

Patrick S Schnable

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

221
papers

17,615
citations

65
h-index

129
g-index

231
ext. papers

20,929
ext. citations

7.8
avg, IF

6.78
L-index

#	Paper	IF	Citations
221	Maize Leaf Appearance Rates: A Synthesis From the United States Corn Belt.. <i>Frontiers in Plant Science</i> , 2022 , 13, 872738	6.2	0
220	Ten simple rules to ruin a collaborative environment.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009957	5	0
219	Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. <i>One Earth</i> , 2021 , 4, 372-383	8.1	3
218	Detection of the Progression of Anthesis in Field-Grown Maize Tassels: A Case Study. <i>Plant Phenomics</i> , 2021 , 2021, 4238701	7	4
217	TWAS results are complementary to and less affected by linkage disequilibrium than GWAS. <i>Plant Physiology</i> , 2021 , 186, 1800-1811	6.6	5
216	Identification and utilization of genetic determinants of trait measurement errors in image-based, high-throughput phenotyping. <i>Plant Cell</i> , 2021 , 33, 2562-2582	11.6	1
215	A Field-Deployable, Wearable Leaf Sensor for Continuous Monitoring of Vapor-Pressure Deficit. <i>Advanced Materials Technologies</i> , 2021 , 6, 2001246	6.8	5
214	Meta-analysis identifies pleiotropic loci controlling phenotypic trade-offs in sorghum. <i>Genetics</i> , 2021 , 218,	4	3
213	Trajectories of Homoeolog-Specific Expression in Allotetraploid Populations of Independent Origins. <i>Frontiers in Plant Science</i> , 2021 , 12, 679047	6.2	0
212	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021 , 22, 175	18.3	5
211	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021 , 14, 874-887	14.4	7
210	Hyppo-X: A Scalable Exploratory Framework for Analyzing Complex Phenomics Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1535-1548	3	3
209	Genome-wide analyses reveal footprints of divergent selection and popping-related traits in CIMMYT's maize inbred lines. <i>Journal of Experimental Botany</i> , 2021 , 72, 1307-1320	7	2
208	KAT4IA: -Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 2021 , 2021, 9805489	7	3
207	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,	3.2	12
206	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2456-2465	11.6	8
205	Multi-trait Genomic Selection Methods for Crop Improvement. <i>Genetics</i> , 2020 , 215, 931-945	4	21

204	Increased Power and Accuracy of Causal Locus Identification in Time Series Genome-wide Association in Sorghum. <i>Plant Physiology</i> , 2020 , 183, 1898-1909	6.6	17
203	Shared Genetic Control of Root System Architecture between and. <i>Plant Physiology</i> , 2020 , 182, 977-991	6.6	19
202	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 2761-2773	6	1
201	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	2.3	16
200	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020 , 60, 62-81	2.4	7
199	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	2.3	6
198	Toward "Smart Canopy" Sorghum: Discovery of the Genetic Control of Leaf Angle Across Layers. <i>Plant Physiology</i> , 2020 , 184, 1927-1940	6.6	6
197	Construction of a dense genetic map of the Malus fusca fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. <i>Scientific Reports</i> , 2020 , 10, 16358	4.9	7
196	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	4.5	11
195	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	11.6	12
194	Novel All-Solid-State Soil Nutrient Sensor Using Nanocomposite of Poly(3-Octyl-Thiophene) and Molybdenum Sulfate 2019 ,		3
193	Development of Decreased-Gluten Wheat Enabled by Determination of the Genetic Basis of Barley. <i>Plant Physiology</i> , 2019 , 179, 1692-1703	6.6	25
192	The genome of broomcorn millet. <i>Nature Communications</i> , 2019 , 10, 436	17.4	61
191	Maize glossy6 is involved in cuticular wax deposition and drought tolerance. <i>Journal of Experimental Botany</i> , 2019 , 70, 3089-3099	7	25
190	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	9.5	33
189	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. <i>Molecular Ecology</i> , 2019 , 28, 3544-3560	5.7	16
188	Linkage disequilibrium mapping of high-throughput image-derived descriptors of plant architecture traits under field conditions. <i>Field Crops Research</i> , 2019 , 244, 107619	5.5	3
187	In-Planta Nitrate Detection Using Insertable Plant Microsensor 2019 ,		1

