

Shawn M Kaeppler

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

12,169
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29994

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103
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153
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153
docs citations

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times ranked

14223
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| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811. | 9.4 | 816 |
| 2 | Epigenetic aspects of somaclonal variation in plants. <i>Plant Molecular Biology</i> , 2000, 43, 179-188. | 2.0 | 593 |
| 3 | Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807. | 9.4 | 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. | 1.8 | 545 |
| 5 | Genome-wide atlas of transcription during maize development. <i>Plant Journal</i> , 2011, 66, 553-563. | 2.8 | 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. | 3.3 | 509 |
| 7 | Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135. | 3.1 | 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. | 1.6 | 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. | 0.8 | 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. | 1.8 | 224 |
| 11 | Maize root growth angles become steeper under low N conditions. <i>Field Crops Research</i> , 2013, 140, 18-31. | 2.3 | 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. | 3.3 | 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. | 1.8 | 218 |
| 14 | Autophagic Recycling Plays a Central Role in Maize Nitrogen Remobilization. <i>Plant Cell</i> , 2015, 27, 1389-1408. | 3.1 | 211 |
| 15 | Marker Density and Read Depth for Genotyping Populations Using Genotyping-by-Sequencing. <i>Genetics</i> , 2013, 193, 1073-1081. | 1.2 | 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. | 3.3 | 197 |
| 17 | Topsoil foraging and phosphorus acquisition efficiency in maize (<i>Zea mays</i>). <i>Functional Plant Biology</i> , 2005, 32, 749. | 1.1 | 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. | 3.1 | 183 |

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|----|--|-----|-----------|
| 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. | 2.3 | 176 |
| 20 | Genetic Perturbation of the Maize Methylome. <i>Plant Cell</i> , 2014, 26, 4602-4616. | 3.1 | 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. | 1.8 | 157 |
| 22 | Maize (<i>Zea mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e33071. | 1.1 | 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. | 1.1 | 152 |
| 24 | 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 |
| 25 | Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. <i>Plant Genome</i> , 2011, 4, 191-203. | 1.6 | 131 |
| 26 | The Genetic Architecture of Maize Stalk Strength. <i>PLoS ONE</i> , 2013, 8, e67066. | 1.1 | 129 |
| 27 | Maize Chromomethylase <i>Zea methyltransferase2</i> Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928. | 3.1 | 120 |
| 28 | The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348. | 5.8 | 105 |
| 29 | Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (Mez) homologs. <i>Plant Journal</i> , 2007, 49, 325-337. | 2.8 | 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. | 1.1 | 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. | 0.8 | 92 |
| 32 | Introduction to a Special Issue on Genotype by Environment Interaction. <i>Crop Science</i> , 2016, 56, 2081-2089. | 0.8 | 92 |
| 33 | The Switchgrass Genome: Tools and Strategies. <i>Plant Genome</i> , 2011, 4, 273-282. | 1.6 | 91 |
| 34 | Transcriptional and Metabolic Analysis of Senescence Induced by Preventing Pollination in Maize. <i>Plant Physiology</i> , 2012, 159, 1730-1744. | 2.3 | 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. | 1.8 | 90 |
| 36 | Induction of maize acid phosphatase activities under phosphorus starvation. <i>Plant and Soil</i> , 2001, 237, 109-115. | 1.8 | 87 |

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|----|--|-----|-----------|
| 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. | 0.5 | 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. | 2.8 | 86 |
| 39 | Maize Chromomethylase <i>Zea methyltransferase2</i> Is Required for CpNpG Methylation. <i>Plant Cell</i> , 2001, 13, 1919-1928. | 3.1 | 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. | 0.5 | 85 |
| 41 | Genetic Diversity of a Maize Association Population with Restricted Phenology. <i>Crop Science</i> , 2011, 51, 704-715. | 0.8 | 81 |
| 42 | Enhanced maize productivity by inoculation with diazotrophic bacteria. <i>Functional Plant Biology</i> , 2001, 28, 829. | 1.1 | 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. | 1.8 | 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. | 2.3 | 79 |
| 45 | Transgene-Induced RNA Interference as a Tool for Plant Functional Genomics. <i>Methods in Enzymology</i> , 2005, 392, 1-24. | 0.4 | 78 |
| 46 | Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45. | 1.6 | 77 |
| 47 | B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690. | 2.3 | 76 |
| 48 | Natural Hybrids and Gene Flow between Upland and Lowland Switchgrass. <i>Crop Science</i> , 2011, 51, 2626-2641. | 0.8 | 76 |
| 49 | Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. <i>Genetics</i> , 2014, 198, 209-218. | 1.2 | 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. | 1.2 | 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. | 1.2 | 63 |
| 53 | Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989. | 3.1 | 63 |
| 54 | Evolutionary Divergence of Monocot and Dicot Methyl-CpG-Binding Domain Proteins. <i>Plant Physiology</i> , 2005, 138, 92-104. | 2.3 | 62 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | TIPS: a system for automated image-based phenotyping of maize tassels. <i>Plant Methods</i> , 2017, 13, 21. | 1.9 | 62 |
| 56 | Heritable Epigenomic Changes to the Maize Methylome Resulting from Tissue Culture. <i>Genetics</i> , 2018, 209, 983-995. | 1.2 | 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. | 0.5 | 57 |
| 58 | Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data. <i>New Phytologist</i> , 2017, 213, 154-169. | 3.5 | 56 |
| 59 | Assessing the Efficiency of RNA Interference for Maize Functional Genomics. <i>Plant Physiology</i> , 2007, 143, 1441-1451. | 2.3 | 55 |
| 60 | 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 |
| 61 | 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 |
| 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, . | 0.8 | 52 |
| 63 | Genotype-by-environment interactions affecting heterosis in maize. <i>PLoS ONE</i> , 2018, 13, e0191321. | 1.1 | 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. | 1.2 | 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. | 1.8 | 49 |
| 66 | Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815. | 2.8 | 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. | 2.4 | 47 |
| 68 | 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 |
| 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. | 2.8 | 46 |
| 70 | Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <i>Genetics</i> , 2018, 210, 1125-1138. | 1.2 | 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. | 1.1 | 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. | 1.8 | 43 |

