

# Patrick S Schnable

## List of Publications by Citations

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221  
papers

17,615  
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65  
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129  
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231  
ext. papers

20,929  
ext. citations

7.8  
avg, IF

6.78  
L-index

#	Paper	IF	Citations
221	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , <b>2009</b> , 326, 1112-5	33.3	2949
220	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , <b>2010</b> , 463, 763-850.4	50.4	1399
219	The molecular basis of cytoplasmic male sterility and fertility restoration. <i>Trends in Plant Science</i> , <b>1998</b> , 3, 175-180	13.1	594
218	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000734	6	389
217	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , <b>2010</b> , 42, 1027-30	36.3	365
216	SNP discovery via 454 transcriptome sequencing. <i>Plant Journal</i> , <b>2007</b> , 51, 910-8	6.9	339
215	Laser-capture microdissection, a tool for the global analysis of gene expression in specific plant cell types: identification of genes expressed differentially in epidermal cells or vascular tissues of maize. <i>Plant Cell</i> , <b>2003</b> , 15, 583-96	11.6	323
214	The rf2 nuclear restorer gene of male-sterile T-cytoplasm maize. <i>Science</i> , <b>1996</b> , 272, 1334-6	33.3	316
213	All possible modes of gene action are observed in a global comparison of gene expression in a maize F1 hybrid and its inbred parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 6805-10	11.5	314
212	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , <b>2014</b> , 15, R40	18.3	308
211	Parallel domestication of the Shattering1 genes in cereals. <i>Nature Genetics</i> , <b>2012</b> , 44, 720-4	36.3	287
210	Gene discovery and annotation using LCM-454 transcriptome sequencing. <i>Genome Research</i> , <b>2007</b> , 17, 69-73	9.7	268
209	Progress toward understanding heterosis in crop plants. <i>Annual Review of Plant Biology</i> , <b>2013</b> , 64, 71-88	30.7	267
208	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , <b>2015</b> , 16, 3	18.3	218
207	Gene mapping via bulked segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , <b>2012</b> , 7, e36406	3.7	212
206	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , <b>2018</b> , 50, 1289-1295	36.3	201
205	Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize. <i>Plant Cell</i> , <b>2001</b> , 13, 1063-78	11.6	198

204	Crop genome sequencing: lessons and rationales. <i>Trends in Plant Science</i> , <b>2011</b> , 16, 77-88	13.1	194
203	The ALDH gene superfamily of Arabidopsis. <i>Trends in Plant Science</i> , <b>2004</b> , 9, 371-7	13.1	181
202	Parent-of-origin effects on gene expression and DNA methylation in the maize endosperm. <i>Plant Cell</i> , <b>2011</b> , 23, 4221-33	11.6	160
201	The relationship between genetic and physical distances in the cloned a1-sh2 interval of the Zea mays L. genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1994</b> , 91, 8268-72	11.5	154
200	Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic marks for open chromatin across the maize genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000733	6	154
199	The roothairless1 gene of maize encodes a homolog of sec3, which is involved in polar exocytosis. <i>Plant Physiology</i> , <b>2005</b> , 138, 1637-43	6.6	151
198	Isolation, characterization, and pericycle-specific transcriptome analyses of the novel maize lateral and seminal root initiation mutant rum1. <i>Plant Physiology</i> , <b>2005</b> , 139, 1255-67	6.6	148
197	Transcriptomic shock generates evolutionary novelty in a newly formed, natural allopolyploid plant. <i>Current Biology</i> , <b>2011</b> , 21, 551-6	6.3	143
196	Characterization of duplicate gene evolution in the recent natural allopolyploid <i>Tragopogon miscellus</i> by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. <i>Molecular Ecology</i> , <b>2010</b> , 19 Suppl 1, 132-46	5.7	143
195	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , <b>2016</b> , 2, 16150	11.5	125
194	Spreading of heterochromatin is limited to specific families of maize retrotransposons. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003127	6	124
193	Rapid, repeated, and clustered loss of duplicate genes in allopolyploid plant populations of independent origin. <i>Current Biology</i> , <b>2012</b> , 22, 248-52	6.3	122
192	Transcriptomic and proteomic analyses of pericycle cells of the maize primary root. <i>Plant Physiology</i> , <b>2007</b> , 145, 575-88	6.6	120
191	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. <i>Nature Communications</i> , <b>2017</b> , 8, 14573	17.4	119
190	Production of transgenic maize from bombarded type II callus: Effect of gold particle size and callus morphology on transformation efficiency. <i>In Vitro Cellular and Developmental Biology - Plant</i> , <b>2000</b> , 36, 21-29	2.3	119
189	Heritable epigenetic variation among maize inbreds. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002372	6	118
188	The maize ( <i>Zea mays</i> L.) roothairless3 gene encodes a putative GPI-anchored, monocot-specific, COBRA-like protein that significantly affects grain yield. <i>Plant Journal</i> , <b>2008</b> , 54, 888-98	6.9	118
187	Regulation of small RNA accumulation in the maize shoot apex. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000320	6	113

