

Z Jeffrey Chen

List of Publications by Year in descending order

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101
papers

14,765
citations

28274

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30922

102
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115
all docs

115
docs citations

115
times ranked

10605
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | Understanding mechanisms of novel gene expression in polyploids. <i>Trends in Genetics</i> , 2003, 19, 141-147. | 6.7 | 812 |
| 4 | Altered circadian rhythms regulate growth vigour in hybrids and allopolyploids. <i>Nature</i> , 2009, 457, 327-331. | 27.8 | 598 |
| 5 | Genomewide Nonadditive Gene Regulation in Arabidopsis Allotetraploids. <i>Genetics</i> , 2006, 172, 507-517. | 2.9 | 527 |
| 6 | Molecular mechanisms of polyploidy and hybrid vigor. <i>Trends in Plant Science</i> , 2010, 15, 57-71. | 8.8 | 510 |
| 7 | Genomic and epigenetic insights into the molecular bases of heterosis. <i>Nature Reviews Genetics</i> , 2013, 14, 471-482. | 16.3 | 444 |
| 8 | Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. <i>Plant Physiology</i> , 2007, 145, 1303-1310. | 4.8 | 390 |
| 9 | Evolution of Genome Size in Brassicaceae. <i>Annals of Botany</i> , 2005, 95, 229-235. | 2.9 | 383 |
| 10 | Mechanisms of genomic rearrangements and gene expression changes in plant polyploids. <i>BioEssays</i> , 2006, 28, 240-252. | 2.5 | 371 |
| 11 | 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 |
| 12 | Gene Expression Changes and Early Events in Cotton Fibre Development. <i>Annals of Botany</i> , 2007, 100, 1391-1401. | 2.9 | 330 |
| 13 | Stochastic and Epigenetic Changes of Gene Expression in Arabidopsis Polyploids. <i>Genetics</i> , 2004, 167, 1961-1973. | 2.9 | 323 |
| 14 | 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 |
| 15 | Genomic and expression plasticity of polyploidy. <i>Current Opinion in Plant Biology</i> , 2010, 13, 153-159. | 7.1 | 283 |
| 16 | <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 |
| 17 | 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 |
| 18 | miR828 and miR858 regulate homoeologous MYB2 gene functions in Arabidopsis trichome and cotton fibre development. <i>Nature Communications</i> , 2014, 5, 3050. | 12.8 | 215 |

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|----|---|------|-----------|
| 19 | Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. <i>Nature Communications</i> , 2014, 5, 5519. | 12.8 | 205 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Epigenetic and developmental regulation in plant polyploids. <i>Current Opinion in Plant Biology</i> , 2015, 24, 101-109. | 7.1 | 173 |
| 24 | 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 |
| 25 | 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 |
| 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 | Coordinated histone modifications are associated with gene expression variation within and between species. <i>Genome Research</i> , 2011, 21, 590-598. | 5.5 | 140 |
| 28 | 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 |
| 29 | A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14. | 28.9 | 133 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33. | 8.8 | 128 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|---|------|-----------|
| 37 | <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 |
| 38 | 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 |
| 39 | Developmental and gene expression analyses of a cotton naked seed mutant. <i>Planta</i> , 2006, 223, 418-432. | 3.2 | 110 |
| 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 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | RNAi of <i>met1</i> Reduces DNA Methylation and Induces Genome-Specific Changes in Gene Expression and Centromeric Small RNA Accumulation in <i>Arabidopsis</i> Allopolyploids. <i>Genetics</i> , 2008, 178, 1845-1858. | 2.9 | 82 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | Polyploidy and small RNA regulation of cotton fiber development. <i>Trends in Plant Science</i> , 2014, 19, 516-528. | 8.8 | 68 |
| 52 | Both maternally and paternally imprinted genes regulate seed development in rice. <i>New Phytologist</i> , 2017, 216, 373-387. | 7.3 | 67 |
| 53 | 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 |
| 54 | Single-cell RNA-seq analysis reveals ploidy-dependent and cell-specific transcriptome changes in <i>Arabidopsis</i> female gametophytes. <i>Genome Biology</i> , 2020, 21, 178. | 8.8 | 63 |

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|----|---|------|-----------|
| 55 | From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020, 6, eaaz7677. | 10.3 | 59 |
| 56 | External factors accelerate expression divergence between duplicate genes. <i>Trends in Genetics</i> , 2007, 23, 162-166. | 6.7 | 58 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in Arabidopsis and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57. | 8.3 | 55 |
| 61 | Altered chromatin architecture and gene expression during polyploidization and domestication of soybean. <i>Plant Cell</i> , 2021, 33, 1430-1446. | 6.6 | 55 |
| 62 | 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 |
| 63 | Activation of Arabidopsis Seed Hair Development by Cotton Fiber-Related Genes. <i>PLoS ONE</i> , 2011, 6, e21301. | 2.5 | 53 |
| 64 | 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 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | 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 |
| 70 | 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 |
| 71 | Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. <i>Nature Ecology and Evolution</i> , 2021, 5, 1382-1393. | 7.8 | 41 |
| 72 | Asymmetrical changes of gene expression, small RNA and chromatin in two resynthesized wheat allotetraploids. <i>Plant Journal</i> , 2018, 93, 828-842. | 5.7 | 40 |

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|----|---|------|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | <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 |
| 76 | Wide-Cross Whole-Genome Radiation Hybrid Mapping of Cotton (<i>Gossypium hirsutum</i> L.). <i>Genetics</i> , 2004, 167, 1317-1329. | 2.9 | 35 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | Histone Modifications Define Expression Bias of Homoeologous Genomes in Allotetraploid Cotton. <i>Plant Physiology</i> , 2016, 172, 1760-1771. | 4.8 | 30 |
| 81 | 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 |
| 82 | Auxin boost for cotton. <i>Nature Biotechnology</i> , 2011, 29, 407-409. | 17.5 | 29 |
| 83 | 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 |
| 84 | Rice Interploidy Crosses Disrupt Epigenetic Regulation, Gene Expression, and Seed Development. <i>Molecular Plant</i> , 2018, 11, 300-314. | 8.3 | 27 |
| 85 | Interactive roles of chromatin regulation and circadian clock function in plants. <i>Genome Biology</i> , 2019, 20, 62. | 8.8 | 26 |
| 86 | 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 |
| 87 | 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 |
| 88 | 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 |
| 89 | Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Overl 7, 15274. | 3.3 | 23 |
| 90 | Diurnal regulation of SDG2 and JM14 by circadian clock oscillators orchestrates histone modification rhythms in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2019, 20, 170. | 8.8 | 22 |

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|-----|--|------|-----------|
| 91 | 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 |
| 92 | Small RNAs mediate transgenerational inheritance of genome-wide trans-acting epialleles in maize. <i>Genome Biology</i> , 2022, 23, 53. | 8.8 | 19 |
| 93 | 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 |
| 94 | Methods for Genome-Wide Analysis of Gene Expression Changes in Polyploids. <i>Methods in Enzymology</i> , 2005, 395, 570-596. | 1.0 | 13 |
| 95 | 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 |
| 96 | 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 |
| 97 | 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 |
| 98 | An epigenetic basis of inbreeding depression in maize. <i>Science Advances</i> , 2021, 7, . | 10.3 | 10 |
| 99 | 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 |
| 100 | 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 |
| 101 | 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 |