

Nathan M Springer

List of Publications by Year in descending order

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152
papers

18,867
citations

22099

59
h-index

14702

127
g-index

192
all docs

192
docs citations

192
times ranked

16065
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2022, 34, 514-534.	3.1	30
2	DNA demethylation affects imprinted gene expression in maize endosperm. <i>Genome Biology</i> , 2022, 23, 77.	3.8	20
3	Genome-wide loss of CHH methylation with limited transcriptome changes in <i>Setaria viridis</i> DOMAINS REARRANGED METHYLTRANSFERASE (DRM) mutants. <i>Plant Journal</i> , 2022, 111, 103-116.	2.8	2
4	Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. <i>The Plant Phenome Journal</i> , 2022, 5, .	1.0	9
5	Epigenetic features drastically impact CRISPR-Cas9 efficacy in plants. <i>Plant Physiology</i> , 2022, 190, 1153-1164.	2.3	25
6	The maize gene maternal derepression of <i>r1</i> encodes a DNA glycosylase that demethylates DNA and reduces siRNA expression in the endosperm. <i>Plant Cell</i> , 2022, 34, 3685-3701.	3.1	16
7	CHH DNA methylation increases at PHAS loci depend on phased small interfering RNAs in maize meiotic anthers. <i>New Phytologist</i> , 2021, 229, 2984-2997.	3.5	29
8	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	2.8	16
9	Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. <i>Plant Physiology</i> , 2021, 186, 420-433.	2.3	16
10	Utilizing temporal measurements from UAVs to assess root lodging in maize and its impact on productivity. <i>Field Crops Research</i> , 2021, 262, 108014.	2.3	18
11	Maize decrease in DNA methylation 1 targets RNA-directed DNA methylation on active chromatin. <i>Plant Cell</i> , 2021, 33, 2183-2196.	3.1	11
12	Widespread imprinting of transposable elements and variable genes in the maize endosperm. <i>PLoS Genetics</i> , 2021, 17, e1009491.	1.5	6
13	A capture-based assay for detection and characterization of transposon polymorphisms in maize. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
14	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
15	Stories that can't be told by SNPs; DNA methylation variation in plant populations. <i>Current Opinion in Plant Biology</i> , 2021, 61, 101989.	3.5	17
16	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	3.8	32
17	Whole-genome variation of transposable element insertions in a maize diversity panel. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	16
18	Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. <i>The Plant Phenome Journal</i> , 2021, 4, e20013.	1.0	3

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19	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
20	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021, 217, 1-13.	1.2	14
21	The genomic ecosystem of transposable elements in maize. <i>PLoS Genetics</i> , 2021, 17, e1009768.	1.5	57
22	Plant height heterosis is quantitatively associated with expression levels of plastid ribosomal proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
23	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.	0.8	21
24	Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in <i>Setaria viridis</i> . <i>Plant Journal</i> , 2020, 104, 828-838.	2.8	48
25	Evolutionary and functional genomics of DNA methylation in maize domestication and improvement. <i>Nature Communications</i> , 2020, 11, 5539.	5.8	59
26	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23991-24000.	3.3	67
27	UAV-based imaging platform for monitoring maize growth throughout development. <i>Plant Direct</i> , 2020, 4, e00230.	0.8	25
28	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	3.1	60
29	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2761-2773.	1.8	2
30	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
31	Using multiple reference genomes to identify and resolve annotation inconsistencies. <i>BMC Genomics</i> , 2020, 21, 281.	1.2	10
32	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331.	2.3	14
33	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
34	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019, 100, 1052-1065.	2.8	76
35	Maize Carbohydrate Partitioning Defective33 Encodes an MCTP Protein and Functions in Sucrose Export from Leaves. <i>Molecular Plant</i> , 2019, 12, 1278-1293.	3.9	26
36	Challenges of Translating Gene Regulatory Information into Agronomic Improvements. <i>Trends in Plant Science</i> , 2019, 24, 1075-1082.	4.3	34

