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	Quantitative Resistance Loci to Southern Rust Mapped in a Temperate Maize Diversity Panel. Phytopathology, 2022, 112, 579-587.	2.2	8
2	A UAVâ€based highâ€throughput phenotyping approach to assess timeâ€series nitrogen responses and identify traitâ€associated genetic components in maize. The Plant Phenome Journal, 2022, 5, .	2.0	16
3	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. Nature Communications, 2022, 13, 820.	12.8	4
4	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
5	Sorghum Association PanelÂwholeâ€genome sequencing establishes cornerstone resource for dissecting genomic diversity. Plant Journal, 2022, 111, 888-904.	5.7	20
6	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
7	Automation of leaf counting in maize and sorghum using deep learning. The Plant Phenome Journal, 2021, 4, e20022.	2.0	14
8	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
9	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
10	Genomic resources in plant breeding for sustainable agriculture. Journal of Plant Physiology, 2021, 257, 153351.	3.5	90
11	*DCT4*â€"A New Member of the Dicarboxylate Transporter Family in C4 Grasses. Genome Biology and Evolution, 2021, 13, .	2.5	1
12	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
13	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
14	Continuous in situ soil nitrate sensors: The importance of highâ€resolution measurements across time and a comparison with salt extractionâ€based methods. Soil Science Society of America Journal, 2021, 85, 677-690.	2.2	9
15	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
16	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
17	Maize Tassel Detection From UAV Imagery Using Deep Learning. Frontiers in Robotics and AI, 2021, 8, 600410.	3.2	17
18	Development of a Gas Sensor for Green Leaf Volatile Detection. , 2021, , .		4

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19	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. Genetics, 2021, 218, .	2.9	24
20	Robotic Technologies for High-Throughput Plant Phenotyping: Contemporary Reviews and Future Perspectives. Frontiers in Plant Science, 2021, 12, 611940.	3.6	50
21	Comparative Transcriptome Analysis Reveals Genetic Mechanisms of Sugarcane Aphid Resistance in Grain Sorghum. International Journal of Molecular Sciences, 2021, 22, 7129.	4.1	10
22	Hyperspectral reflectance-based phenotyping for quantitative genetics in crops: Progress and challenges. Plant Communications, 2021, 2, 100209.	7.7	28
23	qTeller: a tool for comparative multi-genomic gene expression analysis. Bioinformatics, 2021, 38, 236-242.	4.1	15
24	Tandem duplicate expression patterns are conserved between maize haplotypes of the <i>Î±</i>â€zein gene family. Plant Direct, 2021, 5, e346.	1.9	1
25	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
26	Genome-Wide DNA Polymorphism Analysis and Molecular Marker Development for the Setaria italica Variety â€œSSR41â€ and Positional Cloning of the Setaria White Leaf Sheath Gene SiWLS1. Frontiers in Plant Science, 2021, 12, 743782.	3.6	2
27	3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. PeerJ, 2021, 9, e12628.	2.0	4
28	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
29	Genes and gene models, an important distinction. New Phytologist, 2020, 228, 50-55.	7.3	12
30	Leaf Angle eXtractor: A highâ€throughput image processing framework for leaf angle measurements in maize and sorghum. Applications in Plant Sciences, 2020, 8, e11385.	2.1	14
31	Voxel carvingâ€based 3D reconstruction of sorghum identifies genetic determinants of light interception efficiency. Plant Direct, 2020, 4, e00255.	1.9	21
32	Robotic Detection and Grasp of Maize and Sorghum: Stem Measurement with Contact. Robotics, 2020, 9, 58.	3.5	13
33	Advances in plant phenomics: From data and algorithms to biological insights. Applications in Plant Sciences, 2020, 8, e11386.	2.1	1
34	Plant segmentation by supervised machine learning methods. The Plant Phenome Journal, 2020, 3, e20001.	2.0	38
35	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. Plant Cell, 2020, 32, 2457-2473.	6.6	29
36	Nonâ€homologyâ€based prediction of gene functions in maize (Zea mays ssp. mays). Plant Genome, 2020, 13, e20015.	2.8	7

