Peter J Bradbury

List of Publications by Year
in descending order

42 papers	16,369 citations	172207 29 h-index	276539 41 g-index
51 all docs	51 docs citations	51 times ranked	12193 citing authors

#	ARTICLE	IF	CITATIONS
1	TASSEL: software for association mapping of complex traits in diverse samples. Bioinformatics, 2007, 23, 2633-2635.	1.8	6,407
2	Mixed linear model approach adapted for genome-wide association studies. Nature Genetics, 2010, 42, 355-360.	9.4	2,022
3	The Genetic Architecture of Maize Flowering Time. Science, 2009, 325, 714-718.	6.0	1,284
4	Genome-wide association study of leaf architecture in the maize nested association mapping population. Nature Genetics, 2011, 43, 159-162.	9.4	987
5	Genetic Properties of the Maize Nested Association Mapping Population. Science, 2009, 325, 737-740.	6.0	959
6	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	9.4	577
7	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. Nature Genetics, 2011, 43, 163-168.	9.4	553
8	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, 6893-6898.	3.3	350
9	The Genetic Architecture Of Maize Height. Genetics, 2014, 196, 1337-1356.	1.2	329
10	Genetic Architecture of Maize Kernel Composition in the Nested Association Mapping and Inbred Association Panels Â. Plant Physiology, 2012, 158, 824-834.	2.3	307
11	<i>ZmCCT</i> 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.	3.3	290
12	Novel Methods to Optimize Genotypic Imputation for Lowâ€Coverage, Nextâ€Generation Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023.	1.6	241
13	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. PLoS Genetics, 2011, 7, e1002383.	1.5	231
14	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. Nature, 2018, 555, 520-523.	13.7	211
15	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.	3.3	210
16	Association Mapping across Numerous Traits Reveals Patterns of Functional Variation in Maize. PLoS Genetics, 2014, 10, e1004845.	1.5	171
17	Enrichment of statistical power for genome-wide association studies. BMC Biology, 2014, 12, 73.	1.7	160
18	Identification of genetic variants associated with maize flowering time using an extremely large multiâ€genetic background population. Plant Journal, 2016, 86, 391-402.	2.8	122

#	Article	IF	Citations
19	Joint QTL Linkage Mapping for Multiple-Cross Mating Design Sharing One Common Parent. PLoS ONE, 2011, 6, e17573.	1.1	102
20	Software engineering the mixed model for genome-wide association studies on large samples. Briefings in Bioinformatics, 2009, 10, 664-675.	3.2	96
21	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. Plant Cell, 2017, 29, 2374-2392.	3.1	93
22	Genome-Wide Association of Carbon and Nitrogen Metabolism in the Maize Nested Association Mapping Population. Plant Physiology, 2015, 168, 575-583.	2.3	80
23	A Genome-Wide Association Study of the Maize Hypersensitive Defense Response Identifies Genes That Cluster in Related Pathways. PLoS Genetics, 2014, 10, e1004562.	1.5	62
24	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.	3.3	59
25	A sorghum practical haplotype graph facilitates genome€wide imputation and cost€effective genomic prediction. Plant Genome, 2020, 13, e20009.	1.6	54
26	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. Heredity, 2018, 121, 648-662.	1.2	53
27	Assessment of Power and False Discovery Rate in Genome€Wide Association Studies using the BarleyCAP Germplasm. Crop Science, 2011, 51, 52-59.	0.8	45
28	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. BMC Biology, 2015, 13, 78.	1.7	40
29	Genetic Architecture of Domestication-Related Traits in Maize. Genetics, 2016, 204, 99-113.	1.2	39
30	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. Genetics, 2020, 215, 215-230.	1.2	35
31	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. Plant Cell, 2021, 33, 882-900.	3.1	31
32	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. Genome Research, 2021, 31, 1245-1257.	2.4	29
33	The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication. PLoS Genetics, 2020, 16, e1008791.	1.5	27
34	Maize Introgression Library Provides Evidence for the Involvement of <i>liguleless1</i> in Resistance to Northern Leaf Blight. G3: Genes, Genomes, Genetics, 2020, 10, 3611-3622.	0.8	17
35	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.	1.6	16
36	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	14

#	Article	IF	Citations
37	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
38	Genome-wide imputation using the practical haplotype graph in the heterozygous crop cassava. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
39	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	0.8	5
40	Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. PLoS Genetics, 2021, 17, e1009797.	1.5	5
41	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	1.2	4
42	A conserved genetic architecture among populations of the maize progenitor, teosinte, was radically altered by domestication. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	1