

# Edward S Buckler

## List of Publications by Citations

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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	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , <b>2007</b> , 23, 2633-5	7.2	4013
256	A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. <i>PLoS ONE</i> , <b>2011</b> , 6, e19379	3.7	3791
255	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , <b>2006</b> , 38, 203-8	36.3	2595
254	Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , <b>2010</b> , 42, 961-7	36.3	1414
253	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , <b>2010</b> , 42, 355-60	36.3	1259
252	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , <b>2012</b> , 28, 2397-9	7.2	1135
251	Structure of linkage disequilibrium in plants. <i>Annual Review of Plant Biology</i> , <b>2003</b> , 54, 357-74	30.7	1125
250	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
249	The genetic architecture of maize flowering time. <i>Science</i> , <b>2009</b> , 325, 714-8	33.3	1043
248	TASSEL-GBS: a high capacity genotyping by sequencing analysis pipeline. <i>PLoS ONE</i> , <b>2014</b> , 9, e90346	3.7	994
247	Dwarf8 polymorphisms associate with variation in flowering time. <i>Nature Genetics</i> , <b>2001</b> , 28, 286-9	36.3	871
246	A single domestication for maize shown by multilocus microsatellite genotyping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 6080-4	11.5	860
245	Structure of linkage disequilibrium and phenotypic associations in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 11479-84	11.5	854
244	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , <b>2004</b> , 36, 1133-7	36.3	822
243	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , <b>2008</b> , 1,	4.4	818
242	Genetic properties of the maize nested association mapping population. <i>Science</i> , <b>2009</b> , 325, 737-40	33.3	775
241	Genetic design and statistical power of nested association mapping in maize. <i>Genetics</i> , <b>2008</b> , 178, 539-514		753

240	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , <b>2011</b> , 43, 159-62	36.3	746
239	Genetic association mapping and genome organization of maize. <i>Current Opinion in Biotechnology</i> , <b>2006</b> , 17, 155-60	11.4	659
238	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , <b>2005</b> , 44, 1054-64	6.9	633
237	A first-generation haplotype map of maize. <i>Science</i> , <b>2009</b> , 326, 1115-7	33.3	613
236	Association mapping: critical considerations shift from genotyping to experimental design. <i>Plant Cell</i> , <b>2009</b> , 21, 2194-202	11.6	601
235	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , <b>2012</b> , 44, 808-11	36.3	600
234	Natural genetic variation in lycopene epsilon cyclase tapped for maize biofortification. <i>Science</i> , <b>2008</b> , 319, 330-3	33.3	571
233	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
232	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
231	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , <b>2012</b> , 44, 803-7	36.3	470
230	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
229	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
228	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , <b>2011</b> , 43, 163-8	36.3	444
227	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> , <b>2011</b> , 6, e28334	3.7	422
226	Agriculture: Feeding the future. <i>Nature</i> , <b>2013</b> , 499, 23-4	50.4	363
225	Crop genomics: advances and applications. <i>Nature Reviews Genetics</i> , <b>2011</b> , 13, 85-96	30.1	362
224	The evolution of ribosomal DNA: divergent paralogues and phylogenetic implications. <i>Genetics</i> , <b>1997</b> , 145, 821-32	4	357
223	Rare genetic variation at <i>Zea mays</i> crtRB1 increases beta-carotene in maize grain. <i>Nature Genetics</i> , <b>2010</b> , 42, 322-7	36.3	349

222	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , <b>2013</b> , 14, R55	18.3	337
221	Agriculture. Increased food and ecosystem security via perennial grains. <i>Science</i> , <b>2010</b> , 328, 1638-9	33.3	303
220	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
219	Genetic characterization and linkage disequilibrium estimation of a global maize collection using SNP markers. <i>PLoS ONE</i> , <b>2009</b> , 4, e8451	3.7	288
218	Plant molecular diversity and applications to genomics. <i>Current Opinion in Plant Biology</i> , <b>2002</b> , 5, 107-11	9.9	279
217	Dissection of maize kernel composition and starch production by candidate gene association. <i>Plant Cell</i> , <b>2004</b> , 16, 2719-33	11.6	259
216	Architecture of floral branch systems in maize and related grasses. <i>Nature</i> , <b>2005</b> , 436, 1119-26	50.4	253
215	Genetic diversity and selection in the maize starch pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 12959-62	11.5	252
214	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
213	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
212	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
211	Early allelic selection in maize as revealed by ancient DNA. <i>Science</i> , <b>2003</b> , 302, 1206-8	33.3	224
210	The genetic architecture of maize height. <i>Genetics</i> , <b>2014</b> , 196, 1337-56	4	211
209	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
208	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
207	Comparison of mixed-model approaches for association mapping. <i>Genetics</i> , <b>2008</b> , 178, 1745-54	4	199
206	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
205	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