186	Global gene expression analysis of the shoot apical meristem of maize ( <i>Zea mays</i> L.). <i>Plant Journal</i> , <b>2007</b> , 52, 391-404	6.9	108
185	Molecular characterization of meiotic recombination across the 140-kb multigenic a1-sh2 interval of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 6157-62 <sup>11,5</sup>	11.5	104
184	Cloning and characterization of CER2, an Arabidopsis gene that affects cuticular wax accumulation. <i>Plant Cell</i> , <b>1996</b> , 8, 1291-304	11.6	100
183	Refinement of light-responsive transcript lists using rice oligonucleotide arrays: evaluation of gene-redundancy. <i>PLoS ONE</i> , <b>2008</b> , 3, e3337	3.7	99
182	Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. <i>Science</i> , <b>2009</b> , 326, 1118-20	33.3	98
181	Complementation contributes to transcriptome complexity in maize ( <i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , <b>2012</b> , 22, 2445-54	9.7	97
180	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , <b>2012</b> , 22, 2436-44	9.7	96
179	Loss of RNA-dependent RNA polymerase 2 (RDR2) function causes widespread and unexpected changes in the expression of transposons, genes, and 24-nt small RNAs. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000737 <sup>6</sup>	9.7	92
178	Maize Mu transposons are targeted to the 5' untranslated region of the gl8 gene and sequences flanking Mu target-site duplications exhibit nonrandom nucleotide composition throughout the genome. <i>Genetics</i> , <b>2002</b> , 160, 697-716	4	92
177	Tissue specificity and evolution of meristematic WOX3 function. <i>Plant Physiology</i> , <b>2009</b> , 149, 841-50	6.6	89
176	Genetic Isolation, Cloning, and Analysis of a Mutator-Induced, Dominant Antimorph of the Maize amylose extender1 Locus. <i>Plant Cell</i> , <b>1993</b> , 5, 1555-1566	11.6	87
175	A High-Throughput, Field-Based Phenotyping Technology for Tall Biomass Crops. <i>Plant Physiology</i> , <b>2017</b> , 174, 2008-2022	6.6	84
174	The physical and genetic framework of the maize B73 genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000715	6	83
173	Sequence analysis of the cloned glossy8 gene of maize suggests that it may code for a beta-ketoacyl reductase required for the biosynthesis of cuticular waxes. <i>Plant Physiology</i> , <b>1997</b> , 115, 501-10	6.6	83
172	Genetic recombination in plants. <i>Current Opinion in Plant Biology</i> , <b>1998</b> , 1, 123-9	9.9	83
171	FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in Arabidopsis thaliana. <i>Current Biology</i> , <b>2018</b> , 28, 3316-3324.e6	6.3	83
170	Functional specialization of maize mitochondrial aldehyde dehydrogenases. <i>Plant Physiology</i> , <b>2002</b> , 130, 1657-74	6.6	79
169	Genomewide single nucleotide polymorphism discovery in Atlantic salmon ( <i>Salmo salar</i> ): validation in wild and farmed American and European populations. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 1002-11 <sup>8.4</sup>	8.4	79

