Peter J Bradbury

List of Publications by Citations

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	TASSEL: software for association mapping of complex traits in diverse samples. *Bioinformatics*, **2007**, 23, 2633-5	7.2	4013
43	Mixed linear model approach adapted for genome-wide association studies. *Nature Genetics*, **2010**, 42, 355-60	36.3	1259
42	The genetic architecture of maize flowering time. *Science*, **2009**, 325, 714-8	33.3	1043
41	Genetic properties of the maize nested association mapping population. *Science*, **2009**, 325, 737-40	33.3	775
40	Genome-wide association study of leaf architecture in the maize nested association mapping population. *Nature Genetics*, **2011**, 43, 159-62	36.3	746
39	Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics*, **2012**, 44, 803-7	36.3	470
38	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nature Genetics*, **2011**, 43, 163-8	36.3	444
37	Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 6893-8	11.5	288
36	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. *Plant Physiology*, **2012**, 158, 824-34	6.6	242
35	ZmCCT and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E1913-21	11.5	226
34	The genetic architecture of maize height. *Genetics*, **2014**, 196, 1337-56	4	211
33	Novel Methods to Optimize Genotypic Imputation for Low-Coverage, Next-Generation Sequence Data in Crop Plants. *Plant Genome*, **2014**, 7, plantgenome2014.05.0023	4.4	184
32	Distinct genetic architectures for male and female inflorescence traits of maize. *PLoS Genetics*, **2011**, 7, e1002383	6	175
31	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, 3823-8	11.5	147
30	Association mapping across numerous traits reveals patterns of functional variation in maize. *PLoS Genetics*, **2014**, 10, e1004845	6	133
29	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. *Nature*, **2018**, 555, 520-523	50.4	124
28	Joint QTL linkage mapping for multiple-cross mating design sharing one common parent. *PLoS ONE*, **2011**, 6, e17573	3.7	82

27	Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. *Plant Journal*, **2016**, 86, 391-402	6.9	79
26	Genome-wide association of carbon and nitrogen metabolism in the maize nested association mapping population. *Plant Physiology*, **2015**, 168, 575-83	6.6	67
25	Enrichment of statistical power for genome-wide association studies. *BMC Biology*, **2014**, 12, 73	7.3	60
24	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. *Plant Cell*, **2017**, 29, 2374-2392	11.6	57
23	Software engineering the mixed model for genome-wide association studies on large samples. *Briefings in Bioinformatics*, **2009**, 10, 664-75	13.4	50
22	A genome-wide association study of the maize hypersensitive defense response identifies genes that cluster in related pathways. *PLoS Genetics*, **2014**, 10, e1004562	6	43
21	Assessment of Power and False Discovery Rate in Genome-Wide Association Studies using the BarleyCAP Germplasm. *Crop Science*, **2011**, 51, 52-59	2.4	41
20	The genetic architecture of teosinte catalyzed and constrained maize domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 5643-5652	11.5	34
19	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. *Heredity*, **2018**, 121, 648-662	3.6	34
18	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. *BMC Biology*, **2015**, 13, 78	7.3	32
17	Genetic Architecture of Domestication-Related Traits in Maize. *Genetics*, **2016**, 204, 99-113	4	31
16	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. *Plant Genome*, **2020**, 13, e20009	4.4	24
15	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. *PLoS Genetics*, **2020**, 16, e1008791	6	17
14	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. *Genetics*, **2020**, 215, 215-230	4	12
13	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. *Scientific Reports*, **2018**, 8, 6848	4.9	9
12	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	8
11	Maize Introgression Library Provides Evidence for the Involvement of in Resistance to Northern Leaf Blight. *G3: Genes, Genomes, Genetics*, **2020**, 10, 3611-3622	3.2	8
10	A Maize Practical Haplotype Graph Leverages Diverse NAM Assemblies		6

9	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. *Genome Research*, **2021**,	9.7	5
8	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. *Plant Cell*, **2021**, 33, 882-900	11.6	3
7	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2
6	A strategy for building and using a human reference pangenome. *F1000Research*, **2019**, 8, 1751	3.6	2
5	Genome-wide Imputation Using the Practical Haplotype Graph in the Heterozygous Crop Cassava. *G3: Genes, Genomes, Genetics*, **2021**,	3.2	1
4	rTASSEL: an R interface to TASSEL for association mapping of complex traits		1
3	Maize nested introgression library provides evidence for the involvement ofliguleless1in resistance to northern leaf blight		1
2	Joint analysis of days to flowering reveals independent temperate adaptations in maize. *Heredity*, **2021**, 126, 929-941	3.6	1
1	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte.. *PLoS Genetics*, **2021**, 17, e1009797	6	1