186	Optimizing Selection and Mating in Genomic Selection with a Look-Ahead Approach: An Operations Research Framework. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2123-2133	3.2	26
185	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019 , 29, 1962-1973	9.7	26
184	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> , 2019 , 116, 23840-23849	11.5	23
183	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , 2019 , 59, 1406-1410	2.4	10
182	Field-based architectural traits characterisation of maize plant using time-of-flight 3D imaging. <i>Biosystems Engineering</i> , 2019 , 178, 86-101	4.8	21
181	Semiautomated Feature Extraction from RGB Images for Sorghum Panicle Architecture GWAS. <i>Plant Physiology</i> , 2019 , 179, 24-37	6.6	33
180	Field-based robotic phenotyping of sorghum plant architecture using stereo vision. <i>Journal of Field Robotics</i> , 2019 , 36, 397-415	6.7	32
179	ZmMADS69 functions as a flowering activator through the ZmRap2.7-ZCN8 regulatory module and contributes to maize flowering time adaptation. <i>New Phytologist</i> , 2019 , 221, 2335-2347	9.8	48
178	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , 2019 , 97, 530-542	6.9	15
177	FarmCPUpp: Efficient large-scale genomewide association studies. <i>Plant Direct</i> , 2018 , 2, e00053	3.3	13
176	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018 , 50, 1289-1295	36.3	201
175	Exploiting the Genomic Diversity of Rice (L.): SNP-Typing in 11 Early-Backcross Introgression-Breeding Populations. <i>Frontiers in Plant Science</i> , 2018 , 9, 849	6.2	13
174	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	2.3	16
173	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018 , 13, e0191321	3.7	27
172	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018 , 217, 1292-1306	9.8	59
171	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> , 2018 , 8, 3567-3575	3.2	9
170	FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2018 , 28, 3316-3324.e6	6.3	83
169	Harnessing Phenotypic Plasticity to Improve Maize Yields. <i>Frontiers in Plant Science</i> , 2018 , 9, 1377	6.2	19

168	Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , 2018 , 19, 651	4.5	20
167	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2762-2772	8.3	2
166	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 2513-2522	3.2	25
165	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. <i>Nature Communications</i> , 2017 , 8, 14573	17.4	119
164	Improving Response in Genomic Selection with a Population-Based Selection Strategy: Optimal Population Value Selection. <i>Genetics</i> , 2017 , 206, 1675-1682	4	23
163	A High-Throughput, Field-Based Phenotyping Technology for Tall Biomass Crops. <i>Plant Physiology</i> , 2017 , 174, 2008-2022	6.6	84
162	tGBS genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017 , 45, e178	20.1	67
161	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , 2017 , 18, 192	18.3	29
160	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> , 2017 , 2, 1700223	6.8	50
159	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017 , 8, 1348	17.4	58
158	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017 , 8, 694	6.2	43
157	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , 2017 , 3, 715-723	11.5	46
156	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> , 2016 , 6, 34395	4.9	16
155	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , 2016 , 2, 16150	11.5	125
154	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> , 2016 , 16, 1002-11	8.4	79
153	Co-expression network analysis of duplicate genes in maize (<i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016 , 17, 875	4.5	20
152	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015 , 16, 3	18.3	218
151	The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , 2015 , 81, 493-504	6.9	27

150	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> , 2015 , 84, 587-96	6.9	57
149	Laser Microdissection-Mediated Isolation and In Vitro Transcriptional Amplification of Plant RNA. <i>Current Protocols in Molecular Biology</i> , 2015 , 112, 25A.3.1-25A.3.23	2.9	3
148	Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , 2015 , 6, 8974	17.4	58
147	Fast and accurate construction of ultra-dense consensus genetic maps using evolution strategy optimization. <i>PLoS ONE</i> , 2015 , 10, e0122485	3.7	5
146	The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , 2014 , 77, 380-92	6.9	67
145	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> , 2014 , 79, 729-40	6.9	70
144	Histone lysine methyltransferase SDG8 is involved in brassinosteroid-regulated gene expression in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2014 , 7, 1303-1315	14.4	47
143	Genetic control of maize shoot apical meristem architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1327-37	3.7	8
142	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> , 2014 , 42, 5456-67	20.1	14
141	Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. <i>Plant Cell</i> , 2014 , 26, 3939-48	11.6	43
140	The Aux/IAA gene rum1 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> , 2014 , 65, 4919-30	7	44
139	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014 , 15, R40	18.3	308
138	Progress toward understanding heterosis in crop plants. <i>Annual Review of Plant Biology</i> , 2013 , 64, 71-88	30.7	267
137	Integrating Omics Data and Expression QTL to Understand Maize Heterosis 2013 , 85-103		
136	Comparative transcriptome profiling of maize coleoptilar nodes during shoot-borne root initiation. <i>Plant Physiology</i> , 2013 , 163, 419-30	6.6	22
135	The potential of genomics in plant systematics. <i>Taxon</i> , 2013 , 62, 886-898	0.8	45
134	Mendelian and non-Mendelian regulation of gene expression in maize. <i>PLoS Genetics</i> , 2013 , 9, e10032026		66
133	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> , 2013 , 8, e82333	3.7	54