168	Meiotic recombination break points resolve at high rates at the 5' end of a maize coding sequence. <i>Plant Cell</i> , <b>1995</b> , 7, 2151-61	11.6	78
167	Picky: oligo microarray design for large genomes. <i>Bioinformatics</i> , <b>2004</b> , 20, 2893-902	7.2	77
166	Global expression profiling applied to plant development. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 50-6	9.9	74
165	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , <b>2010</b> , 62, 898-909	9.9	73
164	Roothairless5, which functions in maize ( <i>Zea mays</i> L.) root hair initiation and elongation encodes a monocot-specific NADPH oxidase. <i>Plant Journal</i> , <b>2014</b> , 79, 729-40	6.9	70
163	Characterization of two GL8 paralogs reveals that the 3-ketoacyl reductase component of fatty acid elongase is essential for maize ( <i>Zea mays</i> L.) development. <i>Plant Journal</i> , <b>2005</b> , 42, 844-61	6.9	70
162	tGBS genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e178	20.1	67
161	The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , <b>2014</b> , 77, 380-92	6.9	67
160	Next-generation sequencing and genome evolution in allopolyploids. <i>American Journal of Botany</i> , <b>2012</b> , 99, 372-82	2.7	67
159	The glossy1 locus of maize and an epidermis-specific cDNA from <i>Kleinia odora</i> define a class of receptor-like proteins required for the normal accumulation of cuticular waxes. <i>Plant Physiology</i> , <b>1997</b> , 113, 1091-100	6.6	67
158	Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. <i>Genetics</i> , <b>2006</b> , 174, 1671-83	4	67
157	Mendelian and non-Mendelian regulation of gene expression in maize. <i>PLoS Genetics</i> , <b>2013</b> , 9, e10032026		66
156	Functional analysis of maize RAD51 in meiosis and double-strand break repair. <i>Genetics</i> , <b>2007</b> , 176, 1469-82		65
155	Microdissection of shoot meristem functional domains. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000476	6	64
154	The genome of broomcorn millet. <i>Nature Communications</i> , <b>2019</b> , 10, 436	17.4	61
153	Developmental and hormonal regulation of the arabidopsis CER2 gene that codes for a nuclear-localized protein required for the normal accumulation of cuticular waxes. <i>Plant Physiology</i> , <b>1997</b> , 115, 925-37	6.6	61
152	Ontogeny of the maize shoot apical meristem. <i>Plant Cell</i> , <b>2012</b> , 24, 3219-34	11.6	60
151	Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 12282-7	11.5	60

