

Nathan M Springer

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.

161
papers

13,512
citations

56
h-index

115
g-index

192
ext. papers

16,963
ext. citations

8.9
avg, IF

6.36
L-index

#	Paper	IF	Citations
161	DNA demethylation affects imprinted gene expression in maize endosperm.. <i>Genome Biology</i> , 2022 , 23, 77	18.3	2
160	Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. <i>The Plant Phenome Journal</i> , 2022 , 5,	5	0
159	Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. <i>Plant Cell</i> , 2021 ,	11.6	5
158	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,	11.5	2
157	The genomic ecosystem of transposable elements in maize. <i>PLoS Genetics</i> , 2021 , 17, e1009768	6	6
156	Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. <i>Genetics</i> , 2021 , 217, 1-13	4	4
155	Utilizing temporal measurements from UAVs to assess root lodging in maize and its impact on productivity. <i>Field Crops Research</i> , 2021 , 262, 108014	5.5	3
154	Maize decrease in DNA methylation 1 targets RNA-directed DNA methylation on active chromatin. <i>Plant Cell</i> , 2021 , 33, 2183-2196	11.6	5
153	Widespread imprinting of transposable elements and variable genes in the maize endosperm. <i>PLoS Genetics</i> , 2021 , 17, e1009491	6	2
152	Stories that can't be told by SNPs; DNA methylation variation in plant populations. <i>Current Opinion in Plant Biology</i> , 2021 , 61, 101989	9.9	7
151	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021 , 22, 175	18.3	5
150	CHH DNA methylation increases at 24-PHAS loci depend on 24-nt phased small interfering RNAs in maize meiotic anthers. <i>New Phytologist</i> , 2021 , 229, 2984-2997	9.8	6
149	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021 , 105, 93-107	6.9	5
148	Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. <i>Plant Physiology</i> , 2021 , 186, 420-433	6.6	3
147	Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. <i>The Plant Phenome Journal</i> , 2021 , 4, e20013	5	1
146	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
145	UAV-based imaging platform for monitoring maize growth throughout development. <i>Plant Direct</i> , 2020 , 4, e00230	3.3	9

144	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020 , 32, 1377-1396	11.6	20
143	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 2761-2773	6	1
142	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
141	Using multiple reference genomes to identify and resolve annotation inconsistencies. <i>BMC Genomics</i> , 2020 , 21, 281	4.5	6
140	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
139	Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in <i>Setaria viridis</i> . <i>Plant Journal</i> , 2020 , 104, 828-838	6.9	24
138	Evolutionary and functional genomics of DNA methylation in maize domestication and improvement. <i>Nature Communications</i> , 2020 , 11, 5539	17.4	23
137	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	11.5	25
136	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
135	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020 , 182, 318-331	6.6	8
134	Monitoring the interplay between transposable element families and DNA methylation in maize. <i>PLoS Genetics</i> , 2019 , 15, e1008291	6	32
133	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019 , 12, 410-425	14.4	27
132	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019 , 20, 74	18.3	6
131	Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. <i>Molecular Plant</i> , 2019 , 12, 282-284	14.4	11
130	Classifying cold-stress responses of inbred maize seedlings using RGB imaging. <i>Plant Direct</i> , 2019 , 3, e00104	3.3	17
129	Transposable elements contribute to dynamic genome content in maize. <i>Plant Journal</i> , 2019 , 100, 1052-1065	6.5	46
128	Maize Carbohydrate Partitioning Defective33 Encodes an MCTP Protein and Functions in Sucrose Export from Leaves. <i>Molecular Plant</i> , 2019 , 12, 1278-1293	14.4	15
127	Challenges of Translating Gene Regulatory Information into Agronomic Improvements. <i>Trends in Plant Science</i> , 2019 , 24, 1075-1082	13.1	16

