

Edward S Buckler

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3880087/publications.pdf>

Version: 2024-02-01

231
papers

67,776
citations

2440

100
h-index

1333

229
g-index

288
all docs

288
docs citations

288
times ranked

34873
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Genome-wide imputation using the practical haplotype graph in the heterozygous crop cassava. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 0.8 | 7 |
| 2 | QTL mapping and genomic analyses of earliness and fruit ripening traits in a melon recombinant inbred lines population supported by <i>de novo</i> assembly of their parental genomes. <i>Horticulture Research</i> , 2022, 9, . | 2.9 | 12 |
| 3 | AnchorWave: Sensitive alignment of genomes with high sequence diversity, extensive structural polymorphism, and whole-genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, . | 3.3 | 29 |
| 4 | Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112516119. | 3.3 | 10 |
| 5 | Ten simple rules to ruin a collaborative environment. <i>PLoS Computational Biology</i> , 2022, 18, e1009957. | 1.5 | 1 |
| 6 | A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. <i>Plant Genome</i> , 2022, 15, e20204. | 1.6 | 5 |
| 7 | An adaptive teosinte <i>mexicana</i> introgression modulates phosphatidylcholine levels and is associated with maize flowering time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, . | 3.3 | 21 |
| 8 | Local adaptation contributes to gene expression divergence in maize. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 7 |
| 9 | Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941. | 1.2 | 4 |
| 10 | Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 7 |
| 11 | Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257. | 2.4 | 29 |
| 12 | Underground heterosis for yield improvement in melon. <i>Journal of Experimental Botany</i> , 2021, 72, 6205-6218. | 2.4 | 11 |
| 13 | Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. <i>Nature Plants</i> , 2021, 7, 842-855. | 4.7 | 78 |
| 14 | Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185. | 3.8 | 47 |
| 15 | Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , 2021, 7, 954-965. | 4.7 | 48 |
| 16 | Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , 2021, 187, 1481-1500. | 2.3 | 44 |
| 17 | Predicting phenotypes from genetic, environment, management, and historical data using CNNs. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3997-4011. | 1.8 | 20 |
| 18 | Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562. | 2.3 | 23 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 11 |
| 20 | 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 |
| 21 | Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24. | 4.7 | 52 |
| 22 | Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900. | 3.1 | 31 |
| 23 | Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021, 135, 273. | 1.8 | 4 |
| 24 | Haplotype associated RNA expression (HARE) improves prediction of complex traits in maize. <i>PLoS Genetics</i> , 2021, 17, e1009568. | 1.5 | 5 |
| 25 | A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 1 |
| 26 | Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. <i>PLoS Genetics</i> , 2021, 17, e1009797. | 1.5 | 5 |
| 27 | 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 |
| 28 | Identification of miRNA-eQTLs in maize mature leaf by GWAS. <i>BMC Genomics</i> , 2020, 21, 689. | 1.2 | 6 |
| 29 | Reconstructing the maize leaf regulatory network using ChIP-seq data of 104 transcription factors. <i>Nature Communications</i> , 2020, 11, 5089. | 5.8 | 111 |
| 30 | Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 769-781. | 0.8 | 25 |
| 31 | Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , 2020, 6, 1375-1388. | 4.7 | 52 |
| 32 | Building a tRNA thermometer to estimate microbial adaptation to temperature. <i>Nucleic Acids Research</i> , 2020, 48, 12004-12015. | 6.5 | 9 |
| 33 | Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future Directions. <i>Plant Cell</i> , 2020, 32, 2083-2093. | 3.1 | 81 |
| 34 | The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020, 16, e1008791. | 1.5 | 27 |
