

Patrick S Schnable

List of Publications by Year in descending order

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213
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10389
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times ranked

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#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
2	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
3	The molecular basis of cytoplasmic male sterility and fertility restoration. <i>Trends in Plant Science</i> , 1998, 3, 175-180.	8.8	688
4	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.	3.5	484
5	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	21.4	439
6	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	9.6	419
7	Parallel domestication of the <i>Shattering1</i> genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724.	21.4	401
8	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, 6805-6810.	7.1	399
9	Progress Toward Understanding Heterosis in Crop Plants. <i>Annual Review of Plant Biology</i> , 2013, 64, 71-88.	18.7	393
10	The <i>rf2</i> Nuclear Restorer Gene of Male-Sterile T-Cytoplasm Maize. <i>Science</i> , 1996, 272, 1334-1336.	12.6	370
11	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[W]. <i>Plant Cell</i> , 2003, 15, 583-596.	6.6	368
12	SNP discovery via 454 transcriptome sequencing. <i>Plant Journal</i> , 2007, 51, 910-918.	5.7	361
13	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015, 16, 3.	8.8	340
14	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	21.4	335
15	Gene discovery and annotation using LCM-454 transcriptome sequencing. <i>Genome Research</i> , 2006, 17, 69-73.	5.5	321
16	Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406.	2.5	297
17	Mitochondrial Aldehyde Dehydrogenase Activity Is Required for Male Fertility in Maize. <i>Plant Cell</i> , 2001, 13, 1063-1078.	6.6	228
18	Crop genome sequencing: lessons and rationales. <i>Trends in Plant Science</i> , 2011, 16, 77-88.	8.8	222

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19	The ALDH gene superfamily of Arabidopsis. Trends in Plant Science, 2004, 9, 371-377.	8.8	207
20	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. Nature Communications, 2017, 8, 14573.	12.8	202
21	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. PLoS Genetics, 2009, 5, e1000733.	3.5	196
22	Transcriptomic Shock Generates Evolutionary Novelty in a Newly Formed, Natural Allopolyploid Plant. Current Biology, 2011, 21, 551-556.	3.9	192
23	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. Plant Cell, 2011, 23, 4221-4233.	6.6	189
24	The maize (<i>Zea mays</i> L.) <i>roothairless3</i> gene encodes a putative GPI-anchored, monocot-specific, COBRA-like protein that significantly affects grain yield. Plant Journal, 2008, 54, 888-898.	5.7	185
25	The relationship between genetic and physical distances in the cloned <i>a1-sh2</i> interval of the <i>Zea mays</i> L. genome.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 8268-8272.	7.1	184
26	The roothairless1 Gene of Maize Encodes a Homolog of <i>sec3</i> , Which Is Involved in Polar Exocytosis. Plant Physiology, 2005, 138, 1637-1643.	4.8	183
27	Isolation, Characterization, and Pericycle-Specific Transcriptome Analyses of the Novel Maize Lateral and Seminal Root Initiation Mutant <i>rum1</i> . Plant Physiology, 2005, 139, 1255-1267.	4.8	179
28	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. Nature Plants, 2016, 2, 16150.	9.3	179
29	Characterization of duplicate gene evolution in the recent natural allopolyploid <i>Tragopogon miscellus</i> by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. Molecular Ecology, 2010, 19, 132-146.	3.9	167
30	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. PLoS Genetics, 2012, 8, e1003127.	3.5	166
31	Rapid, Repeated, and Clustered Loss of Duplicate Genes in Allopolyploid Plant Populations of Independent Origin. Current Biology, 2012, 22, 248-252.	3.9	159
32	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. Genome Research, 2012, 22, 2445-2454.	5.5	154
33	FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in <i>Arabidopsis thaliana</i> . Current Biology, 2018, 28, 3316-3324.e6.	3.9	154
34	Production of transgenic maize from bombarded type II callus: Effect of gold particle size and callus morphology on transformation efficiency. In Vitro Cellular and Developmental Biology - Plant, 2000, 36, 21-29.	2.1	152
35	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	3.5	150
36	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. Plant Physiology, 2007, 145, 575-588.	4.8	144

