

# Edward S Buckler

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

257  
papers

47,478  
citations

92  
h-index

217  
g-index

288  
ext. papers

61,276  
ext. citations

10.7  
avg, IF

7.34  
L-index

#	Paper	IF	Citations
257	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> , <b>2022</b> , 119,	11.5	2
256	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> , <b>2022</b> , 119, e2112516119	11.5	1
255	Ten simple rules to ruin a collaborative environment.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009957	5	0
254	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants.. <i>Plant Genome</i> , <b>2022</b> , e20204	4.4	0
253	Genome-wide Imputation Using the Practical Haplotype Graph in the Heterozygous Crop Cassava. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> ,	3.2	1
252	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 135, 273	6	0
251	Haplotype associated RNA expression (HARE) improves prediction of complex traits in maize. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009568	6	0
250	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , <b>2021</b> , 33, 882-900	11.6	3
249	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , <b>2021</b> , 126, 929-941	3.6	1
248	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> , <b>2021</b> , 11,	3.2	2
247	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , <b>2021</b> ,	9.7	5
246	Underground heterosis for yield improvement in melon. <i>Journal of Experimental Botany</i> , <b>2021</b> , 72, 6205-6218	3	
245	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. <i>Nature Plants</i> , <b>2021</b> , 7, 842-855	11.5	7
244	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , <b>2021</b> , 22, 185	18.3	9
243	Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , <b>2021</b> , 7, 954-965	11.5	5
242	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , <b>2021</b> , 187, 1481-1500	6.6	3
241	Local adaptation contributes to gene expression divergence in maize. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	1

240	Predicting phenotypes from genetic, environment, management, and historical data using CNNs. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 3997-4011	6	0
239	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , <b>2021</b> , 187, 2544-2562	6.6	3
238	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
237	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> , <b>2021</b> , 11,	3.2	12
236	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , <b>2021</b> , 7, 17-24	11.5	12
235	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte.. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009797	6	1
234	Building a tRNA thermometer to estimate microbial adaptation to temperature. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 12004-12015	20.1	2
233	Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future Directions. <i>Plant Cell</i> , <b>2020</b> , 32, 2083-2093	11.6	33
232	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008791	6	17
231	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. <i>Plant Genome</i> , <b>2020</b> , 13, e20008	4.4	17
230	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2020</b> , 13, 71	2.3	16
229	Deep learning for plant genomics and crop improvement. <i>Current Opinion in Plant Biology</i> , <b>2020</b> , 54, 34-41	19	50
228	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , <b>2020</b> , 13, e20009	4.4	24
227	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , <b>2020</b> , 215, 215-230	4	12
226	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , <b>2020</b> , 60, 62-81	2.4	7
225	Identification of miRNA-eQTLs in maize mature leaf by GWAS. <i>BMC Genomics</i> , <b>2020</b> , 21, 689	4.5	1
224	Reconstructing the maize leaf regulatory network using ChIP-seq data of 104 transcription factors. <i>Nature Communications</i> , <b>2020</b> , 11, 5089	17.4	34
223	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 769-781	3.2	10

222	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , <b>2020</b> , 6, 1375-1388	11.5	23
221	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> , <b>2020</b> , 11, 592769	4.5	11
220	The multi-allelic APRR2 gene is associated with fruit pigment accumulation in melon and watermelon. <i>Journal of Experimental Botany</i> , <b>2019</b> , 70, 3781-3794	7	33
219	A k-mer grammar analysis to uncover maize regulatory architecture. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 103	5.3	18
218	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> , <b>2019</b> , 116, 5542-5549	11.5	56
217	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> , <b>2019</b> , 116, 5643-5652	11.5	34
216	Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Maize Specialized Metabolites. <i>Plant Cell</i> , <b>2019</b> , 31, 937-955	11.6	41
215	Transcriptome-Wide Association Supplements Genome-Wide Association in. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 3023-3033	3.2	28
214	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , <b>2019</b> , 5, 1237-1249	11.5	127
213	In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , <b>2019</b> , 2, 1-11	5	11
212	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , <b>2019</b> , 5, 1043-1056	11.5	36
211	Breaking the curse of dimensionality to identify causal variants in Breeding 4. <i>Theoretical and Applied Genetics</i> , <b>2019</b> , 132, 559-567	6	36
210	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (). <i>Genetics</i> , <b>2019</b> , 211, 1075-1087	4	27
209	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , <b>2019</b> , 12, 180038	4.4	20
208	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> , <b>2019</b> , 221, 2096-2111	9.8	26
207	Diverse Chromosomal Locations of Quantitative Trait Loci for Tolerance to Maize chlorotic mottle virus in Five Maize Populations. <i>Phytopathology</i> , <b>2018</b> , 108, 748-758	3.8	14
206	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , <b>2018</b> , 7, 1-12	7.6	127
205	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. <i>Scientific Reports</i> , <b>2018</b> , 8, 6848	4.9	9