| 35 | Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. <i>Plant Genome</i> , 2020, 13, e20008. | 1.6 | 34 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Deep learning for plant genomics and crop improvement. <i>Current Opinion in Plant Biology</i> , 2020, 54, 34-41. | 3.5 | 108 |
| 38 | A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009. | 1.6 | 54 |
| 39 | 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 |
| 40 | Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020, 215, 215-230. | 1.2 | 35 |
| 41 | The multi-allelic APRR2 gene is associated with fruit pigment accumulation in melon and watermelon. <i>Journal of Experimental Botany</i> , 2019, 70, 3781-3794. | 2.4 | 84 |
| 42 | A k-mer grammar analysis to uncover maize regulatory architecture. <i>BMC Plant Biology</i> , 2019, 19, 103. | 1.6 | 35 |
| 43 | Evolutionarily informed deep learning methods for predicting relative transcript abundance from DNA sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5542-5549. | 3.3 | 121 |
| 44 | The genetic architecture of teosinte catalyzed and constrained maize domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5643-5652. | 3.3 | 59 |
| 45 | Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Maize Specialized Metabolites. <i>Plant Cell</i> , 2019, 31, 937-955. | 3.1 | 75 |
| 46 | Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3023-3033. | 0.8 | 64 |
| 47 | Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249. | 4.7 | 250 |
| 48 | In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , 2019, 2, 1-11. | 1.0 | 23 |
| 49 | Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056. | 4.7 | 60 |
| 50 | Breaking the curse of dimensionality to identify causal variants in Breeding 4. <i>Theoretical and Applied Genetics</i> , 2019, 132, 559-567. | 1.8 | 68 |
| 51 | Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (<i>Sorghum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1.2 51 | 1.2 | 51 |
| 52 | Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038. | 1.6 | 37 |
| 53 | Ethylene signaling regulates natural variation in the abundance of antifungal acetylated diferuloylsucroses and <i>Fusarium graminearum</i> resistance in maize seedling roots. <i>New Phytologist</i> , 2019, 221, 2096-2111. | 3.5 | 42 |
| 54 | Diverse Chromosomal Locations of Quantitative Trait Loci for Tolerance to Maize chlorotic mottle virus in Five Maize Populations. <i>Phytopathology</i> , 2018, 108, 748-758. | 1.1 | 26 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , 2018, 7, 1-12. | 3.3 | 191 |
| 56 | Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. <i>Scientific Reports</i> , 2018, 8, 6848. | 1.6 | 16 |
| 57 | Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. <i>Nature</i> , 2018, 555, 520-523. | 13.7 | 211 |
| 58 | Quantitative Genetics of the Maize Leaf Microbiome. <i>Phytobiomes Journal</i> , 2018, 2, 208-224. | 1.4 | 110 |
| 59 | A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , 2018, 1, 1-13. | 1.0 | 7 |
| 60 | <i>Tripsacum</i> De novo Transcriptome Assemblies Reveal Parallel Gene Evolution with Maize after Ancient Polyploidy. <i>Plant Genome</i> , 2018, 11, 180012. | 1.6 | 9 |
| 61 | On the Road to Breeding 4.0: Unraveling the Good, the Bad, and the Boring of Crop Quantitative Genomics. <i>Annual Review of Genetics</i> , 2018, 52, 421-444. | 3.2 | 182 |
| 62 | Coregulation of ribosomal RNA with hundreds of genes contributes to phenotypic variation. <i>Genome Research</i> , 2018, 28, 1555-1565. | 2.4 | 16 |
| 63 | Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018, 121, 648-662. | 1.2 | 53 |
| 64 | Large-scale replicated field study of maize rhizosphere identifies heritable microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7368-7373. | 3.3 | 435 |
| 65 | The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288. | 9.4 | 183 |
| 66 | Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295. | 9.4 | 335 |
| 67 | 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 |
| 68 | A study of allelic diversity underlying flowering-time adaptation in maize landraces. <i>Nature Genetics</i> , 2017, 49, 476-480. | 9.4 | 254 |
| 69 | Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. <i>Nature Genetics</i> , 2017, 49, 959-963. | 9.4 | 208 |
| 70 | Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2315-2326. | 0.8 | 92 |