126	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	11.5	20
125	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	4	6
124	Dynamic Patterns of Transcript Abundance of Transposable Element Families in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3673-3682	3.2	17
123	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019 , 5, 1237-1249	11.5	127
122	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	18.3	26
121	Idea Factory: the Maize Genomes to Fields Initiative. <i>Crop Science</i> , 2019 , 59, 1406-1410	2.4	10
120	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	3.2	14
119	Potential roles for transposable elements in creating imprinted expression. <i>Current Opinion in Genetics and Development</i> , 2018 , 49, 8-14	4.9	11
118	Weeding out bad alleles. <i>Nature Plants</i> , 2018 , 4, 193-194	11.5	2
117	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018 , 50, 1282-1288	36.3	114
116	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
115	Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018 , 209, 983-995	4	31
114	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018 , 13, e0191321	3.7	27
113	Detection of DNA Methylation by Whole-Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018 , 1676, 185-196	1.4	24
112	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	6.9	31
111	The Plant Genome: Decoding the Transcriptional Hardwiring 2018 , 196-228		
110	The Maize Methylome. <i>Compendium of Plant Genomes</i> , 2018 , 81-96	0.8	3
109	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2762-2772	8.3	2

108	Transposable element influences on gene expression in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 157-165	6	106
107	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	4.9	3
106	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017 , 546, 524-527	50.4	643
105	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	11.5	59
104	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , 2017 , 18, 137	18.3	88
103	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017 , 8, 22	4.4	33
102	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017 , 8, 1348	17.4	58
101	Exploiting induced and natural epigenetic variation for crop improvement. <i>Nature Reviews Genetics</i> , 2017 , 18, 563-575	30.1	121
100	Natural variation for gene expression responses to abiotic stress in maize. <i>Plant Journal</i> , 2017 , 89, 706-717	6.7	63
99	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017 , 8, 694	6.2	43
98	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016 , 28, 2700-2714	11.6	139
97	Advancing Crop Transformation in the Era of Genome Editing. <i>Plant Cell</i> , 2016 , 28, 1510-20	11.6	309
96	Creating Order from Chaos: Epigenome Dynamics in Plants with Complex Genomes. <i>Plant Cell</i> , 2016 , 28, 314-25	11.6	60
95	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
94	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016 , 17, 194	18.3	289
93	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
92	Reassess the t Test: Interact with All Your Data via ANOVA. <i>Plant Cell</i> , 2015 , 27, 2088-94	11.6	40
91	Examining the Causes and Consequences of Context-Specific Differential DNA Methylation in Maize. <i>Plant Physiology</i> , 2015 , 168, 1262-74	6.6	51

90	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2015 , 43, e81	20.1	52
89	Transposable elements contribute to activation of maize genes in response to abiotic stress. <i>PLoS Genetics</i> , 2015 , 11, e1004915	6	239
88	Paramutation in evolution, population genetics and breeding. <i>Seminars in Cell and Developmental Biology</i> , 2015 , 44, 33-8	7.5	8
87	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, 14728-33	11.5	126
86	Transposable elements: Microbiomes in the genomes. <i>Nature Plants</i> , 2015 , 1, 15004	11.5	1
85	Genomic limitations to RNA sequencing expression profiling. <i>Plant Journal</i> , 2015 , 84, 491-503	6.9	17
84	Minimal evidence for consistent changes in maize DNA methylation patterns following environmental stress. <i>Frontiers in Plant Science</i> , 2015 , 6, 308	6.2	61
83	Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. <i>Plant Physiology</i> , 2014 , 165, 933-947	6.6	101
82	Insights into the effects of long-term artificial selection on seed size in maize. <i>Genetics</i> , 2014 , 198, 409-21		25
81	Inheritance patterns and stability of DNA methylation variation in maize near-isogenic lines. <i>Genetics</i> , 2014 , 196, 667-76	4	47
80	Consistent and heritable alterations of DNA methylation are induced by tissue culture in maize. <i>Genetics</i> , 2014 , 198, 209-18	4	53
79	Utilization of deletion bins to anchor and order sequences along the wheat 7B chromosome. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2029-40	6	8
78	Discovering functional modules across diverse maize transcriptomes using COB, the Co-expression Browser. <i>PLoS ONE</i> , 2014 , 9, e99193	3.7	19
77	Genomic distribution of H3K9me2 and DNA methylation in a maize genome. <i>PLoS ONE</i> , 2014 , 9, e105267	3.7	108
76	Genetic control of maize shoot apical meristem architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1327-37	3.7	8
75	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	6.6	39
74	Genetic perturbation of the maize methylome. <i>Plant Cell</i> , 2014 , 26, 4602-16	11.6	126
73	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014 , 15, R40	18.3	308

