James C Schnable

List of Publications by Year
in descending order

123 papers	8,614 citations

81900
39 h-index	53230 85 g-index

161 all docs	161 docs citations

161 times ranked	9880 citing authors

#	Article	IF	Citations
1	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	27.8	1,685
2	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4069-4074.	7.1	644
3	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	12.6	411
4	ALLMAPS: robust scaffold ordering based on multiple maps. Genome Biology, 2015, 16, 3.	8.8	340
5	Following Tetraploidy in Maize, a Short Deletion Mechanism Removed Genes Preferentially from One of the Two Homeologs. PLoS Biology, 2010, 8, e1000409.	5.6	260
6	Temporal dynamics of maize plant growth, water use, and leaf water content using automated high throughput RGB and hyperspectral imaging. Computers and Electronics in Agriculture, 2016, 127, 625-632.	7.7	219
7	High-resolution mapping of open chromatin in the rice genome. Genome Research, 2012, 22, 151-162.	5.5	205
8	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. Current Opinion in Plant Biology, 2012, 15, 131-139.	7.1	194
9	High Throughput In vivo Analysis of Plant Leaf Chemical Properties Using Hyperspectral Imaging. Frontiers in Plant Science, 2017, 8, 1348.	3.6	181
10	Towards a multiscale crop modelling framework for climate change adaptation assessment. Nature Plants, 2020, 6, 338-348.	9.3	181
11	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. Genetics, 2012, 190, 1563-1574.	2.9	163
12	Two Evolutionarily Distinct Classes of Paleopolyploidy. Molecular Biology and Evolution, 2014, 31, 448-454.	8.9	159
13	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	3.5	150
14	Genes Identified by Visible Mutant Phenotypes Show Increased Bias toward One of Two Subgenomes of Maize. PLoS ONE, 2011, 6, e17855.	2.5	145
15	Screening synteny blocks in pairwise genome comparisons through integer programming. BMC Bioinformatics, 2011, 12, 102.	2.6	142
16	The genome of broomcorn millet. Nature Communications, 2019, 10, 436.	12.8	130
17	Genome-Wide Analysis of Syntenic Gene Deletion in the Grasses. Genome Biology and Evolution, 2012, 4, 265-277.	2.5	126
18	tGBSÂ® genotyping-by-sequencing enables reliable genotyping of heterozygous loci. Nucleic Acids Research, 2017, 45, e178-e178.	14.5	115

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19	High-throughput analysis of leaf physiological and chemical traits with VIS–NIR–SWIR spectroscopy: a case study with a maize diversity panel. Plant Methods, 2019, 15, 66.	4.3	115
20	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. Frontiers in Plant Science, 2017, 8, 694.	3.6	109
21	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
22	Epigenetic regulation of subgenome dominance following whole genome triplication in *Brassica rapa*. New Phytologist, 2016, 211, 288-299.	7.3	100
23	Initiation of Setaria as a model plant. Frontiers of Agricultural Science and Engineering, 2014, 1, 16.	1.4	91
24	Genomic resources in plant breeding for sustainable agriculture. Journal of Plant Physiology, 2021, 257, 153351.	3.5	90
25	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. Plant Cell, 2014, 26, 3939-3948.	6.6	80
26	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. Frontiers in Plant Science, 2012, 3, 94.	3.6	73
27	Functional Divergence between Subgenomes and Gene Pairs after Whole Genome Duplications. Molecular Plant, 2018, 11, 388-397.	8.3	73
28	SynFind: Compiling Syntenic Regions across Any Set of Genomes on Demand. Genome Biology and Evolution, 2015, 7, 3286-3298.	2.5	70
29	Low-temperature tolerance in land plants: Are transcript and membrane responses conserved?. Plant Science, 2018, 276, 73-86.	3.6	70
30	Differentially Regulated Orthologs in Sorghum and the Subgenomes of Maize. Plant Cell, 2017, 29, 1938-1951.	6.6	68
31	Continuous Monitoring of Soil Nitrate Using a Miniature Sensor with Poly(3-octyl-thiophene) and Molybdenum Disulfide Nanocomposite. ACS Applied Materials & Interfaces, 2019, 11, 29195-29206.	8.0	66
32	Genome Evolution in Maize: From Genomes Back to Genes. Annual Review of Plant Biology, 2015, 66, 329-343.	18.7	65
33	NU-Spidercam: A large-scale, cable-driven, integrated sensing and robotic system for advanced phenotyping, remote sensing, and agronomic research. Computers and Electronics in Agriculture, 2019, 160, 71-81.	7.7	63
34	Mapping of Quantitative Trait Locus (QTLs) that Contribute to Germination and Early Seedling Drought Tolerance in the Interspecific Cross Setaria italicaÃ—Setaria viridis. PLoS ONE, 2014, 9, e101868.	2.5	62
35	Cross species selection scans identify components of C_4 photosynthesis in the grasses. Journal of Experimental Botany, 2017, 68, 127-135.	4.8	61
36	Phylogeny and photosynthesis of the grass tribe Paniceae. American Journal of Botany, 2015, 102, 1493-1505.	1.7	58

