

Shawn M Kaeppler

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

12,169
citations

29994

54
h-index

30010

103
g-index

153
all docs

153
docs citations

153
times ranked

14223
citing authors

#	ARTICLE	IF	CITATIONS
1	Root angle in maize influences nitrogen capture and is regulated by calcineurin B-like protein <sc>(CBL)</sc>-interacting serine/threonine-protein kinase 15 (<sc>i>ZmCIPK15</i></sc>). Plant, Cell and Environment, 2022, 45, 837-853.	2.8	46
2	Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. Genetics, 2022, 221, .	1.2	5
3	Strong parallel evidence of selection during switchgrass sward establishment in hybrid and lowland ecotypes. , 2022, 1, 31-42.		3
4	A novel high-throughput hyperspectral scanner and analytical methods for predicting maize kernel composition and physical traits. Food Chemistry, 2022, 391, 133264.	4.2	4
5	IntegrateNet: A Deep Learning Network for Maize Stand Counting From UAV Imagery by Integrating Density and Local Count Maps. IEEE Geoscience and Remote Sensing Letters, 2022, 19, 1-5.	1.4	3
6	Estimation of Maize Yield and Flowering Time Using Multi-Temporal UAV-Based Hyperspectral Data. Remote Sensing, 2022, 14, 3052.	1.8	13
7	Single-parent expression drives dynamic gene expression complementation in maize hybrids. Plant Journal, 2021, 105, 93-107.	2.8	16
8	Chromosome-level genome assembly of a regenerable maize inbred line A188. Genome Biology, 2021, 22, 175.	3.8	32
9	Genomic variation within the maize stiff-stalk heterotic germplasm pool. Plant Genome, 2021, 14, e20114.	1.6	14
10	Testcross vs. randomly paired single-cross progeny tests for genomic prediction of new inbreds and hybrids derived from multiparent maize populations. Crop Science, 2021, 61, 3425-3435.	0.8	4
11	Generating novel plant genetic variation via genome editing to escape the breeding lottery. In Vitro Cellular and Developmental Biology - Plant, 2021, 57, 627.	0.9	3
12	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	52
13	Genetic loci associated with winter survivorship in diverse lowland switchgrass populations. Plant Genome, 2021, 14, e20159.	1.6	5
14	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. Crop Science, 2020, 60, 62-81.	0.8	21
15	Plant science decadal vision 2020-2030: Reimagining the potential of plants for a healthy and sustainable future. Plant Direct, 2020, 4, e00252.	0.8	26
16	Genetic control of root anatomical plasticity in maize. Plant Genome, 2020, 13, e20003.	1.6	39
17	Diversity and heterotic patterns in North American proprietary dent maize germplasm. Crop Science, 2020, 60, 100-114.	0.8	42
18	Characterizing introgression-by-environment interactions using maize near isogenic lines. Theoretical and Applied Genetics, 2020, 133, 2761-2773.	1.8	2

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19	Genetic control of root architectural plasticity in maize. <i>Journal of Experimental Botany</i> , 2020, 71, 3185-3197.	2.4	37
20	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
21	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 2012-2024.	3.6	54
22	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 1922-1922.	3.6	0
23	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331.	2.3	14
24	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
25	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	1.6	37
26	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989.	3.1	63
27	Predicting Zea mays Flowering Time, Yield, and Kernel Dimensions by Analyzing Aerial Images. <i>Frontiers in Plant Science</i> , 2019, 10, 1251.	1.7	20
28	Maize <i>sugary enhancer1</i> (<i>se1</i>) is a gene affecting endosperm starch metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20776-20785.	3.3	36
29	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	1.6	77
30	Genomic Prediction for Winter Survival of Lowland Switchgrass in the Northern USA. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1921-1931.	0.8	22
31	Quantitative Trait Loci for Freezing Tolerance in a Lowland x Upland Switchgrass Population. <i>Frontiers in Plant Science</i> , 2019, 10, 372.	1.7	19
32	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <i>Genetics</i> , 2018, 210, 1125-1138.	1.2	45
33	Candidate Variants for Additive and Interactive Effects on Bioenergy Traits in Switchgrass (<i>Panicum virgatum</i> L.) Identified by Genome-Wide Association Analyses. <i>Plant Genome</i> , 2018, 11, 180002.	1.6	8
34	A machine vision platform for measuring imbibition of maize kernels: quantification of genetic effects and correlations with germination. <i>Plant Methods</i> , 2018, 14, 115.	1.9	6
35	Genetic Analysis of <i>Sugarcane mosaic virus</i> Resistance in the Wisconsin Diversity Panel of Maize. <i>Crop Science</i> , 2018, 58, 1853-1865.	0.8	20
36	Quantitative Trait Locus Mapping for Flowering Time in a Lowland × Upland Switchgrass Pseudo-F 2 Population. <i>Plant Genome</i> , 2018, 11, 170093.	1.6	35

