

Peter J Bradbury

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.

44
papers

11,194
citations

28
h-index

51
g-index

51
ext. papers

14,895
ext. citations

11.3
avg, IF

5.67
L-index

#	Paper	IF	Citations
44	Genome-wide Imputation Using the Practical Haplotype Graph in the Heterozygous Crop Cassava. <i>G3: Genes, Genomes, Genetics</i> , 2021 ,	3.2	1
43	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021 , 33, 882-900	11.6	3
42	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021 , 126, 929-941	3.6	1
41	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021 ,	9.7	5
40	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	6	1
39	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. <i>PLoS Genetics</i> , 2020 , 16, e1008791	6	17
38	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020 , 13, e20009	4.4	24
37	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. <i>Genetics</i> , 2020 , 215, 215-230	4	12
36	Maize Introgression Library Provides Evidence for the Involvement of in Resistance to Northern Leaf Blight. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3611-3622	3.2	8
35	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	11.5	34
34	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019 , 8, 1751	3.6	8
33	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019 , 8, 1751	3.6	2
32	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	4.9	9
31	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. <i>Nature</i> , 2018 , 555, 520-523	50.4	124
30	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018 , 121, 648-662	3.6	34
29	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017 , 29, 2374-2392	11.6	57
28	Genetic Architecture of Domestication-Related Traits in Maize. <i>Genetics</i> , 2016 , 204, 99-113	4	31

27	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	6.9	79
26	Genome-wide association of carbon and nitrogen metabolism in the maize nested association mapping population. <i>Plant Physiology</i> , 2015 , 168, 575-83	6.6	67
25	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, 3823-8	11.5	147
24	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015 , 13, 78	7.3	32
23	Novel Methods to Optimize Genotypic Imputation for Low-Coverage, Next-Generation Sequence Data in Crop Plants. <i>Plant Genome</i> , 2014 , 7, plantgenome2014.05.0023	4.4	184
22	A genome-wide association study of the maize hypersensitive defense response identifies genes that cluster in related pathways. <i>PLoS Genetics</i> , 2014 , 10, e1004562	6	43
21	Association mapping across numerous traits reveals patterns of functional variation in maize. <i>PLoS Genetics</i> , 2014 , 10, e1004845	6	133
20	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014 , 12, 73	7.3	60
19	The genetic architecture of maize height. <i>Genetics</i> , 2014 , 196, 1337-56	4	211
18	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. <i>Plant Physiology</i> , 2012 , 158, 824-34	6.6	242
17	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
16	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> , 2012 , 109, E1913-21	11.5	226
15	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, 6893-8	11.5	288
14	Assessment of Power and False Discovery Rate in Genome-Wide Association Studies using the BarleyCAP Germplasm. <i>Crop Science</i> , 2011 , 51, 52-59	2.4	41
13	Joint QTL linkage mapping for multiple-cross mating design sharing one common parent. <i>PLoS ONE</i> , 2011 , 6, e17573	3.7	82
12	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 159-62	36.3	746
11	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <i>Nature Genetics</i> , 2011 , 43, 163-8	36.3	444
10	Distinct genetic architectures for male and female inflorescence traits of maize. <i>PLoS Genetics</i> , 2011 , 7, e1002383	6	175

9	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010 , 42, 355-60	36.3	1259
8	Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , 2009 , 10, 664-75	13.4	50
7	Genetic properties of the maize nested association mapping population. <i>Science</i> , 2009 , 325, 737-40	33.3	775
6	The genetic architecture of maize flowering time. <i>Science</i> , 2009 , 325, 714-8	33.3	1043
5	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007 , 23, 2633-5	7.2	4013
4	rTASSEL: an R interface to TASSEL for association mapping of complex traits		1
3	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2
2	A Maize Practical Haplotype Graph Leverages Diverse NAM Assemblies		6
1	Maize nested introgression library provides evidence for the involvement of <i>flguleless1</i> in resistance to northern leaf blight		1