

Z Jeffrey Chen

List of Publications by Year in descending order

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101
papers

14,765
citations

28274

55
h-index

30922

102
g-index

115
all docs

115
docs citations

115
times ranked

10605
citing authors

#	ARTICLE	IF	CITATIONS
1	Small RNAs mediate transgenerational inheritance of genome-wide trans-acting epialleles in maize. <i>Genome Biology</i> , 2022, 23, 53.	8.8	19
2	Histone H3K27 dimethylation landscapes contribute to genome stability and genetic recombination during wheat polyploidization. <i>Plant Journal</i> , 2021, 105, 678-690.	5.7	24
3	DNA hypomethylation in tetraploid rice potentiates stress-responsive gene expression for salt tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	44
4	Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. <i>Plant Cell</i> , 2021, 33, 1430-1446.	6.6	55
5	LCM and RNA-seq analyses revealed roles of cell cycle and translational regulation and homoeolog expression bias in cotton fiber cell initiation. <i>BMC Genomics</i> , 2021, 22, 309.	2.8	7
6	An epigenetic basis of inbreeding depression in maize. <i>Science Advances</i> , 2021, 7, .	10.3	10
7	Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. <i>Nature Ecology and Evolution</i> , 2021, 5, 1382-1393.	7.8	41
8	Comparison of <i>Arachis monticola</i> with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. <i>Advanced Science</i> , 2020, 7, 1901672.	11.2	43
9	Temporal Regulation of the Metabolome and Proteome in Photosynthetic and Photorespiratory Pathways Contributes to Maize Heterosis. <i>Plant Cell</i> , 2020, 32, 3706-3722.	6.6	45
10	Dynamic and reversible DNA methylation changes induced by genome separation and merger of polyploid wheat. <i>BMC Biology</i> , 2020, 18, 171.	3.8	26
11	Single-cell RNA-seq analysis reveals ploidy-dependent and cell-specific transcriptome changes in Arabidopsis female gametophytes. <i>Genome Biology</i> , 2020, 21, 178.	8.8	63
12	The Rice Circadian Clock Regulates Tiller Growth and Panicle Development Through Strigolactone Signaling and Sugar Sensing. <i>Plant Cell</i> , 2020, 32, 3124-3138.	6.6	112
13	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020, 6, eaaz7677.	10.3	59
14	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14.	28.9	133
15	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
16	Diurnal regulation of SDG2 and JM14 by circadian clock oscillators orchestrates histone modification rhythms in Arabidopsis. <i>Genome Biology</i> , 2019, 20, 170.	8.8	22
17	Maternal small RNAs mediate spatial-temporal regulation of gene expression, imprinting, and seed development in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2761-2766.	7.1	54
18	Interactive roles of chromatin regulation and circadian clock function in plants. <i>Genome Biology</i> , 2019, 20, 62.	8.8	26

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19	Epigenetic perspectives on the evolution and domestication of polyploid plant and crops. <i>Current Opinion in Plant Biology</i> , 2018, 42, 37-48.	7.1	74
20	Asymmetrical changes of gene expression, small <sc>RNA</sc>s and chromatin in two resynthesized wheat allotetraploids. <i>Plant Journal</i> , 2018, 93, 828-842.	5.7	40
21	Rice Interploidy Crosses Disrupt Epigenetic Regulation, Gene Expression, and Seed Development. <i>Molecular Plant</i> , 2018, 11, 300-314.	8.3	27
22	COP1 SUPPRESSOR 4 promotes seedling photomorphogenesis by repressing <i>CCA1</i> and <i>PIF4</i> expression in <i>Arabidopsis</i>. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11631-11636.	7.1	12
23	Diurnal down-regulation of ethylene biosynthesis mediates biomass heterosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5606-5611.	7.1	49
24	B-BOX DOMAIN PROTEIN28 Negatively Regulates Photomorphogenesis by Repressing the Activity of Transcription Factor HY5 and Undergoes COP1-Mediated Degradation. <i>Plant Cell</i> , 2018, 30, 2006-2019.	6.6	105
25	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	8.8	128
26	Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 99.	8.8	153
27	Heterologous protein-DNA interactions lead to biased allelic expression of circadian clock genes in interspecific hybrids. <i>Scientific Reports</i> , 2017, 7, 45087.	3.3	10
28	Both maternally and paternally imprinted genes regulate seed development in rice. <i>New Phytologist</i> , 2017, 216, 373-387.	7.3	67
29	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Over 7, 15274.	3.3	23
30	Temporal Shift of Circadian-Mediated Gene Expression and Carbon Fixation Contributes to Biomass Heterosis in Maize Hybrids. <i>PLoS Genetics</i> , 2016, 12, e1006197.	3.5	100
31	Histone Modifications Define Expression Bias of Homoeologous Genomes in Allotetraploid Cotton. <i>Plant Physiology</i> , 2016, 172, 1760-1771.	4.8	30
32	<i>Gossypium barbadense</i> genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. <i>Scientific Reports</i> , 2015, 5, 14139.	3.3	271
33	A Long-Read Transcriptome Assembly of Cotton (<i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	2.8	12
34	Phytohormonal Networks Promote Differentiation of Fiber Initials on Pre-Anthesis Cotton Ovules Grown In Vitro and In Planta. <i>PLoS ONE</i> , 2015, 10, e0125046.	2.5	24
35	Genome-Wide Dosage-Dependent and -Independent Regulation Contributes to Gene Expression and Evolutionary Novelty in Plant Polyploids. <i>Molecular Biology and Evolution</i> , 2015, 32, 2351-2366.	8.9	57
36	Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall synthesis, represses lignification, and prolongs elongation. <i>BMC Genomics</i> , 2015, 16, 477.	2.8	72

