

Edward S Buckler

List of Publications by Year in descending order

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231
papers

67,776
citations

2101
100
h-index

1158
229
g-index

288
all docs

288
docs citations

288
times ranked

31400
citing authors

#	ARTICLE	IF	CITATIONS
1	TASSEL: software for association mapping of complex traits in diverse samples. Bioinformatics, 2007, 23, 2633-2635.	4.1	6,407
2	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. PLoS ONE, 2011, 6, e19379.	2.5	5,470
3	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nature Genetics, 2006, 38, 203-208.	21.4	3,622
4	Mixed linear model approach adapted for genome-wide association studies. Nature Genetics, 2010, 42, 355-360.	21.4	2,022
5	GAPIT: genome association and prediction integrated tool. Bioinformatics, 2012, 28, 2397-2399.	4.1	2,016
6	Genome-wide association studies of 14 agronomic traits in rice landraces. Nature Genetics, 2010, 42, 961-967.	21.4	1,978
7	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.	7.1	1,594
8	TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline. PLoS ONE, 2014, 9, e90346.	2.5	1,511
9	Structure of Linkage Disequilibrium in Plants. Annual Review of Plant Biology, 2003, 54, 357-374.	18.7	1,456
10	The Genetic Architecture of Maize Flowering Time. Science, 2009, 325, 714-718.	12.6	1,284
11	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.	7.1	1,143
12	Status and Prospects of Association Mapping in Plants. Plant Genome, 2008, 1, .	2.8	1,118
13	Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. PLoS Genetics, 2016, 12, e1005767.	3.5	1,095
14	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.	7.1	1,060
15	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
16	Genome-wide association study of leaf architecture in the maize nested association mapping population. Nature Genetics, 2011, 43, 159-162.	21.4	987
17	Dwarf8 polymorphisms associate with variation in flowering time. Nature Genetics, 2001, 28, 286-289.	21.4	960
18	Genetic Properties of the Maize Nested Association Mapping Population. Science, 2009, 325, 737-740.	12.6	959

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19	Genetic Design and Statistical Power of Nested Association Mapping in Maize. <i>Genetics</i> , 2008, 178, 539-551.	2.9	939
20	Genetic association mapping and genome organization of maize. <i>Current Opinion in Biotechnology</i> , 2006, 17, 155-160.	6.6	869
21	Maize association population: a high-resolution platform for quantitative trait locus dissection. <i>Plant Journal</i> , 2005, 44, 1054-1064.	5.7	821
22	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	21.4	816
23	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202.	6.6	786
24	A First-Generation Haplotype Map of Maize. <i>Science</i> , 2009, 326, 1115-1117.	12.6	747
25	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> , 2013, 110, 453-458.	7.1	743
26	Natural Genetic Variation in <i>Lycopene Epsilon Cyclase</i> Tapped for Maize Biofortification. <i>Science</i> , 2008, 319, 330-333.	12.6	692
27	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.	7.1	684
28	Switchgrass Genomic Diversity, Ploidy, and Evolution: Novel Insights from a Network-Based SNP Discovery Protocol. <i>PLoS Genetics</i> , 2013, 9, e1003215.	3.5	608
29	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
30	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.	21.4	553
31	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.	2.5	523
32	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	27.8	464
33	The Evolution of Ribosomal DNA Divergent Paralogues and Phylogenetic Implications. <i>Genetics</i> , 1997, 145, 821-832.	2.9	463
34	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013, 14, R55.	8.8	458
35	Crop genomics: advances and applications. <i>Nature Reviews Genetics</i> , 2012, 13, 85-96.	16.3	439
36	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.	7.1	435