204	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. <i>Nature</i> , <b>2018</b> , 555, 520-523	50.4	124
203	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , <b>2018</b> , 50, 1282-1288	36.3	114
202	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , <b>2018</b> , 50, 1289-1295	36.3	201
201	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2018</b> , 11, 452	2.3	16
200	Quantitative Genetics of the Maize Leaf Microbiome. <i>Phytobiomes Journal</i> , <b>2018</b> , 2, 208-224	4.8	65
199	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , <b>2018</b> , 1, 1-13	5	5
198	De novo Transcriptome Assemblies Reveal Parallel Gene Evolution with Maize after Ancient Polyploidy. <i>Plant Genome</i> , <b>2018</b> , 11, 180012	4.4	4
197	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> , <b>2018</b> , 52, 421-444	14.5	87
196	Coregulation of ribosomal RNA with hundreds of genes contributes to phenotypic variation. <i>Genome Research</i> , <b>2018</b> , 28, 1555-1565	9.7	10
195	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , <b>2018</b> , 121, 648-662	3.6	34
194	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> , <b>2018</b> , 115, 7368-7373	11.5	230
193	A study of allelic diversity underlying flowering-time adaptation in maize landraces. <i>Nature Genetics</i> , <b>2017</b> , 49, 476-480	36.3	155
192	Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. <i>Nature Genetics</i> , <b>2017</b> , 49, 959-963	36.3	118
191	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 2315-2326	3.2	47
190	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> , <b>2017</b> , 114, 12231-12236	11.5	59
189	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , <b>2017</b> , 29, 2374-2392	11.6	57
188	Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007019	6	74
187	Non-Mendelian Single-Nucleotide Polymorphism Inheritance and Atypical Meiotic Configurations are Prevalent in Hop. <i>Plant Genome</i> , <b>2017</b> , 10, plantgenome2017.04.0032	4.4	12

186	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 969-976	44.5	197
185	Patterns of genomic and phenomic diversity in wine and table grapes. <i>Horticulture Research</i> , <b>2017</b> , 4, 17035	7.7	40
184	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , <b>2017</b> , 357, 512-515	33.3	110
183	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , <b>2017</b> , 8, 1348	17.4	58
182	Maize Genes and Regulate Plant Architecture. <i>Plant Cell</i> , <b>2017</b> , 29, 1622-1641	11.6	69
181	Fast-Flowering Mini-Maize: Seed to Seed in 60 Days. <i>Genetics</i> , <b>2016</b> , 204, 35-42	4	19
180	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , <b>2016</b> , 28, 2700-2714	11.6	139
179	Biosynthesis of 8-O-Methylated Benzoxazinoid Defense Compounds in Maize. <i>Plant Cell</i> , <b>2016</b> , 28, 1682-1700	11.6	63
178	Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. <i>Plant Biotechnology Journal</i> , <b>2016</b> , 14, 1551-62	11.6	64
177	A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , <b>2016</b> , 28, 606-9	11.6	25
176	Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005767	6	469
175	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> , <b>2016</b> , 7, 1022	6.2	15
174	Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. <i>Plant Journal</i> , <b>2016</b> , 86, 391-402	6.9	79
173	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> , <b>2016</b> , 129, 1775-84	6	9
172	Development of a High-Density Linkage Map and Tagging Leaf Spot Resistance in Pearl Millet Using Genotyping-by-Sequencing Markers. <i>Plant Genome</i> , <b>2016</b> , 9, plantgenome2015.10.0106	4.4	18
171	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. <i>BMC Genomics</i> , <b>2016</b> , 17, 894	4.5	31
170	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> , <b>2016</b> , 56, 2365-2378	2.4	45
169	GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. <i>Plant Genome</i> , <b>2016</b> , 9, plantgenome2015.11.0120	4.4	198