150	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , <b>2018</b> , 217, 1292-1306	9.8	59
149	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , <b>2017</b> , 8, 1348	17.4	58
148	Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , <b>2015</b> , 6, 8974	17.4	58
147	Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. <i>PLoS Genetics</i> , <b>2007</b> , 3, e101	6	58
146	Characterization of the aldehyde dehydrogenase gene families of <i>Zea mays</i> and <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , <b>2002</b> , 48, 751-64	4.6	58
145	The Endoplasmic reticulum-associated maize GL8 protein is a component of the acyl-coenzyme A elongase involved in the production of cuticular waxes. <i>Plant Physiology</i> , <b>2002</b> , 128, 924-34	6.6	58
144	Rf8 and Rf* mediate unique T-urf13-transcript accumulation, revealing a conserved motif associated with RNA processing and restoration of pollen fertility in T-cytoplasm maize. <i>Genetics</i> , <b>1997</b> , 147, 1367-79	4	58
143	Extreme-phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. <i>Plant Journal</i> , <b>2015</b> , 84, 587-96	6.9	57
142	The roles of aldehyde dehydrogenases (ALDHs) in the PDH bypass of <i>Arabidopsis</i> . <i>BMC Biochemistry</i> , <b>2009</b> , 10, 7	4.8	57
141	B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. <i>Plant Physiology</i> , <b>2011</b> , 156, 1679-90	6.6	57
140	High-throughput genetic mapping of mutants via quantitative single nucleotide polymorphism typing. <i>Genetics</i> , <b>2010</b> , 184, 19-26	4	56
139	Analyses of mutants of three genes that influence root hair development in <i>Zea mays</i> (Gramineae) suggest that root hairs are dispensable. <i>American Journal of Botany</i> , <b>1994</b> , 81, 833-842	2.7	56
138	The maize glossy13 gene, cloned via BSR-Seq and Seq-walking encodes a putative ABC transporter required for the normal accumulation of epicuticular waxes. <i>PLoS ONE</i> , <b>2013</b> , 8, e82333	3.7	54
137	Nearly identical paralogs: implications for maize ( <i>Zea mays</i> L.) genome evolution. <i>Genetics</i> , <b>2007</b> , 175, 429-39	4	51
136	High-Resolution Patterning and Transferring of Graphene-Based Nanomaterials onto Tape toward Roll-to-Roll Production of Tape-Based Wearable Sensors. <i>Advanced Materials Technologies</i> , <b>2017</b> , 2, 1700223	6.8	50
135	ZmMADS69 functions as a flowering activator through the ZmRap2.7-ZCN8 regulatory module and contributes to maize flowering time adaptation. <i>New Phytologist</i> , <b>2019</b> , 221, 2335-2347	9.8	48
134	Histone lysine methyltransferase SDG8 is involved in brassinosteroid-regulated gene expression in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , <b>2014</b> , 7, 1303-1315	14.4	47
133	A strategy for assembling the maize ( <i>Zea mays</i> L.) genome. <i>Bioinformatics</i> , <b>2004</b> , 20, 140-7	7.2	47

132	Mitochondrial transcript processing and restoration of male fertility in T-cytoplasm maize. <i>Journal of Heredity</i> , <b>1999</b> , 90, 380-5	2.4	46
131	Analyses of mutants of three genes that influence root hair development in <i>Zea mays</i> (Gramineae) suggest that root hairs are dispensable <b>1994</b> , 81, 833		46
130	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , <b>2017</b> , 3, 715-723	11.5	46
129	The potential of genomics in plant systematics. <i>Taxon</i> , <b>2013</b> , 62, 886-898	0.8	45
128	Cytoplasmic regulation of the accumulation of nuclear-encoded proteins in the mitochondrial proteome of maize. <i>Plant Journal</i> , <b>2004</b> , 37, 199-208	6.9	45
127	DNA sequence analyses support the role of interrupted gap repair in the origin of internal deletions of the maize transposon, MuDR. <i>Genetics</i> , <b>1996</b> , 142, 603-18	4	45
126	The Aux/IAA gene <i>rum1</i> involved in seminal and lateral root formation controls vascular patterning in maize ( <i>Zea mays</i> L.) primary roots. <i>Journal of Experimental Botany</i> , <b>2014</b> , 65, 4919-30	7	44
125	Lateral roots affect the proteome of the primary root of maize ( <i>Zea mays</i> L.). <i>Plant Molecular Biology</i> , <b>2004</b> , 56, 397-412	4.6	44
124	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 694	6.2	43
123	Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. <i>Plant Cell</i> , <b>2014</b> , 26, 3939-48	11.6	43
122	Cell type-specific gene expression profiling in plants by using a combination of laser microdissection and high-throughput technologies. <i>Plant and Cell Physiology</i> , <b>2007</b> , 48, 3-7	4.9	43
121	The <i>bz-rcy</i> allele of the <i>Cy</i> transposable element system of <i>Zea mays</i> contains a Mu-like element insertion. <i>Molecular Genetics and Genomics</i> , <b>1989</b> , 217, 459-63		43
120	The Genetics, Pathology, and Molecular Biology of T-Cytoplasm Male Sterility in Maize. <i>Advances in Agronomy</i> , <b>1999</b> , 65, 79-130	7.7	41
119	The accumulation of abundant soluble proteins changes early in the development of the primary roots of maize ( <i>Zea mays</i> L.). <i>Proteomics</i> , <b>2005</b> , 5, 4885-93	4.8	40
118	Ecological genomics: making the leap from model systems in the lab to native populations in the field. <i>Frontiers in Ecology and the Environment</i> , <b>2007</b> , 5, 19-24	5.5	39
117	The <i>Etched1</i> gene of <i>Zea mays</i> (L.) encodes a zinc ribbon protein that belongs to the transcriptionally active chromosome (TAC) of plastids and is similar to the transcription factor TFIIIS. <i>Plant Journal</i> , <b>2004</b> , 38, 923-39	6.9	39
116	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. <i>Plant Molecular Biology</i> , <b>2005</b> , 57, 445-60	4.6	39
115	Mapping complementary genes in maize: positioning the <i>rf1</i> and <i>rf2</i> nuclear-fertility restorer loci of Texas (T) cytoplasm relative to RFLP and visible markers. <i>Theoretical and Applied Genetics</i> , <b>1994</b> , 88, 785-95	6.5	37