72	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013 , 14, R58	18.3	81
71	Epigenetics and crop improvement. <i>Trends in Genetics</i> , 2013 , 29, 241-7	8.5	88
70	Genomic distribution of maize facultative heterochromatin marked by trimethylation of H3K27. <i>Plant Cell</i> , 2013 , 25, 780-93	11.6	77
69	Variation in DNA Methylation Patterns is More Common among Maize Inbreds than among Tissues. <i>Plant Genome</i> , 2013 , 6, plantgenome2012.06.0009	4.4	24
68	Progress toward understanding heterosis in crop plants. <i>Annual Review of Plant Biology</i> , 2013 , 64, 71-88	30.7	267
67	Mendelian and non-Mendelian regulation of gene expression in maize. <i>PLoS Genetics</i> , 2013 , 9, e10032026		66
66	Epigenetic and genetic influences on DNA methylation variation in maize populations. <i>Plant Cell</i> , 2013 , 25, 2783-97	11.6	174
65	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, 19639-44	11.5	93
64	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	3.7	125
63	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012 , 72, 390-9	6.9	21
62	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012 , 44, 808-11	36.3	600
61	Spreading of heterochromatin is limited to specific families of maize retrotransposons. <i>PLoS Genetics</i> , 2012 , 8, e1003127	6	124
60	Reshaping of the maize transcriptome by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 11878-83	11.5	113
59	Brd1 gene in maize encodes a brassinosteroid C-6 oxidase. <i>PLoS ONE</i> , 2012 , 7, e30798	3.7	89
58	Density Stress has Minimal Impacts on the Barley or Maize Seedling Transcriptome. <i>Plant Genome</i> , 2011 , 4,	4.4	7
57	B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. <i>Plant Physiology</i> , 2011 , 156, 1679-90	6.6	57
56	The composition and origins of genomic variation among individuals of the soybean reference cultivar Williams 82. <i>Plant Physiology</i> , 2011 , 155, 645-55	6.6	111
55	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

54	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 4069-74	11.5	462
53	Heritable epigenetic variation among maize inbreds. <i>PLoS Genetics</i> , 2011 , 7, e1002372	6	118
52	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010 , 62, 898-909	9.9	73
51	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010 , 42, 1027-30	36.3	365
50	High-throughput genetic mapping of mutants via quantitative single nucleotide polymorphism typing. <i>Genetics</i> , 2010 , 184, 19-26	4	56
49	ragged seedling2 Encodes an ARGONAUTE7-like protein required for mediolateral expansion, but not dorsiventrality, of maize leaves. <i>Plant Cell</i> , 2010 , 22, 1441-51	11.6	65
48	Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. <i>Genome Research</i> , 2010 , 20, 1689-99	9.7	236
47	Isolation of plant DNA for PCR and genotyping using organic extraction and CTAB. <i>Cold Spring Harbor Protocols</i> , 2010 , 2010, pdb.prot5515	1.2	32
46	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. <i>PLoS ONE</i> , 2010 , 5, e14178	3.7	10
45	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
44	Heterosis is prevalent for multiple traits in diverse maize germplasm. <i>PLoS ONE</i> , 2009 , 4, e7433	3.7	116
43	A recommendation for naming transcription factor proteins in the grasses. <i>Plant Physiology</i> , 2009 , 149, 4-6	6.6	35
42	Reciprocal silencing, transcriptional bias and functional divergence of homeologs in polyploid cotton (<i>gossypium</i>). <i>Genetics</i> , 2009 , 182, 503-17	4	174
41	Disruption of imprinting by mutator transposon insertions in the 5Tproximal regions of the <i>Zea mays</i> <i>Mez1</i> locus. <i>Genetics</i> , 2009 , 181, 1229-37	4	12
40	Small RNAs: how seeds remember to obey their mother. <i>Current Biology</i> , 2009 , 19, R649-51	6.3	7
39	Imprinting in Maize 2009 , 429-440		1
38	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
37	Epigenetic Phenomena and Epigenomics in Maize 2009 , 119-147		1

