Brian L Browning

List of Publications by Year
in descending order

70	22,023	76326	88630
papers	citations	40 h-index	70 g-index

78	78	78	38622
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genotype error biases trio-based estimates of haplotype phase accuracy. American Journal of Human Genetics, 2022, 109, 1016-1025.	6.2	5
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
3	Fast two-stage phasing of large-scale sequence data. American Journal of Human Genetics, 2021, 108, 1880-1890.	6.2	250
4	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.	5.0	9
5	Probabilistic Estimation of Identity by Descent Segment Endpoints and Detection of Recent Selection. American Journal of Human Genetics, 2020, 107, 895-910.	6.2	22
6	A Fast and Simple Method for Detecting Identity-by-Descent Segments in Large-Scale Data. American Journal of Human Genetics, 2020, 106, 426-437.	6.2	89
7	Population-Specific Recombination Maps from Segments of Identity by Descent. American Journal of Human Genetics, 2020, 107, 137-148.	6.2	24
8	IBDkin: fast estimation of kinship coefficients from identity by descent segments. Bioinformatics, 2020, 36, 4519-4520.	4.1	15
9	Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. American Journal of Human Genetics, 2019, 105, 883-893.	6.2	38
10	Genetic history of the population of Crete. Annals of Human Genetics, 2019, 83, 373-388.	0.8	2
11	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. Cell, 2018, 173, 53-61.e9.	28.9	271
12	POPdemog: visualizing population demographic history from simulation scripts. Bioinformatics, 2018, 34, 2854-2855.	4.1	9
13	Ancestry-specific recent effective population size in the Americas. PLoS Genetics, 2018, 14, e1007385.	3.5	87
14	Genotype Imputation from Large Reference Panels. Annual Review of Genomics and Human Genetics, 2018, 19, 73-96.	6.2	158
15	A One-Penny Imputed Genome from Next-Generation Reference Panels. American Journal of Human Genetics, 2018, 103, 338-348.	6.2	1,168
16	Genetics of the peloponnesean populations and the theory of extinction of the medieval peloponnesean Greeks. European Journal of Human Genetics, 2017, 25, 637-645.	2.8	22
17	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.	2.9	38
18	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18

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19	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.	3.5	53
20	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, 1525-1534.	1.8	51
21	Robust Inference of Identity by Descent from Exome-Sequencing Data. American Journal of Human Genetics, 2016, 99, 1106-1116.	6.2	8
22	ASAFE: ancestry-specific allele frequency estimation. Bioinformatics, 2016, 32, 2227-2229.	4.1	7
23	Consideration of Cosegregation in the Pathogenicity Classification of Genomic Variants. American Journal of Human Genetics, 2016, 98, 1077-1081.	6.2	205
24	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
25	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, 165-184.	6.2	266
26	Genotype Imputation with Millions of Reference Samples. American Journal of Human Genetics, 2016, 98, 116-126.	6.2	1,013
27	Accurate Non-parametric Estimation of Recent Effective Population Size from Segments of Identity by Descent. American Journal of Human Genetics, 2015, 97, 404-418.	6.2	263
28	Genome-wide haplotypic testing in a Finnish cohort identifies a novel association with low-density lipoprotein cholesterol. European Journal of Human Genetics, 2015, 23, 672-677.	2.8	9
29	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. Genetics in Medicine, 2014, 16, 529-534.	2.4	21
30	Efficient clustering of identity-by-descent between multiple individuals. Bioinformatics, 2014, 30, 915-922.	4.1	9
31	Detecting Identity by Descent and Estimating Genotype Error Rates in Sequence Data. American Journal of Human Genetics, 2013, 93, 840-851.	6.2	162
32	Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. Human Genetics, 2013, 132, 129-138.	3.8	34
33	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. American Journal of Human Genetics, 2013, 93, 463-470.	6.2	72
34	Improving the Accuracy and Efficiency of Identity-by-Descent Detection in Population Data. Genetics, 2013, 194, 459-471.	2.9	536
35	Exome Sequencing Reveals Novel Rare Variants in the Ryanodine Receptor and Calcium Channel Genes in Malignant Hyperthermia Families. Anesthesiology, 2013, 119, 1054-1065.	2.5	56
36	Genome-Wide Association Study Identifies Novel Loci Associated With Concentrations of Four Plasma Phospholipid Fatty Acids in the De Novo Lipogenesis Pathway. Circulation: Cardiovascular Genetics, 2013, 6, 171-183.	5.1	91