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37	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	1.6	35
38	Genetic Fineâ€Mapping of a Quantitative Trait Locus (QTL) Associated with Embryogenic Tissue Culture Response and Plant Regeneration Ability in Maize (<i>Zea mays</i> L.). <i>Plant Genome</i> , 2018, 11, 170111.	1.6	17
39	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
40	Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018, 209, 983-995.	1.2	57
41	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321.	1.1	51
42	DNA methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i> . <i>New Phytologist</i> , 2017, 214, 1213-1229.	3.5	47
43	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
44	Prediction of Cell Wall Properties and Response to Deconstruction Using Alkaline Pretreatment in Diverse Maize Genotypes Using Py-MBMS and NIR. <i>Bioenergy Research</i> , 2017, 10, 329-343.	2.2	8
45	Transcriptional Analysis of Flowering Time in Switchgrass. <i>Bioenergy Research</i> , 2017, 10, 700-713.	2.2	19
46	TIPS: a system for automated image-based phenotyping of maize tassels. <i>Plant Methods</i> , 2017, 13, 21.	1.9	62
47	Suppression of CINNAMOYL-CoA REDUCTASE increases the level of monolignol ferulates incorporated into maize lignins. <i>Biotechnology for Biofuels</i> , 2017, 10, 109.	6.2	32
48	A robust, highâ€throughput method for computing maize ear, cob, and kernel attributes automatically from images. <i>Plant Journal</i> , 2017, 89, 169-178.	2.8	86
49	Genomeâ€wide associations with flowering time in switchgrass using exomeâ€capture sequencing data. <i>New Phytologist</i> , 2017, 213, 154-169.	3.5	56
50	Registration of the NyH (Ny821Ã—H99) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 101-104.	0.4	2
51	Registration of the OhW (Oh43Ã—W64A) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 97-100.	0.4	0
52	Introduction to a Special Issue on Genotype by Environment Interaction. <i>Crop Science</i> , 2016, 56, 2081-2089.	0.8	92
53	Selection Signatures in Four Lignin Genes from Switchgrass Populations Divergently Selected for In Vitro Dry Matter Digestibility. <i>PLoS ONE</i> , 2016, 11, e0167005.	1.1	5
54	Stover Composition in Maize and Sorghum Reveals Remarkable Genetic Variation and Plasticity for Carbohydrate Accumulation. <i>Frontiers in Plant Science</i> , 2016, 7, 822.	1.7	29

