

James C Schnable

List of Publications by Year in descending order

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123
papers

8,614
citations

81743

39
h-index

53109

85
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161
all docs

161
docs citations

161
times ranked

9880
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
2	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4069-4074.	3.3	644
3	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	6.0	411
4	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015, 16, 3.	3.8	340
5	Following Tetraploidy in Maize, a Short Deletion Mechanism Removed Genes Preferentially from One of the Two Homeologs. <i>PLoS Biology</i> , 2010, 8, e1000409.	2.6	260
6	Temporal dynamics of maize plant growth, water use, and leaf water content using automated high throughput RGB and hyperspectral imaging. <i>Computers and Electronics in Agriculture</i> , 2016, 127, 625-632.	3.7	219
7	High-resolution mapping of open chromatin in the rice genome. <i>Genome Research</i> , 2012, 22, 151-162.	2.4	205
8	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. <i>Current Opinion in Plant Biology</i> , 2012, 15, 131-139.	3.5	194
9	High Throughput In vivo Analysis of Plant Leaf Chemical Properties Using Hyperspectral Imaging. <i>Frontiers in Plant Science</i> , 2017, 8, 1348.	1.7	181
10	Towards a multiscale crop modelling framework for climate change adaptation assessment. <i>Nature Plants</i> , 2020, 6, 338-348.	4.7	181
11	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	1.2	163
12	Two Evolutionarily Distinct Classes of Paleopolyploidy. <i>Molecular Biology and Evolution</i> , 2014, 31, 448-454.	3.5	159
13	Heritable Epigenetic Variation among Maize Inbreds. <i>PLoS Genetics</i> , 2011, 7, e1002372.	1.5	150
14	Genes Identified by Visible Mutant Phenotypes Show Increased Bias toward One of Two Subgenomes of Maize. <i>PLoS ONE</i> , 2011, 6, e17855.	1.1	145
15	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.	1.2	142
16	The genome of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 436.	5.8	130
17	Genome-Wide Analysis of Syntenic Gene Deletion in the Grasses. <i>Genome Biology and Evolution</i> , 2012, 4, 265-277.	1.1	126
18	tGBS [®] genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017, 45, e178-e178.	6.5	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. <i>Plant Methods</i> , 2019, 15, 66.	1.9	115
20	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	1.7	109
21	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
22	Epigenetic regulation of subgenome dominance following whole genome triplication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2016, 211, 288-299.	3.5	100
23	Initiation of <i>Setaria</i> as a model plant. <i>Frontiers of Agricultural Science and Engineering</i> , 2014, 1, 16.	0.9	91
24	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	1.6	90
25	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	3.1	80
26	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	1.7	73
27	Functional Divergence between Subgenomes and Gene Pairs after Whole Genome Duplications. <i>Molecular Plant</i> , 2018, 11, 388-397.	3.9	73
28	SynFind: Compiling Syntenic Regions across Any Set of Genomes on Demand. <i>Genome Biology and Evolution</i> , 2015, 7, 3286-3298.	1.1	70
29	Low-temperature tolerance in land plants: Are transcript and membrane responses conserved?. <i>Plant Science</i> , 2018, 276, 73-86.	1.7	70
30	Differentially Regulated Orthologs in Sorghum and the Subgenomes of Maize. <i>Plant Cell</i> , 2017, 29, 1938-1951.	3.1	68
31	Continuous Monitoring of Soil Nitrate Using a Miniature Sensor with Poly(3-octyl-thiophene) and Molybdenum Disulfide Nanocomposite. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 29195-29206.	4.0	66
32	Genome Evolution in Maize: From Genomes Back to Genes. <i>Annual Review of Plant Biology</i> , 2015, 66, 329-343.	8.6	65
33	NU-Spidercam: A large-scale, cable-driven, integrated sensing and robotic system for advanced phenotyping, remote sensing, and agronomic research. <i>Computers and Electronics in Agriculture</i> , 2019, 160, 71-81.	3.7	63
34	Mapping of Quantitative Trait Locus (QTLs) that Contribute to Germination and Early Seedling Drought Tolerance in the Interspecific Cross <i>Setaria italica</i> – <i>Setaria viridis</i> . <i>PLoS ONE</i> , 2014, 9, e101868.	1.1	62
35	Cross species selection scans identify components of C ₄ photosynthesis in the grasses. <i>Journal of Experimental Botany</i> , 2017, 68, 127-135.	2.4	61
36	Phylogeny and photosynthesis of the grass tribe Paniceae. <i>American Journal of Botany</i> , 2015, 102, 1493-1505.	0.8	58