114	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000728	6	34
113	DNA sequence-based "bar codes" for tracking the origins of expressed sequence tags from a maize cDNA library constructed using multiple mRNA sources. <i>Plant Physiology</i> , <b>2003</b> , 133, 475-81	6.6	34
112	Continuous Monitoring of Soil Nitrate Using a Miniature Sensor with Poly(3-octyl-thiophene) and Molybdenum Disulfide Nanocomposite. <i>ACS Applied Materials &amp; Interfaces</i> , <b>2019</b> , 11, 29195-29206	9.5	33
111	Cis-effects on meiotic recombination across distinct a1-sh2 intervals in a common Zea genetic background. <i>Genetics</i> , <b>2005</b> , 170, 1929-44	4	33
110	Semiautomated Feature Extraction from RGB Images for Sorghum Panicle Architecture GWAS. <i>Plant Physiology</i> , <b>2019</b> , 179, 24-37	6.6	33
109	Recent advances in plant recombination. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 131-5	9.9	32
108	Field-based robotic phenotyping of sorghum plant architecture using stereo vision. <i>Journal of Field Robotics</i> , <b>2019</b> , 36, 397-415	6.7	32
107	DLA-based strategies for cloning insertion mutants: cloning the gl4 locus of maize using Mu transposon tagged alleles. <i>Genetics</i> , <b>2009</b> , 183, 1215-25	4	31
106	Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , <b>2008</b> , 56, 1045-57	6.9	31
105	Mutator-induced mutations of the rf1 nuclear fertility restorer of T-cytoplasm maize alter the accumulation of T-urf13 mitochondrial transcripts. <i>Genetics</i> , <b>1996</b> , 143, 1383-94	4	31
104	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , <b>2017</b> , 18, 192	18.3	29
103	Parallel short sequence assembly of transcriptomes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 1, S14	3.6	29
102	Temperature gradient capillary electrophoresis (TGCE)--a tool for the high-throughput discovery and mapping of SNPs and IDPs. <i>Theoretical and Applied Genetics</i> , <b>2005</b> , 111, 218-25	6	29
101	Genetic Isolation, Cloning, and Analysis of a Mutator-Induced, Dominant Antimorph of the Maize amylose extender1 Locus. <i>Plant Cell</i> , <b>1993</b> , 5, 1555	11.6	29
100	The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , <b>2015</b> , 81, 493-504	6.9	27
99	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , <b>2018</b> , 13, e0191321	3.7	27
98	Variation in gene expression of <i>Andropogon gerardii</i> in response to altered environmental conditions associated with climate change. <i>Journal of Ecology</i> , <b>2010</b> , 98, 374-383	6	27
97	Unequal sister chromatid and homolog recombination at a tandem duplication of the A1 locus in maize. <i>Genetics</i> , <b>2006</b> , 173, 2211-26	4	27