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37	Rare genetic variation at <i>Zea mays crtRB1</i> increases β -carotene in maize grain. <i>Nature Genetics</i> , 2010, 42, 322-327.	21.4	421
38	GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0120.	2.8	421
39	Increased Food and Ecosystem Security via Perennial Grains. <i>Science</i> , 2010, 328, 1638-1639.	12.6	397
40	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
41	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.	7.1	350
42	Architecture of floral branch systems in maize and related grasses. <i>Nature</i> , 2005, 436, 1119-1126.	27.8	348
43	Genetic Characterization and Linkage Disequilibrium Estimation of a Global Maize Collection Using SNP Markers. <i>PLoS ONE</i> , 2009, 4, e8451.	2.5	338
44	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	21.4	335
45	Plant molecular diversity and applications to genomics. <i>Current Opinion in Plant Biology</i> , 2002, 5, 107-111.	7.1	333
46	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	2.9	329
47	Genetic Architecture of Maize Kernel Composition in the Nested Association Mapping and Inbred Association Panels A. <i>Plant Physiology</i> , 2012, 158, 824-834.	4.8	307
48	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.	7.1	298
49	Dissection of Maize Kernel Composition and Starch Production by Candidate Gene Association. <i>Plant Cell</i> , 2004, 16, 2719-2733.	6.6	291
50	<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.	7.1	290
51	A SUPER Powerful Method for Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e107684.	2.5	289
52	Early Allelic Selection in Maize as Revealed by Ancient DNA. <i>Science</i> , 2003, 302, 1206-1208.	12.6	287
53	Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.	2.9	273
54	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.	7.1	265

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55	Molecular Diversity, Structure and Domestication of Grasses. Genetical Research, 2001, 77, 213-8.	0.9	262
56	Genome-environment associations in sorghum landraces predict adaptive traits. Science Advances, 2015, 1, e1400218.	10.3	257
57	A study of allelic diversity underlying flowering-time adaptation in maize landraces. Nature Genetics, 2017, 49, 476-480.	21.4	254
58	Natural Variation in Maize Aphid Resistance Is Associated with 2,4-Dihydroxy-7-Methoxy-1,4-Benzoxazin-3-One Glucoside Methyltransferase Activity. Plant Cell, 2013, 25, 2341-2355.	6.6	251
59	Widespread long-range cis-regulatory elements in the maize genome. Nature Plants, 2019, 5, 1237-1249.	9.3	250
60	Can genomics boost productivity of orphan crops?. Nature Biotechnology, 2012, 30, 1172-1176.	17.5	248
61	Novel Methods to Optimize Genotypic Imputation for Low-Coverage, Next-Generation Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023.	2.8	241
62	A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. Plant Physiology, 2014, 164, 259-272.	4.8	233
63	Open chromatin reveals the functional maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3177-84.	7.1	233
64	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. PLoS Genetics, 2011, 7, e1002383.	3.5	231
65	Population genetics of genomics-based crop improvement methods. Trends in Genetics, 2011, 27, 98-106.	6.7	230
66	High-resolution genetic mapping of maize pan-genome sequence anchors. Nature Communications, 2015, 6, 6914.	12.8	213
67	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. Nature, 2018, 555, 520-523.	27.8	211
68	Recombination in diverse maize is stable, predictable, and associated with genetic load. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3823-3828.	7.1	210
69	Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. Nature Genetics, 2017, 49, 959-963.	21.4	208
70	Empirical Comparison of Simple Sequence Repeats and Single Nucleotide Polymorphisms in Assessment of Maize Diversity and Relatedness. PLoS ONE, 2007, 2, e1367.	2.5	204
71	Rapid Genomic Characterization of the Genus Vitis. PLoS ONE, 2010, 5, e8219.	2.5	203
72	Zea systematics: ribosomal ITS evidence. Molecular Biology and Evolution, 1996, 13, 612-622.	8.9	202

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73	Molecular and functional diversity of maize. <i>Current Opinion in Plant Biology</i> , 2006, 9, 172-176.	7.1	201
74	Construction of the third-generation Zea mays haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	6.4	191
75	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.	2.6	187
76	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. <i>Plant Cell</i> , 2016, 28, 2700-2714.	6.6	183
77	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288.	21.4	183
78	Genetic Diversity and Population Structure of Teosinte. <i>Genetics</i> , 2005, 169, 2241-2254.	2.9	182
79	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.	7.6	182
80	A Foundation for Provitamin A Biofortification of Maize: Genome-Wide Association and Genomic Prediction Models of Carotenoid Levels. <i>Genetics</i> , 2014, 198, 1699-1716.	2.9	180
81	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723.	14.5	177
82	Heterosis Is Prevalent for Multiple Traits in Diverse Maize Germplasm. <i>PLoS ONE</i> , 2009, 4, e7433.	2.5	173
83	Meiotic Drive of Chromosomal Knobs Reshaped the Maize Genome. <i>Genetics</i> , 1999, 153, 415-426.	2.9	173
84	Association Mapping across Numerous Traits Reveals Patterns of Functional Variation in Maize. <i>PLoS Genetics</i> , 2014, 10, e1004845.	3.5	171
85	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017, 357, 512-515.	12.6	169
86	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014, 12, 73.	3.8	160
87	Genome-Wide Association Study and Pathway-Level Analysis of Tocochromanol Levels in Maize Grain. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1287-1299.	1.8	152
88	Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , 2007, 36, D947-D953.	14.5	151
89	Entering the second century of maize quantitative genetics. <i>Heredity</i> , 2014, 112, 30-38.	2.6	142
90	Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize. <i>PLoS Genetics</i> , 2017, 13, e1007019.	3.5	136