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37	Shared Genetic Control of Root System Architecture between <i>Zea mays</i> and <i>Sorghum bicolor</i> . <i>Plant Physiology</i> , 2020, 182, 977-991.	2.3	57
38	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	52
39	Robotic Technologies for High-Throughput Plant Phenotyping: Contemporary Reviews and Future Perspectives. <i>Frontiers in Plant Science</i> , 2021, 12, 611940.	1.7	50
40	The draft genome of the C3 panicoid grass species <i>Dichanthelium oligosanthes</i> . <i>Genome Biology</i> , 2016, 17, 223.	3.8	48
41	Evolutionarily Conserved Alternative Splicing Across Monocots. <i>Genetics</i> , 2017, 207, 465-480.	1.2	47
42	Mapping QTLs for morpho-agronomic traits in proso millet (<i>Panicum miliaceum</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	46
43	Predicting transcriptional responses to cold stress across plant species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	46
44	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	1.1	44
45	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2513-2522.	0.8	41
46	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. <i>Plant Physiology</i> , 2020, 183, 1898-1909.	2.3	39
47	Plant segmentation by supervised machine learning methods. <i>The Plant Phenome Journal</i> , 2020, 3, e20001.	1.0	38
48	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	0.6	38
49	Co-option of the polarity gene network shapes filament morphology in angiosperms. <i>Scientific Reports</i> , 2014, 4, 6194.	1.6	37
50	Multiscale computational models can guide experimentation and targeted measurements for crop improvement. <i>Plant Journal</i> , 2020, 103, 21-31.	2.8	36
51	Dose–Sensitivity, Conserved Non-Coding Sequences, and Duplicate Gene Retention Through Multiple Tetraploidies in the Grasses. <i>Frontiers in Plant Science</i> , 2011, 2, 2.	1.7	35
52	Conventional and hyperspectral time-series imaging of maize lines widely used in field trials. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	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). <i>Journal of Experimental Botany</i> , 2016, 67, 3237-3249.	2.4	33
54	Automated conserved non-coding sequence (CNS) discovery reveals differences in gene content and promoter evolution among grasses. <i>Frontiers in Plant Science</i> , 2013, 4, 170.	1.7	32

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55	Semantic Segmentation of Sorghum Using Hyperspectral Data Identifies Genetic Associations. <i>Plant Phenomics</i> , 2020, 2020, 4216373.	2.5	32
56	Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , 2018, 19, 651.	1.2	31
57	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. <i>Plant Biotechnology Journal</i> , 2020, 18, 389-401.	4.1	30
58	Optimising the identification of causal variants across varying genetic architectures in crops. <i>Plant Biotechnology Journal</i> , 2019, 17, 893-905.	4.1	29
59	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. <i>Plant Cell</i> , 2020, 32, 2457-2473.	3.1	29
60	Interspecific analysis of diurnal gene regulation in panicoid grasses identifies known and novel regulatory motifs. <i>BMC Genomics</i> , 2020, 21, 428.	1.2	29
61	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
62	Hyperspectral reflectance-based phenotyping for quantitative genetics in crops: Progress and challenges. <i>Plant Communications</i> , 2021, 2, 100209.	3.6	28
63	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27
64	A co-opted steroid synthesis gene, maintained in sorghum but not maize, is associated with a divergence in leaf wax chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
65	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	0.6	25
66	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. <i>Genetics</i> , 2021, 218, .	1.2	24
67	Enhancing Hybrid Prediction in Pearl Millet Using Genomic and/or Multi-Environment Phenotypic Information of Inbreds. <i>Frontiers in Genetics</i> , 2019, 10, 1294.	1.1	23
68	RNA-Seq Based Analysis of Population Structure within the Maize Inbred B73. <i>PLoS ONE</i> , 2016, 11, e0157942.	1.1	23
69	Genotype-Corrector: improved genotype calls for genetic mapping in F2 and RIL populations. <i>Scientific Reports</i> , 2018, 8, 10088.	1.6	22
70	Voxel carving-based 3D reconstruction of sorghum identifies genetic determinants of light interception efficiency. <i>Plant Direct</i> , 2020, 4, e00255.	0.8	21
71	Largely unlinked gene sets targeted by selection for domestication syndrome phenotypes in maize and sorghum. <i>Plant Journal</i> , 2018, 93, 843-855.	2.8	20
72	Sorghum Association Panel-whole-genome sequencing establishes cornerstone resource for dissecting genomic diversity. <i>Plant Journal</i> , 2022, 111, 888-904.	2.8	20