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37	Shared Genetic Control of Root System Architecture between <i>Zea mays</i> and <i>Sorghum bicolor</i>. Plant Physiology, 2020, 182, 977-991.	4.8	57
38	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	52
39	Robotic Technologies for High-Throughput Plant Phenotyping: Contemporary Reviews and Future Perspectives. Frontiers in Plant Science, 2021, 12, 611940.	3.6	50
40	The draft genome of the C3 panicoid grass species Dichanthelium oligosanthes. Genome Biology, 2016, 17, 223.	8.8	48
41	Evolutionarily Conserved Alternative Splicing Across Monocots. Genetics, 2017, 207, 465-480.	2.9	47
42	Mapping QTLs for morpho-agronomic traits in proso millet (Panicum miliaceum L.). Molecular Breeding, 2016, 36, 1.	2.1	46
43	Predicting transcriptional responses to cold stress across plant species. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	46
44	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. Frontiers in Genetics, 2020, 11, 592769.	2.3	44
45	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. G3: Genes, Genomes, Genetics, 2018, 8, 2513-2522.	1.8	41
46	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. Plant Physiology, 2020, 183, 1898-1909.	4.8	39
47	Plant segmentation by supervised machine learning methods. The Plant Phenome Journal, 2020, 3, e20001.	2.0	38
48	Maize genomes to fields (G2F): 2014â€"2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	1.4	38
49	Co-option of the polarity gene network shapes filament morphology in angiosperms. Scientific Reports, 2014, 4, 6194.	3.3	37
50	Multiscale computational models can guide experimentation and targeted measurements for crop improvement. Plant Journal, 2020, 103, 21-31.	5.7	36
51	Doseâ€"Sensitivity, Conserved Non-Coding Sequences, and Duplicate Gene Retention Through Multiple Tetraploidies in the Grasses. Frontiers in Plant Science, 2011, 2, 2.	3.6	35
52	Conventional and hyperspectral time-series imaging of maize lines widely used in field trials. GigaScience, 2018, 7, 1-11.	6.4	34
53	The C-terminal motif of SiAGO1b is required for the regulation of growth, development and stress responses in foxtail millet (<i>Setaria italica</i>(L.) P. Beauv). Journal of Experimental Botany, 2016, 67, 3237-3249.	4.8	33
54	Automated conserved non-coding sequence (CNS) discovery reveals differences in gene content and promoter evolution among grasses. Frontiers in Plant Science, 2013, 4, 170.	3.6	32

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55	Semantic Segmentation of Sorghum Using Hyperspectral Data Identifies Genetic Associations. Plant Phenomics, 2020, 2020, 4216373.	5.9	32
56	Linked read technology for assembling large complex and polyploid genomes. BMC Genomics, 2018, 19, 651.	2.8	31
57	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. Plant Biotechnology Journal, 2020, 18, 389-401.	8.3	30
58	Optimising the identification of causal variants across varying genetic architectures in crops. Plant Biotechnology Journal, 2019, 17, 893-905.	8.3	29
59	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. Plant Cell, 2020, 32, 2457-2473.	6.6	29
60	Interspecific analysis of diurnal gene regulation in panicoid grasses identifies known and novel regulatory motifs. BMC Genomics, 2020, 21, 428.	2.8	29
61	A near complete snapshot of the Zea mays seedling transcriptome revealed from ultra-deep sequencing. Scientific Reports, 2015, 4, 4519.	3.3	28
62	Hyperspectral reflectance-based phenotyping for quantitative genetics in crops: Progress and challenges. Plant Communications, 2021, 2, 100209.	7.7	28
63	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	3.3	27
64	A co-opted steroid synthesis gene, maintained in sorghum but not maize, is associated with a divergence in leaf wax chemistry. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
65	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. BMC Research Notes, 2018, 11, 452.	1.4	25
66	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. Genetics, 2021, 218, .	2.9	24
67	Enhancing Hybrid Prediction in Pearl Millet Using Genomic and/or Multi-Environment Phenotypic Information of Inbreds. Frontiers in Genetics, 2019, 10, 1294.	2.3	23
68	RNA-Seq Based Analysis of Population Structure within the Maize Inbred B73. PLoS ONE, 2016, 11, e0157942.	2.5	23
69	Genotype-Corrector: improved genotype calls for genetic mapping in F2 and RIL populations. Scientific Reports, 2018, 8, 10088.	3.3	22
70	Voxel carving€based 3D reconstruction of sorghum identifies genetic determinants of light interception efficiency. Plant Direct, 2020, 4, e00255.	1.9	21
71	Largely unlinked gene sets targeted by selection for domestication syndrome phenotypes in maize and sorghum. Plant Journal, 2018, 93, 843-855.	5.7	20
72	Sorghum Association Panel whole€genome sequencing establishes cornerstone resource for dissecting genomic diversity. Plant Journal, 2022, 111, 888-904.	5.7	20