96	Alternative transcription initiation sites and polyadenylation sites are recruited during Mu suppression at the rf2a locus of maize. <i>Genetics</i> , <b>2003</b> , 163, 685-98	4	27
95	MuDR transposase increases the frequency of meiotic crossovers in the vicinity of a Mu insertion in the maize a1 gene. <i>Genetics</i> , <b>2005</b> , 169, 917-29	4	26
94	Optimizing Selection and Mating in Genomic Selection with a Look-Ahead Approach: An Operations Research Framework. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 2123-2133	3.2	26
93	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , <b>2019</b> , 29, 1962-1973	9.7	26
92	Development of Decreased-Gluten Wheat Enabled by Determination of the Genetic Basis of Barley. <i>Plant Physiology</i> , <b>2019</b> , 179, 1692-1703	6.6	25
91	Maize glossy6 is involved in cuticular wax deposition and drought tolerance. <i>Journal of Experimental Botany</i> , <b>2019</b> , 70, 3089-3099	7	25
90	Consensus genetic maps as median orders from inconsistent sources. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2008</b> , 5, 161-71	3	25
89	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 2513-2522	3.2	25
88	Effects of trans-acting genetic modifiers on meiotic recombination across the a1-sh2 interval of maize. <i>Genetics</i> , <b>2006</b> , 174, 101-12	4	24
87	Improving Response in Genomic Selection with a Population-Based Selection Strategy: Optimal Population Value Selection. <i>Genetics</i> , <b>2017</b> , 206, 1675-1682	4	23
86	The Early Stages of Polyploidy: Rapid and Repeated Evolution in <i>Tragopogon</i> <b>2012</b> , 271-292		23
85	Comprehensive mapping of abiotic stress inputs into the soybean circadian clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 23840-23849	11.5	23
84	Comparative transcriptome profiling of maize coleoptilar nodes during shoot-borne root initiation. <i>Plant Physiology</i> , <b>2013</b> , 163, 419-30	6.6	22
83	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. <i>Bioinformatics</i> , <b>2006</b> , 22, 1863-70	7.2	22
82	Types and frequencies of sequencing errors in methyl-filtered and high c0t maize genome survey sequences. <i>Plant Physiology</i> , <b>2004</b> , 135, 2040-5	6.6	22
81	Multi-trait Genomic Selection Methods for Crop Improvement. <i>Genetics</i> , <b>2020</b> , 215, 931-945	4	21
80	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , <b>2012</b> , 72, 390-9	6.9	21
79	Field-based architectural traits characterisation of maize plant using time-of-flight 3D imaging. <i>Biosystems Engineering</i> , <b>2019</b> , 178, 86-101	4.8	21

78	Co-expression network analysis of duplicate genes in maize ( <i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , <b>2016</b> , 17, 875	4.5	20
77	Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , <b>2018</b> , 19, 651	4.5	20
76	Shared Genetic Control of Root System Architecture between and. <i>Plant Physiology</i> , <b>2020</b> , 182, 977-991	6.6	19
75	Harnessing Phenotypic Plasticity to Improve Maize Yields. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1377	6.2	19
74	Laser microdissection-mediated isolation and in vitro transcriptional amplification of plant RNA. <i>Current Protocols in Molecular Biology</i> , <b>2009</b> , Chapter 25, Unit 25A.3	2.9	18
73	Genetic evidence of a relationship between two maize transposable element systems: Cy and Mutator. <i>Molecular Genetics and Genomics</i> , <b>1989</b> , 215, 317-321		18
72	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. <i>Plant Physiology</i> , <b>2020</b> , 183, 1898-1909	6.6	17
71	SNP discovery by transcriptome pyrosequencing. <i>Methods in Molecular Biology</i> , <b>2011</b> , 729, 225-46	1.4	17
70	Involving undergraduates in the annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database. <i>Genetics</i> , <b>2007</b> , 176, 741-7	4	17
69	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2020</b> , 13, 71	2.3	16
68	Characterization of maize roothairless6 which encodes a D-type cellulose synthase and controls the switch from bulge formation to tip growth. <i>Scientific Reports</i> , <b>2016</b> , 6, 34395	4.9	16
67	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2018</b> , 11, 452	2.3	16
66	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. <i>Molecular Ecology</i> , <b>2019</b> , 28, 3544-3560	5.7	16
65	On the origins of species: does evolution repeat itself in polyploid populations of independent origin?. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>2009</b> , 74, 215-23	3.9	16
64	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , <b>2019</b> , 97, 530-542	6.9	15
63	Genome-wide analysis of regulation of gene expression and H3K9me2 distribution by JIL-1 kinase mediated histone H3S10 phosphorylation in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 5456-67	20.1	14
62	FarmCPUpp: Efficient large-scale genomewide association studies. <i>Plant Direct</i> , <b>2018</b> , 2, e00053	3.3	13
61	Exploiting the Genomic Diversity of Rice ( <i>L.</i> ): SNP-Typing in 11 Early-Backcross Introgression-Breeding Populations. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 849	6.2	13

