of soybean. Plant Biotechnology Journal, 2022, , .	8.3	6
4	Histone H3K27 dimethylation landscapes contribute to genome stability and genetic recombination during wheat polyploidization. Plant Journal, 2021, 105, 678-690.	5.7	24
5	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
6	Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. Plant Cell, 2021, 33, 1430-1446.	6.6	55
7	An epigenetic basis of inbreeding depression in maize. Science Advances, 2021, 7, .	10.3	10
8	Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. Nature Ecology and Evolution, 2021, 5, 1382-1393.	7.8	41
9	Comparison of <i>Arachis monticola</i> with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced Science, 2020, 7, 1901672.	11.2	43
10	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
11	Dynamic and reversible DNA methylation changes induced by genome separation and merger of polyploid wheat. BMC Biology, 2020, 18, 171.	3.8	26
12	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
13	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
14	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249
15	Diurnal regulation of SDG2 and JMJ14 by circadian clock oscillators orchestrates histone modification rhythms in Arabidopsis. Genome Biology, 2019, 20, 170.	8.8	22
16	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
17	Selection for a Zinc-Finger Protein Contributes to Seed Oil Increase during Soybean Domestication. Plant Physiology, 2017, 173, 2208-2224.	4.8	73
18	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

#	ARTICLE	IF	CITATIONS
19	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (Gossypium hirsutum) Tj ETQq1 1 0.784314 rgBT /Overl 7, 15274.	3.3	23
20	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
21	Histone Modifications Define Expression Bias of Homoeologous Genomes in Allotetraploid Cotton. Plant Physiology, 2016, 172, 1760-1771.	4.8	30
22	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
23	Epigenetic and developmental regulation in plant polyploids. Current Opinion in Plant Biology, 2015, 24, 101-109.	7.1	173
24	Natural variation in timing of stress-responsive gene expression predicts heterosis in intraspecific hybrids of Arabidopsis. Nature Communications, 2015, 6, 7453.	12.8	109
25	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
26	Dynamic Roles for Small RNAs and DNA Methylation during Ovule and Fiber Development in Allotetraploid Cotton. PLoS Genetics, 2015, 11, e1005724.	3.5	57
27	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
28	Soybean GmMYB73 promotes lipid accumulation in transgenic plants. BMC Plant Biology, 2014, 14, 73.	3.6	83
29	Polyploidy and small RNA regulation of cotton fiber development. Trends in Plant Science, 2014, 19, 516-528.	8.8	68
30	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
31	Genome-Wide Analysis of DNA Methylation in Soybean. Molecular Plant, 2013, 6, 1961-1974.	8.3	143
32	The transcription factor AtDOF4.2 regulates shoot branching and seed coat formation in <i>Arabidopsis</i>. Biochemical Journal, 2013, 449, 373-388.	3.7	48
33	Soybean GmbZIP123 gene enhances lipid content in the seeds of transgenic Arabidopsis plants. Journal of Experimental Botany, 2013, 64, 4329-4341.	4.8	81
34	Soybean NAC transcription factors promote abiotic stress tolerance and lateral root formation in transgenic plants. Plant Journal, 2011, 68, 302-313.	5.7	471
35	Identification of miRNAs and their target genes in developing soybean seeds by deep sequencing. BMC Plant Biology, 2011, 11, 5.	3.6	287
36	Plant NAC-type transcription factor proteins contain a NARD domain for repression of transcriptional activation. Planta, 2010, 232, 1033-1043.	3.2	135