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37	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , 2019, 15, e1008291.	1.5	56
38	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019, 12, 410-425.	3.9	69
39	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019, 20, 74.	3.8	13
40	Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. <i>Molecular Plant</i> , 2019, 12, 282-284.	3.9	12
41	Classifying cold stress responses of inbred maize seedlings using <i>RGB</i> imaging. <i>Plant Direct</i> , 2019, 3, e00104.	0.8	34
42	Identification of the expressome by machine learning on omics data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18119-18125.	3.3	47
43	Hybrid Decay: A Transgenerational Epigenetic Decline in Vigor and Viability Triggered in Backcross Populations of Teosinte with Maize. <i>Genetics</i> , 2019, 213, 143-160.	1.2	7
44	Dynamic Patterns of Transcript Abundance of Transposable Element Families in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3673-3682.	0.8	32
45	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	4.7	250
46	Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. <i>Genome Biology</i> , 2019, 20, 243.	3.8	65
47	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , 2019, 59, 1406-1410.	0.8	18
48	Subtle Perturbations of the Maize Methylome Reveal Genes and Transposons Silenced by Chromomethylase or RNA-Directed DNA Methylation Pathways. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1921-1932.	0.8	19
49	Potential roles for transposable elements in creating imprinted expression. <i>Current Opinion in Genetics and Development</i> , 2018, 49, 8-14.	1.5	21
50	Weeding out bad alleles. <i>Nature Plants</i> , 2018, 4, 193-194.	4.7	3
51	The limited role of differential fractionation in genome content variation and function in maize (<i>Zea mays</i> L.) inbred lines. <i>Plant Journal</i> , 2018, 93, 131-141.	2.8	42
52	The Maize Methylome. <i>Compendium of Plant Genomes</i> , 2018, , 81-96.	0.3	3
53	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018, 35, 2762-2772.	3.5	4
54	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288.	9.4	183

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55	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
56	Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018, 209, 983-995.	1.2	57
57	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321.	1.1	51
58	Detection of DNA Methylation by Whole-Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1676, 185-196.	0.4	39
59	Transposable element influences on gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 157-165.	0.9	188
60	A comparative genomic hybridization approach to study gene copy number variations among chinese hamster cell lines. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1903-1908.	1.7	5
61	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527.	13.7	1,113
62	Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12231-12236.	3.3	91
63	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
64	Exploiting induced and natural epigenetic variation for crop improvement. <i>Nature Reviews Genetics</i> , 2017, 18, 563-575.	7.7	183
65	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017, 89, 706-717.	2.8	145
66	News from the plant world: Listening to transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 1-2.	0.9	8
67	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	1.7	109
68	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , 2017, 18, 137.	3.8	134
69	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	49
70	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.	1.2	36
71	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	3.8	436
72	Bisulfite Sequence Analyses Using CyVerse Discovery Environment: From Mapping to DMRs. <i>Current Protocols in Plant Biology</i> , 2016, 1, 510-529.	2.8	4

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73	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	3.1	183
74	Advancing Crop Transformation in the Era of Genome Editing. <i>Plant Cell</i> , 2016, 28, tpc.00196.2016.	3.1	429
75	Creating Order from Chaos: Epigenome Dynamics in Plants with Complex Genomes. <i>Plant Cell</i> , 2016, 28, 314-325.	3.1	89
76	Transposable elements: Microbiomes in the genomes. <i>Nature Plants</i> , 2015, 1, 15004.	4.7	1
77	Genomic limitations to <scp>RNA</scp> sequencing expression profiling. <i>Plant Journal</i> , 2015, 84, 491-503.	2.8	34
78	Minimal evidence for consistent changes in maize DNA methylation patterns following environmental stress. <i>Frontiers in Plant Science</i> , 2015, 6, 308.	1.7	82
79	Reassess the <i>t</i> Test: Interact with All Your Data via ANOVA. <i>Plant Cell</i> , 2015, 27, 2088-2094.	3.1	48
80	Examining the Causes and Consequences of Context-Specific Differential DNA Methylation in Maize. <i>Plant Physiology</i> , 2015, 168, 1262-1274.	2.3	62
81	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2015, 43, e81-e81.	6.5	62
82	Transposable Elements Contribute to Activation of Maize Genes in Response to Abiotic Stress. <i>PLoS Genetics</i> , 2015, 11, e1004915.	1.5	346
83	Paramutation in evolution, population genetics and breeding. <i>Seminars in Cell and Developmental Biology</i> , 2015, 44, 33-38.	2.3	10
84	RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14728-14733.	3.3	179
85	Discovering Functional Modules across Diverse Maize Transcriptomes Using COB, the Co-Expression Browser. <i>PLoS ONE</i> , 2014, 9, e99193.	1.1	25
86	Genomic Distribution of H3K9me2 and DNA Methylation in a Maize Genome. <i>PLoS ONE</i> , 2014, 9, e105267.	1.1	137
87	Genetic Control of Maize Shoot Apical Meristem Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1327-1337.	0.8	13
88	Genetic Determinants for Enzymatic Digestion of Lignocellulosic Biomass Are Independent of Those for Lignin Abundance in a Maize Recombinant Inbred Population. <i>Plant Physiology</i> , 2014, 165, 1475-1487.	2.3	51
89	Genetic Perturbation of the Maize Methylome. <i>Plant Cell</i> , 2014, 26, 4602-4616.	3.1	158
90	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419

