Sharon R Browning

List of Publications by Year
in descending order

69 papers	28,604 citations	101543 36 h-index	91884 69 g-index
84 all docs	84 docs citations	84 times ranked	46390 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	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
3	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
4	A One-Penny Imputed Genome from Next-Generation Reference Panels. American Journal of Human Genetics, 2018, 103, 338-348.	6.2	1,168
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	Genotype Imputation with Millions of Reference Samples. American Journal of Human Genetics, 2016, 98, 116-126.	6.2	1,013
7	A Groupwise Association Test for Rare Mutations Using a Weighted Sum Statistic. PLoS Genetics, 2009, 5, e1000384.	3.5	989
8	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	21.4	539
9	Haplotype phasing: existing methods and new developments. Nature Reviews Genetics, 2011, 12, 703-714.	16.3	537
10	Improving the Accuracy and Efficiency of Identity-by-Descent Detection in Population Data. Genetics, 2013, 194, 459-471.	2.9	536
11	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. Nature Genetics, 2009, 41, 824-828.	21.4	501
12	A Fast, Powerful Method for Detecting Identity by Descent. American Journal of Human Genetics, 2011, 88, 173-182.	6.2	321
13	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. Cell, 2018, 173, 53-61.e9.	28.9	271
14	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
15	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
16	Fast two-stage phasing of large-scale sequence data. American Journal of Human Genetics, 2021, 108, 1880-1890.	6.2	250
17	High-Resolution Detection of Identity by Descent in Unrelated Individuals. American Journal of Human Genetics, 2010, 86, 526-539.	6.2	196
18	Detecting Identity by Descent and Estimating Genotype Error Rates in Sequence Data. American Journal of Human Genetics, 2013, 93, 840-851.	6.2	162

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19	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. Genetic Epidemiology, 2007, 31, 365-375.	1.3	151
20	Identity by Descent Between Distant Relatives: Detection and Applications. Annual Review of Genetics, 2012, 46, 617-633.	7.6	145
21	Missing data imputation and haplotype phase inference for genome-wide association studies. Human Genetics, 2008, 124, 439-450.	3.8	142
22	Multilocus Association Mapping Using Variable-Length Markov Chains. American Journal of Human Genetics, 2006, 78, 903-913.	6.2	119
23	Detecting Rare Variant Associations by Identity-by-Descent Mapping in Case-Control Studies. Genetics, 2012, 190, 1521-1531.	2.9	103
24	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
25	Ancestry-specific recent effective population size in the Americas. PLoS Genetics, 2018, 14, e1007385.	3.5	87
26	Population Structure Can Inflate SNP-Based Heritability Estimates. American Journal of Human Genetics, 2011, 89, 191-193.	6.2	83
27	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
28	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	7.1	71
29	Haplotypic analysis of Wellcome Trust Case Control Consortium data. Human Genetics, 2008, 123, 273-280.	3.8	65
30	Estimation of Pairwise Identity by Descent From Dense Genetic Marker Data in a Population Sample of Haplotypes. Genetics, 2008, 178, 2123-2132.	2.9	65
31	A Polymorphism in the HLA-DPB1 Gene Is Associated with Susceptibility to Multiple Sclerosis. PLoS ONE, 2010, 5, e13454.	2.5	55
32	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
33	Saliva-Derived DNA Performs Well in Large-Scale, High-Density Single-Nucleotide Polymorphism Microarray Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 794-798.	2.5	52
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, 1525-1534.	1.8	51
35	Performance of Genotype Imputation for Rare Variants Identified in Exons and Flanking Regions of Genes. PLoS ONE, 2011, 6, e24945.	2.5	49
36	Case-control single-marker and haplotypic association analysis of pedigree data. Genetic Epidemiology, 2005, 28, 110-122.	1.3	48