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91	Tracking footprints of maize domestication and evidence for a massive selective sweep on chromosome 10. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9979-9986.	7.1	133
92	The Genetic Architecture of Maize Stalk Strength. PLoS ONE, 2013, 8, e67066.	2.5	129
93	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. Heredity, 2012, 108, 490-499.	2.6	128
94	Maize <i>YABBY</i> Genes <i>drooping leaf1</i> and <i>drooping leaf2</i> Regulate Plant Architecture. Plant Cell, 2017, 29, 1622-1641.	6.6	128
95	Genic and nongenic contributions to natural variation of quantitative traits in maize. Genome Research, 2012, 22, 2436-2444.	5.5	125
96	Association analysis of candidate genes for maysin and chlorogenic acid accumulation in maize silks. Theoretical and Applied Genetics, 2005, 110, 1324-1333.	3.6	124
97	Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. Plant Journal, 2016, 86, 391-402.	5.7	122
98	Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. Plant Biotechnology Journal, 2016, 14, 1551-1562.	8.3	121
99	Evolutionarily informed deep learning methods for predicting relative transcript abundance from DNA sequence. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5542-5549.	7.1	121
100	Lessons from Dwarf8 on the Strengths and Weaknesses of Structured Association Mapping. PLoS Genetics, 2013, 9, e1003246.	3.5	115
101	Reconstructing the maize leaf regulatory network using ChIP-seq data of 104 transcription factors. Nature Communications, 2020, 11, 5089.	12.8	111
102	Genetic association mapping identifies single nucleotide polymorphisms in genes that affect abscisic acid levels in maize floral tissues during drought. Journal of Experimental Botany, 2011, 62, 701-716.	4.8	110
103	Quantitative Genetics of the Maize Leaf Microbiome. Phytobiomes Journal, 2018, 2, 208-224.	2.7	110
104	Deep learning for plant genomics and crop improvement. Current Opinion in Plant Biology, 2020, 54, 34-41.	7.1	108
105	Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . Plant Cell, 2016, 28, 2651-2665.	6.6	105
106	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
107	Joint QTL Linkage Mapping for Multiple-Cross Mating Design Sharing One Common Parent. PLoS ONE, 2011, 6, e17573.	2.5	102
108	Zea ribosomal repeat evolution and substitution patterns. Molecular Biology and Evolution, 1996, 13, 623-632.	8.9	98

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109	Software engineering the mixed model for genome-wide association studies on large samples. Briefings in Bioinformatics, 2009, 10, 664-675.	6.5	96
110	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. , 2007, , 97-119.		95
111	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. Plant Cell, 2017, 29, 2374-2392.	6.6	93
112	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326.	1.8	92
113	Association and Linkage Analysis of Aluminum Tolerance Genes in Maize. PLoS ONE, 2010, 5, e9958.	2.5	91
114	Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12231-12236.	7.1	91
115	Panzea: a database and resource for molecular and functional diversity in the maize genome. Nucleic Acids Research, 2006, 34, D752-D757.	14.5	89
116	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. Crop Science, 2016, 56, 2365-2378.	1.8	88
117	Biosynthesis of 8-O-methylated benzoxazinoid defense compounds in maize. Plant Cell, 2016, 28, tpc.00065.2016.	6.6	87
118	Patterns of genomic and phenomic diversity in wine and table grapes. Horticulture Research, 2017, 4, 17035.	6.3	87
119	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. BMC Plant Biology, 2014, 14, 372.	3.6	85
120	The multi-allelic APRR2 gene is associated with fruit pigment accumulation in melon and watermelon. Journal of Experimental Botany, 2019, 70, 3781-3794.	4.8	84
121	Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future Directions. Plant Cell, 2020, 32, 2083-2093.	6.6	81
122	Genome-Wide Association of Carbon and Nitrogen Metabolism in the Maize Nested Association Mapping Population. Plant Physiology, 2015, 168, 575-583.	4.8	80
123	Quantitative trait loci analysis of growth response to varying nitrogen sources in Arabidopsis thaliana. Theoretical and Applied Genetics, 2002, 104, 743-750.	3.6	78
124	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. Nature Plants, 2021, 7, 842-855.	9.3	78
125	Genome-size Variation in Switchgrass (Panicum virgatum): Flow Cytometry and Cytology Reveal Rampant Aneuploidy. Plant Genome, 2010, 3, .	2.8	77
126	Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Maize Specialized Metabolites. Plant Cell, 2019, 31, 937-955.	6.6	75