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91	Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. <i>Plant Physiology</i> , 2014, 165, 933-947.	2.3	126
92	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
93	Inheritance Patterns and Stability of DNA Methylation Variation in Maize Near-Isogenic Lines. <i>Genetics</i> , 2014, 196, 667-676.	1.2	58
94	Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. <i>Genetics</i> , 2014, 198, 209-218.	1.2	76
95	Utilization of deletion bins to anchor and order sequences along the wheat 7B chromosome. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2029-2040.	1.8	8
96	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
97	Epigenetics and crop improvement. <i>Trends in Genetics</i> , 2013, 29, 241-247.	2.9	110
98	Genomic Distribution of Maize Facultative Heterochromatin Marked by Trimethylation of H3K27. <i>Plant Cell</i> , 2013, 25, 780-793.	3.1	91
99	Progress Toward Understanding Heterosis in Crop Plants. <i>Annual Review of Plant Biology</i> , 2013, 64, 71-88.	8.6	393
100	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003202.	1.5	84
101	Epigenetic and Genetic Influences on DNA Methylation Variation in Maize Populations. <i>Plant Cell</i> , 2013, 25, 2783-2797.	3.1	227
102	Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19639-19644.	3.3	131
103	Maize Gene Atlas Developed by RNA Sequencing and Comparative Evaluation of Transcriptomes Based on RNA Sequencing and Microarrays. <i>PLoS ONE</i> , 2013, 8, e61005.	1.1	152
104	Variation in DNA Methylation Patterns is More Common among Maize Inbreds than among Tissues. <i>Plant Genome</i> , 2013, 6, plantgenome2012.06.0009.	1.6	28
105	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127.	1.5	166
106	Reshaping of the maize transcriptome by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11878-11883.	3.3	154
107	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012, 72, 390-399.	2.8	24
108	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	9.4	816

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109	Brd1 Gene in Maize Encodes a Brassinosteroid C-6 Oxidase. PLoS ONE, 2012, 7, e30798.	1.1	116
110	Density Stress has Minimal Impacts on the Barley or Maize Seedling Transcriptome. Plant Genome, 2011, 4, .	1.6	9
111	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. Plant Physiology, 2011, 156, 1679-1690.	2.3	76
112	The Composition and Origins of Genomic Variation among Individuals of the Soybean Reference Cultivar Williams 82. Plant Physiology, 2011, 155, 645-655.	2.3	137
113	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. Plant Cell, 2011, 23, 4221-4233.	3.1	189
114	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4069-4074.	3.3	644
115	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	1.5	150
116	Repeat subtraction-mediated sequence capture from a complex genome. Plant Journal, 2010, 62, 898-909.	2.8	89
117	Genome-wide patterns of genetic variation among elite maize inbred lines. Nature Genetics, 2010, 42, 1027-1030.	9.4	439
118	Shaping a better rice plant. Nature Genetics, 2010, 42, 475-476.	9.4	27
119	Realizing the potential of genomics for crop improvement. Briefings in Functional Genomics, 2010, 9, 93-94.	1.3	3
120	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. Genetics, 2010, 184, 19-26.	1.2	66
121	<i>ragged seedling2</i> Encodes an ARGONAUTE7-Like Protein Required for Mediolateral Expansion, but Not Dorsiventrality, of Maize Leaves. Plant Cell, 2010, 22, 1441-1451.	3.1	85
122	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. Genome Research, 2010, 20, 1689-1699.	2.4	309
123	Isolation of Plant DNA for PCR and Genotyping Using Organic Extraction and CTAB. Cold Spring Harbor Protocols, 2010, 2010, pdb.prot5515.	0.2	50
124	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. PLoS ONE, 2010, 5, e14178.	1.1	11
125	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. PLoS Genetics, 2009, 5, e1000734.	1.5	484
126	Heterosis Is Prevalent for Multiple Traits in Diverse Maize Germplasm. PLoS ONE, 2009, 4, e7433.	1.1	173