204	Molecular diversity, structure and domestication of grasses. <i>Genetical Research</i> , <b>2001</b> , 77, 213-8	1.1	197
203	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 1172-6	44.5	192
202	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
201	Population genetics of genomics-based crop improvement methods. <i>Trends in Genetics</i> , <b>2011</b> , 27, 98-106	68.5	181
200	Empirical comparison of Simple Sequence Repeats and single nucleotide polymorphisms in assessment of maize diversity and relatedness. <i>PLoS ONE</i> , <b>2007</b> , 2, e1367	3.7	176
199	Distinct genetic architectures for male and female inflorescence traits of maize. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002383	6	175
198	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
197	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
196	Molecular and functional diversity of maize. <i>Current Opinion in Plant Biology</i> , <b>2006</b> , 9, 172-6	9.9	168
195	Rapid genomic characterization of the genus vitis. <i>PLoS ONE</i> , <b>2010</b> , 5, e8219	3.7	166
194	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D717-23	20.1	162
193	Genome-environment associations in sorghum landraces predict adaptive traits. <i>Science Advances</i> , <b>2015</b> , 1, e1400218	14.3	160
192	Zea systematics: ribosomal ITS evidence. <i>Molecular Biology and Evolution</i> , <b>1996</b> , 13, 612-22	8.3	157
191	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
190	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
189	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , <b>2015</b> , 6, 6914	17.4	142
188	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
187	Association mapping across numerous traits reveals patterns of functional variation in maize. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004845	6	133

186	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
185	Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D947-53	20.1	130
184	Genetic diversity and population structure of teosinte. <i>Genetics</i> , <b>2005</b> , 169, 2241-54	4	130
183	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
182	Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , <b>2018</b> , 7, 1-12	7.6	127
181	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , <b>2019</b> , 5, 1237-1249	11.5	127
180	Meiotic drive of chromosomal knobs reshaped the maize genome. <i>Genetics</i> , <b>1999</b> , 153, 415-26	4	126
179	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
178	Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. <i>Nature Genetics</i> , <b>2017</b> , 49, 959-963	36.3	118
177	Association analysis of candidate genes for maysin and chlorogenic acid accumulation in maize silks. <i>Theoretical and Applied Genetics</i> , <b>2005</b> , 110, 1324-33	6	117
176	Heterosis is prevalent for multiple traits in diverse maize germplasm. <i>PLoS ONE</i> , <b>2009</b> , 4, e7433	3.7	116
175	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
174	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
173	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
172	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
171	A SUPER powerful method for genome wide association study. <i>PLoS ONE</i> , <b>2014</b> , 9, e107684	3.7	109
170	Entering the second century of maize quantitative genetics. <i>Heredity</i> , <b>2014</b> , 112, 30-8	3.6	107
169	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> , <b>2009</b> , 106 Suppl 1, 9979-86	11.5	106

168	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> , <b>2011</b> , 62, 701-76	96
167	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
166	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
165	Lessons from Dwarf8 on the strengths and weaknesses of structured association mapping. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003246	6 88
164	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
163	Zea ribosomal repeat evolution and substitution patterns. <i>Molecular Biology and Evolution</i> , <b>1996</b> , 13, 623-32	8.3 86
162	Joint QTL linkage mapping for multiple-cross mating design sharing one common parent. <i>PLoS ONE</i> , <b>2011</b> , 6, e17573	3.7 82
161	The genetic architecture of maize stalk strength. <i>PLoS ONE</i> , <b>2013</b> , 8, e67066	3.7 81
160	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
159	Association and linkage analysis of aluminum tolerance genes in maize. <i>PLoS ONE</i> , <b>2010</b> , 5, e9958	3.7 75
158	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants <b>2007</b> , 97-119	75
157	Quantitative trait loci analysis of growth response to varying nitrogen sources in <i>Arabidopsis thaliana</i> . <i>Theoretical and Applied Genetics</i> , <b>2002</b> , 104, 743-750	6 75
156	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
155	Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D752-7	20.1 74
154	Maize Genes and Regulate Plant Architecture. <i>Plant Cell</i> , <b>2017</b> , 29, 1622-1641	11.6 69
153	Genome-size Variation in Switchgrass ( <i>Panicum virgatum</i> ): Flow Cytometry and Cytology Reveal Rampant Aneuploidy. <i>Plant Genome</i> , <b>2010</b> , 3,	4.4 69
152	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
151	The genetic architecture of complex traits in teosinte ( <i>Zea mays</i> ssp. <i>parviglumis</i> ): new evidence from association mapping. <i>Genetics</i> , <b>2008</b> , 180, 1221-32	4 66

150	Quantitative Genetics of the Maize Leaf Microbiome. <i>Phytobiomes Journal</i> , <b>2018</b> , 2, 208-224	4.8	65
149	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
148	Biosynthesis of 8-O-Methylated Benzoxazinoid Defense Compounds in Maize. <i>Plant Cell</i> , <b>2016</b> , 28, 1682-700	11.6	63
147	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
146	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. <i>Plant Genome</i> , <b>2009</b> , 2,	4.4	62
145	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , <b>2014</b> , 12, 73	7.3	60
144	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
143	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , <b>2017</b> , 8, 1348	17.4	58
142	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
141	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
140	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
139	Using natural allelic diversity to evaluate gene function. <i>Methods in Molecular Biology</i> , <b>2003</b> , 236, 123-40	1.4	55
138	Fine quantitative trait loci mapping of carbon and nitrogen metabolism enzyme activities and seedling biomass in the maize IBM mapping population. <i>Plant Physiology</i> , <b>2010</b> , 154, 1753-65	6.6	52
137	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
136	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , <b>2015</b> , 200, 1297-312	11.6	50
135	Deep learning for plant genomics and crop improvement. <i>Current Opinion in Plant Biology</i> , <b>2020</b> , 54, 34-41	11.9	50
134	Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , <b>2009</b> , 10, 664-75	13.4	50
133	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , <b>2013</b> , 53, 189-200	2.4	49