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73	A High-Throughput Phenotyping Pipeline for Image Processing and Functional Growth Curve Analysis. <i>Plant Phenomics</i> , 2020, 2020, 7481687.	2.5	19
74	Impacts of Whole-Genome Triplication on <i>MIRNA</i> Evolution in <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3085-3096.	1.1	18
75	Genome-wide characterization of non-reference transposable element insertion polymorphisms reveals genetic diversity in tropical and temperate maize. <i>BMC Genomics</i> , 2017, 18, 702.	1.2	18
76	Parallels between natural selection in the cold-adapted crop wild relative <i>Tripsacum dactyloides</i> and artificial selection in temperate adapted maize. <i>Plant Journal</i> , 2019, 99, 965-977.	2.8	18
77	Rhizosphere Microbiomes in a Historical Maize-Soybean Rotation System Respond to Host Species and Nitrogen Fertilization at the Genus and Subgenus Levels. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0313220.	1.4	17
78	Maize Tassel Detection From UAV Imagery Using Deep Learning. <i>Frontiers in Robotics and AI</i> , 2021, 8, 600410.	2.0	17
79	STAG-CNS: An Order-Aware Conserved Noncoding Sequences Discovery Tool for Arbitrary Numbers of Species. <i>Molecular Plant</i> , 2017, 10, 990-999.	3.9	16
80	In vivo human-like robotic phenotyping of leaf traits in maize and sorghum in greenhouse. <i>Computers and Electronics in Agriculture</i> , 2019, 163, 104854.	3.7	16
81	High Density Genetic Maps of Seashore <i>Paspalum</i> Using Genotyping-By-Sequencing and Their Relationship to The Sorghum Bicolor Genome. <i>Scientific Reports</i> , 2019, 9, 12183.	1.6	16
82	A UAV-based high-throughput phenotyping approach to assess time-series nitrogen responses and identify trait-associated genetic components in maize. <i>The Plant Phenome Journal</i> , 2022, 5, .	1.0	16
83	Functional Modeling of Plant Growth Dynamics. <i>The Plant Phenome Journal</i> , 2018, 1, 1-10.	1.0	15
84	qTeller: a tool for comparative multi-genomic gene expression analysis. <i>Bioinformatics</i> , 2021, 38, 236-242.	1.8	15
85	Microsatellite Variations of Elite <i>Setaria</i> Varieties Released during Last Six Decades in China. <i>PLoS ONE</i> , 2015, 10, e0125688.	1.1	15
86	FractBias: a graphical tool for assessing fractionation bias following polyploidy. <i>Bioinformatics</i> , 2017, 33, 552-554.	1.8	14
87	Leaf Angle eXtractor: A high-throughput image processing framework for leaf angle measurements in maize and sorghum. <i>Applications in Plant Sciences</i> , 2020, 8, e11385.	0.8	14
88	Genome-Phenome Wide Association in Maize and <i>Arabidopsis</i> Identifies a Common Molecular and Evolutionary Signature. <i>Molecular Plant</i> , 2020, 13, 907-922.	3.9	14
89	Automation of leaf counting in maize and sorghum using deep learning. <i>The Plant Phenome Journal</i> , 2021, 4, e20022.	1.0	14
90	Robotic Detection and Grasp of Maize and Sorghum: Stem Measurement with Contact. <i>Robotics</i> , 2020, 9, 58.	2.1	13