| 71 | Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12231-12236. | 3.3 | 91 |
| 72 | Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392. | 3.1 | 93 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976. | 9.4 | 356 |
| 74 | Patterns of genomic and phenomic diversity in wine and table grapes. <i>Horticulture Research</i> , 2017, 4, 17035. | 2.9 | 87 |
| 75 | Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515. | 6.0 | 169 |
| 76 | The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348. | 5.8 | 105 |
| 77 | Maize <i>YABBY</i> Genes <i>drooping leaf1</i> and <i>drooping leaf2</i> Regulate Plant Architecture. <i>Plant Cell</i> , 2017, 29, 1622-1641. | 3.1 | 128 |
| 78 | Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize. <i>PLoS Genetics</i> , 2017, 13, e1007019. | 1.5 | 136 |
| 79 | Non-Mendelian Single Nucleotide Polymorphism Inheritance and Atypical Meiotic Configurations are Prevalent in Hop. <i>Plant Genome</i> , 2017, 10, plantgenome2017.04.0032. | 1.6 | 20 |
| 80 | Correlation-Based Network Analysis of Metabolite and Enzyme Profiles Reveals a Role of Citrate Biosynthesis in Modulating N and C Metabolism in <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1022. | 1.7 | 20 |
| 81 | Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. <i>Plant Journal</i> , 2016, 86, 391-402. | 2.8 | 122 |
| 82 | Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1775-1784. | 1.8 | 9 |
| 83 | Development of a High-Density Linkage Map and Tagging Leaf Spot Resistance in Pearl Millet Using Genotyping-by-Sequencing Markers. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0106. | 1.6 | 20 |
| 84 | Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. <i>BMC Genomics</i> , 2016, 17, 894. | 1.2 | 63 |
| 85 | Genome-wide Association for Plant Height and Flowering Time across 15 Tropical Maize Populations under Managed Drought Stress and Well-Watered Conditions in Sub-Saharan Africa. <i>Crop Science</i> , 2016, 56, 2365-2378. | 0.8 | 88 |
| 86 | GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0120. | 1.6 | 421 |
| 87 | Open chromatin reveals the functional maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3177-84. | 3.3 | 233 |
| 88 | Genome-wide association mapping of provitamin A carotenoid content in cassava. <i>Euphytica</i> , 2016, 212, 97-110. | 0.6 | 36 |
| 89 | Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . <i>Plant Cell</i> , 2016, 28, 2651-2665. | 3.1 | 105 |
| 90 | Fast-Flowering Mini-Maize: Seed to Seed in 60 Days. <i>Genetics</i> , 2016, 204, 35-42. | 1.2 | 25 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | 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 |
| 92 | Biosynthesis of 8-O-methylated benzoxazinoid defense compounds in maize. <i>Plant Cell</i> , 2016, 28, tpc.00065.2016. | 3.1 | 87 |
| 93 | Joint linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. <i>Plant Biotechnology Journal</i> , 2016, 14, 1551-1562. | 4.1 | 121 |
| 94 | A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , 2016, 28, 606-609. | 3.1 | 31 |
| 95 | Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005767. | 1.5 | 1,095 |
| 96 | Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015, 13, 78. | 1.7 | 40 |
| 97 | The Genetic Makeup of a Global Barnyard Millet Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0067. | 1.6 | 36 |
| 98 | Population Genetics and Structure of a Global Foxtail Millet Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.07.0054. | 1.6 | 28 |
| 99 | Genetic mapping in grapevine using SNP microarray intensity values. <i>Molecular Breeding</i> , 2015, 35, 1. | 1.0 | 17 |
| 100 | Genome-Wide Association Study Based on Multiple Imputation with Low-Depth Sequencing Data: Application to Biofuel Traits in Reed Canarygrass. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 891-909. | 0.8 | 10 |
| 101 | Genome-environment associations in sorghum landraces predict adaptive traits. <i>Science Advances</i> , 2015, 1, e1400218. | 4.7 | 257 |
| 102 | Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , 2015, 114, 291-299. | 1.2 | 187 |
| 103 | Genome-Wide Association of Carbon and Nitrogen Metabolism in the Maize Nested Association Mapping Population. <i>Plant Physiology</i> , 2015, 168, 575-583. | 2.3 | 80 |