60	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 389-401	11.6	12
59	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> , <b>2021</b> , 11,	3.2	12
58	Role of RAD51 in the repair of MuDR-induced double-strand breaks in maize ( <i>Zea mays</i> L.). <i>Genetics</i> , <b>2008</b> , 178, 57-66	4	11
57	Consensus genetic maps: a graph theoretic approach <b>2005</b> , 35-43		11
56	Tunable Genotyping-By-Sequencing (tGBS) Enables Reliable Genotyping of Heterozygous Loci		11
55	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> , <b>2020</b> , 11, 592769	4.5	11
54	Floret-specific differences in gene expression and support for the hypothesis that tapetal degeneration of <i>Zea mays</i> L. occurs via programmed cell death. <i>Journal of Genetics and Genomics</i> , <b>2008</b> , 35, 603-16	4	10
53	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. <i>PLoS ONE</i> , <b>2010</b> , 5, e14178	3.7	10
52	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , <b>2019</b> , 59, 1406-1410	2.4	10
51	Assessing probe-specific dye and slide biases in two-color microarray data. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 314	3.6	9
50	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 3567-3575	3.2	9
49	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 2456-2465	11.6	8
48	Genetic control of maize shoot apical meristem architecture. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 1327-37	5.2	8
47	Direct calibration of PICKY-designed microarrays. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 347	3.6	8
46	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , <b>2020</b> , 60, 62-81	2.4	7
45	Construction of a dense genetic map of the <i>Malus fusca</i> fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. <i>Scientific Reports</i> , <b>2020</b> , 10, 16358	4.9	7
44	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , <b>2021</b> , 14, 874-887	14.4	7
43	Punctate vascular expression1 is a novel maize gene required for leaf pattern formation that functions downstream of the trans-acting small interfering RNA pathway. <i>Plant Physiology</i> , <b>2012</b> , 159, 1453-62	6.6	6

42	GRAMA: genetic mapping analysis of temperature gradient capillary electrophoresis data. <i>Theoretical and Applied Genetics</i> , <b>2006</b> , 113, 156-62	6	6
41	Leaf Angle eXtractor: A high-throughput image processing framework for leaf angle measurements in maize and sorghum. <i>Applications in Plant Sciences</i> , <b>2020</b> , 8, e11385	2.3	6
40	Toward "Smart Canopy" Sorghum: Discovery of the Genetic Control of Leaf Angle Across Layers. <i>Plant Physiology</i> , <b>2020</b> , 184, 1927-1940	6.6	6
39	Fast and accurate construction of ultra-dense consensus genetic maps using evolution strategy optimization. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122485	3.7	5
38	TWAS results are complementary to and less affected by linkage disequilibrium than GWAS. <i>Plant Physiology</i> , <b>2021</b> , 186, 1800-1811	6.6	5
37	A Field-Deployable, Wearable Leaf Sensor for Continuous Monitoring of Vapor-Pressure Deficit. <i>Advanced Materials Technologies</i> , <b>2021</b> , 6, 2001246	6.8	5
36	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , <b>2021</b> , 22, 175	18.3	5
35	Detection of the Progression of Anthesis in Field-Grown Maize Tassels: A Case Study. <i>Plant Phenomics</i> , <b>2021</b> , 2021, 4238701	7	4
34	Novel All-Solid-State Soil Nutrient Sensor Using Nanocomposite of Poly(3-Octyl-Thiophene) and Molybdenum Sulfate <b>2019</b> ,		3
33	Linkage disequilibrium mapping of high-throughput image-derived descriptors of plant architecture traits under field conditions. <i>Field Crops Research</i> , <b>2019</b> , 244, 107619	5.5	3
32	Laser Microdissection-Mediated Isolation and In Vitro Transcriptional Amplification of Plant RNA. <i>Current Protocols in Molecular Biology</i> , <b>2015</b> , 112, 25A.3.1-25A.3.23	2.9	3
31	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies <b>2011</b> ,		3
30	Expression and nucleotide diversity of the maize RIK gene. <i>Journal of Heredity</i> , <b>2008</b> , 99, 407-16	2.4	3
29	T7-based RNA amplification for genotyping from maize shoot apical meristem. <i>Cold Spring Harbor Protocols</i> , <b>2007</b> , 2007, pdb.prot4785	1.2	3
28	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. <i>One Earth</i> , <b>2021</b> , 4, 372-383	8.1	3
27	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. <i>Genetics</i> , <b>2021</b> , 218,	4	3
26	Hyppo-X: A Scalable Exploratory Framework for Analyzing Complex Phenomics Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 1535-1548	3	3
25	KAT4IA: -Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , <b>2021</b> , 2021, 9805489	7	3