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37	Imputation-Based Genomic Coverage Assessments of Current Human Genotyping Arrays. G3: Genes, Genomes, Genetics, 2013, 3, 1795-1807.	1.8	43
38	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
39	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
40	Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. American Journal of Human Genetics, 2019, 105, 883-893.	6.2	38
41	Deletion at the SLC1A1 glutamate transporter gene coâ€segregates with schizophrenia and bipolar schizoaffective disorder in a 5â€generation family. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 87-95.	1.7	36
42	Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. Human Genetics, 2013, 132, 129-138.	3.8	34
43	Admixture Mapping Identifies an Amerindian Ancestry Locus Associated with Albuminuria in Hispanics in the United States. Journal of the American Society of Nephrology: JASN, 2017, 28, 2211-2220.	6.1	33
44	Admixture mapping in the Hispanic Community Health Study/Study of Latinos reveals regions of genetic associations with blood pressure traits. PLoS ONE, 2017, 12, e0188400.	2.5	29
45	Population Structure With Localized Haplotype Clusters. Genetics, 2010, 185, 1337-1344.	2.9	28
46	Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465.	6.2	25
47	Population-Specific Recombination Maps from Segments of Identity by Descent. American Journal of Human Genetics, 2020, 107, 137-148.	6.2	24
48	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
49	A Canine Model of Inherited Myopia: Familial Aggregation of Refractive Error in Labrador Retrievers. , 2008, 49, 4784.		18
50	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
51	Relationship Information Contained in Gamete Identity by Descent Data. Journal of Computational Biology, 1998, 5, 323-334.	1.6	16
52	A neurodegenerative disease landscape of rare mutations in Colombia due to founder effects. Genome Medicine, 2022, 14, 27.	8.2	16
53	IBDkin: fast estimation of kinship coefficients from identity by descent segments. Bioinformatics, 2020, 36, 4519-4520.	4.1	15
54	Phenotypic population screen identifies a new mutation in bovine DGAT1 responsible for unsaturated milk fat. Scientific Reports, 2015, 5, 8484.	3.3	14

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55	Evolutionary history of modern Samoans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9458-9465.	7.1	14
56	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
57	On Reducing the Statespace of Hidden Markov Models for the Identity by Descent Process. Theoretical Population Biology, 2002, 62, 1-8.	1.1	13
58	The Relationship Between Count-Location and Stationary Renewal Models for the Chiasma Process. Genetics, 2000, 155, 1955-1960.	2.9	12
59	Efficient clustering of identity-by-descent between multiple individuals. Bioinformatics, 2014, 30, 915-922.	4.1	9
60	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
61	POPdemog: visualizing population demographic history from simulation scripts. Bioinformatics, 2018, 34, 2854-2855.	4.1	9
62	Robust Inference of Identity by Descent from Exome-Sequencing Data. American Journal of Human Genetics, 2016, 99, 1106-1116.	6.2	8
63	ASAFE: ancestry-specific allele frequency estimation. Bioinformatics, 2016, 32, 2227-2229.	4.1	7
64	Protocol for detecting introgressed archaic variants with SPrime. STAR Protocols, 2021, 2, 100550.	1.2	6
65	Genotype error biases trio-based estimates of haplotype phase accuracy. American Journal of Human Genetics, 2022, 109, 1016-1025.	6.2	5
66	A Monte Carlo approach to calculating probabilities for continuous identity by descent data. Journal of Applied Probability, 2000, 37, 850-864.	0.7	4
67	A Monte Carlo approach to calculating probabilities for continuous identity by descent data. Journal of Applied Probability, 2000, 37, 850-864.	0.7	4
68	Multilocus analysis of GAW15 NARAC chromosome 18 case-control data. BMC Proceedings, 2007, 1, S11.	1.6	2
69	AFA: Ancestry-specific allele frequency estimation in admixed populations: The Hispanic Community Health Study/Study of Latinos. Human Genetics and Genomics Advances, 2022, 3, 100096.	1.7	2