| 104 | High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015, 6, 6914. | 5.8 | 213 |
| 105 | Accumulation of 5-hydroxynorvaline in maize (<i>Zea mays</i>) leaves is induced by insect feeding and abiotic stress. <i>Journal of Experimental Botany</i> , 2015, 66, 593-602. | 2.4 | 36 |
| 106 | Recombination in diverse maize is stable, predictable, and associated with genetic load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3823-3828. | 3.3 | 210 |
| 107 | Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312. | 1.2 | 67 |
| 108 | Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. <i>PLoS ONE</i> , 2015, 10, e0121624. | 1.1 | 69 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 109 | A SUPER Powerful Method for Genome Wide Association Study. PLoS ONE, 2014, 9, e107684. | 1.1 | 289 |
| 110 | Accelerating the Switchgrass (<i>Panicum virgatum</i> L.) Breeding Cycle Using Genomic Selection Approaches. PLoS ONE, 2014, 9, e112227. | 1.1 | 65 |
| 111 | A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. Plant Physiology, 2014, 164, 259-272. | 2.3 | 233 |
| 112 | Association Mapping across Numerous Traits Reveals Patterns of Functional Variation in Maize. PLoS Genetics, 2014, 10, e1004845. | 1.5 | 171 |
| 113 | TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline. PLoS ONE, 2014, 9, e90346. | 1.1 | 1,511 |
| 114 | Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. BMC Plant Biology, 2014, 14, 372. | 1.6 | 85 |
| 115 | Enrichment of statistical power for genome-wide association studies. BMC Biology, 2014, 12, 73. | 1.7 | 160 |
| 116 | The Genetic Architecture Of Maize Height. Genetics, 2014, 196, 1337-1356. | 1.2 | 329 |
| 117 | Entering the second century of maize quantitative genetics. Heredity, 2014, 112, 30-38. | 1.2 | 142 |
| 118 | Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. Genetics, 2014, 198, 409-421. | 1.2 | 38 |
| 119 | A Foundation for Provitamin A Biofortification of Maize: Genome-Wide Association and Genomic Prediction Models of Carotenoid Levels. Genetics, 2014, 198, 1699-1716. | 1.2 | 180 |
| 120 | Novel Methods to Optimize Genotypic Imputation for Lowâ€œCoverage, Nextâ€œGeneration Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023. | 1.6 | 241 |
| 121 | Comprehensive genotyping of the USA national maize inbred seed bank. Genome Biology, 2013, 14, R55. | 3.8 | 458 |
| 122 | Mining conifersâ€™ mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. Tree Genetics and Genomes, 2013, 9, 1537-1544. | 0.6 | 54 |
| 123 | Diversity and heritability of the maize rhizosphere microbiome under field conditions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6548-6553. | 3.3 | 1,594 |
| 124 | Feeding the future. Nature, 2013, 499, 23-24. | 13.7 | 464 |
| 125 | Population genomic and genome-wide association studies of agroclimatic traits in sorghum. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 453-458. | 3.3 | 743 |
| 126 | Switchgrass Genomic Diversity, Ploidy, and Evolution: Novel Insights from a Network-Based SNP Discovery Protocol. PLoS Genetics, 2013, 9, e1003215. | 1.5 | 608 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Lessons from Dwarf8 on the Strengths and Weaknesses of Structured Association Mapping. <i>PLoS Genetics</i> , 2013, 9, e1003246. | 1.5 | 115 |
| 128 | Genome-Wide Association Study and Pathway-Level Analysis of Tocochromanol Levels in Maize Grain. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1287-1299. | 0.8 | 152 |
| 129 | Dissecting Genome-Wide Association Signals for Loss-of-Function Phenotypes in Sorghum Flavonoid Pigmentation Traits. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2085-2094. | 0.8 | 65 |
| 130 | Natural Variation in Maize Aphid Resistance Is Associated with 2,4-Dihydroxy-7-Methoxy-1,4-Benzoxazin-3-One Glucoside Methyltransferase Activity. <i>Plant Cell</i> , 2013, 25, 2341-2355. | 3.1 | 251 |
| 131 | Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5241-5246. | 3.3 | 265 |
| 132 | Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200. | 0.8 | 66 |
| 133 | The Genetic Architecture of Maize Stalk Strength. <i>PLoS ONE</i> , 2013, 8, e67066. | 1.1 | 129 |
| 134 | Vitis Phylogenomics: Hybridization Intensities from a SNP Array Outperform Genotype Calls. <i>PLoS ONE</i> , 2013, 8, e78680. | 1.1 | 55 |
