

Shawn M Kaeppler

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5250305/publications.pdf>

Version: 2024-02-01

138
papers

12,169
citations

30070

54
h-index

30087

103
g-index

153
all docs

153
docs citations

153
times ranked

14223
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	21.4	816
2	Epigenetic aspects of somaclonal variation in plants. <i>Plant Molecular Biology</i> , 2000, 43, 179-188.	3.9	593
3	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
4	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.	3.7	545
5	Genome-wide atlas of transcription during maize development. <i>Plant Journal</i> , 2011, 66, 553-563.	5.7	515
6	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.	7.1	509
7	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	6.6	498
8	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.	2.8	289
9	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.	1.8	231
10	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.	3.6	224
11	Maize root growth angles become steeper under low N conditions. <i>Field Crops Research</i> , 2013, 140, 18-31.	5.1	223
12	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.	7.1	222
13	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.	3.7	218
14	Autophagic Recycling Plays a Central Role in Maize Nitrogen Remobilization. <i>Plant Cell</i> , 2015, 27, 1389-1408.	6.6	211
15	Marker Density and Read Depth for Genotyping Populations Using Genotyping-by-Sequencing. <i>Genetics</i> , 2013, 193, 1073-1081.	2.9	206
16	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.	7.1	197
17	Topsoil foraging and phosphorus acquisition efficiency in maize (<i>Zea mays</i>). <i>Functional Plant Biology</i> , 2005, 32, 749.	2.1	191
18	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	6.6	183

#	ARTICLE	IF	CITATIONS
19	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.	4.8	176
20	Genetic Perturbation of the Maize Methylome. <i>Plant Cell</i> , 2014, 26, 4602-4616.	6.6	158
21	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.	3.6	157
22	Maize (<i>Zea mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e33071.	2.5	153
23	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.	2.5	152
24	Genome-wide association analysis reveals new targets for carotenoid biofortification in maize. <i>Theoretical and Applied Genetics</i> , 2015, 128, 851-864.	3.6	146
25	Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. <i>Plant Genome</i> , 2011, 4, 191-203.	2.8	131
26	The Genetic Architecture of Maize Stalk Strength. <i>PLoS ONE</i> , 2013, 8, e67066.	2.5	129
27	Maize Chromomethylase <i>Zea methyltransferase2</i> Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928.	6.6	120
28	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
29	Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (<i>Mez</i>) homologs. <i>Plant Journal</i> , 2007, 49, 325-337.	5.7	97
30	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.	2.5	96
31	Formation of Heterotic Groups and Understanding Genetic Effects in a Provitamin A Biofortified Maize Breeding Program. <i>Crop Science</i> , 2014, 54, 14-24.	1.8	92
32	Introduction to a Special Issue on Genotype by Environment Interaction. <i>Crop Science</i> , 2016, 56, 2081-2089.	1.8	92
33	The Switchgrass Genome: Tools and Strategies. <i>Plant Genome</i> , 2011, 4, 273-282.	2.8	91
34	Transcriptional and Metabolic Analysis of Senescence Induced by Preventing Pollination in Maize. <i>Plant Physiology</i> , 2012, 159, 1730-1744.	4.8	90
35	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.	3.6	90
36	Induction of maize acid phosphatase activities under phosphorus starvation. <i>Plant and Soil</i> , 2001, 237, 109-115.	3.7	87

#	ARTICLE	IF	CITATIONS
37	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.	1.0	87
38	A robust, high-throughput method for computing maize ear, cob, and kernel attributes automatically from images. <i>Plant Journal</i> , 2017, 89, 169-178.	5.7	86
39	Maize Chromomethylase Zea methyltransferase2 Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928.	6.6	86
40	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.	1.1	85
41	Genetic Diversity of a Maize Association Population with Restricted Phenology. <i>Crop Science</i> , 2011, 51, 704-715.	1.8	81
42	Enhanced maize productivity by inoculation with diazotrophic bacteria. <i>Functional Plant Biology</i> , 2001, 28, 829.	2.1	80
43	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.	3.6	80
44	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.	4.8	79
45	Transgene-Induced RNA Interference as a Tool for Plant Functional Genomics. <i>Methods in Enzymology</i> , 2005, 392, 1-24.	1.0	78
46	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	3.6	77
47	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690.	4.8	76
48	Natural Hybrids and Gene Flow between Upland and Lowland Switchgrass. <i>Crop Science</i> , 2011, 51, 2626-2641.	1.8	76
49	Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. <i>Genetics</i> , 2014, 198, 209-218.	2.9	76
50	Heterosis: Many Genes, Many Mechanisms—End the Search for an Undiscovered Unifying Theory. <i>ISRN Botany</i> , 2012, 2012, 1-12.	0.8	73
51	Defining window-boundaries for genomic analyses using smoothing spline techniques. <i>Genetics Selection Evolution</i> , 2015, 47, 30.	3.0	72
52	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.	2.9	63
53	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989.	6.6	63
54	Evolutionary Divergence of Monocot and Dicot Methyl-CpG-Binding Domain Proteins. <i>Plant Physiology</i> , 2005, 138, 92-104.	4.8	62