132	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> , 2013 , 1057, 167-76	1.4	2
131	Rapid, repeated, and clustered loss of duplicate genes in allopolyploid plant populations of independent origin. <i>Current Biology</i> , 2012 , 22, 248-52	6.3	122
130	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012 , 72, 390-9	6.9	21
129	Next-generation sequencing and genome evolution in allopolyploids. <i>American Journal of Botany</i> , 2012 , 99, 372-82	2.7	67
128	The Early Stages of Polyploidy: Rapid and Repeated Evolution in <i>Tragopogon</i> 2012 , 271-292		23
127	Parallel domestication of the Shattering1 genes in cereals. <i>Nature Genetics</i> , 2012 , 44, 720-4	36.3	287
126	Spreading of heterochromatin is limited to specific families of maize retrotransposons. <i>PLoS Genetics</i> , 2012 , 8, e1003127	6	124
125	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , 2012 , 22, 2445-54	9.7	97
124	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012 , 22, 2436-44	9.7	96
123	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> , 2012 , 159, 1453-62	6.6	6
122	Ontogeny of the maize shoot apical meristem. <i>Plant Cell</i> , 2012 , 24, 3219-34	11.6	60
121	Gene mapping via bulked segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012 , 7, e36406	3.7	212
120	SNP discovery by transcriptome pyrosequencing. <i>Methods in Molecular Biology</i> , 2011 , 729, 225-46	1.4	17
119	Crop genome sequencing: lessons and rationales. <i>Trends in Plant Science</i> , 2011 , 16, 77-88	13.1	194
118	Transcriptomic shock generates evolutionary novelty in a newly formed, natural allopolyploid plant. <i>Current Biology</i> , 2011 , 21, 551-6	6.3	143
117	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies 2011 ,		3
116	B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. <i>Plant Physiology</i> , 2011 , 156, 1679-90	6.6	57
115	Parent-of-origin effects on gene expression and DNA methylation in the maize endosperm. <i>Plant Cell</i> , 2011 , 23, 4221-33	11.6	160

114	Heritable epigenetic variation among maize inbreds. <i>PLoS Genetics</i> , 2011 , 7, e1002372	6	118
113	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010 , 62, 898-909	6.9	73
112	Variation in gene expression of <i>Andropogon gerardii</i> in response to altered environmental conditions associated with climate change. <i>Journal of Ecology</i> , 2010 , 98, 374-383	6	27
111	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> , 2010 , 19 Suppl 1, 132-46	5.7	143
110	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010 , 463, 763-850.4	5.4	1399
109	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010 , 42, 1027-30	36.3	365
108	High-throughput genetic mapping of mutants via quantitative single nucleotide polymorphism typing. <i>Genetics</i> , 2010 , 184, 19-26	4	56
107	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. <i>PLoS ONE</i> , 2010 , 5, e14178	3.7	10
106	Microdissection of shoot meristem functional domains. <i>PLoS Genetics</i> , 2009 , 5, e1000476	6	64
105	The physical and genetic framework of the maize B73 genome. <i>PLoS Genetics</i> , 2009 , 5, e1000715	6	83
104	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000728	6	34
103	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. <i>PLoS Genetics</i> , 2009 , 5, e1000734	6	389
102	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> , 2009 , 5, e1000737	6	92
101	Regulation of small RNA accumulation in the maize shoot apex. <i>PLoS Genetics</i> , 2009 , 5, e1000320	6	113
100	DLA-based strategies for cloning insertion mutants: cloning the gl4 locus of maize using Mu transposon tagged alleles. <i>Genetics</i> , 2009 , 183, 1215-25	4	31
99	Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. <i>Science</i> , 2009 , 326, 1118-20	33.3	98
98	Tissue specificity and evolution of meristematic WOX3 function. <i>Plant Physiology</i> , 2009 , 149, 841-50	6.6	89
97	Direct calibration of PICKY-designed microarrays. <i>BMC Bioinformatics</i> , 2009 , 10, 347	3.6	8