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37	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
38	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
39	Genome–Phenome Wide Association in Maize and Arabidopsis Identifies a Common Molecular and Evolutionary Signature. Molecular Plant, 2020, 13, 907-922.	8.3	14
40	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
41	Shared Genetic Control of Root System Architecture between *Zea mays* and *Sorghum bicolor*. Plant Physiology, 2020, 182, 977-991.	4.8	57
42	Interspecific analysis of diurnal gene regulation in panicoid grasses identifies known and novel regulatory motifs. BMC Genomics, 2020, 21, 428.	2.8	29
43	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	1.4	38
44	Multiscale computational models can guide experimentation and targeted measurements for crop improvement. Plant Journal, 2020, 103, 21-31.	5.7	36
45	Towards a multiscale crop modelling framework for climate change adaptation assessment. Nature Plants, 2020, 6, 338-348.	9.3	181
46	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
47	Sorghum Segmentation by Skeleton Extraction. Lecture Notes in Computer Science, 2020, , 296-311.	1.3	13
48	Investigating the potential of satellite imagery for high-throughput field phenotyping applications. , 2020, , .		7
49	Semantic Segmentation of Sorghum Using Hyperspectral Data Identifies Genetic Associations. Plant Phenomics, 2020, 2020, 4216373.	5.9	32
50	A High-Throughput Phenotyping Pipeline for Image Processing and Functional Growth Curve Analysis. Plant Phenomics, 2020, 2020, 7481687.	5.9	19
51	Faster-R-CNN based deep learning for locating corn tassels in UAV imagery. , 2020, , .		2
52	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
53	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
54	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

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55	In-Planta Nitrate Detection Using Insertable Plant Microsensor. , 2019, , .		3
56	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
57	Novel All-Solid-State Soil Nutrient Sensor Using Nanocomposite of Poly(3-Octyl-Thiophene) and Molybdenum Sulfate. , 2019, , .		5
58	The genome of broomcorn millet. Nature Communications, 2019, 10, 436.	12.8	130
59	Parallels between natural selection in the cold�sadapted crop�swild relative <i>Tripsacum dactyloides</i> and artificial selection in temperate adapted maize. Plant Journal, 2019, 99, 965-977.	5.7	18
60	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
61	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
62	Optimising the identification of causal variants across varying genetic architectures in crops. Plant Biotechnology Journal, 2019, 17, 893-905.	8.3	29
63	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
64	Location of low copy genes in chromosomes of Brachiaria spp.. Molecular Biology Reports, 2018, 45, 109-118.	2.3	7
65	Conventional and hyperspectral time-series imaging of maize lines widely used in field trials. GigaScience, 2018, 7, 1-11.	6.4	34
66	Largely unlinked gene sets targeted by selection for domestication syndrome phenotypes in maize and sorghum. Plant Journal, 2018, 93, 843-855.	5.7	20
67	Functional Divergence between Subgenomes and Gene Pairs after Whole Genome Duplications. Molecular Plant, 2018, 11, 388-397.	8.3	73
68	Functional Modeling of Plant Growth Dynamics. The Plant Phenome Journal, 2018, 1, 1-10.	2.0	15
69	Linked read technology for assembling large complex and polyploid genomes. BMC Genomics, 2018, 19, 651.	2.8	31
70	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. Molecular Biology and Evolution, 2018, 35, 2762-2772.	8.9	4
71	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. G3: Genes, Genomes, Genetics, 2018, 8, 2513-2522.	1.8	41
72	Genotype-Corrector: improved genotype calls for genetic mapping in F2 and RIL populations. Scientific Reports, 2018, 8, 10088.	3.3	22