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37	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
38	Identity by Descent Between Distant Relatives: Detection and Applications. Annual Review of Genetics, 2012, 46, 617-633.	7.6	145
39	Performance of Genotype Imputation for Rare Variants Identified in Exons and Flanking Regions of Genes. PLoS ONE, 2011, 6, e24945.	2.5	49
40	Haplotype phasing: existing methods and new developments. Nature Reviews Genetics, 2011, 12, 703-714.	16.3	537
41	A Fast, Powerful Method for Detecting Identity by Descent. American Journal of Human Genetics, 2011, 88, 173-182.	6.2	321
42	Population Structure Can Inflate SNP-Based Heritability Estimates. American Journal of Human Genetics, 2011, 89, 191-193.	6.2	83
43	Genomeâ€wide metaâ€analysis identifies novel multiple sclerosis susceptibility loci. Annals of Neurology, 2011, 70, 897-912.	5.3	314
44	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.	3.5	324
45	High-Resolution Detection of Identity by Descent in Unrelated Individuals. American Journal of Human Genetics, 2010, 86, 526-539.	6.2	196
46	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	21.4	539
47	The multiple sclerosis whole blood mRNA transcriptome and genetic associations indicate dysregulation of specific T cell pathways in pathogenesis. Human Molecular Genetics, 2010, 19, 2134-2143.	2.9	128
48	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.	1.4	22
49	Genetic analysis of MDR1 and inflammatory bowel disease reveals protective effect of heterozygous variants for ulcerative colitis. Inflammatory Bowel Diseases, 2009, 15, 1784-1793.	1.9	36
50	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, S64-S68.	4.1	23
51	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. Nature Genetics, 2009, 41, 824-828.	21.4	501
52	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, 210-223.	6.2	1,441
53	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, 847-861.	6.2	186
54	Interactions among genes influencing bacterial recognition increase IBD risk in a population-based New Zealand cohort. Human Immunology, 2009, 70, 440-446.	2.4	25

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55	Haplotypic analysis of Wellcome Trust Case Control Consortium data. Human Genetics, 2008, 123, 273-280.	3.8	65
56	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.	2.6	43
57	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, 723-730.	0.9	22
58	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, 2504-2512.	0.4	116
59	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, 1185-1192.	2.5	49
60	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, 1084-1097.	6.2	2,845
61	Interactions among genes in the ErbB-Neuregulin signalling network are associated with increased susceptibility to schizophrenia. Behavioral and Brain Functions, 2007, 3, 31.	3.3	107
62	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, 1069-1076.	1.9	25
63	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. Genetic Epidemiology, 2007, 31, 365-375.	1.3	151
64	Genes, diet and inflammatory bowel disease. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 622, 70-83.	1.0	85
65	FLOSS: flexible ordered subset analysis for linkage mapping of complex traits. Bioinformatics, 2006, 22, 512-513.	4.1	22
66	Time domain electromagnetic scattering using finite elements and perfectly matched layers. Computer Methods in Applied Mechanics and Engineering, 2005, 194, 149-168.	6.6	5
67	Evaluation of Nyholtâ€™s Procedure for Multiple Testing Correction. Human Heredity, 2005, 60, 19-25.	0.8	45
68	Linkage Analysis Using Single Nucleotide Polymorphisms. Human Heredity, 2004, 57, 220-227.	0.8	9
69	On Reducing the Statespace of Hidden Markov Models for the Identity by Descent Process. Theoretical Population Biology, 2002, 62, 1-8.	1.1	13
70	Time and frequency domain scattering for the one-dimensional wave equation. Inverse Problems, 2000, 16, 1377-1403.	2.0	5