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73	A High-Throughput Phenotyping Pipeline for Image Processing and Functional Growth Curve Analysis. Plant Phenomics, 2020, 2020, 7481687.	5.9	19
74	Impacts of Whole-Genome Triplication on *MIRNA* Evolution in *Brassica rapa*. Genome Biology and Evolution, 2015, 7, 3085-3096.	2.5	18
75	Genome-wide characterization of non-reference transposable element insertion polymorphisms reveals genetic diversity in tropical and temperate maize. BMC Genomics, 2017, 18, 702.	2.8	18
76	Parallels between natural selection in the cold–adapted crop–wild relative *Tripsacum dactyloides* and artificial selection in temperate adapted maize. Plant Journal, 2019, 99, 965-977.	5.7	18
77	Rhizosphere Microbiomes in a Historical Maize-Soybean Rotation System Respond to Host Species and Nitrogen Fertilization at the Genus and Subgenus Levels. Applied and Environmental Microbiology, 2021, 87, e0313220.	3.1	17
78	Maize Tassel Detection From UAV Imagery Using Deep Learning. Frontiers in Robotics and AI, 2021, 8, 600410.	3.2	17
79	STAG-CNS: An Order-Aware Conserved Noncoding Sequences Discovery Tool for Arbitrary Numbers of Species. Molecular Plant, 2017, 10, 990-999.	8.3	16
80	In vivo human-like robotic phenotyping of leaf traits in maize and sorghum in greenhouse. Computers and Electronics in Agriculture, 2019, 163, 104854.	7.7	16
81	High Density Genetic Maps of Seashore Paspalum Using Genotyping-By-Sequencing and Their Relationship to The Sorghum Bicolor Genome. Scientific Reports, 2019, 9, 12183.	3.3	16
82	A UAV–based high–throughput phenotyping approach to assess time–series nitrogen responses and identify trait–associated genetic components in maize. The Plant Phenome Journal, 2022, 5, .	2.0	16
83	Functional Modeling of Plant Growth Dynamics. The Plant Phenome Journal, 2018, 1, 1-10.	2.0	15
84	qTeller: a tool for comparative multi-genomic gene expression analysis. Bioinformatics, 2021, 38, 236-242.	4.1	15
85	Microsatellite Variations of Elite Setaria Varieties Released during Last Six Decades in China. PLoS ONE, 2015, 10, e0125688.	2.5	15
86	FractBias: a graphical tool for assessing fractionation bias following polyploidy. Bioinformatics, 2017, 33, 552-554.	4.1	14
87	Leaf Angle eXtractor: A high–throughput image processing framework for leaf angle measurements in maize and sorghum. Applications in Plant Sciences, 2020, 8, e11385.	2.1	14
88	Genome–Phenome Wide Association in Maize and Arabidopsis Identifies a Common Molecular and Evolutionary Signature. Molecular Plant, 2020, 13, 907-922.	8.3	14
89	Automation of leaf counting in maize and sorghum using deep learning. The Plant Phenome Journal, 2021, 4, e20022.	2.0	14
90	Robotic Detection and Grasp of Maize and Sorghum: Stem Measurement with Contact. Robotics, 2020, 9, 58.	3.5	13