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37	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton (<i>Gossypium</i>) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1095-1105.	1.8	20
38	Epigenetic and developmental regulation in plant polyploids. <i>Current Opinion in Plant Biology</i> , 2015, 24, 101-109.	7.1	173
39	SCARECROW-LIKE15 interacts with HISTONE DEACETYLASE19 and is essential for repressing the seed maturation programme. <i>Nature Communications</i> , 2015, 6, 7243.	12.8	58
40	Natural variation in timing of stress-responsive gene expression predicts heterosis in intraspecific hybrids of <i>Arabidopsis</i> . <i>Nature Communications</i> , 2015, 6, 7453.	12.8	109
41	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
42	An Epigenetic Role for Disrupted Paternal Gene Expression in Postzygotic Seed Abortion in <i>Arabidopsis</i> Interspecific Hybrids. <i>Molecular Plant</i> , 2015, 8, 1766-1775.	8.3	39
43	Dynamic Roles for Small RNAs and DNA Methylation during Ovule and Fiber Development in Allotetraploid Cotton. <i>PLoS Genetics</i> , 2015, 11, e1005724.	3.5	57
44	Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. <i>Nature Communications</i> , 2014, 5, 5519.	12.8	205
45	A Role for CHH Methylation in the Parent-of-Origin Effect on Altered Circadian Rhythms and Biomass Heterosis in <i>Arabidopsis</i> Intraspecific Hybrids. <i>Plant Cell</i> , 2014, 26, 2430-2440.	6.6	69
46	miR828 and miR858 regulate homoeologous MYB2 gene functions in <i>Arabidopsis</i> trichome and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050.	12.8	215
47	Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. <i>BMC Research Notes</i> , 2014, 7, 493.	1.4	9
48	Polyploidy and small RNA regulation of cotton fiber development. <i>Trends in Plant Science</i> , 2014, 19, 516-528.	8.8	68
49	Genomic and epigenetic insights into the molecular bases of heterosis. <i>Nature Reviews Genetics</i> , 2013, 14, 471-482.	16.3	444
50	Ploidy and Hybridity Effects on Growth Vigor and Gene Expression in <i>Arabidopsis thaliana</i> Hybrids and Their Parents. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 505-513.	1.8	127
51	Maternal siRNAs as regulators of parental genome imbalance and gene expression in endosperm of <i>Arabidopsis</i> seeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5529-5534.	7.1	133
52	Cis- and trans-regulatory divergence between progenitor species determines gene-expression novelty in <i>Arabidopsis</i> allopolyploids. <i>Nature Communications</i> , 2012, 3, 950.	12.8	186
53	Roles of target site location and sequence complementarity in trans-acting siRNA formation in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2012, 69, 217-226.	5.7	32
54	Big roles for small RNAs in polyploidy, hybrid vigor, and hybrid incompatibility. <i>Current Opinion in Plant Biology</i> , 2012, 15, 154-161.	7.1	132

