

# Brian L Browning

## 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.

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	Genotype error biases trio-based estimates of haplotype phase accuracy. <i>American Journal of Human Genetics</i> , <b>2022</b> , 109, 1016-1025	11	0
73	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , <b>2021</b> , 590, 290-299	50.4	268
72	Fast two-stage phasing of large-scale sequence data. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1880-1890	11	8
71	Probabilistic Estimation of Identity by Descent Segment Endpoints and Detection of Recent Selection. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 895-910	11	4
70	A Fast and Simple Method for Detecting Identity-by-Descent Segments in Large-Scale Data. <i>American Journal of Human Genetics</i> , <b>2020</b> , 106, 426-437	11	28
69	Population-Specific Recombination Maps from Segments of Identity by Descent. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 137-148	11	5
68	IBDkin: fast estimation of kinship coefficients from identity by descent segments. <i>Bioinformatics</i> , <b>2020</b> , 36, 4519-4520	7.2	2
67	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. <i>Breast Cancer Research</i> , <b>2020</b> , 22, 108	8.3	0
66	Genetic history of the population of Crete. <i>Annals of Human Genetics</i> , <b>2019</b> , 83, 373-388	2.2	1
65	Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. <i>American Journal of Human Genetics</i> , <b>2019</b> , 105, 883-893	11	20
64	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. <i>Cell</i> , <b>2018</b> , 173, 53-61.e9	56.2	152
63	POPdemog: visualizing population demographic history from simulation scripts. <i>Bioinformatics</i> , <b>2018</b> , 34, 2854-2855	7.2	4
62	A One-Penny Imputed Genome from Next-Generation Reference Panels. <i>American Journal of Human Genetics</i> , <b>2018</b> , 103, 338-348	11	433
61	Ancestry-specific recent effective population size in the Americas. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007385	6	51
60	Genotype Imputation from Large Reference Panels. <i>Annual Review of Genomics and Human Genetics</i> , <b>2018</b> , 19, 73-96	9.7	68
59	Genetics of the peloponnesean populations and the theory of extinction of the medieval peloponnesean Greeks. <i>European Journal of Human Genetics</i> , <b>2017</b> , 25, 637-645	5.3	7
58	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 1193-1204	5.6	23

57	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. <i>Heart Rhythm</i> , <b>2017</b> , 14, 1675-1684	6.7	11
56	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006760	6	38
55	Robust Inference of Identity by Descent from Exome-Sequencing Data. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 1106-1116	11	6
54	ASAFE: ancestry-specific allele frequency estimation. <i>Bioinformatics</i> , <b>2016</b> , 32, 2227-9	7.2	5
53	Consideration of Cosegregation in the Pathogenicity Classification of Genomic Variants. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 1077-1081	11	127
52	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 229-42	11	54
51	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 165-84	11	181
50	Genotype Imputation with Millions of Reference Samples. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 116-26	11	612
49	Local Ancestry Inference in a Large US-Based Hispanic/Latino Study: Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 1525-34	3.2	34
48	Genome-wide haplotypic testing in a Finnish cohort identifies a novel association with low-density lipoprotein cholesterol. <i>European Journal of Human Genetics</i> , <b>2015</b> , 23, 672-7	5.3	7
47	Accurate Non-parametric Estimation of Recent Effective Population Size from Segments of Identity by Descent. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 404-18	11	142
46	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. <i>Genetics in Medicine</i> , <b>2014</b> , 16, 529-34	8.1	16
45	Efficient clustering of identity-by-descent between multiple individuals. <i>Bioinformatics</i> , <b>2014</b> , 30, 915-22	7.2	2
44	Detecting identity by descent and estimating genotype error rates in sequence data. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 840-51	11	102
43	Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. <i>Human Genetics</i> , <b>2013</b> , 132, 129-38	6.3	25
42	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 463-70	11	55
41	Improving the accuracy and efficiency of identity-by-descent detection in population data. <i>Genetics</i> , <b>2013</b> , 194, 459-71	4	320
40	Exome sequencing reveals novel rare variants in the ryanodine receptor and calcium channel genes in malignant hyperthermia families. <i>Anesthesiology</i> , <b>2013</b> , 119, 1054-65	4.3	45

