

Brenna Henn

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

9,359
citations

109321

35
h-index

144013

57
g-index

72
all docs

72
docs citations

72
times ranked

12983
citing authors

#	ARTICLE	IF	CITATIONS
1	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
2	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
3	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
4	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	7.1	589
5	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5154-5162.	7.1	394
6	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , 2012, 3, 698.	12.8	382
7	The great human expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17758-17764.	7.1	364
8	Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?. <i>Trends in Ecology and Evolution</i> , 2018, 33, 582-594.	8.7	315
9	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	12.6	293
10	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	3.5	275
11	The genetic prehistory of southern Africa. <i>Nature Communications</i> , 2012, 3, 1143.	12.8	271
12	Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females. <i>Science</i> , 2013, 341, 562-565.	12.6	235
13	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 333-343.	16.3	233
14	Rapid, global demographic expansions after the origins of agriculture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6044-6049.	7.1	225
15	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E440-9.	7.1	224
16	History of Click-Speaking Populations of Africa Inferred from mtDNA and Y Chromosome Genetic Variation. <i>Molecular Biology and Evolution</i> , 2007, 24, 2180-2195.	8.9	202
17	Cryptic Distant Relatives Are Common in Both Isolated and Cosmopolitan Genetic Samples. <i>PLoS ONE</i> , 2012, 7, e34267.	2.5	184
18	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11791-11796.	7.1	174

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19	African Y Chromosome and mtDNA Divergence Provides Insight into the History of Click Languages. <i>Current Biology</i> , 2003, 13, 464-473.	3.9	173
20	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	28.9	134
21	Y-chromosomal evidence of a pastoralist migration through Tanzania to southern Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10693-10698.	7.1	133
22	Characterizing the Time Dependency of Human Mitochondrial DNA Mutation Rate Estimates. <i>Molecular Biology and Evolution</i> , 2008, 26, 217-230.	8.9	111
23	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. <i>Genetics</i> , 2016, 204, 303-314.	2.9	93
24	Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans. <i>PLoS Genetics</i> , 2017, 13, e1006560.	3.5	87
25	Population Genomic Analysis of Ancient and Modern Genomes Yields New Insights into the Genetic Ancestry of the Tyrolean Iceman and the Genetic Structure of Europe. <i>PLoS Genetics</i> , 2014, 10, e1004353.	3.5	86
26	Localization of adaptive variants in human genomes using averaged one-dependence estimation. <i>Nature Communications</i> , 2018, 9, 703.	12.8	83
27	A Panel of Ancestry Informative Markers for the Complex Five-Way Admixed South African Coloured Population. <i>PLoS ONE</i> , 2013, 8, e82224.	2.5	74
28	Limited Evidence for Classic Selective Sweeps in African Populations. <i>Genetics</i> , 2012, 192, 1049-1064.	2.9	72
29	The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. <i>European Journal of Human Genetics</i> , 2010, 18, 348-353.	2.8	71
30	Population and Evolutionary Genomics of <i>Amblyomma americanum</i> , an Expanding Arthropod Disease Vector. <i>Genome Biology and Evolution</i> , 2016, 8, 1351-1360.	2.5	70
31	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017, 206, 1659-1674.	2.9	69
32	Clarifying distinct models of modern human origins in Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 148-156.	3.3	51
33	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13865-13870.	7.1	49
34	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. <i>PLoS Genetics</i> , 2014, 10, e1004549.	3.5	49
35	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. <i>PLoS ONE</i> , 2013, 8, e73971.	2.5	42
36	Loss and Gain of Natural Killer Cell Receptor Function in an African Hunter-Gatherer Population. <i>PLoS Genetics</i> , 2015, 11, e1005439.	3.5	42

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37	High rate of extrapair paternity in a human population demonstrates diversity in human reproductive strategies. <i>Science Advances</i> , 2020, 6, eaay6195.	10.3	41
38	Worldwide patterns of human epigenetic variation. <i>Nature Ecology and Evolution</i> , 2017, 1, 1577-1583.	7.8	40
39	Exome capture from saliva produces high quality genomic and metagenomic data. <i>BMC Genomics</i> , 2014, 15, 262.	2.8	34
40	Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA-C in Two Indigenous Human Populations in Southern Africa. <i>Journal of Immunology</i> , 2018, 200, 2640-2655.	0.8	32
41	A Sex-Stratified Genome-Wide Association Study of Tuberculosis Using a Multi-Ethnic Genotyping Array. <i>Frontiers in Genetics</i> , 2018, 9, 678.	2.3	28
42	Diversity of KIR, HLA Class I, and Their Interactions in Seven Populations of Sub-Saharan Africans. <i>Journal of Immunology</i> , 2019, 202, 2636-2647.	0.8	26
43	Fine-scale population structure and the era of next-generation sequencing. <i>Human Molecular Genetics</i> , 2010, 19, R221-R226.	2.9	25
44	Admixed Populations Improve Power for Variant Discovery and Portability in Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 673167.	2.3	22
45	Population structure and infectious disease risk in southern Africa. <i>Molecular Genetics and Genomics</i> , 2017, 292, 499-509.	2.1	21
46	A post-GWAS analysis of predicted regulatory variants and tuberculosis susceptibility. <i>PLoS ONE</i> , 2017, 12, e0174738.	2.5	19
47	Rapid evolution of a skin-lightening allele in southern African KhoeSan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13324-13329.	7.1	17
48	Hunter-gatherer genomes reveal diverse demographic trajectories during the rise of farming in Eastern Africa. <i>Current Biology</i> , 2022, 32, 1852-1860.e5.	3.9	15
49	Shadows of early migrations. <i>Nature</i> , 2010, 468, 1044-1045.	27.8	9
50	Worldwide variation in hip fracture incidence weakly aligns with genetic divergence between populations. <i>Osteoporosis International</i> , 2016, 27, 2867-2872.	3.1	9
51	Inferring archaic introgression from hominin genetic data. <i>Evolutionary Anthropology</i> , 2021, 30, 199-220.	3.4	9
52	IMPUTOR: Phylogenetically Aware Software for Imputation of Errors in Next-Generation Sequencing. <i>Genome Biology and Evolution</i> , 2018, 10, 1248-1254.	2.5	7
53	Inferring recombination patterns in African populations. <i>Human Molecular Genetics</i> , 2021, 30, R11-R16.	2.9	6
54	Reply to Hublin and Klein: Locating a geographic point of dispersion in Africa for contemporary humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, .	7.1	5

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55	The great human expansion. <i>Resonance</i> , 2019, 24, 711-718.	0.3	5
56	The ethics and logistics of field-based genetic paternity studies. <i>Evolutionary Human Sciences</i> , 2020, 2, .	1.7	3
57	Molecular Anthropology is dead, long live Molecular Anthropology. <i>Journal of Anthropological Sciences</i> , 2021, 99, .	0.4	0