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91	Sorghum Segmentation by Skeleton Extraction. Lecture Notes in Computer Science, 2020, , 296-311.	1.3	13
92	Genes and gene models, an important distinction. New Phytologist, 2020, 228, 50-55.	7.3	12
93	Comparative Transcriptome Analysis Reveals Genetic Mechanisms of Sugarcane Aphid Resistance in Grain Sorghum. International Journal of Molecular Sciences, 2021, 22, 7129.	4.1	10
94	Can High-Resolution Satellite Multispectral Imagery Be Used to Phenotype Canopy Traits and Yield Potential in Field Conditions?. Transactions of the ASABE, 2021, 64, 879-891.	1.1	9
95	Continuous in situ soil nitrate sensors: The importance of high‐resolution measurements across time and a comparison with salt extraction‐based methods. Soil Science Society of America Journal, 2021, 85, 677-690.	2.2	9
96	RGPDB: database of root-associated genes and promoters in maize, soybean, and sorghum. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	8
97	Kinetic variation in grass phospho*enol*pyruvate carboxylases provides opportunity to enhance C_4 photosynthetic efficiency. Plant Journal, 2021, 105, 1677-1688.	5.7	8
98	Quantitative Resistance Loci to Southern Rust Mapped in a Temperate Maize Diversity Panel. Phytopathology, 2022, 112, 579-587.	2.2	8
99	Location of low copy genes in chromosomes of Brachiaria spp.. Molecular Biology Reports, 2018, 45, 109-118.	2.3	7
100	Integrating Phylogenetic and Network Approaches to Study Gene Family Evolution: The Case of the *AGAMOUS* Family of Floral Genes. Evolutionary Bioinformatics, 2018, 14, 117693431876468.	1.2	7
101	QTL identification and epistatic effect analysis of seed size- and weight-related traits in Zea mays L. Molecular Breeding, 2019, 39, 1.	2.1	7
102	Non‐homology‐based prediction of gene functions in maize (Zea mays ssp. mays). Plant Genome, 2020, 13, e20015.	2.8	7
103	Investigating the potential of satellite imagery for high-throughput field phenotyping applications. , 2020, , .		7
104	The Evolution of Plant Gene and Genome Sequencing. Advances in Botanical Research, 2014, , 47-90.	1.1	6
105	Early History of the Angiosperms. Advances in Botanical Research, 2014, 69, 195-222.	1.1	6
106	Identification and utilization of genetic determinants of trait measurement errors in image-based, high-throughput phenotyping. Plant Cell, 2021, 33, 2562-2582.	6.6	6
107	Maize (Zea Mays) as a Model for Studying the Impact of Gene and Regulatory Sequence Loss Following Whole-Genome Duplication. , 2012, , 137-145.		5
108	Novel All-Solid-State Soil Nutrient Sensor Using Nanocomposite of Poly(3-Octyl-Thiophene) and Molybdenum Sulfate. , 2019, , .		5

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109	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. Molecular Biology and Evolution, 2018, 35, 2762-2772.	8.9	4
110	Development of a Gas Sensor for Green Leaf Volatile Detection. , 2021, , .		4
111	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. Nature Communications, 2022, 13, 820.	12.8	4
112	3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. PeerJ, 2021, 9, e12628.	2.0	4
113	In-Planta Nitrate Detection Using Insertable Plant Microsensor. , 2019, , .		3
114	Harnessing the Potential of the Tea Tree Genome. Molecular Plant, 2017, 10, 788-790.	8.3	2
115	IsoSeq transcriptome assembly of C_3 panicoid grasses provides tools to study evolutionary change in the Panicoideae. Plant Direct, 2020, 4, e00203.	1.9	2
116	Faster-R-CNN based deep learning for locating corn tassels in UAV imagery. , 2020, , .		2
117	Genome-Wide DNA Polymorphism Analysis and Molecular Marker Development for the Setaria italica Variety "SSR41"and Positional Cloning of the Setaria White Leaf Sheath Gene SiWLS1. Frontiers in Plant Science, 2021, 12, 743782.	3.6	2
118	DiCE: Discovery of conserved noncoding sequences efficiently. , 2017, , .		1
119	Advances in plant phenomics: From data and algorithms to biological insights. Applications in Plant Sciences, 2020, 8, e11386.	2.1	1
120	72-h diurnal RNA-seq analysis of fully expanded third leaves from maize, sorghum, and foxtail millet at 3-h resolution. BMC Research Notes, 2021, 14, 24.	1.4	1
121	*DCT4*—A New Member of the Dicarboxylate Transporter Family in C4 Grasses. Genome Biology and Evolution, 2021, 13, .	2.5	1
122	Tandem duplicate expression patterns are conserved between maize haplotypes of the *α*-zein gene family. Plant Direct, 2021, 5, e346.	1.9	1
123	Can the Grains Offer Each Other Helping Hands? Convergent Molecular Mechanisms Associated with Domestication and Crop Improvement in Rice and Maize. Molecular Plant, 2022, , .	8.3	1