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73	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
74	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
75	Low-temperature tolerance in land plants: Are transcript and membrane responses conserved?. Plant Science, 2018, 276, 73-86.	3.6	70
76	FractBias: a graphical tool for assessing fractionation bias following polyploidy. Bioinformatics, 2017, 33, 552-554.	4.1	14
77	STAG-CNS: An Order-Aware Conserved Noncoding Sequences Discovery Tool for Arbitrary Numbers of Species. Molecular Plant, 2017, 10, 990-999.	8.3	16
78	Harnessing the Potential of the Tea Tree Genome. Molecular Plant, 2017, 10, 788-790.	8.3	2
79	tGBSÂ® genotyping-by-sequencing enables reliable genotyping of heterozygous loci. Nucleic Acids Research, 2017, 45, e178-e178.	14.5	115
80	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	3.3	27
81	Evolutionarily Conserved Alternative Splicing Across Monocots. Genetics, 2017, 207, 465-480.	2.9	47
82	Differentially Regulated Orthologs in Sorghum and the Subgenomes of Maize. Plant Cell, 2017, 29, 1938-1951.	6.6	68
83	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
84	Cross species selection scans identify components of C_4 photosynthesis in the grasses. Journal of Experimental Botany, 2017, 68, 127-135.	4.8	61
85	DiCE: Discovery of conserved noncoding sequences efficiently. , 2017, , .		1
86	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. Frontiers in Plant Science, 2017, 8, 694.	3.6	109
87	High Throughput In vivo Analysis of Plant Leaf Chemical Properties Using Hyperspectral Imaging. Frontiers in Plant Science, 2017, 8, 1348.	3.6	181
88	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
89	Epigenetic regulation of subgenome dominance following whole genome triplication in *Brassica rapa*. New Phytologist, 2016, 211, 288-299.	7.3	100
90	The C-terminal motif of SiAGO1b is required for the regulation of growth, development and stress responses in foxtail millet (*Setaria italica* (L.) P. Beauv). Journal of Experimental Botany, 2016, 67, 3237-3249.	4.8	33

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91	Mapping QTLs for morpho-agronomic traits in proso millet (Panicum miliaceum L.). Molecular Breeding, 2016, 36, 1.	2.1	46
92	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
93	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	12.6	411
94	The draft genome of the C3 panicoid grass species Dichanthelium oligosanthes. Genome Biology, 2016, 17, 223.	8.8	48
95	RNA-Seq Based Analysis of Population Structure within the Maize Inbred B73. PLoS ONE, 2016, 11, e0157942.	2.5	23
96	Impacts of Whole-Genome Triplication on *MIRNA* Evolution in *Brassica rapa*. Genome Biology and Evolution, 2015, 7, 3085-3096.	2.5	18
97	SynFind: Compiling Syntenic Regions across Any Set of Genomes on Demand. Genome Biology and Evolution, 2015, 7, 3286-3298.	2.5	70
98	ALLMAPS: robust scaffold ordering based on multiple maps. Genome Biology, 2015, 16, 3.	8.8	340
99	Phylogeny and photosynthesis of the grass tribe Paniceae. American Journal of Botany, 2015, 102, 1493-1505.	1.7	58
100	Genome Evolution in Maize: From Genomes Back to Genes. Annual Review of Plant Biology, 2015, 66, 329-343.	18.7	65
101	A near complete snapshot of the Zea mays seedling transcriptome revealed from ultra-deep sequencing. Scientific Reports, 2015, 4, 4519.	3.3	28
102	Microsatellite Variations of Elite Setaria Varieties Released during Last Six Decades in China. PLoS ONE, 2015, 10, e0125688.	2.5	15
103	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
104	The Evolution of Plant Gene and Genome Sequencing. Advances in Botanical Research, 2014, , 47-90.	1.1	6
105	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. Plant Cell, 2014, 26, 3939-3948.	6.6	80
106	Early History of the Angiosperms. Advances in Botanical Research, 2014, 69, 195-222.	1.1	6
107	Two Evolutionarily Distinct Classes of Paleopolyploidy. Molecular Biology and Evolution, 2014, 31, 448-454.	8.9	159
108	Co-option of the polarity gene network shapes filament morphology in angiosperms. Scientific Reports, 2014, 4, 6194.	3.3	37

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109	Initiation of Setaria as a model plant. Frontiers of Agricultural Science and Engineering, 2014, 1, 16.	1.4	91
110	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
111	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. Frontiers in Plant Science, 2012, 3, 94.	3.6	73
112	High-resolution mapping of open chromatin in the rice genome. Genome Research, 2012, 22, 151-162.	5.5	205
113	Genome-Wide Analysis of Syntenic Gene Deletion in the Grasses. Genome Biology and Evolution, 2012, 4, 265-277.	2.5	126
114	Maize (Zea Mays) as a Model for Studying the Impact of Gene and Regulatory Sequence Loss Following Whole-Genome Duplication. , 2012, , 137-145.		5
115	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
116	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
117	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
118	Screening synteny blocks in pairwise genome comparisons through integer programming. BMC Bioinformatics, 2011, 12, 102.	2.6	142
119	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
120	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	3.5	150
121	Genes Identified by Visible Mutant Phenotypes Show Increased Bias toward One of Two Subgenomes of Maize. PLoS ONE, 2011, 6, e17855.	2.5	145
122	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	27.8	1,685
123	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