168	Open chromatin reveals the functional maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E3177-84	11.5	169
167	Genome-wide association mapping of provitamin A carotenoid content in cassava. <i>Euphytica</i> , <b>2016</b> , 212, 97-110	2.1	27
166	Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . <i>Plant Cell</i> , <b>2016</b> , 28, 2651-2665	11.6	56
165	Genetic mapping in grapevine using SNP microarray intensity values. <i>Molecular Breeding</i> , <b>2015</b> , 35, 1	3.4	14
164	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> , <b>2015</b> , 5, 891-909	3.2	9
163	Genome-environment associations in sorghum landraces predict adaptive traits. <i>Science Advances</i> , <b>2015</b> , 1, e1400218	14.3	160
162	Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , <b>2015</b> , 114, 291-9	3.6	131
161	Genome-wide association of carbon and nitrogen metabolism in the maize nested association mapping population. <i>Plant Physiology</i> , <b>2015</b> , 168, 575-83	6.6	67
160	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , <b>2015</b> , 6, 6914	17.4	142
159	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> , <b>2015</b> , 66, 593-602	7	28
158	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> , <b>2015</b> , 112, 3823-8	11.5	147
157	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , <b>2015</b> , 200, 1297-314		50
156	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , <b>2015</b> , 13, 78	7.3	32
155	The Genetic Makeup of a Global Barnyard Millet Germplasm Collection. <i>Plant Genome</i> , <b>2015</b> , 8, eplantgenome2014.10.001		10
154	Population Genetics and Structure of a Global Foxtail Millet Germplasm Collection. <i>Plant Genome</i> , <b>2015</b> , 8, eplantgenome2015.07.0054	4.4	19
153	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> , <b>2015</b> , 10, e0121624	3.7	52
152	Entering the second century of maize quantitative genetics. <i>Heredity</i> , <b>2014</b> , 112, 30-8	3.6	107
151	Insights into the effects of long-term artificial selection on seed size in maize. <i>Genetics</i> , <b>2014</b> , 198, 409-24		25



150	A foundation for provitamin A biofortification of maize: genome-wide association and genomic prediction models of carotenoid levels. <i>Genetics</i> , <b>2014</b> , 198, 1699-716	4	129
149	Novel Methods to Optimize Genotypic Imputation for Low-Coverage, Next-Generation Sequence Data in Crop Plants. <i>Plant Genome</i> , <b>2014</b> , 7, plantgenome2014.05.0023	4.4	184
148	A SUPER powerful method for genome wide association study. <i>PLoS ONE</i> , <b>2014</b> , 9, e107684	3.7	109
147	Accelerating the switchgrass ( <i>Panicum virgatum</i> L.) breeding cycle using genomic selection approaches. <i>PLoS ONE</i> , <b>2014</b> , 9, e112227	3.7	45
146	A modern ampelography: a genetic basis for leaf shape and venation patterning in grape. <i>Plant Physiology</i> , <b>2014</b> , 164, 259-72	6.6	110
145	Association mapping across numerous traits reveals patterns of functional variation in maize. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004845	6	133
144	TASSEL-GBS: a high capacity genotyping by sequencing analysis pipeline. <i>PLoS ONE</i> , <b>2014</b> , 9, e90346	3.7	994
143	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. <i>BMC Plant Biology</i> , <b>2014</b> , 14, 372	5.3	62
142	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , <b>2014</b> , 12, 73	7.3	60
141	The genetic architecture of maize height. <i>Genetics</i> , <b>2014</b> , 196, 1337-56	4	211
140	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , <b>2013</b> , 14, R55	18.3	337
139	Mining conifers' mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. <i>Tree Genetics and Genomes</i> , <b>2013</b> , 9, 1537-1544 <sup>2.1</sup>		45
138	Diversity and heritability of the maize rhizosphere microbiome under field conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 6548-53	11.5	1067
137	Agriculture: Feeding the future. <i>Nature</i> , <b>2013</b> , 499, 23-4	50.4	363
136	Population genomic and genome-wide association studies of agroclimatic traits in sorghum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 453-8	11.5	556
135	Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003215	6	481
134	Lessons from Dwarf8 on the strengths and weaknesses of structured association mapping. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003246	6	88
133	Genome-wide association study and pathway-level analysis of tocochromanol levels in maize grain. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 1287-99	3.2	111