| 135 | Genomics Assisted Ancestry Deconvolution in Grape. <i>PLoS ONE</i> , 2013, 8, e80791. | 1.1 | 43 |
| 136 | <i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1913-21. | 3.3 | 290 |
| 137 | The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , 2012, 108, 490-499. | 1.2 | 128 |
| 138 | Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444. | 2.4 | 125 |
| 139 | Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012, 30, 1172-1176. | 9.4 | 248 |
| 140 | GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399. | 1.8 | 2,016 |
| 141 | Genetic Architecture of Maize Kernel Composition in the Nested Association Mapping and Inbred Association Panels. <i>Plant Physiology</i> , 2012, 158, 824-834. | 2.3 | 307 |
| 142 | Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807. | 9.4 | 577 |
| 143 | SNP Discovery with EST and NextGen Sequencing in Switchgrass (<i>Panicum virgatum</i> L.). <i>PLoS ONE</i> , 2012, 7, e44112. | 1.1 | 16 |
| 144 | PICARA, an Analytical Pipeline Providing Probabilistic Inference about A Priori Candidates Genes Underlying Genome-Wide Association QTL in Plants. <i>PLoS ONE</i> , 2012, 7, e46596. | 1.1 | 23 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811. | 9.4 | 816 |
| 146 | Crop genomics: advances and applications. <i>Nature Reviews Genetics</i> , 2012, 13, 85-96. | 7.7 | 439 |
| 147 | Genetic structure and domestication history of the grape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3530-3535. | 3.3 | 684 |
| 148 | Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6893-6898. | 3.3 | 350 |
| 149 | Joint QTL Linkage Mapping for Multiple-Cross Mating Design Sharing One Common Parent. <i>PLoS ONE</i> , 2011, 6, e17573. | 1.1 | 102 |
| 150 | Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 159-162. | 9.4 | 987 |
| 151 | Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 163-168. | 9.4 | 553 |
| 152 | Population genetics of genomics-based crop improvement methods. <i>Trends in Genetics</i> , 2011, 27, 98-106. | 2.9 | 230 |
| 153 | A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. <i>PLoS ONE</i> , 2011, 6, e19379. | 1.1 | 5,470 |
| 154 | Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. <i>PLoS Genetics</i> , 2011, 7, e1002383. | 1.5 | 231 |
| 155 | Genetic association mapping identifies single nucleotide polymorphisms in genes that affect abscisic acid levels in maize floral tissues during drought. <i>Journal of Experimental Botany</i> , 2011, 62, 701-716. | 2.4 | 110 |
| 156 | A Large Maize (<i>Zea mays</i> L.) SNP Genotyping Array: Development and Germplasm Genotyping, and Genetic Mapping to Compare with the B73 Reference Genome. <i>PLoS ONE</i> , 2011, 6, e28334. | 1.1 | 523 |
| 157 | Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360. | 9.4 | 2,022 |
| 158 | Rare genetic variation at <i>Zea mays crtRB1</i> increases β -carotene in maize grain. <i>Nature Genetics</i> , 2010, 42, 322-327. | 9.4 | 421 |
| 159 | Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , 2010, 42, 961-967. | 9.4 | 1,978 |
| 160 | The Gramene Genetic Diversity Module: a resource for genotype-phenotype association analysis in grass species. <i>Nature Precedings</i> , 2010, , . | 0.1 | 3 |
| 161 | Rapid Genomic Characterization of the Genus <i>Vitis</i> . <i>PLoS ONE</i> , 2010, 5, e8219. | 1.1 | 203 |
| 162 | Association and Linkage Analysis of Aluminum Tolerance Genes in Maize. <i>PLoS ONE</i> , 2010, 5, e9958. | 1.1 | 91 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | Genetic Analysis of Central Carbon Metabolism Unveils an Amino Acid Substitution That Alters Maize NAD-Dependent Isocitrate Dehydrogenase Activity. <i>PLoS ONE</i> , 2010, 5, e9991. | 1.1 | 30 |
| 164 | Genome Size Variation in Switchgrass (<i>Panicum virgatum</i>): Flow Cytometry and Cytology Reveal Rampant Aneuploidy. <i>Plant Genome</i> , 2010, 3, . | 1.6 | 77 |
| 165 | Increased Food and Ecosystem Security via Perennial Grains. <i>Science</i> , 2010, 328, 1638-1639. | 6.0 | 397 |
| 166 | Fine Quantitative Trait Loci Mapping of Carbon and Nitrogen Metabolism Enzyme Activities and Seedling Biomass in the Maize IBM Mapping Population Å Å. <i>Plant Physiology</i> , 2010, 154, 1753-1765. | 2.3 | 58 |