36	Maternal and paternal alleles exhibit differential histone methylation and acetylation at maize imprinted genes. <i>Plant Journal</i> , 2008 , 56, 903-12	6.9	38
35	Profiling expression changes caused by a segmental aneuploid in maize. <i>BMC Genomics</i> , 2008 , 9, 7	4.5	32
34	Gene expression analyses in maize inbreds and hybrids with varying levels of heterosis. <i>BMC Plant Biology</i> , 2008 , 8, 33	5.3	111
33	Chapter 3 Epigenetics. <i>Advances in Agronomy</i> , 2008 , 100, 59-80	7.7	1
32	Allelic variation and heterosis in maize: how do two halves make more than a whole?. <i>Genome Research</i> , 2007 , 17, 264-75	9.7	248
31	Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (Mez) homologs. <i>Plant Journal</i> , 2007 , 49, 325-37	6.9	86
30	Nonadditive expression and parent-of-origin effects identified by microarray and allele-specific expression profiling of maize endosperm. <i>Plant Physiology</i> , 2007 , 145, 411-25	6.6	57
29	Assessing the efficiency of RNA interference for maize functional genomics. <i>Plant Physiology</i> , 2007 , 143, 1441-51	6.6	45
28	Allele-specific expression patterns reveal biases and embryo-specific parent-of-origin effects in hybrid maize. <i>Plant Cell</i> , 2007 , 19, 2391-402	11.6	113
27	Natural variation for alleles under epigenetic control by the maize chromomethylase zmet2. <i>Genetics</i> , 2007 , 177, 749-60	4	28
26	Cis-transcriptional variation in maize inbred lines B73 and Mo17 leads to additive expression patterns in the F1 hybrid. <i>Genetics</i> , 2006 , 173, 2199-210	4	201
25	Evolutionary divergence of monocot and dicot methyl-CpG-binding domain proteins. <i>Plant Physiology</i> , 2005 , 138, 92-104	6.6	53
24	Transgene-induced RNA interference as a tool for plant functional genomics. <i>Methods in Enzymology</i> , 2005 , 392, 1-24	1.7	69
23	Discovery of induced point mutations in maize genes by TILLING. <i>BMC Plant Biology</i> , 2004 , 4, 12	5.3	282
22	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, 907-25	6.6	136
21	Sequence relationships, conserved domains, and expression patterns for maize homologs of the polycomb group genes E(z), esc, and E(Pc). <i>Plant Physiology</i> , 2002 , 128, 1332-45	6.6	70
20	Maize chromomethylase Zea methyltransferase2 is required for CpNpG methylation. <i>Plant Cell</i> , 2001 , 13, 1919-28	11.6	106
19	Using multiple reference genomes to identify and resolve annotation inconsistencies		1

18	Genetic and epigenetic contributions to variation in transposable element expression responses to abiotic stress in maize	2
17	Widespread natural variation of DNA methylation within angiosperms	7
16	Improved maize reference genome with single molecule technologies	10
15	Utilizing top-down hyperspectral imaging for monitoring genotype and growth conditions in maize	4
14	Evolutionary and functional genomics of DNA methylation in maize domestication and improvement	4
13	Cis-regulatory elements within TEs can influence expression of nearby maize genes	5
12	Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes	2
11	Chromosome-level Genome Assembly of a Regenerable Maize Inbred Line A188	2
10	Whole Genome Variation of Transposable Element Insertions in a Maize Diversity Panel	2
9	Subtle perturbations of the maize methylome reveal genes and transposons silenced by DNA methylation	4
8	Targeted epigenomic changes to the maize methylome resulting from tissue culture	1
7	Transposable elements contribute to dynamic genome content in maize	5
6	The Genomic Ecosystem of Transposable Elements in Maize	25
5	UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development	1
4	Limited role of differential fractionation in genome content variation and function in maize (<i>Zea mays</i> L.) inbred lines	1
3	BII-Implementation: The causes and consequences of plant biodiversity across scales in a rapidly changing world. <i>Research Ideas and Outcomes</i> ,7,	2.5 2
2	Plant trait heterosis is quantitatively associated with expression heterosis of the plastid ribosomal proteins	2
1	The Plant Genome: Decoding the Transcriptional Hardwiring196-228	2