132	Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 2085-94	3.2	45
131	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> , <b>2013</b> , 25, 2341-55	11.6	171
130	Aluminum tolerance in maize is associated with higher MATE1 gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 5241-6	11.5	199
129	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , <b>2013</b> , 53, 189-200	2.4	49
128	The genetic architecture of maize stalk strength. <i>PLoS ONE</i> , <b>2013</b> , 8, e67066	3.7	81
127	Vitis phylogenomics: hybridization intensities from a SNP array outperform genotype calls. <i>PLoS ONE</i> , <b>2013</b> , 8, e78680	3.7	36
126	Genomics assisted ancestry deconvolution in grape. <i>PLoS ONE</i> , <b>2013</b> , 8, e80791	3.7	25
125	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 1172-6	44.5	192
124	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , <b>2012</b> , 28, 2397-9	7.2	1135
123	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. <i>Plant Physiology</i> , <b>2012</b> , 158, 824-34	6.6	242
122	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , <b>2012</b> , 44, 803-7	36.3	470
121	SNP discovery with EST and NextGen sequencing in switchgrass ( <i>Panicum virgatum</i> L.). <i>PLoS ONE</i> , <b>2012</b> , 7, e44112	3.7	16
120	PICARA, an analytical pipeline providing probabilistic inference about a priori candidates genes underlying genome-wide association QTL in plants. <i>PLoS ONE</i> , <b>2012</b> , 7, e46596	3.7	20
119	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , <b>2012</b> , 44, 808-11	36.3	600
118	ZmCCT 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> , <b>2012</b> , 109, E1913-21	11.5	226
117	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <i>Heredity</i> , <b>2012</b> , 108, 490-9	3.6	96
116	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , <b>2012</b> , 22, 2436-44	9.7	96
115	Crop genomics: advances and applications. <i>Nature Reviews Genetics</i> , <b>2011</b> , 13, 85-96	30.1	362

114	Genetic structure and domestication history of the grape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 3530-5	11.5	468
113	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> , <b>2011</b> , 108, 6893-8	11.5	288
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29	<i>Tripsacum</i> de novo transcriptome assemblies reveal parallel gene evolution with maize after ancient polyploidy		3
28	Quantitative Genetic Analysis of the Maize Leaf Microbiome		3
27	Genetic elucidation of complex biochemical traits mediating maize innate immunity		1
26	rTASSEL: an R interface to TASSEL for association mapping of complex traits		1
25	Independent molecular basis of convergent highland adaptation in maize		3

24	Construction of the third generation Zea mays haplotype map	19
23	Non-Mendelian inheritance of SNP markers reveals extensive chromosomal translocations in dioecious hops ( <i>Humulus lupulus</i> L.)	2
22	Cassava HapMap: Masking deleterious mutations in a clonal crop species	2
21	A Large Scale Joint Analysis of Flowering Time Reveals Independent Temperate Adaptations in Maize	2
20	Incomplete Dominance of Deleterious Alleles Contributes Substantially to Trait Variation and Heterosis in Maize	2
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18	Genetic Analysis of Lodging in Diverse Maize Hybrids	4
17	Constrained non-coding sequence provides insights into regulatory elements and loss of gene expression in maize	5
16	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain	2
15	A Maize Practical Haplotype Graph Leverages Diverse NAM Assemblies	6
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11	Transcriptome-wide association supplements genome-wide association in Zea mays	3
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4	A multiple genome alignment workflow shows the impact of repeat masking and parameter tuning on alignment of functional regions in plants	1
3	Synthetic Promoter Designs Enabled by a Comprehensive Analysis of Plant Core Promoters	1
2	Teosinte introgression modulates phosphatidylcholine levels and induces early maize flowering time	3
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