#	ARTICLE	IF	CITATIONS
55	TIPS: a system for automated image-based phenotyping of maize tassels. <i>Plant Methods</i> , 2017, 13, 21.	4.3	62
56	Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018, 209, 983-995.	2.9	57
57	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.	1.0	57
58	Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data. <i>New Phytologist</i> , 2017, 213, 154-169.	7.3	56
59	Assessing the Efficiency of RNA Interference for Maize Functional Genomics. <i>Plant Physiology</i> , 2007, 143, 1441-1451.	4.8	55
60	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 2012-2024.	6.8	54
61	Variability of chromosomal DNA contents in maize (<i>Zea mays</i> L.) inbred and hybrid lines. <i>Planta</i> , 2002, 215, 666-671.	3.2	52
62	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
63	Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321.	2.5	51
64	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.	2.9	49
65	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.	3.6	49
66	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	47
67	Evidence for maternal control of seed size in maize from phenotypic and transcriptional analysis. <i>Journal of Experimental Botany</i> , 2016, 67, 1907-1917.	4.8	47
68	DNA methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i> . <i>New Phytologist</i> , 2017, 214, 1213-1229.	7.3	47
69	Root angle in maize influences nitrogen capture and is regulated by calcineurin B-like protein (CBL)-interacting serine/threonine-protein kinase 15 (<i>ZmCIPK15</i>). <i>Plant, Cell and Environment</i> , 2022, 45, 837-853.	5.7	46
70	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <i>Genetics</i> , 2018, 210, 1125-1138.	2.9	45
71	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
72	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.	3.6	43

#	ARTICLE	IF	CITATIONS
73	Diversity and heterotic patterns in North American proprietary dent maize germplasm. <i>Crop Science</i> , 2020, 60, 100-114.	1.8	42
74	Image analysis of anatomical traits in stalk transections of maize and other grasses. <i>Plant Methods</i> , 2015, 11, 26.	4.3	40
75	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.	5.7	39
76	Genetic control of root anatomical plasticity in maize. <i>Plant Genome</i> , 2020, 13, e20003.	2.8	39
77	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	2.9	38
78	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.	1.4	38
79	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.	4.8	37
80	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.	1.8	37
81	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.	2.8	37
82	Genetic control of root architectural plasticity in maize. <i>Journal of Experimental Botany</i> , 2020, 71, 3185-3197.	4.8	37
83	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.	7.1	36
84	Quantitative Trait Locus Mapping for Flowering Time in a Lowland–Upland Switchgrass Pseudo-2 Population. <i>Plant Genome</i> , 2018, 11, 170093.	2.8	35
85	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	35
86	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
87	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	8.8	32
88	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	2.9	31
89	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.	1.8	31
90	Impacts of Agricultural Nitrogen on the Environment and Strategies to Reduce these Impacts. <i>Procedia Environmental Sciences</i> , 2015, 29, 303.	1.4	29

#	ARTICLE	IF	CITATIONS
91	Stover Composition in Maize and Sorghum Reveals Remarkable Genetic Variation and Plasticity for Carbohydrate Accumulation. <i>Frontiers in Plant Science</i> , 2016, 7, 822.	3.6	29
92	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.	4.8	28
93	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.	3.6	28
94	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	3.3	28
95	Genetic Analysis of Cell Wall Traits Relevant to Cellulosic Ethanol Production in Maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2015, 66, 4305-4315.	1.8	26
96	Plant science decadal vision 2020–2030: Reimagining the potential of plants for a healthy and sustainable future. <i>Plant Direct</i> , 2020, 4, e00252.	1.9	26
97	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.	1.4	25
98	Use of near-isogenic lines derived by backcrossing or selfing to map qualitative traits. <i>Theoretical and Applied Genetics</i> , 1993, 87, 233-237.	3.6	23
99	TCUP: A Novel hAT Transposon Active in Maize Tissue Culture. <i>Frontiers in Plant Science</i> , 2012, 3, 6.	3.6	22
100	Genomic Prediction for Winter Survival of Lowland Switchgrass in the Northern USA. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1921-1931.	1.8	22
101	The Scientific Grand Challenges of the 21st Century for the Crop Science Society of America. <i>Crop Science</i> , 2012, 52, 1003-1010.	1.8	21
102	Relative utility of agronomic, phenological, and morphological traits for assessing genotype × environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	1.8	21
103	Genetic Analysis of Sugarcane mosaic virus Resistance in the Wisconsin Diversity Panel of Maize. <i>Crop Science</i> , 2018, 58, 1853-1865.	1.8	20
104	Predicting <i>Zea mays</i> Flowering Time, Yield, and Kernel Dimensions by Analyzing Aerial Images. <i>Frontiers in Plant Science</i> , 2019, 10, 1251.	3.6	20
105	Response to Selection and Genetic Drift in Three Populations Derived from the Golden Glow Maize Population. <i>Crop Science</i> , 2004, 44, 1527-1534.	1.8	19
106	Transcriptional Analysis of Flowering Time in Switchgrass. <i>Bioenergy Research</i> , 2017, 10, 700-713.	3.9	19
107	Quantitative Trait Loci for Freezing Tolerance in a Lowland x Upland Switchgrass Population. <i>Frontiers in Plant Science</i> , 2019, 10, 372.	3.6	19
108	Genetic Fine-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.	2.8	17

