Brian L Browning

List of Publications by Citations

74 papers	15,823 citations	39 h-index	78 g-index
78 ext. papers	19,659 ext. citations	9.7 avg, IF	7.08 L-index

#	Paper	IF	Citations
74	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
73	Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *American Journal of Human Genetics*, **2007**, 81, 1084-97	11	2043
72	A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. *American Journal of Human Genetics*, **2009**, 84, 210-23	11	1203
71	Genotype Imputation with Millions of Reference Samples. *American Journal of Human Genetics*, **2016**, 98, 116-26	11	612
70	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. *Nature Genetics*, **2010**, 42, 203-9	36.3	461
69	A One-Penny Imputed Genome from Next-Generation Reference Panels. *American Journal of Human Genetics*, **2018**, 103, 338-348	11	433
68	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. *Nature Genetics*, **2009**, 41, 824-8	36.3	432
67	Haplotype phasing: existing methods and new developments. *Nature Reviews Genetics*, **2011**, 12, 703-14	30.1	406
66	Improving the accuracy and efficiency of identity-by-descent detection in population data. *Genetics*, **2013**, 194, 459-71	4	320
65	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
64	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. *Annals of Neurology*, **2011**, 70, 897-912	9.4	263
63	Genetic loci associated with plasma phospholipid n-3 fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. *PLoS Genetics*, **2011**, 7, e1002193	6	257
62	A fast, powerful method for detecting identity by descent. *American Journal of Human Genetics*, **2011**, 88, 173-82	11	252
61	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. *American Journal of Human Genetics*, **2016**, 98, 165-84	11	181
60	High-resolution detection of identity by descent in unrelated individuals. *American Journal of Human Genetics*, **2010**, 86, 526-39	11	169
59	Simultaneous genotype calling and haplotype phasing improves genotype accuracy and reduces false-positive associations for genome-wide association studies. *American Journal of Human Genetics*, **2009**, 85, 847-61	11	165
58	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. *Cell*, **2018**, 173, 53-61.e9	56.2	152

57	Accurate Non-parametric Estimation of Recent Effective Population Size from Segments of Identity by Descent. *American Journal of Human Genetics*, **2015**, 97, 404-18	11	142
56	Consideration of Cosegregation in the Pathogenicity Classification of Genomic Variants. *American Journal of Human Genetics*, **2016**, 98, 1077-1081	11	127
55	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. *Genetic Epidemiology*, **2007**, 31, 365-75	2.6	121
54	The multiple sclerosis whole blood mRNA transcriptome and genetic associations indicate dysregulation of specific T cell pathways in pathogenesis. *Human Molecular Genetics*, **2010**, 19, 2134-43	5.6	103
53	Detecting identity by descent and estimating genotype error rates in sequence data. *American Journal of Human Genetics*, **2013**, 93, 840-51	11	102
52	Has toll-like receptor 4 been prematurely dismissed as an inflammatory bowel disease gene? Association study combined with meta-analysis shows strong evidence for association. *American Journal of Gastroenterology*, **2007**, 102, 2504-12	0.7	102
51	Identity by descent between distant relatives: detection and applications. *Annual Review of Genetics*, **2012**, 46, 617-33	14.5	97
50	Interactions among genes in the ErbB-Neuregulin signalling network are associated with increased susceptibility to schizophrenia. *Behavioral and Brain Functions*, **2007**, 3, 31	4.1	96
49	Population structure can inflate SNP-based heritability estimates. *American Journal of Human Genetics*, **2011**, 89, 191-3; author reply 193-5	11	69
48	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
47	Genotype Imputation from Large Reference Panels. *Annual Review of Genomics and Human Genetics* , **2018**, 19, 73-96	9.7	68
46	Genome-wide association study identifies novel loci associated with concentrations of four plasma phospholipid fatty acids in the de novo lipogenesis pathway: results from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Circulation: Cardiovascular Genetics*, **2013**, 6, 171-83		65
45	Genes, diet and inflammatory bowel disease. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2007**, 622, 70-83	3.3	64
44	Haplotypic analysis of Wellcome Trust Case Control Consortium data. *Human Genetics*, **2008**, 123, 273-80	6.3	60
43	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. *American Journal of Human Genetics*, **2013**, 93, 463-70	11	55
42	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. *American Journal of Human Genetics*, **2016**, 98, 229-42	11	54
41	Ancestry-specific recent effective population size in the Americas. *PLoS Genetics*, **2018**, 14, e1007385	6	51
40	Performance of genotype imputation for rare variants identified in exons and flanking regions of genes. *PLoS ONE*, **2011**, 6, e24945	3.7	46