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55	An Expanded Maize Gene Expression Atlas based on RNA Sequencing and its Use to Explore Root Development. <i>Plant Genome</i> , 2016, 9, plantgenome2015.04.0025.	1.6	289
56	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
57	Accuracy of Genomic Prediction in Switchgrass (<i>Panicum virgatum</i> L.) Improved by Accounting for Linkage Disequilibrium. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1049-1062.	0.8	31
58	Evidence for maternal control of seed size in maize from phenotypic and transcriptional analysis. <i>Journal of Experimental Botany</i> , 2016, 67, 1907-1917.	2.4	47
59	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	2.8	47
60	Cell-wall properties contributing to improved deconstruction by alkaline pre-treatment and enzymatic hydrolysis in diverse maize (<i>Zea mays</i> L.) lines. <i>Journal of Experimental Botany</i> , 2015, 66, 4305-4315.	2.4	28
61	Image analysis of anatomical traits in stalk transections of maize and other grasses. <i>Plant Methods</i> , 2015, 11, 26.	1.9	40
62	Impacts of Agricultural Nitrogen on the Environment and Strategies to Reduce these Impacts. <i>Procedia Environmental Sciences</i> , 2015, 29, 303.	1.3	29
63	Large effect QTL explain natural phenotypic variation for the developmental timing of vegetative phase change in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 529-538.	1.8	28
64	Genome-wide association analysis reveals new targets for carotenoid biofortification in maize. <i>Theoretical and Applied Genetics</i> , 2015, 128, 851-864.	1.8	146
65	Shared Genomic Regions Between Derivatives of a Large Segregating Population of Maize Identified Using Bulk Segregant Analysis Sequencing and Traditional Linkage Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1593-1602.	0.8	37
66	Defining window-boundaries for genomic analyses using smoothing spline techniques. <i>Genetics Selection Evolution</i> , 2015, 47, 30.	1.2	72
67	Autophagic Recycling Plays a Central Role in Maize Nitrogen Remobilization. <i>Plant Cell</i> , 2015, 27, 1389-1408.	3.1	211
68	QTL mapping and phenotypic variation of root anatomical traits in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 93-106.	1.8	49
69	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
70	Whole Transcriptome Profiling of Maize during Early Somatic Embryogenesis Reveals Altered Expression of Stress Factors and Embryogenesis-Related Genes. <i>PLoS ONE</i> , 2014, 9, e111407.	1.1	96
71	Conserved Transcriptional Regulatory Programs Underlying Rice and Barley Germination. <i>PLoS ONE</i> , 2014, 9, e87261.	1.1	6
72	Phenotypic and Transcriptional Analysis of Divergently Selected Maize Populations Reveals the Role of Developmental Timing in Seed Size Determination. <i>Plant Physiology</i> , 2014, 165, 658-669.	2.3	37

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73	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	3.1	498
74	Genetic Perturbation of the Maize Methylome. <i>Plant Cell</i> , 2014, 26, 4602-4616.	3.1	158
75	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	1.2	38
76	QTL mapping and phenotypic variation for root architectural traits in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 2293-2311.	1.8	90
77	Nucleotide polymorphism and copy number variant detection using exome capture and next-generation sequencing in the polyploid grass <i>Panicum virgatum</i> . <i>Plant Journal</i> , 2014, 79, 993-1008.	2.8	39
78	Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. <i>Genetics</i> , 2014, 198, 209-218.	1.2	76
79	A Genome-Wide Scan for Evidence of Selection in a Maize Population Under Long-Term Artificial Selection for Ear Number. <i>Genetics</i> , 2014, 196, 829-840.	1.2	63
80	Formation of Heterotic Groups and Understanding Genetic Effects in a Provitamin A Biofortified Maize Breeding Program. <i>Crop Science</i> , 2014, 54, 14-24.	0.8	92
81	Generation of Transcript Assemblies and Identification of Single Nucleotide Polymorphisms from Seven Lowland and Upland Cultivars of Switchgrass. <i>Plant Genome</i> , 2014, 7, plantgenome2013.12.0041.	1.6	6
82	Maize (<i>Zea Mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. , 2014, , 299-325.		0
83	Maize root growth angles become steeper under low N conditions. <i>Field Crops Research</i> , 2013, 140, 18-31.	2.3	223
84	Marker Density and Read Depth for Genotyping Populations Using Genotyping-by-Sequencing. <i>Genetics</i> , 2013, 193, 1073-1081.	1.2	206
85	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
86	The Genetic Architecture of Maize Stalk Strength. <i>PLoS ONE</i> , 2013, 8, e67066.	1.1	129
87	Transcriptional and Metabolic Analysis of Senescence Induced by Preventing Pollination in Maize. <i>Plant Physiology</i> , 2012, 159, 1730-1744.	2.3	90
88	A high-throughput core sampling device for the evaluation of maize stalk composition. <i>Biotechnology for Biofuels</i> , 2012, 5, 27.	6.2	9
89	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
90	Maize (<i>Zea mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e33071.	1.1	153