| 167 | Perennial Questions of Hydrology and Climate Response. <i>Science</i> , 2010, 330, 33-34. | 6.0 | 1 |
| 168 | Large Scale Discovery of Gene Enriched SNPs. <i>Plant Genome</i> , 2009, 2, . | 1.6 | 55 |
| 169 | Heterosis Is Prevalent for Multiple Traits in Diverse Maize Germplasm. <i>PLoS ONE</i> , 2009, 4, e7433. | 1.1 | 173 |
| 170 | Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202. | 3.1 | 786 |
| 171 | Tracking footprints of maize domestication and evidence for a massive selective sweep on chromosome 10. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9979-9986. | 3.3 | 133 |
| 172 | Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , 2009, 10, 664-675. | 3.2 | 96 |
| 173 | Genetic Characterization and Linkage Disequilibrium Estimation of a Global Maize Collection Using SNP Markers. <i>PLoS ONE</i> , 2009, 4, e8451. | 1.1 | 338 |
| 174 | Discovery and mapping of single feature polymorphisms in wheat using Affymetrix arrays. <i>BMC Genomics</i> , 2009, 10, 251. | 1.2 | 34 |
| 175 | Natural variation in maize architecture is mediated by allelic differences at the PINOID co ortholog <i>barren inflorescence2</i> . <i>Plant Journal</i> , 2009, 58, 618-628. | 2.8 | 36 |
| 176 | A First-Generation Haplotype Map of Maize. <i>Science</i> , 2009, 326, 1115-1117. | 6.0 | 747 |
| 177 | Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 173-195. | 0.2 | 41 |
| 178 | Genetic Properties of the Maize Nested Association Mapping Population. <i>Science</i> , 2009, 325, 737-740. | 6.0 | 959 |
| 179 | The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718. | 6.0 | 1,284 |
| 180 | Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. <i>Plant Genome</i> , 2009, 2, . | 1.6 | 66 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 181 | Genetic Design and Statistical Power of Nested Association Mapping in Maize. <i>Genetics</i> , 2008, 178, 539-551. | 1.2 | 939 |
| 182 | Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008, 1, . | 1.6 | 1,118 |
| 183 | Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754. | 1.2 | 273 |
| 184 | Natural Genetic Variation in <i>Lycopene Epsilon Cyclase</i> Tapped for Maize Biofortification. <i>Science</i> , 2008, 319, 330-333. | 6.0 | 692 |
| 185 | The Genetic Architecture of Complex Traits in Teosinte (<i>Zea mays</i> ssp. <i>parviglumis</i>): New Evidence From Association Mapping. <i>Genetics</i> , 2008, 180, 1221-1232. | 1.2 | 73 |
| 186 | Using Crossover Breakpoints in Recombinant Inbred Lines to Identify Quantitative Trait Loci Controlling the Global Recombination Frequency. <i>Genetics</i> , 2007, 177, 1851-1858. | 1.2 | 53 |
| 187 | TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007, 23, 2633-2635. | 1.8 | 6,407 |
| 188 | Panzea: an update on new content and features. <i>Nucleic Acids Research</i> , 2007, 36, D1041-D1043. | 6.5 | 30 |
| 189 | Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. <i>Genetics</i> , 2007, 176, 563-570. | 1.2 | 43 |
| 190 | Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. , 2007, , 97-119. | | 95 |
| 191 | Empirical Comparison of Simple Sequence Repeats and Single Nucleotide Polymorphisms in Assessment of Maize Diversity and Relatedness. <i>PLoS ONE</i> , 2007, 2, e1367. | 1.1 | 204 |
| 192 | Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood. <i>Journal of Animal Science</i> , 2007, 85, 881-885. | 0.2 | 58 |
| 193 | Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , 2007, 47, S-135. | 0.8 | 36 |
| 194 | An Arabidopsis haplotype map takes root. <i>Nature Genetics</i> , 2007, 39, 1056-1057. | 9.4 | 32 |
| 195 | Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , 2007, 36, D947-D953. | 6.5 | 151 |
| 196 | Recurrent Mutation and Genome Evolution: Example of <i>Sugary1</i> and the Origin of Sweet Maize. <i>Crop Science</i> , 2006, 46, S-49. | 0.8 | 38 |
| 197 | 4. Maize Origins, Domestication, and Selection. , 2006, , 67-90. | | 30 |
| 198 | Genetic diversity contribution to errors in short oligonucleotide microarray analysis. <i>Plant Biotechnology Journal</i> , 2006, 4, 060615010054001-???. | 4.1 | 26 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 199 | A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006, 38, 203-208. | 9.4 | 3,622 |