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127	A Recommendation for Naming Transcription Factor Proteins in the Grasses. <i>Plant Physiology</i> , 2009, 149, 4-6.	2.3	45
128	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2009, 182, 503-517.	1.2	212
129	Disruption of Imprinting by <i>Mutator</i> Transposon Insertions in the 5' Proximal Regions of the <i>Zea mays</i> <i>Mez1</i> Locus. <i>Genetics</i> , 2009, 181, 1229-1237.	1.2	16
130	Small RNAs: How Seeds Remember To Obey Their Mother. <i>Current Biology</i> , 2009, 19, R649-R651.	1.8	8
131	Imprinting in Maize. , 2009, , 429-440.		1
132	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
133	Epigenetic Phenomena and Epigenomics in Maize. , 2009, , 119-147.		2
134	Maternal and paternal alleles exhibit differential histone methylation and acetylation at maize imprinted genes. <i>Plant Journal</i> , 2008, 56, 903-912.	2.8	43
135	Profiling expression changes caused by a segmental aneuploid in maize. <i>BMC Genomics</i> , 2008, 9, 7.	1.2	38
136	Gene expression analyses in maize inbreds and hybrids with varying levels of heterosis. <i>BMC Plant Biology</i> , 2008, 8, 33.	1.6	145
137	Chapter 3 Epigenetics. <i>Advances in Agronomy</i> , 2008, 100, 59-80.	2.4	1
138	Nonadditive Expression and Parent-of-Origin Effects Identified by Microarray and Allele-Specific Expression Profiling of Maize Endosperm. <i>Plant Physiology</i> , 2007, 145, 411-425.	2.3	64
139	Assessing the Efficiency of RNA Interference for Maize Functional Genomics. <i>Plant Physiology</i> , 2007, 143, 1441-1451.	2.3	55
140	Allele-Specific Expression Patterns Reveal Biases and Embryo-Specific Parent-of-Origin Effects in Hybrid Maize. <i>Plant Cell</i> , 2007, 19, 2391-2402.	3.1	157
141	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	1.2	31
142	Allelic variation and heterosis in maize: How do two halves make more than a whole?. <i>Genome Research</i> , 2007, 17, 264-275.	2.4	306
143	Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (<i>Mez</i>) homologs. <i>Plant Journal</i> , 2007, 49, 325-337.	2.8	97
144	Cis-transcriptional Variation in Maize Inbred Lines B73 and Mo17 Leads to Additive Expression Patterns in the F1 Hybrid. <i>Genetics</i> , 2006, 173, 2199-2210.	1.2	253

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145	Evolutionary Divergence of Monocot and Dicot Methyl-CpG-Binding Domain Proteins. <i>Plant Physiology</i> , 2005, 138, 92-104.	2.3	62
146	Transgene-Induced RNA Interference as a Tool for Plant Functional Genomics. <i>Methods in Enzymology</i> , 2005, 392, 1-24.	0.4	78
147	Discovery of induced point mutations in maize genes by TILLING. <i>BMC Plant Biology</i> , 2004, 4, 12.	1.6	342
148	Comparative Analysis of SET Domain Proteins in Maize and Arabidopsis Reveals Multiple Duplications Preceding the Divergence of Monocots and Dicots. <i>Plant Physiology</i> , 2003, 132, 907-925.	2.3	176
149	Sequence Relationships, Conserved Domains, and Expression Patterns for Maize Homologs of the Polycomb Group Genes <i>E(z)</i> , <i>esc</i> , and <i>E(Pc)</i> . <i>Plant Physiology</i> , 2002, 128, 1332-1345.	2.3	79
150	Maize Chromomethylase <i>Zea methyltransferase2</i> Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928.	3.1	120
151	BI-Implementation: The causes and consequences of plant biodiversity across scales in a rapidly changing world. <i>Research Ideas and Outcomes</i> , 0, 7, .	1.0	5
152	The Plant Genome: Decoding the Transcriptional Hardwiring. , 0, , 196-228.		4