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37	Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. <i>Science</i> , 2009, 326, 1118-1120.	12.6	137
38	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, 1002-1011.	4.8	134
39	The genome of broomcorn millet. <i>Nature Communications</i> , 2019, 10, 436.	12.8	130
40	Regulation of Small RNA Accumulation in the Maize Shoot Apex. <i>PLoS Genetics</i> , 2009, 5, e1000320.	3.5	127
41	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444.	5.5	125
42	Global gene expression analysis of the shoot apical meristem of maize (<i>Zea mays</i> L.). <i>Plant Journal</i> , 2007, 52, 391-404.	5.7	123
43	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> , 2002, 99, 6157-6162.	7.1	120
44	<i>Roothairless5</i> , 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, 729-740.	5.7	118
45	A High-Throughput, Field-Based Phenotyping Technology for Tall Biomass Crops. <i>Plant Physiology</i> , 2017, 174, 2008-2022.	4.8	118
46	tGBS® genotyping-by-sequencing enables reliable genotyping of heterozygous loci. <i>Nucleic Acids Research</i> , 2017, 45, e178-e178.	14.5	115
47	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	3.6	109
48	Cloning and characterization of CER2, an Arabidopsis gene that affects cuticular wax accumulation.. <i>Plant Cell</i> , 1996, 8, 1291-1304.	6.6	108
49	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> , 1997, 115, 501-510.	4.8	108
50	Tissue Specificity and Evolution of Meristematic WOX3 Function. <i>Plant Physiology</i> , 2009, 149, 841-850.	4.8	108
51	Maize <i>Mu</i> Transposons Are Targeted to the 5' Untranslated Region of the <i>gl8</i> Gene and Sequences Flanking <i>Mu</i> Target-Site Duplications Exhibit Nonrandom Nucleotide Composition Throughout the Genome. <i>Genetics</i> , 2002, 160, 697-716.	2.9	108
52	Genetic Isolation, Cloning, and Analysis of a Mutator-Induced, Dominant Antimorph of the Maize amylose extender1 Locus.. <i>Plant Cell</i> , 1993, 5, 1555-1566.	6.6	107
53	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.	3.5	106
54	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105

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55	Refinement of Light-Responsive Transcript Lists Using Rice Oligonucleotide Arrays: Evaluation of Gene-Redundancy. PLoS ONE, 2008, 3, e3337.	2.5	104
56	Genetic recombination in plants. Current Opinion in Plant Biology, 1998, 1, 123-129.	7.1	102
57	Genetic control of morphometric diversity in the maize shoot apical meristem. Nature Communications, 2015, 6, 8974.	12.8	100
58	<i>ZmMADS69</i> functions as a flowering activator through the <i>ZmRap2.7</i> - <i>ZCN8</i> regulatory module and contributes to maize flowering time adaptation. New Phytologist, 2019, 221, 2335-2347.	7.3	100
59	Meiotic recombination break points resolve at high rates at the 5' end of a maize coding sequence.. Plant Cell, 1995, 7, 2151-2161.	6.6	98
60	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . Nature Plants, 2017, 3, 715-723.	9.3	98
61	The Physical and Genetic Framework of the Maize B73 Genome. PLoS Genetics, 2009, 5, e1000715.	3.5	95
62	The maize <i>brown midrib2</i> (<i>bm2</i>) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. Plant Journal, 2014, 77, 380-392.	5.7	94
63	Extreme phenotype genome-wide association study (<i>XP-GWAS</i>): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. Plant Journal, 2015, 84, 587-596.	5.7	93
64	Analyses of mutants of three genes that influence root hair development in <i>Zea mays</i> (Gramineae) suggest that root hairs are dispensable. American Journal of Botany, 1994, 81, 833-842.	1.7	92
65	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. New Phytologist, 2018, 217, 1292-1306.	7.3	92
66	Repeat subtraction-mediated sequence capture from a complex genome. Plant Journal, 2010, 62, 898-909.	5.7	89
67	Picky: oligo microarray design for large genomes. Bioinformatics, 2004, 20, 2893-2902.	4.1	88
68	Functional Analysis of Maize RAD51 in Meiosis and Double-Strand Break Repair. Genetics, 2007, 176, 1469-1482.	2.9	86
69	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. PLoS Genetics, 2013, 9, e1003202.	3.5	84
70	Functional Specialization of Maize Mitochondrial Aldehyde Dehydrogenases. Plant Physiology, 2002, 130, 1657-1674.	4.8	83
71	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. Plant Journal, 2005, 42, 844-861.	5.7	82
72	Global expression profiling applied to plant development. Current Opinion in Plant Biology, 2004, 7, 50-56.	7.1	81

