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 neurodegenerative disease landscape of rare mutations in Colombia due to founder effects. Genome Medicine, 2022, 14, 27.	8.2	16
2	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
3	Genotype error biases trio-based estimates of haplotype phase accuracy. American Journal of Human Genetics, 2022, 109, 1016-1025.	6.2	5
4	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
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	Protocol for detecting introgressed archaic variants with SPrime. STAR Protocols, 2021, 2, 100550.	1.2	6
7	Fast two-stage phasing of large-scale sequence data. American Journal of Human Genetics, 2021, 108, 1880-1890.	6.2	250
8	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
9	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
10	Population-Specific Recombination Maps from Segments of Identity by Descent. American Journal of Human Genetics, 2020, 107, 137-148.	6.2	24
11	IBDkin: fast estimation of kinship coefficients from identity by descent segments. Bioinformatics, 2020, 36, 4519-4520.	4.1	15
12	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
13	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
14	Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. American Journal of Human Genetics, 2019, 105, 883-893.	6.2	38
15	Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465.	6.2	25
16	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	2.9	41
17	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. Cell, 2018, 173, 53-61.e9.	28.9	271
18	POPdemog: visualizing population demographic history from simulation scripts. Bioinformatics, 2018, 34, 2854-2855.	4.1	9

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19	Ancestry-specific recent effective population size in the Americas. PLoS Genetics, 2018, 14, e1007385.	3.5	87
20	A One-Penny Imputed Genome from Next-Generation Reference Panels. American Journal of Human Genetics, 2018, 103, 338-348.	6.2	1,168
21	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
22	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
23	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
24	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
25	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
26	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
27	Robust Inference of Identity by Descent from Exome-Sequencing Data. American Journal of Human Genetics, 2016, 99, 1106-1116.	6.2	8
28	ASAFE: ancestry-specific allele frequency estimation. Bioinformatics, 2016, 32, 2227-2229.	4.1	7
29	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
30	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
31	Genotype Imputation with Millions of Reference Samples. American Journal of Human Genetics, 2016, 98, 116-126.	6.2	1,013
32	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
33	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
34	Phenotypic population screen identifies a new mutation in bovine DGAT1 responsible for unsaturated milk fat. Scientific Reports, 2015, 5, 8484.	3.3	14
35	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
36	Efficient clustering of identity-by-descent between multiple individuals. Bioinformatics, 2014, 30, 915-922.	4.1	9

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37	Detecting Identity by Descent and Estimating Genotype Error Rates in Sequence Data. American Journal of Human Genetics, 2013, 93, 840-851.	6.2	162
38	Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. Human Genetics, 2013, 132, 129-138.	3.8	34
39	Improving the Accuracy and Efficiency of Identity-by-Descent Detection in Population Data. Genetics, 2013, 194, 459-471.	2.9	536
40	Imputation-Based Genomic Coverage Assessments of Current Human Genotyping Arrays. G3: Genes, Genomes, Genetics, 2013, 3, 1795-1807.	1.8	43
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	Detecting Rare Variant Associations by Identity-by-Descent Mapping in Case-Control Studies. Genetics, 2012, 190, 1521-1531.	2.9	103
43	Identity by Descent Between Distant Relatives: Detection and Applications. Annual Review of Genetics, 2012, 46, 617-633.	7.6	145
44	Performance of Genotype Imputation for Rare Variants Identified in Exons and Flanking Regions of Genes. PLoS ONE, 2011, 6, e24945.	2.5	49
45	Haplotype phasing: existing methods and new developments. Nature Reviews Genetics, 2011, 12, 703-714.	16.3	537
46	A Fast, Powerful Method for Detecting Identity by Descent. American Journal of Human Genetics, 2011, 88, 173-182.	6.2	321
47	Population Structure Can Inflate SNP-Based Heritability Estimates. American Journal of Human Genetics, 2011, 89, 191-193.	6.2	83
48	High-Resolution Detection of Identity by Descent in Unrelated Individuals. American Journal of Human Genetics, 2010, 86, 526-539.	6.2	196
49	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	21.4	539
50	A Polymorphism in the HLA-DPB1 Gene Is Associated with Susceptibility to Multiple Sclerosis. PLoS ONE, 2010, 5, e13454.	2.5	55
51	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
52	Population Structure With Localized Haplotype Clusters. Genetics, 2010, 185, 1337-1344.	2.9	28
53	A Groupwise Association Test for Rare Mutations Using a Weighted Sum Statistic. PLoS Genetics, 2009, 5, e1000384.	3.5	989
54	Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. Nature Genetics, 2009, 41, 824-828.	21.4	501

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55	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
56	Haplotypic analysis of Wellcome Trust Case Control Consortium data. Human Genetics, 2008, 123, 273-280.	3.8	65
57	Missing data imputation and haplotype phase inference for genome-wide association studies. Human Genetics, 2008, 124, 439-450.	3.8	142
58	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
59	A Canine Model of Inherited Myopia: Familial Aggregation of Refractive Error in Labrador Retrievers. , 2008, 49, 4784.		18
60	Multilocus analysis of GAW15 NARAC chromosome 18 case-control data. BMC Proceedings, 2007, 1, S11.	1.6	2
61	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
62	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. Genetic Epidemiology, 2007, 31, 365-375.	1.3	151
63	Multilocus Association Mapping Using Variable-Length Markov Chains. American Journal of Human Genetics, 2006, 78, 903-913.	6.2	119
64	Case-control single-marker and haplotypic association analysis of pedigree data. Genetic Epidemiology, 2005, 28, 110-122.	1.3	48
65	On Reducing the Statespace of Hidden Markov Models for the Identity by Descent Process. Theoretical Population Biology, 2002, 62, 1-8.	1.1	13
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	The Relationship Between Count-Location and Stationary Renewal Models for the Chiasma Process. Genetics, 2000, 155, 1955-1960.	2.9	12
69	Relationship Information Contained in Gamete Identity by Descent Data. Journal of Computational Biology, 1998, 5, 323-334.	1.6	16