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127	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.	2.9	73
128	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.	2.5	69
129	Breaking the curse of dimensionality to identify causal variants in Breeding 4. <i>Theoretical and Applied Genetics</i> , 2019, 132, 559-567.	3.6	68
130	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312.	2.9	67
131	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. <i>Plant Genome</i> , 2009, 2, .	2.8	66
132	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200.	1.8	66
133	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.	1.8	65
134	Accelerating the Switchgrass (<i>Panicum virgatum</i> L.) Breeding Cycle Using Genomic Selection Approaches. <i>PLoS ONE</i> , 2014, 9, e112227.	2.5	65
135	Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3023-3033.	1.8	64
136	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. <i>BMC Genomics</i> , 2016, 17, 894.	2.8	63
137	Molecular Evolution of Type 1 Serine/Threonine Protein Phosphatases. <i>Molecular Phylogenetics and Evolution</i> , 1999, 12, 57-66.	2.7	61
138	Using Natural Allelic Diversity to Evaluate Gene Function. , 2003, 236, 123-140.		60
139	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056.	9.3	60
140	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.	7.1	59
141	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.	0.5	58
142	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.	4.8	58
143	Large-scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , 2009, 2, .	2.8	55
144	Vitis Phylogenomics: Hybridization Intensities from a SNP Array Outperform Genotype Calls. <i>PLoS ONE</i> , 2013, 8, e78680.	2.5	55

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145	Mining conifersâ€™ mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. <i>Tree Genetics and Genomes</i> , 2013, 9, 1537-1544.	1.6	54
146	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
147	Using Crossover Breakpoints in Recombinant Inbred Lines to Identify Quantitative Trait Loci Controlling the Global Recombination Frequency. <i>Genetics</i> , 2007, 177, 1851-1858.	2.9	53
148	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018, 121, 648-662.	2.6	53
149	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , 2020, 6, 1375-1388.	9.3	52
150	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	52
151	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24.	9.3	52
152	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (<i>Sorghum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	2.9	51
153	Climate, Plant Ecology, and Central Mexican Archaic Subsistence. <i>Current Anthropology</i> , 1998, 39, 152-164.	1.6	49
154	Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , 2021, 7, 954-965.	9.3	48
155	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	8.8	47
156	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	2.3	44
157	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.	4.8	44
158	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. <i>Genetics</i> , 2007, 176, 563-570.	2.9	43
159	Genomics Assisted Ancestry Deconvolution in Grape. <i>PLoS ONE</i> , 2013, 8, e80791.	2.5	43
160	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.	7.3	42
161	Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 173-195.	0.2	41
162	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015, 13, 78.	3.8	40

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163	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , 2001, 12, 84-86.	0.6	39
164	Recurrent Mutation and Genome Evolution: Example of <i>Sugary1</i> and the Origin of Sweet Maize. <i>Crop Science</i> , 2006, 46, S-49.	1.8	38
165	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	2.9	38
166	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	1.4	38
167	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038.	2.8	37
168	Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , 2007, 47, S-135.	1.8	36
169	Natural variation in maize architecture is mediated by allelic differences at the <i>PINOID</i> ortholog <i>barren inflorescence2</i> . <i>Plant Journal</i> , 2009, 58, 618-628.	5.7	36
170	The Genetic Makeup of a Global Barnyard Millet Germplasm Collection. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0067.	2.8	36
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