96	Parallel short sequence assembly of transcriptomes. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S14	3.6	29
95	The roles of aldehyde dehydrogenases (ALDHs) in the PDH bypass of Arabidopsis. <i>BMC Biochemistry</i> , 2009 , 10, 7	4.8	57
94	Laser microdissection-mediated isolation and in vitro transcriptional amplification of plant RNA. <i>Current Protocols in Molecular Biology</i> , 2009 , Chapter 25, Unit 25A.3	2.9	18
93	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
92	On the origins of species: does evolution repeat itself in polyploid populations of independent origin?. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2009 , 74, 215-23	3.9	16
91	Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic marks for open chromatin across the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000733	6	154
90	Homologous Recombination in Maize 2009 , 377-403		2
89	Molecular Markers. <i>Biotechnology in Agriculture and Forestry</i> , 2009 , 231-240		
88	Assembly of Large Genomes from Paired Short Reads. <i>Lecture Notes in Computer Science</i> , 2009 , 30-43	0.9	2
87	Heterosis 2009 , 457-467		2
86	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> , 2008 , 54, 888-98	6.9	118
85	Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , 2008 , 56, 1045-57	6.9	31
84	Assessing probe-specific dye and slide biases in two-color microarray data. <i>BMC Bioinformatics</i> , 2008 , 9, 314	3.6	9
83	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> , 2008 , 35, 603-16	4	10
82	Consensus genetic maps as median orders from inconsistent sources. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008 , 5, 161-71	3	25
81	Expression and nucleotide diversity of the maize RIK gene. <i>Journal of Heredity</i> , 2008 , 99, 407-16	2.4	3
80	Role of RAD51 in the repair of MuDR-induced double-strand breaks in maize (<i>Zea mays</i> L.). <i>Genetics</i> , 2008 , 178, 57-66	4	11
79	Refinement of light-responsive transcript lists using rice oligonucleotide arrays: evaluation of gene-redundancy. <i>PLoS ONE</i> , 2008 , 3, e3337	3.7	99

78	SNP discovery via 454 transcriptome sequencing. <i>Plant Journal</i> , 2007 , 51, 910-8	6.9	339
77	Global gene expression analysis of the shoot apical meristem of maize (<i>Zea mays</i> L.). <i>Plant Journal</i> , 2007 , 52, 391-404	6.9	108
76	Recent advances in plant recombination. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 131-5	9.9	32
75	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> , 2007 , 48, 3-7	4.9	43
74	Gene discovery and annotation using LCM-454 transcriptome sequencing. <i>Genome Research</i> , 2007 , 17, 69-73	9.7	268
73	Involving undergraduates in the annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database. <i>Genetics</i> , 2007 , 176, 741-7	4	17
72	Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. <i>PLoS Genetics</i> , 2007 , 3, e101	6	58
71	Functional analysis of maize RAD51 in meiosis and double-strand break repair. <i>Genetics</i> , 2007 , 176, 1469-82	6.5	65
70	Transcriptomic and proteomic analyses of pericycle cells of the maize primary root. <i>Plant Physiology</i> , 2007 , 145, 575-88	6.6	120
69	Nearly identical paralogs: implications for maize (<i>Zea mays</i> L.) genome evolution. <i>Genetics</i> , 2007 , 175, 429-39	4	51
68	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> , 2007 , 5, 19-24	5.5	39
67	T7-based RNA amplification for genotyping from maize shoot apical meristem. <i>Cold Spring Harbor Protocols</i> , 2007 , 2007, pdb.prot4785	1.2	3
66	Temperature Gradient Capillary Electrophoresis (TGCE) Assay. <i>Cold Spring Harbor Protocols</i> , 2007 , 2007, pdb.prot4845	1.2	
65	Maize tissue preparation and extraction of RNA from target cells for genotyping. <i>Cold Spring Harbor Protocols</i> , 2007 , 2007, pdb.prot4784	1.2	2
64	GRAMA: genetic mapping analysis of temperature gradient capillary electrophoresis data. <i>Theoretical and Applied Genetics</i> , 2006 , 113, 156-62	6	6
63	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. <i>Bioinformatics</i> , 2006 , 22, 1863-70	7.2	22
62	Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. <i>Genetics</i> , 2006 , 174, 1671-83	4	67
61	Effects of trans-acting genetic modifiers on meiotic recombination across the a1-sh2 interval of maize. <i>Genetics</i> , 2006 , 174, 101-12	4	24

60	Unequal sister chromatid and homolog recombination at a tandem duplication of the A1 locus in maize. <i>Genetics</i> , 2006 , 173, 2211-26	4	27
59	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> , 2006 , 103, 6805-10	11.5	314
58	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> , 2005 , 42, 844-61	6.9	70
57	Temperature gradient capillary electrophoresis (TGCE)--a tool for the high-throughput discovery and mapping of SNPs and IDPs. <i>Theoretical and Applied Genetics</i> , 2005 , 111, 218-25	6	29
56	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. <i>Plant Molecular Biology</i> , 2005 , 57, 445-60	4.6	39
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9	Functional principal component based time-series genome-wide association in sorghum		1
8	Meta-Analysis Identifies Pleiotropic Loci Controlling Phenotypic Trade-offs in Sorghum		1
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