#	ARTICLE	IF	CITATIONS
109	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	5.7	16
110	Heterosis: one boat at a time, or a rising tide?. <i>New Phytologist</i> , 2011, 189, 900-902.	7.3	15
111	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331.	4.8	14
112	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
113	Estimation of Maize Yield and Flowering Time Using Multi-Temporal UAV-Based Hyperspectral Data. <i>Remote Sensing</i> , 2022, 14, 3052.	4.0	13
114	Power analysis for quantitative trait locus mapping in populations derived by multiple backcrosses. <i>Theoretical and Applied Genetics</i> , 1997, 95, 618-621.	3.6	12
115	Genetic Control of Prolificacy and Related Traits in the Golden Glow Maize Population: I. Phenotypic Evaluation. <i>Crop Science</i> , 2005, 45, 1361-1369.	1.8	10
116	Lax leaf maize: cell wall composition and nutritional value. <i>Journal of the Science of Food and Agriculture</i> , 2000, 80, 255-262.	3.5	9
117	A high-throughput core sampling device for the evaluation of maize stalk composition. <i>Biotechnology for Biofuels</i> , 2012, 5, 27.	6.2	9
118	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.	3.9	8
119	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.	2.8	8
120	Loss-of-function of DELLA protein SLN1 activates GA signaling in barley aleurone. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 789-800.	2.1	7
121	Conserved Transcriptional Regulatory Programs Underlying Rice and Barley Germination. <i>PLoS ONE</i> , 2014, 9, e87261.	2.5	6
122	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.	4.3	6
123	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.	2.8	6
124	Selection Signatures in Four Lignin Genes from Switchgrass Populations Divergently Selected for In Vitro Dry Matter Digestibility. <i>PLoS ONE</i> , 2016, 11, e0167005.	2.5	5
125	Genetic loci associated with winter survivorship in diverse lowland switchgrass populations. <i>Plant Genome</i> , 2021, 14, e20159.	2.8	5
126	Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. <i>Genetics</i> , 2022, 221, .	2.9	5

#	ARTICLE	IF	CITATIONS
127	Testcross vs. randomly paired singleâ€cross progeny tests for genomic prediction of new inbreds and hybrids derived from multiparent maize populations. <i>Crop Science</i> , 2021, 61, 3425-3435.	1.8	4
128	A novel high-throughput hyperspectral scanner and analytical methods for predicting maize kernel composition and physical traits. <i>Food Chemistry</i> , 2022, 391, 133264.	8.2	4
129	Generating novel plant genetic variation via genome editing to escape the breeding lottery. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2021, 57, 627.	2.1	3
130	Strong parallel evidence of selection during switchgrass sward establishment in hybrid and lowland ecotypes. , 2022, 1, 31-42.		3
131	IntegrateNet: A Deep Learning Network for Maize Stand Counting From UAV Imagery by Integrating Density and Local Count Maps. <i>IEEE Geoscience and Remote Sensing Letters</i> , 2022, 19, 1-5.	3.1	3
132	Registration of the NyH (Ny821Ã—H99) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 101-104.	0.5	2
133	Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2761-2773.	3.6	2
134	Chapter 3 Epigenetics. <i>Advances in Agronomy</i> , 2008, 100, 59-80.	5.2	1
135	Registration of the OhW (Oh43Ã—W64A) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 97-100.	0.5	0
136	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 1922-1922.	6.8	0
137	Maize (<i>Zea Mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. , 2014, , 299-325.		0
138	Chromatin, DNA Methylation, RNAi and Epigenetic Regulation. , 2009, , 441-458.		0