| 200 | Genetic association mapping and genome organization of maize. <i>Current Opinion in Biotechnology</i> , 2006, 17, 155-160. | 3.3 | 869 |
| 201 | Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723. | 6.5 | 177 |
| 202 | Molecular and functional diversity of maize. <i>Current Opinion in Plant Biology</i> , 2006, 9, 172-176. | 3.5 | 201 |
| 203 | Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , 2006, 34, D752-D757. | 6.5 | 89 |
| 204 | Genetic and Biochemical Analysis of Iron Bioavailability in Maize. <i>FASEB Journal</i> , 2006, 20, A623. | 0.2 | 2 |
| 205 | Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005, 44, 1054-1064. | 2.8 | 821 |
| 206 | Architecture of floral branch systems in maize and related grasses. <i>Nature</i> , 2005, 436, 1119-1126. | 13.7 | 348 |
| 207 | Association analysis of candidate genes for maysin and chlorogenic acid accumulation in maize silks. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1324-1333. | 1.8 | 124 |
| 208 | Genetic Diversity and Population Structure of Teosinte. <i>Genetics</i> , 2005, 169, 2241-2254. | 1.2 | 182 |
| 209 | GDPC: connecting researchers with multiple integrated data sources. <i>Bioinformatics</i> , 2004, 20, 2839-2840. | 1.8 | 9 |
| 210 | The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137. | 9.4 | 1,034 |
| 211 | Dissection of Maize Kernel Composition and Starch Production by Candidate Gene Association. <i>Plant Cell</i> , 2004, 16, 2719-2733. | 3.1 | 291 |
| 212 | Development of a Maize Molecular Evolutionary Genomic Database. <i>Comparative and Functional Genomics</i> , 2003, 4, 246-249. | 2.0 | 5 |
| 213 | Structure of Linkage Disequilibrium in Plants. <i>Annual Review of Plant Biology</i> , 2003, 54, 357-374. | 8.6 | 1,456 |
| 214 | Early Allelic Selection in Maize as Revealed by Ancient DNA. <i>Science</i> , 2003, 302, 1206-1208. | 6.0 | 287 |
| 215 | Using Natural Allelic Diversity to Evaluate Gene Function. , 2003, 236, 123-140. | | 60 |
| 216 | Genetic diversity and selection in the maize starch pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12959-12962. | 3.3 | 298 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 217 | A single domestication for maize shown by multilocus microsatellite genotyping. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6080-6084. | 3.3 | 1,143 |
| 218 | Plant molecular diversity and applications to genomics. Current Opinion in Plant Biology, 2002, 5, 107-111. | 3.5 | 333 |
| 219 | Quantitative trait loci analysis of growth response to varying nitrogen sources in Arabidopsis thaliana. Theoretical and Applied Genetics, 2002, 104, 743-750. | 1.8 | 78 |
| 220 | Molecular Diversity, Structure and Domestication of Grasses. Genetical Research, 2001, 77, 213-8. | 0.3 | 262 |
| 221 | Genetic Evidence and the Origin of Maize. Latin American Antiquity, 2001, 12, 84-86. | 0.3 | 39 |
| 222 | Dwarf8 polymorphisms associate with variation in flowering time. Nature Genetics, 2001, 28, 286-289. | 9.4 | 960 |
| 223 | Structure of linkage disequilibrium and phenotypic associations in the maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11479-11484. | 3.3 | 1,060 |
| 224 | Patterns of molecular evolution among paralogous floral homeotic genes. Molecular Biology and Evolution, 1999, 16, 1037-1045. | 3.5 | 30 |
| 225 | Molecular Evolution of Type 1 Serine/Threonine Protein Phosphatases. Molecular Phylogenetics and Evolution, 1999, 12, 57-66. | 1.2 | 61 |
| 226 | Meiotic Drive of Chromosomal Knobs Reshaped the Maize Genome. Genetics, 1999, 153, 415-426. | 1.2 | 173 |
| 227 | Climate, Plant Ecology, and Central Mexican Archaic Subsistence. Current Anthropology, 1998, 39, 152-164. | 0.8 | 49 |
| 228 | The Evolution of Ribosomal DNA Divergent Paralogues and Phylogenetic Implications. Genetics, 1997, 145, 821-832. | 1.2 | 463 |
| 229 | Zea systematics: ribosomal ITS evidence. Molecular Biology and Evolution, 1996, 13, 612-622. | 3.5 | 202 |
| 230 | A Hierarchical View of Genetic Structure in the Rare Annual Plant Clarkia springvillensis. Conservation Biology, 1996, 10, 1425-1434. | 2.4 | 19 |
| 231 | Zea ribosomal repeat evolution and substitution patterns. Molecular Biology and Evolution, 1996, 13, 623-632. | 3.5 | 98 |