39	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. <i>Circulation: Cardiovascular Genetics</i> , <b>2013</b> , 6, 171-83		65
38	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , <b>2012</b> , 491, 56-65	50.4	6049
37	Identity by descent between distant relatives: detection and applications. <i>Annual Review of Genetics</i> , <b>2012</b> , 46, 617-33	14.5	97
36	Performance of genotype imputation for rare variants identified in exons and flanking regions of genes. <i>PLoS ONE</i> , <b>2011</b> , 6, e24945	3.7	46
35	Haplotype phasing: existing methods and new developments. <i>Nature Reviews Genetics</i> , <b>2011</b> , 12, 703-14	30.1	406
34	A fast, powerful method for detecting identity by descent. <i>American Journal of Human Genetics</i> , <b>2011</b> , 88, 173-82	11	252
33	Population structure can inflate SNP-based heritability estimates. <i>American Journal of Human Genetics</i> , <b>2011</b> , 89, 191-3; author reply 193-5	11	69
32	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. <i>Annals of Neurology</i> , <b>2011</b> , 70, 897-912	9.4	263
31	Genetic loci associated with plasma phospholipid n-3 fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002193	6	257
30	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. <i>Nature Genetics</i> , <b>2010</b> , 42, 203-9	36.3	461
29	The multiple sclerosis whole blood mRNA transcriptome and genetic associations indicate dysregulation of specific T cell pathways in pathogenesis. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2134-43	5.6	103
28	High-resolution detection of identity by descent in unrelated individuals. <i>American Journal of Human Genetics</i> , <b>2010</b> , 86, 526-39	11	169
27	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. <i>BMC Research Notes</i> , <b>2009</b> , 2, 52	2.3	18
26	Genetic analysis of MDR1 and inflammatory bowel disease reveals protective effect of heterozygous variants for ulcerative colitis. <i>Inflammatory Bowel Diseases</i> , <b>2009</b> , 15, 1784-93	4.5	27
25	Evaluation of IL12B as a candidate type I diabetes susceptibility gene using data from the Type I Diabetes Genetics Consortium. <i>Genes and Immunity</i> , <b>2009</b> , 10 Suppl 1, S64-8	4.4	20
24	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. <i>Nature Genetics</i> , <b>2009</b> , 41, 824-8	36.3	432
23	A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. <i>American Journal of Human Genetics</i> , <b>2009</b> , 84, 210-23	11	1203
22	Simultaneous genotype calling and haplotype phasing improves genotype accuracy and reduces false-positive associations for genome-wide association studies. <i>American Journal of Human Genetics</i> , <b>2009</b> , 85, 847-61	11	165

21	Interactions among genes influencing bacterial recognition increase IBD risk in a population-based New Zealand cohort. <i>Human Immunology</i> , <b>2009</b> , 70, 440-6	2.3	23
20	PRESTO: rapid calculation of order statistic distributions and multiple-testing adjusted P-values via permutation for one and two-stage genetic association studies. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 309	3.6	36
19	Single nucleotide polymorphisms in human Paneth cell defensin A5 may confer susceptibility to inflammatory bowel disease in a New Zealand Caucasian population. <i>Digestive and Liver Disease</i> , <b>2008</b> , 40, 723-30	3.3	18
18	Haplotypic analysis of Wellcome Trust Case Control Consortium data. <i>Human Genetics</i> , <b>2008</b> , 123, 273-80	6.3	60
17	Interactions among genes in the ErbB-Neuregulin signalling network are associated with increased susceptibility to schizophrenia. <i>Behavioral and Brain Functions</i> , <b>2007</b> , 3, 31	4.1	96
16	Association of DLG5 variants with inflammatory bowel disease in the New Zealand Caucasian population and meta-analysis of the DLG5 R30Q variant. <i>Inflammatory Bowel Diseases</i> , <b>2007</b> , 13, 1069-76	4.5	18
15	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. <i>Genetic Epidemiology</i> , <b>2007</b> , 31, 365-75	2.6	121
14	Genes, diet and inflammatory bowel disease. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , <b>2007</b> , 622, 70-83	3.3	64
13	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. <i>American Journal of Gastroenterology</i> , <b>2007</b> , 102, 2504-12	0.7	102
12	Triallelic single nucleotide polymorphisms and genotyping error in genetic epidemiology studies: MDR1 (ABCB1) G2677/T/A as an example. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2007</b> , 16, 1185-92	4	45
11	Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. <i>American Journal of Human Genetics</i> , <b>2007</b> , 81, 1084-97	11	2043
10	FLOSS: flexible ordered subset analysis for linkage mapping of complex traits. <i>Bioinformatics</i> , <b>2006</b> , 22, 512-3	7.2	21
9	Evaluation of Nyholt's procedure for multiple testing correction. <i>Human Heredity</i> , <b>2005</b> , 60, 19-25; discussion 61-2	1.1	39
8	Time domain electromagnetic scattering using finite elements and perfectly matched layers. <i>Computer Methods in Applied Mechanics and Engineering</i> , <b>2005</b> , 194, 149-168	5.7	3
7	Linkage analysis using single nucleotide polymorphisms. <i>Human Heredity</i> , <b>2004</b> , 57, 220-7	1.1	9
6	On reducing the statespace of hidden Markov models for the identity by descent process. <i>Theoretical Population Biology</i> , <b>2002</b> , 62, 1-8	1.2	12
5	Time and frequency domain scattering for the one-dimensional wave equation. <i>Inverse Problems</i> , <b>2000</b> , 16, 1377-1403	2.3	5
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	A fast and simple method for detecting identity by descent segments in large-scale data	2
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program	68