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91	TCUP: A Novel hAT Transposon Active in Maize Tissue Culture. <i>Frontiers in Plant Science</i> , 2012, 3, 6.	1.7	22
92	The Scientific Grand Challenges of the 21st Century for the Crop Science Society of America. <i>Crop Science</i> , 2012, 52, 1003-1010.	0.8	21
93	Heterosis: Many Genes, Many Mechanisms—End the Search for an Undiscovered Unifying Theory. <i>ISRN Botany</i> , 2012, 2012, 1-12.	0.8	73
94	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	9.4	816
95	Genetic Diversity of a Maize Association Population with Restricted Phenology. <i>Crop Science</i> , 2011, 51, 704-715.	0.8	81
96	The Switchgrass Genome: Tools and Strategies. <i>Plant Genome</i> , 2011, 4, 273-282.	1.6	91
97	Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. <i>Plant Genome</i> , 2011, 4, 191-203.	1.6	131
98	Genome-wide atlas of transcription during maize development. <i>Plant Journal</i> , 2011, 66, 553-563.	2.8	515
99	Heterosis: one boat at a time, or a rising tide?. <i>New Phytologist</i> , 2011, 189, 900-902.	3.5	15
100	Post-glacial evolution of <i>Panicum virgatum</i> : centers of diversity and gene pools revealed by SSR markers and cpDNA sequences. <i>Genetica</i> , 2011, 139, 933-948.	0.5	85
101	Shovelomics: high throughput phenotyping of maize (<i>Zea mays</i> L.) root architecture in the field. <i>Plant and Soil</i> , 2011, 341, 75-87.	1.8	545
102	Hierarchical classification of switchgrass genotypes using SSR and chloroplast sequences: ecotypes, ploidies, gene pools, and cultivars. <i>Theoretical and Applied Genetics</i> , 2011, 122, 805-817.	1.8	80
103	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690.	2.3	76
104	Natural Hybrids and Gene Flow between Upland and Lowland Switchgrass. <i>Crop Science</i> , 2011, 51, 2626-2641.	0.8	76
105	Genetic Analysis of Cell Wall Traits Relevant to Cellulosic Ethanol Production in Maize (<i>Zea mays</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 1078-1086.	0.8	26
106	Loss-of-function of DELLA protein SLN1 activates GA signaling in barley aleurone. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 789-800.	1.0	7
107	Tissue Culture-Induced Novel Epialleles of a <i>Myb</i> Transcription Factor Encoded by <i>pericarp color1</i> in Maize. <i>Genetics</i> , 2010, 186, 843-855.	1.2	49
108	Chromatin, DNA Methylation, RNAi and Epigenetic Regulation. <i>Plant Science</i> , 2009, 176, 441-458.		0