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55	Auxin boost for cotton. <i>Nature Biotechnology</i> , 2011, 29, 407-409.	17.5	29
56	<i>cis</i> - and <i>trans</i> -Regulation of miR163 and Target Genes Confers Natural Variation of Secondary Metabolites in Two <i>Arabidopsis</i> Species and Their Allopolyploids. <i>Plant Cell</i> , 2011, 23, 1729-1740.	6.6	121
57	Coordinated histone modifications are associated with gene expression variation within and between species. <i>Genome Research</i> , 2011, 21, 590-598.	5.5	140
58	Activation of <i>Arabidopsis</i> Seed Hair Development by Cotton Fiber-Related Genes. <i>PLoS ONE</i> , 2011, 6, e21301.	2.5	53
59	Unstable Transcripts in <i>Arabidopsis</i> Allotetraploids Are Associated with Nonadditive Gene Expression in Response to Abiotic and Biotic Stresses. <i>PLoS ONE</i> , 2011, 6, e24251.	2.5	32
60	Near-isogenic cotton germplasm lines that differ in fiber-bundle strength have temporal differences in fiber gene expression patterns as revealed by comparative high-throughput profiling. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1347-1366.	3.6	48
61	Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. <i>Chromosoma</i> , 2010, 119, 255-266.	2.2	32
62	Genomic and expression plasticity of polyploidy. <i>Current Opinion in Plant Biology</i> , 2010, 13, 153-159.	7.1	283
63	Tandem duplication of the <i>FLC</i> locus and the origin of a new gene in <i>Arabidopsis</i> related species and their functional implications in allopolyploids. <i>New Phytologist</i> , 2010, 186, 228-238.	7.3	29
64	RNAi-mediated down-regulation of <i>DCL1</i> and <i>AGO1</i> induces developmental changes in resynthesized <i>Arabidopsis</i> allotetraploids. <i>New Phytologist</i> , 2010, 186, 207-215.	7.3	15
65	Differential sensitivity of the <i>Arabidopsis thaliana</i> transcriptome and enhancers to the effects of genome doubling. <i>New Phytologist</i> , 2010, 186, 194-206.	7.3	39
66	Apyrase (Nucleoside Triphosphate-Diphosphohydrolase) and Extracellular Nucleotides Regulate Cotton Fiber Elongation in Cultured Ovules. <i>Plant Physiology</i> , 2010, 152, 1073-1083.	4.8	75
67	Molecular mechanisms of polyploidy and hybrid vigor. <i>Trends in Plant Science</i> , 2010, 15, 57-71.	8.8	510
68	Small RNAs serve as a genetic buffer against genomic shock in <i>Arabidopsis</i> interspecific hybrids and allopolyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17835-17840.	7.1	320
69	Duplicate genes increase expression diversity in closely related species and allopolyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2295-2300.	7.1	122
70	Altered circadian rhythms regulate growth vigour in hybrids and allopolyploids. <i>Nature</i> , 2009, 457, 327-331.	27.8	598
71	Genome-wide analysis reveals rapid and dynamic changes in miRNA and siRNA sequence and expression during ovule and fiber development in allotetraploid cotton (<i>Gossypium hirsutum</i> L.). <i>Genome Biology</i> , 2009, 10, R122.	9.6	128
72	Analysis of Gene Expression in Resynthesized <i>Brassica napus</i> Allopolyploids Using <i>Arabidopsis</i> 70mer Oligo Microarrays. <i>PLoS ONE</i> , 2009, 4, e4760.	2.5	64