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|----|---|-----|-----------|
| 73 | Diversity and heterotic patterns in North American proprietary dent maize germplasm. <i>Crop Science</i> , 2020, 60, 100-114. | 0.8 | 42 |
| 74 | Image analysis of anatomical traits in stalk transections of maize and other grasses. <i>Plant Methods</i> , 2015, 11, 26. | 1.9 | 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. | 2.8 | 39 |
| 76 | Genetic control of root anatomical plasticity in maize. <i>Plant Genome</i> , 2020, 13, e20003. | 1.6 | 39 |
| 77 | Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421. | 1.2 | 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. | 0.6 | 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. | 2.3 | 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. | 0.8 | 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. | 1.6 | 37 |
| 82 | Genetic control of root architectural plasticity in maize. <i>Journal of Experimental Botany</i> , 2020, 71, 3185-3197. | 2.4 | 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. | 3.3 | 36 |
| 84 | Quantitative Trait Locus Mapping for Flowering Time in a Lowland–Upland Switchgrass Pseudo-2 Population. <i>Plant Genome</i> , 2018, 11, 170093. | 1.6 | 35 |
| 85 | Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055. | 1.6 | 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. | 3.8 | 32 |
| 88 | Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760. | 1.2 | 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. | 0.8 | 31 |
| 90 | Impacts of Agricultural Nitrogen on the Environment and Strategies to Reduce these Impacts. <i>Procedia Environmental Sciences</i> , 2015, 29, 303. | 1.3 | 29 |

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|-----|--|-----|-----------|
| 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. | 1.7 | 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. | 2.4 | 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. | 1.8 | 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. | 1.6 | 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. | 0.8 | 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. | 0.8 | 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. | 0.6 | 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. | 1.8 | 23 |
| 99 | TCUP: A Novel hAT Transposon Active in Maize Tissue Culture. <i>Frontiers in Plant Science</i> , 2012, 3, 6. | 1.7 | 22 |
| 100 | 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 |
| 101 | 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 |
| 102 | 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 |
| 103 | Genetic Analysis of Sugarcane mosaic virus Resistance in the Wisconsin Diversity Panel of Maize. <i>Crop Science</i> , 2018, 58, 1853-1865. | 0.8 | 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. | 1.7 | 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. | 0.8 | 19 |
| 106 | Transcriptional Analysis of Flowering Time in Switchgrass. <i>Bioenergy Research</i> , 2017, 10, 700-713. | 2.2 | 19 |
| 107 | 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 |
| 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. | 1.6 | 17 |

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|-----|--|-----|-----------|
| 109 | Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107. | 2.8 | 16 |
| 110 | Heterosis: one boat at a time, or a rising tide?. <i>New Phytologist</i> , 2011, 189, 900-902. | 3.5 | 15 |
| 111 | Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , 2020, 182, 318-331. | 2.3 | 14 |
| 112 | Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114. | 1.6 | 14 |
| 113 | Estimation of Maize Yield and Flowering Time Using Multi-Temporal UAV-Based Hyperspectral Data. <i>Remote Sensing</i> , 2022, 14, 3052. | 1.8 | 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. | 1.8 | 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. | 0.8 | 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. | 1.7 | 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. | 2.2 | 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. | 1.6 | 8 |
| 120 | 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 |
| 121 | Conserved Transcriptional Regulatory Programs Underlying Rice and Barley Germination. <i>PLoS ONE</i> , 2014, 9, e87261. | 1.1 | 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. | 1.9 | 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. | 1.6 | 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. | 1.1 | 5 |
| 125 | Genetic loci associated with winter survivorship in diverse lowland switchgrass populations. <i>Plant Genome</i> , 2021, 14, e20159. | 1.6 | 5 |
| 126 | Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. <i>Genetics</i> , 2022, 221, . | 1.2 | 5 |

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|-----|--|-----|-----------|
| 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. | 0.8 | 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. | 4.2 | 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. | 0.9 | 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. | 1.4 | 3 |
| 132 | Registration of the NyH (Ny821Ã—H99) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 101-104. | 0.4 | 2 |
| 133 | Characterizing introgression-by-environment interactions using maize near isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2761-2773. | 1.8 | 2 |
| 134 | Chapter 3 Epigenetics. <i>Advances in Agronomy</i> , 2008, 100, 59-80. | 2.4 | 1 |
| 135 | Registration of the OhW (Oh43Ã—W64A) Maize Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2016, 10, 97-100. | 0.4 | 0 |
| 136 | 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 |
| 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 |