39	Exome sequencing reveals novel rare variants in the ryanodine receptor and calcium channel genes in malignant hyperthermia families. *Anesthesiology*, **2013**, 119, 1054-65	4.3	45
38	Triallelic single nucleotide polymorphisms and genotyping error in genetic epidemiology studies: MDR1 (ABCB1) G2677/T/A as an example. *Cancer Epidemiology Biomarkers and Prevention*, **2007**, 16, 1185-92	4	45
37	Evaluation of Nyholt's procedure for multiple testing correction. *Human Heredity*, **2005**, 60, 19-25; discussion 61-2	1.1	39
36	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. *PLoS Genetics*, **2017**, 13, e1006760	6	38
35	PRESTO: rapid calculation of order statistic distributions and multiple-testing adjusted P-values via permutation for one and two-stage genetic association studies. *BMC Bioinformatics*, **2008**, 9, 309	3.6	36
34	Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). *G3: Genes, Genomes, Genetics*, **2016**, 6, 1525-34	3.2	34
33	A Fast and Simple Method for Detecting Identity-by-Descent Segments in Large-Scale Data. *American Journal of Human Genetics*, **2020**, 106, 426-437	11	28
32	Genetic analysis of MDR1 and inflammatory bowel disease reveals protective effect of heterozygous variants for ulcerative colitis. *Inflammatory Bowel Diseases*, **2009**, 15, 1784-93	4.5	27
31	Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. *Human Genetics*, **2013**, 132, 129-38	6.3	25
30	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. *Human Molecular Genetics*, **2017**, 26, 1193-1204	5.6	23
29	Interactions among genes influencing bacterial recognition increase IBD risk in a population-based New Zealand cohort. *Human Immunology*, **2009**, 70, 440-6	2.3	23
28	FLOSS: flexible ordered subset analysis for linkage mapping of complex traits. *Bioinformatics*, **2006**, 22, 512-3	7.2	21
27	Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. *American Journal of Human Genetics*, **2019**, 105, 883-893	11	20
26	Evaluation of IL12B as a candidate type I diabetes susceptibility gene using data from the Type I Diabetes Genetics Consortium. *Genes and Immunity*, **2009**, 10 Suppl 1, S64-8	4.4	20
25	Nucleotide-binding oligomerization domain containing 1 (NOD1) haplotypes and single nucleotide polymorphisms modify susceptibility to inflammatory bowel diseases in a New Zealand caucasian population: a case-control study. *BMC Research Notes*, **2009**, 2, 52	2.3	18
24	Single nucleotide polymorphisms in human Paneth cell defensin A5 may confer susceptibility to inflammatory bowel disease in a New Zealand Caucasian population. *Digestive and Liver Disease*, **2008**, 40, 723-30	3.3	18
23	Association of DLG5 variants with inflammatory bowel disease in the New Zealand Caucasian population and meta-analysis of the DLG5 R30Q variant. *Inflammatory Bowel Diseases*, **2007**, 13, 1069-76	4.5	18
22	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. *Genetics in Medicine*, **2014**, 16, 529-34	8.1	16

21	On reducing the statespace of hidden Markov models for the identity by descent process. *Theoretical Population Biology*, **2002**, 62, 1-8	1.2	12
20	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, **2017**, 14, 1675-1684	6.7	11
19	Linkage analysis using single nucleotide polymorphisms. *Human Heredity*, **2004**, 57, 220-7	1.1	9
18	Fast two-stage phasing of large-scale sequence data. *American Journal of Human Genetics*, **2021**, 108, 1880-1890	11	8
17	Genetics of the peloponnesean populations and the theory of extinction of the medieval peloponnesean Greeks. *European Journal of Human Genetics*, **2017**, 25, 637-645	5.3	7
16	Genome-wide haplotypic testing in a Finnish cohort identifies a novel association with low-density lipoprotein cholesterol. *European Journal of Human Genetics*, **2015**, 23, 672-7	5.3	7
15	Robust Inference of Identity by Descent from Exome-Sequencing Data. *American Journal of Human Genetics*, **2016**, 99, 1106-1116	11	6
14	Population-Specific Recombination Maps from Segments of Identity by Descent. *American Journal of Human Genetics*, **2020**, 107, 137-148	11	5
13	ASAFE: ancestry-specific allele frequency estimation. *Bioinformatics*, **2016**, 32, 2227-9	7.2	5
12	Time and frequency domain scattering for the one-dimensional wave equation. *Inverse Problems*, **2000**, 16, 1377-1403	2.3	5
11	Probabilistic Estimation of Identity by Descent Segment Endpoints and Detection of Recent Selection. *American Journal of Human Genetics*, **2020**, 107, 895-910	11	4
10	POPdemog: visualizing population demographic history from simulation scripts. *Bioinformatics*, **2018**, 34, 2854-2855	7.2	4
9	Time domain electromagnetic scattering using finite elements and perfectly matched layers. *Computer Methods in Applied Mechanics and Engineering*, **2005**, 194, 149-168	5.7	3
8	IBDkin: fast estimation of kinship coefficients from identity by descent segments. *Bioinformatics*, **2020**, 36, 4519-4520	7.2	2
7	Efficient clustering of identity-by-descent between multiple individuals. *Bioinformatics*, **2014**, 30, 915-22	7.2	2
6	A fast and simple method for detecting identity by descent segments in large-scale data		2
5	Genetic history of the population of Crete. *Annals of Human Genetics*, **2019**, 83, 373-388	2.2	1
4	A one penny imputed genome from next generation reference panels		1

3	Population-specific recombination maps from segments of identity by descent		1
2	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. *Breast Cancer Research*, **2020**, 22, 108	8.3	0
1	Genotype error biases trio-based estimates of haplotype phase accuracy. *American Journal of Human Genetics*, **2022**, 109, 1016-1025	11	0