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73	RNAi of <i>met1</i> Reduces DNA Methylation and Induces Genome-Specific Changes in Gene Expression and Centromeric Small RNA Accumulation in Arabidopsis Allopolyploids. <i>Genetics</i> , 2008, 178, 1845-1858.	2.9	82
74	Genetic and Epigenetic Mechanisms for Gene Expression and Phenotypic Variation in Plant Polyploids. <i>Annual Review of Plant Biology</i> , 2007, 58, 377-406.	18.7	838
75	Gene Expression Changes and Early Events in Cotton Fibre Development. <i>Annals of Botany</i> , 2007, 100, 1391-1401.	2.9	330
76	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310.	4.8	390
77	Roles of dynamic and reversible histone acetylation in plant development and polyploidy. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007, 1769, 295-307.	2.4	195
78	External factors accelerate expression divergence between duplicate genes. <i>Trends in Genetics</i> , 2007, 23, 162-166.	6.7	58
79	Analysis of gene expression profiles in response to <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>Planta</i> , 2007, 227, 13-24.	3.2	131
80	The Expression of Genes Encoding Lipodepsipeptide Phytotoxins by <i>Pseudomonas syringae</i> pv. <i>syringae</i> Is Coordinated in Response to Plant Signal Molecules. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 257-269.	2.6	28
81	<i>Arabidopsis thaliana</i> histone deacetylase 1 (AtHD1) is localized in euchromatic regions and demonstrates histone deacetylase activity in vitro. <i>Cell Research</i> , 2006, 16, 479-488.	12.0	37
82	Accumulation of genome-specific transcripts, transcription factors and phytohormonal regulators during early stages of fiber cell development in allotetraploid cotton. <i>Plant Journal</i> , 2006, 47, 761-775.	5.7	191
83	Developmental and gene expression analyses of a cotton naked seed mutant. <i>Planta</i> , 2006, 223, 418-432.	3.2	110
84	Mechanisms of genomic rearrangements and gene expression changes in plant polyploids. <i>BioEssays</i> , 2006, 28, 240-252.	2.5	371
85	Genomewide Nonadditive Gene Regulation in <i>Arabidopsis</i> Allotetraploids. <i>Genetics</i> , 2006, 172, 507-517.	2.9	527
86	Nonadditive Regulation of <i>FRI</i> and <i>FLC</i> Loci Mediates Flowering-Time Variation in <i>Arabidopsis</i> Allopolyploids. <i>Genetics</i> , 2006, 173, 965-974.	2.9	125
87	Evolution and Expression of Homeologous Loci in <i>Tragopogon miscellus</i> (Asteraceae), a Recent and Reciprocally Formed Allopolyploid. <i>Genetics</i> , 2006, 173, 1599-1611.	2.9	166
88	Oligonucleotide Microarray Analysis of the SalA Regulon Controlling Phytotoxin Production by <i>Pseudomonas syringae</i> pv. <i>syringae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 324-333.	2.6	44
89	Reversible Histone Acetylation and Deacetylation Mediate Genome-Wide, Promoter-Dependent and Locus-Specific Changes in Gene Expression During Plant Development. <i>Genetics</i> , 2005, 169, 337-345.	2.9	157
90	Detecting Differential Expression of Parental or Progenitor Alleles in Genetic Hybrids and Allopolyploids. <i>Methods in Enzymology</i> , 2005, 395, 554-569.	1.0	4

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91	Evolution of Genome Size in Brassicaceae. <i>Annals of Botany</i> , 2005, 95, 229-235.	2.9	383
92	Methods for Genome-Wide Analysis of Gene Expression Changes in Polyploids. <i>Methods in Enzymology</i> , 2005, 395, 570-596.	1.0	13
93	Wide-Cross Whole-Genome Radiation Hybrid Mapping of Cotton (<i>Gossypium hirsutum</i> L.). <i>Genetics</i> , 2004, 167, 1317-1329.	2.9	35
94	The development of an <i>Arabidopsis</i> model system for genome-wide analysis of polyploidy effects. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 689-700.	1.6	69
95	Stochastic and Epigenetic Changes of Gene Expression in <i>Arabidopsis</i> Polyploids. <i>Genetics</i> , 2004, 167, 1961-1973.	2.9	323
96	Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in <i>Arabidopsis</i> and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57.	8.3	55
97	A Concerted DNA Methylation/Histone Methylation Switch Regulates rRNA Gene Dosage Control and Nucleolar Dominance. <i>Molecular Cell</i> , 2004, 13, 599-609.	9.7	336
98	Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147.	6.7	812
99	Natural variation in nucleolar dominance reveals the relationship between nucleolus organizer chromatin topology and rRNA gene transcription in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11418-11423.	7.1	85
100	Genetic Control of Developmental Changes Induced by Disruption of <i>Arabidopsis</i> Histone Deacetylase 1 (<i>AtHD1</i>) Expression. <i>Genetics</i> , 2003, 165, 399-409.	2.9	105
101	RNA Polymerase I Transcription in a Brassica Interspecific Hybrid and Its Progenitors: Tests of Transcription Factor Involvement in Nucleolar Dominance. <i>Genetics</i> , 1999, 152, 451-460.	2.9	45