132	Large-Scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , <b>2009</b> , 2,	4.4	48
131	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
130	Using crossover breakpoints in recombinant inbred lines to identify quantitative trait loci controlling the global recombination frequency. <i>Genetics</i> , <b>2007</b> , 177, 1851-8	4	47
129	Molecular evolution of type 1 serine/threonine protein phosphatases. <i>Molecular Phylogenetics and Evolution</i> , <b>1999</b> , 12, 57-66	4.1	46
128	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	2.1	45
127	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
126	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
125	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
124	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
123	Power to detect higher-order epistatic interactions in a metabolic pathway using a new mapping strategy. <i>Genetics</i> , <b>2007</b> , 176, 563-70	4	41
122	Patterns of genomic and phenomic diversity in wine and table grapes. <i>Horticulture Research</i> , <b>2017</b> , 4, 17035	7.7	40
121	Vitis phylogenomics: hybridization intensities from a SNP array outperform genotype calls. <i>PLoS ONE</i> , <b>2013</b> , 8, e78680	3.7	36
120	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , <b>2019</b> , 5, 1043-1056	11.5	36
119	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
118	Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , <b>2009</b> , 173-195		35
117	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
116	Discovery and mapping of single feature polymorphisms in wheat using Affymetrix arrays. <i>BMC Genomics</i> , <b>2009</b> , 10, 251	4.5	34
115	Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood. <i>Journal of Animal Science</i> , <b>2007</b> , 85, 881-5	0.7	34

114	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , <b>2001</b> , 12, 84-86	0.5	34
113	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
112	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
111	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
110	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
109	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
108	Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , <b>2007</b> , 47, S-135	2.4	32
107	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
106	Recurrent Mutation and Genome Evolution: Example of Sugary1 and the Origin of Sweet Maize. <i>Crop Science</i> , <b>2006</b> , 46, S-49	2.4	30
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> , <b>2015</b> , 66, 593-602	7	28
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49	Genetic Analysis of Lodging in Diverse Maize Hybrids		4
48	Evolutionarily informed deep learning methods: Predicting transcript abundance from DNA sequence		4
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42	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
41	Independent molecular basis of convergent highland adaptation in maize		3
40	Leveraging mutational burden for complex trait prediction in sorghum		3
39	Transcriptome-wide association supplements genome-wide association in <i>Zea mays</i>		3
38	In-field whole plant maize architecture characterized by Latent Space Phenotyping		3
37	Underground heterosis for yield improvement in melon. <i>Journal of Experimental Botany</i> , <b>2021</b> , 72, 6205-6218		3
36	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
35	Teosinte introgression modulates phosphatidylcholine levels and induces early maize flowering time		3
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30	Non-Mendelian inheritance of SNP markers reveals extensive chromosomal translocations in dioecious hops ( <i>Humulus lupulus</i> L.)		2
29	Cassava HapMap: Masking deleterious mutations in a clonal crop species		2
28	A Large Scale Joint Analysis of Flowering Time Reveals Independent Temperate Adaptations in Maize		2
27	Incomplete Dominance of Deleterious Alleles Contributes Substantially to Trait Variation and Heterosis in Maize		2
26	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2
25	k-mer grammar uncovers maize regulatory architecture		2

24	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
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21	Perennial Questions of Hydrology and Climate--Response. <i>Science</i> , <b>2010</b> , 330, 33-34	33.3	1
20	The transcription regulatory code of a plant leaf		1
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18	Genetic elucidation of complex biochemical traits mediating maize innate immunity		1
17	rTASSEL: an R interface to TASSEL for association mapping of complex traits		1
16	Machine learning enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions		1
15	Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize		1
14	Identifying the diamond in the rough: a study of allelic diversity underlying flowering time adaptation in maize landraces		1
13	Identification of miRNA-eQTLs in maize mature leaf by GWAS. <i>BMC Genomics</i> , <b>2020</b> , 21, 689	4.5	1
12	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , <b>2021</b> , 126, 929-941	3.6	1
11	A multiple genome alignment workflow shows the impact of repeat masking and parameter tuning on alignment of functional regions in plants		1
10	Synthetic Promoter Designs Enabled by a Comprehensive Analysis of Plant Core Promoters		1
9	Local adaptation contributes to gene expression divergence in maize. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	1
8	AnchorWave: sensitive alignment of genomes with high diversity, structural polymorphism and whole-genome duplication variation		1
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4	Haplotype associated RNA expression (HARE) improves prediction of complex traits in maize. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009568	6	0
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2	Ten simple rules to ruin a collaborative environment.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009957	5	0
1	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