24	Homologous Recombination in Maize <b>2009</b> , 377-403		2
23	Development of reduced gluten wheat enabled by determination of the genetic basis of thely3alow hordein barley mutant		2
22	Digestion-ligation-amplification (DLA): a simple genome walking method to amplify unknown sequences flanking mutator (Mu) transposons and thereby facilitate gene cloning. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1057, 167-76	1.4	2
21	Assembly of Large Genomes from Paired Short Reads. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 30-43	0.9	2
20	Chromosome-level Genome Assembly of a Regenerable Maize Inbred Line A188		2
19	Automatic Traits Extraction and Fitting for Field High-throughput Phenotyping Systems		2
18	Maize tissue preparation and extraction of RNA from target cells for genotyping. <i>Cold Spring Harbor Protocols</i> , <b>2007</b> , 2007, pdb.prot4784	1.2	2
17	Genome-wide analyses reveal footprints of divergent selection and popping-related traits in CIMMYT's maize inbred lines. <i>Journal of Experimental Botany</i> , <b>2021</b> , 72, 1307-1320	7	2
16	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 2762-2772	8.3	2
15	Heterosis <b>2009</b> , 457-467		2
14	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , <b>2020</b> , 133, 2761-2773	6	1
13	In-Planta Nitrate Detection Using Insertable Plant Microsensor <b>2019</b> ,		1
12	Functional principal component based time-series genome-wide association in sorghum		1
11	Meta-Analysis Identifies Pleiotropic Loci Controlling Phenotypic Trade-offs in Sorghum		1
10	Transposons modulate transcriptomic and phenotypic variation via the formation of circular RNAs in maize		1
9	Hyppo-X: A Scalable Exploratory Framework for Analyzing Complex Phenomics Data		1
8	A novel maize gene, glossy6 involved in epicuticular wax deposition and drought tolerance		1
7	Identification and utilization of genetic determinants of trait measurement errors in image-based, high-throughput phenotyping. <i>Plant Cell</i> , <b>2021</b> , 33, 2562-2582	11.6	1

- 6 Trajectories of Homoeolog-Specific Expression in Allotetraploid Populations of Independent Origins. *Frontiers in Plant Science*, **2021**, 12, 679047 6.2 o
- 5 Maize Leaf Appearance Rates: A Synthesis From the United States Corn Belt.. *Frontiers in Plant Science*, **2022**, 13, 872738 6.2 o
- 4 Ten simple rules to ruin a collaborative environment.. *PLoS Computational Biology*, **2022**, 18, e1009957 5 o
- 3 Integrating Omics Data and Expression QTL to Understand Maize Heterosis **2013**, 85-103
- 2 Molecular Markers. *Biotechnology in Agriculture and Forestry*, **2009**, 231-240
- 1 Temperature Gradient Capillary Electrophoresis (TGCE) Assay. *Cold Spring Harbor Protocols*, **2007**, 2007, pdb.prot4845 1.2