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109	Chapter 3 Epigenetics. <i>Advances in Agronomy</i> , 2008, 100, 59-80.	2.4	1
110	Assessing the Efficiency of RNA Interference for Maize Functional Genomics. <i>Plant Physiology</i> , 2007, 143, 1441-1451.	2.3	55
111	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	1.2	31
112	Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (Mez) homologs. <i>Plant Journal</i> , 2007, 49, 325-337.	2.8	97
113	Detection of quantitative trait loci for seminal root traits in maize (<i>Zea mays</i> L.) seedlings grown under differential phosphorus levels. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1-10.	1.8	157
114	Mapping of QTLs for lateral root branching and length in maize (<i>Zea mays</i> L.) under differential phosphorus supply. <i>Theoretical and Applied Genetics</i> , 2005, 111, 688-695.	1.8	224
115	Mapping of QTL controlling root hair length in maize (<i>Zea mays</i> L.) under phosphorus deficiency. <i>Plant and Soil</i> , 2005, 270, 299-310.	1.8	218
116	Genetic Control of Prolificacy and Related Traits in the Golden Glow Maize Population: I. Phenotypic Evaluation. <i>Crop Science</i> , 2005, 45, 1361-1369.	0.8	10
117	Topsoil foraging and phosphorus acquisition efficiency in maize (<i>Zea mays</i>). <i>Functional Plant Biology</i> , 2005, 32, 749.	1.1	191
118	Evolutionary Divergence of Monocot and Dicot Methyl-CpG-Binding Domain Proteins. <i>Plant Physiology</i> , 2005, 138, 92-104.	2.3	62
119	Transgene-Induced RNA Interference as a Tool for Plant Functional Genomics. <i>Methods in Enzymology</i> , 2005, 392, 1-24.	0.4	78
120	Response to Selection and Genetic Drift in Three Populations Derived from the Golden Glow Maize Population. <i>Crop Science</i> , 2004, 44, 1527-1534.	0.8	19
121	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
122	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
123	Variability of chromosomal DNA contents in maize (<i>Zea mays</i> L.) inbred and hybrid lines. <i>Planta</i> , 2002, 215, 666-671.	1.6	52
124	Enhanced maize productivity by inoculation with diazotrophic bacteria. <i>Functional Plant Biology</i> , 2001, 28, 829.	1.1	80
125	Induction of maize acid phosphatase activities under phosphorus starvation. <i>Plant and Soil</i> , 2001, 237, 109-115.	1.8	87
126	Maize Chromomethylase <i>Zea methyltransferase2</i> Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928.	3.1	120

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127	Maize Chromomethylase Zea methyltransferase2 Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928.	3.1	86
128	Variation among Maize Inbred Lines and Detection of Quantitative Trait Loci for Growth at Low Phosphorus and Responsiveness to Arbuscular Mycorrhizal Fungi. <i>Crop Science</i> , 2000, 40, 358-364.	0.8	231
129	Lax leaf maize: cell wall composition and nutritional value. <i>Journal of the Science of Food and Agriculture</i> , 2000, 80, 255-262.	1.7	9
130	Epigenetic aspects of somaclonal variation in plants. <i>Plant Molecular Biology</i> , 2000, 43, 179-188.	2.0	593
131	Conserved plant genes with similarity to mammalian de novo DNA methyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 4979-4984.	3.3	222
132	Quantitative trait locus mapping using sets of near-isogenic lines: relative power comparisons and technical considerations. <i>Theoretical and Applied Genetics</i> , 1997, 95, 384-392.	1.8	43
133	Power analysis for quantitative trait locus mapping in populations derived by multiple backcrosses. <i>Theoretical and Applied Genetics</i> , 1997, 95, 618-621.	1.8	12
134	Molecular-marker-based Genetic Analysis of Tepary Bean-derived Common Bacterial Blight Resistance in Different Developmental Stages of Common Bean. <i>Journal of the American Society for Horticultural Science</i> , 1997, 122, 329-337.	0.5	57
135	Molecular Markers Associated with Plant Architecture and Resistance to Common Blight, Web Blight, and Rust in Common Beans. <i>Journal of the American Society for Horticultural Science</i> , 1996, 121, 794-803.	0.5	87
136	Genetic instability of plant tissue cultures: breakdown of normal controls.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 5222-5226.	3.3	509
137	Use of near-isogenic lines derived by backcrossing or selfing to map qualitative traits. <i>Theoretical and Applied Genetics</i> , 1993, 87, 233-237.	1.8	23
138	Tissue culture-induced DNA methylation variation in maize.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 8773-8776.	3.3	197