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91	Sorghum Segmentation by Skeleton Extraction. Lecture Notes in Computer Science, 2020, , 296-311.	1.0	13
92	Genes and gene models, an important distinction. New Phytologist, 2020, 228, 50-55.	3.5	12
93	Comparative Transcriptome Analysis Reveals Genetic Mechanisms of Sugarcane Aphid Resistance in Grain Sorghum. International Journal of Molecular Sciences, 2021, 22, 7129.	1.8	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.	1.2	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, .	1.4	8
97	Kinetic variation in grass phosphoenolpyruvate carboxylases provides opportunity to enhance C ₄ photosynthetic efficiency. Plant Journal, 2021, 105, 1677-1688.	2.8	8
98	Quantitative Resistance Loci to Southern Rust Mapped in a Temperate Maize Diversity Panel. Phytopathology, 2022, 112, 579-587.	1.1	8
99	Location of low copy genes in chromosomes of Brachiaria spp.. Molecular Biology Reports, 2018, 45, 109-118.	1.0	7
100	Integrating Phylogenetic and Network Approaches to Study Gene Family Evolution: The Case of the <i>AGAMOUS</i> Family of Floral Genes. Evolutionary Bioinformatics, 2018, 14, 117693431876468.	0.6	7
101	QTL identification and epistatic effect analysis of seed size- and weight-related traits in <i>Zea mays</i> L. Molecular Breeding, 2019, 39, 1.	1.0	7
102	Non-homology-based prediction of gene functions in maize (<i>Zea mays</i> ssp. <i>mays</i>). Plant Genome, 2020, 13, e20015.	1.6	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.	0.5	6
105	Early History of the Angiosperms. Advances in Botanical Research, 2014, 69, 195-222.	0.5	6
106	Identification and utilization of genetic determinants of trait measurement errors in image-based, high-throughput phenotyping. Plant Cell, 2021, 33, 2562-2582.	3.1	6
107	Maize (<i>Zea Mays</i>) 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

#	ARTICLE	IF	CITATIONS
109	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018, 35, 2762-2772.	3.5	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. <i>Nature Communications</i> , 2022, 13, 820.	5.8	4
112	3D reconstruction identifies loci linked to variation in angle of individual sorghum leaves. <i>PeerJ</i> , 2021, 9, e12628.	0.9	4
113	In-Planta Nitrate Detection Using Insertable Plant Microsensor. , 2019, , .		3
114	Harnessing the Potential of the Tea Tree Genome. <i>Molecular Plant</i> , 2017, 10, 788-790.	3.9	2
115	IsoSeq transcriptome assembly of <i>C₃</i> panicoid grasses provides tools to study evolutionary change in the Panicoideae. <i>Plant Direct</i> , 2020, 4, e00203.	0.8	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 <i>Setaria italica</i> Variety "SSR41" and Positional Cloning of the <i>Setaria</i> White Leaf Sheath Gene <i>StWLS1</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 743782.	1.7	2
118	DiCE: Discovery of conserved noncoding sequences efficiently. , 2017, , .		1
119	Advances in plant phenomics: From data and algorithms to biological insights. <i>Applications in Plant Sciences</i> , 2020, 8, e11386.	0.8	1
120	72-h diurnal RNA-seq analysis of fully expanded third leaves from maize, sorghum, and foxtail millet at 3-h resolution. <i>BMC Research Notes</i> , 2021, 14, 24.	0.6	1
121	"DCT4" A New Member of the Dicarboxylate Transporter Family in C4 Grasses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
122	Tandem duplicate expression patterns are conserved between maize haplotypes of the <i>z</i> gene family. <i>Plant Direct</i> , 2021, 5, e346.	0.8	1
123	Can the Grains Offer Each Other Helping Hands? Convergent Molecular Mechanisms Associated with Domestication and Crop Improvement in Rice and Maize. <i>Molecular Plant</i> , 2022, , .	3.9	1