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73	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	6.6	80
74	Genetic Dissection of Intermated Recombinant Inbred Lines Using a New Genetic Map of Maize. <i>Genetics</i> , 2006, 174, 1671-1683.	2.9	79
75	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.	5.8	79
76	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> , 1997, 113, 1091-1100.	4.8	77
77	Next-generation sequencing and genome evolution in allopolyploids. <i>American Journal of Botany</i> , 2012, 99, 372-382.	1.7	77
78	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690.	4.8	76
79	The roles of aldehyde dehydrogenases (ALDHs) in the PDH bypass of Arabidopsis. <i>BMC Biochemistry</i> , 2009, 10, 7.	4.4	75
80	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.	2.5	75
81	<i>T-RF8</i> and <i>T-RF13</i> * Mediate Unique T-RF13-Transcript Accumulation, Revealing a Conserved Motif Associated With RNA Processing and Restoration of Pollen Fertility in T-Cytoplasm Maize. <i>Genetics</i> , 1997, 147, 1367-1379.	2.9	75
82	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> , 1997, 115, 925-937.	4.8	74
83	Characterization of the aldehyde dehydrogenase gene families of <i>Zea mays</i> and Arabidopsis. <i>Plant Molecular Biology</i> , 2002, 48, 751-764.	3.9	73
84	Laser Microdissection of Narrow Sheath Mutant Maize Uncovers Novel Gene Expression in the Shoot Apical Meristem. <i>PLoS Genetics</i> , 2007, 3, e101.	3.5	73
85	Microdissection of Shoot Meristem Functional Domains. <i>PLoS Genetics</i> , 2009, 5, e1000476.	3.5	73
86	Ontogeny of the Maize Shoot Apical Meristem. <i>Plant Cell</i> , 2012, 24, 3219-3234.	6.6	72
87	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, 4919-4930.	4.8	69
88	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> , 2002, 128, 924-934.	4.8	67
89	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> , 2005, 102, 12282-12287.	7.1	67
90	The potential of genomics in plant systematics. <i>Taxon</i> , 2013, 62, 886-898.	0.7	67

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91	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. <i>Genetics</i> , 2010, 184, 19-26.	2.9	66
92	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.	8.0	66
93	Histone Lysine Methyltransferase SDG8 Is Involved in Brassinosteroid-Regulated Gene Expression in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2014, 7, 1303-1315.	8.3	64
94	DNA Sequence Analyses Support the Role of Interrupted Gap Repair in the Origin of Internal Deletions of the Maize Transposon, <i>μ</i> DR. <i>Genetics</i> , 1996, 142, 603-618.	2.9	63
95	Maize glossy6 is involved in cuticular wax deposition and drought tolerance. <i>Journal of Experimental Botany</i> , 2019, 70, 3089-3099.	4.8	62
96	Nearly Identical Paralogs: Implications for Maize (<i>Zea mays</i> L.) Genome Evolution. <i>Genetics</i> , 2007, 175, 429-439.	2.9	60
97	The bz-rcy allele of the Cy transposable element system of <i>Zea mays</i> contains a Mu-like element insertion. <i>Molecular Genetics and Genomics</i> , 1989, 217, 459-463.	2.4	59
98	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.	4.8	57
99	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.	8.8	56
100	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021, 14, 874-887.	8.3	56
101	The Genetics, Pathology, and Molecular Biology of T-Cytoplasm Male Sterility in Maize. <i>Advances in Agronomy</i> , 1999, 65, 79-130.	5.2	55
102	A strategy for assembling the maize (<i>Zea mays</i> L.) genome. <i>Bioinformatics</i> , 2004, 20, 140-147.	4.1	55
103	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> , 2006, 48, 3-7.	3.1	55
104	Field-based robotic phenotyping of sorghum plant architecture using stereo vision. <i>Journal of Field Robotics</i> , 2019, 36, 397-415.	6.0	55
105	Mitochondrial transcript processing and restoration of male fertility in T-cytoplasm maize. , 1999, 90, 380-385.		54
106	Semiautomated Feature Extraction from RGB Images for Sorghum Panicle Architecture GWAS. <i>Plant Physiology</i> , 2019, 179, 24-37.	4.8	53
107	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, .	1.8	52
108	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321.	2.5	51

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109	Lateral roots affect the proteome of the primary root of maize (<i>Zea mays</i> L.). <i>Plant Molecular Biology</i> , 2004, 56, 397-412.	3.9	50
110	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.	7.1	49
111	Field-based architectural traits characterisation of maize plant using time-of-flight 3D imaging. <i>Biosystems Engineering</i> , 2019, 178, 86-101.	4.3	48
112	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> , 1994, 81, 833.	1.7	48
113	Cytoplasmic regulation of the accumulation of nuclear-encoded proteins in the mitochondrial proteome of maize. <i>Plant Journal</i> , 2004, 37, 199-208.	5.7	47
114	FarmCPU: Efficient large-scale genomewide association studies. <i>Plant Direct</i> , 2018, 2, e00053.	1.9	46
115	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.	1.8	46
116	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. <i>Plant Molecular Biology</i> , 2005, 57, 445-460.	3.9	45
117	Mapping complementary genes in maize: positioning the rf1 and rf2 nuclear-fertility restorer loci of Texas (T) cytoplasm relative to RFLP and visible markers. <i>Theoretical and Applied Genetics</i> , 1994, 88, 785-795.	3.6	44
118	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.	2.3	44
119	Mutator-Induced Mutations of the rf1 Nuclear Fertility Restorer of T-Cytoplasm Maize Alter the Accumulation of T-urfl3 Mitochondrial Transcripts. <i>Genetics</i> , 1996, 143, 1383-1394.	2.9	44
120	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.	4.0	43
121	Improving Response in Genomic Selection with a Population-Based Selection Strategy: Optimal Population Value Selection. <i>Genetics</i> , 2017, 206, 1675-1682.	2.9	43
122	The Etched1 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> , 2004, 38, 923-939.	5.7	42
123	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> , 2005, 5, 4885-4893.	2.2	42
124	The maize brown midrib4 (bm4) gene encodes a functional polyglutamate synthase. <i>Plant Journal</i> , 2015, 81, 493-504.	5.7	42
125	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2513-2522.	1.8	41
126	Cis-effects on Meiotic Recombination Across Distinct a1-sh2 Intervals in a Common <i>Zea</i> Genetic Background Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY656756, AY656757, AY656758 and AY662984, AY662985, AY662986, AY662987.. <i>Genetics</i> , 2005, 170, 1929-1944.	2.9	40

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127	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	3.5	39
128	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
129	DNA Sequence-Based â€žBar Codesâ€•for Tracking the Origins of Expressed Sequence Tags from a Maize cDNA Library Constructed Using Multiple mRNA Sources. Plant Physiology, 2003, 133, 475-481.	4.8	38
130	Recent advances in plant recombination. Current Opinion in Plant Biology, 2007, 10, 131-135.	7.1	38
131	DLA-Based Strategies for Cloning Insertion Mutants: Cloning the <i>gl4</i> Locus of Maize Using <i>Mu</i> Transposon Tagged Alleles. Genetics, 2009, 183, 1215-1225.	2.9	38
132	Development of Decreased-Gluten Wheat Enabled by Determination of the Genetic Basis of <i>lys3a</i> Barley. Plant Physiology, 2019, 179, 1692-1703.	4.8	38
133	Multi-trait Genomic Selection Methods for Crop Improvement. Genetics, 2020, 215, 931-945.	2.9	38
134	Maize genomes to fields (G2F): 2014â€“2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	1.4	38
135	Microarray analysis of vegetative phase change in maize. Plant Journal, 2008, 56, 1045-1057.	5.7	37
136	Harnessing Phenotypic Plasticity to Improve Maize Yields. Frontiers in Plant Science, 2018, 9, 1377.	3.6	37
137	Alternative Transcription Initiation Sites and Polyadenylation Sites Are Recruited During <i>Mu</i> Suppression at the <i>rf2a</i> Locus of Maize. Genetics, 2003, 163, 685-698.	2.9	37
138	The Early Stages of Polyploidy: Rapid and Repeated Evolution in Tragopogon. , 2012, , 271-292.		36
139	Co-expression network analysis of duplicate genes in maize (<i>Zea mays</i> L.) reveals no subgenome bias. BMC Genomics, 2016, 17, 875.	2.8	36
140	Genetic Isolation, Cloning, and Analysis of a Mutator-Induced, Dominant Antimorph of the Maize amylose extender1 Locus. Plant Cell, 1993, 5, 1555.	6.6	35
141	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. Genome Research, 2019, 29, 1962-1973.	5.5	35
142	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. Plant Journal, 2019, 97, 530-542.	5.7	34
143	Temperature gradient capillary electrophoresis (TGCE)â€•a tool for the high-throughput discovery and mapping of SNPs and IDPs. Theoretical and Applied Genetics, 2005, 111, 218-225.	3.6	33
144	Parallel short sequence assembly of transcriptomes. BMC Bioinformatics, 2009, 10, S14.	2.6	33

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145	TWAS results are complementary to and less affected by linkage disequilibrium than GWAS. <i>Plant Physiology</i> , 2021, 186, 1800-1811.	4.8	33
146	Identifying loci with breeding potential across temperate and tropical adaptation via EigenGWAS and EnvGWAS. <i>Molecular Ecology</i> , 2019, 28, 3544-3560.	3.9	32
147	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	8.8	32
148	Unequal Sister Chromatid and Homolog Recombination at a Tandem Duplication of the <i>a1</i> Locus in Maize. <i>Genetics</i> , 2006, 173, 2211-2226.	2.9	31
149	Consensus Genetic Maps as Median Orders from Inconsistent Sources. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 161-171.	3.0	31
150	Characterization of maize <i>roothairless6</i> which encodes a D-type cellulose synthase and controls the switch from bulge formation to tip growth. <i>Scientific Reports</i> , 2016, 6, 34395.	3.3	31
151	Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , 2018, 19, 651.	2.8	31
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