Daniel Shriner

List of Publications by Year
in descending order

101 papers	6,677 citations	81839 39 h-index	66879 78 g-index
111 all docs	111 docs citations	111 times ranked	12969 citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
2	Moving toward System Genetics through Multiple Trait Analysis in Genome-Wide Association Studies. Frontiers in Genetics, 2012, 3, 1.	1.1	231
3	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
4	High-depth African genomes inform human migration and health. Nature, 2020, 586, 741-748.	13.7	197
5	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
6	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189
7	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
8	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
9	Detection of Gene Ã— Gene Interactions in Genome-Wide Association Studies of Human Population Data. Human Heredity, 2007, 63, 67-84.	0.4	164
10	Potential impact of recombination on sitewise approaches for detecting positive natural selection. Genetical Research, 2003, 81, 115-121.	0.3	158
11	Pervasive Genomic Recombination of HIV-1 in VivoSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY496645, AY496646, AY496647, AY496648, AY496649, AY496650, AY496651, AY496652, AY496653, AY496654, AY496655, AY496656, AY496657, AY496658, AY496659, AY496660, AY496661, AY496662, AY496663, AY496664, AY496665, AY496666, AY496667, AY496668, AY496669, AY496670, AY496671, AY496672, AY496673, AY496674, AY496675, AY496676, AY496677, AY496678, AY496679, AY49. Genetics, 2004, 167, 1573-1583.	1.2	139
12	Selection on the Human Immunodeficiency Virus Type 1 Proteome following Primary Infection. Journal of Virology, 2006, 80, 9519-9529.	1.5	118
13	R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. Bioinformatics, 2007, 23, 641-643.	1.8	115
14	Genetic Association for Renal Traits among Participants of African Ancestry Reveals New Loci for Renal Function. PLoS Genetics, 2011, 7, e1002264.	1.5	109
15	Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. PLoS Genetics, 2013, 9, e1003681.	1.5	109
16	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. Human Molecular Genetics, 2011, 20, 4056-4068.	1.4	101
17	Evolutionary Indicators of Human Immunodeficiency Virus Type 1 Reservoirs and Compartments. Journal of Virology, 2003, 77, 5540-5546.	1.5	97
18	<i>FTO</i> Genetic Variation and Association With Obesity in West Africans and African Americans. Diabetes, 2010, 59, 1549-1554.	0.3	94

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19	Genome-wide association of anthropometric traits in African- and African-derived populations. Human Molecular Genetics, 2010, 19, 2725-2738.	1.4	90
20	Ancient familial Mediterranean fever mutations in human pyrin and resistance to Yersinia pestis. Nature Immunology, 2020, 21, 857-867.	7.0	90
21	Joint Ancestry and Association Testing in Admixed Individuals. PLoS Computational Biology, 2011, 7, e1002325.	1.5	88
22	A genome-wide association study of serum uric acid in African Americans. BMC Medical Genomics, 2011, 4, 17.	0.7	82
23	Genome-wide association study identifies novel loci association with fasting insulin and insulin resistance in African Americans. Human Molecular Genetics, 2012, 21, 4530-4536.	1.4	80
24	Whole-Genome-Sequence-Based Haplotypes Reveal Single Origin of the Sickle Allele during the Holocene Wet Phase. American Journal of Human Genetics, 2018, 102, 547-556.	2.6	77
25	Overview of Admixture Mapping. Current Protocols in Human Genetics, 2013, 76, Unit 1.23.	3.5	76
26	An Efficient Bayesian Model Selection Approach for Interacting Quantitative Trait Loci Models With Many Effects. Genetics, 2007, 176, 1865-1877.	1.2	73
27	ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. Nature Communications, 2019, 10, 3195.	5.8	69
28	Human ancestry correlates with language and reveals that race is not an objective genomic classifier. Scientific Reports, 2017, 7, 1572.	1.6	66
29	Influence of Random Genetic Drift on Human Immunodeficiency Virus Type 1 env Evolution During Chronic Infection. Genetics, 2004, 166, 1155-1164.	1.2	65
30	The genomic landscape of African populations in health and disease. Human Molecular Genetics, 2017, 26, R225-R236.	1.4	64
31	UGT1A1 is a major locus influencing bilirubin levels in African Americans. European Journal of Human Genetics, 2012, 20, 463-468.	1.4	63
32	The Roles of IL-6, IL-10, and IL-1RA in Obesity and Insulin Resistance in African-Americans. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E2018-E2022.	1.8	59
33	Type 2 diabetes complications and comorbidity in Sub-Saharan Africans. EClinicalMedicine, 2019, 16, 30-41.	3.2	58
34	Genome-wide genotype and sequence-based reconstruction of the 140,000 year history of modern human ancestry. Scientific Reports, 2015, 4, 6055.	1.6	54
35	Mapping of disease-associated variants in admixed populations. Genome Biology, 2011, 12, 223.	13.9	53
36	*HLA* and autoantibodies define scleroderma subtypes and risk in African and European Americans and suggest a role for molecular mimicry. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 552-562.	3.3	52

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37	Evaluation of Genome Wide Association Study Associated Type 2 Diabetes Susceptibility Loci in Sub Saharan Africans. Frontiers in Genetics, 2015, 6, 335.	1.1	50
38	Transferability and Fine-Mapping of Genome-Wide Associated Loci for Adult Height across Human Populations. PLoS ONE, 2009, 4, e8398.	1.1	47
39	Importance and detection of virus reservoirs and compartments of HIV infection. Current Opinion in Microbiology, 2003, 6, 410-416.	2.3	46
40	The African diaspora: history, adaptation and health. Current Opinion in Genetics and Development, 2016, 41, 77-84.	1.5	44
41	Genome-wide association study identifies African-ancestry specific variants for metabolic syndrome. Molecular Genetics and Metabolism, 2015, 116, 305-313.	0.5	41
42	Circulating Adiponectin Is Associated with Obesity and Serum Lipids in West Africans. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3517-3521.	1.8	37
43	Analyses of genome wide association data, cytokines, and gene expression in African-Americans with benign ethnic neutropenia. PLoS ONE, 2018, 13, e0194400.	1.1	36
44	Gene-Based Sequencing Identifies Lipid-Influencing Variants with Ethnicity-Specific Effects in African Americans. PLoS Genetics, 2014, 10, e1004190.	1.5	34
45	Overview of Admixture Mapping. Current Protocols in Human Genetics, 2017, 94, 1.23.1-1.23.8.	3.5	34
46	Transferability and Fine Mapping of genome-wide associated loci for lipids in African Americans. BMC Medical Genetics, 2012, 13, 88.	2.1	33
47	Practical considerations for imputation of untyped markers in admixed populations. Genetic Epidemiology, 2010, 34, 258-265.	0.6	32
48	C-reactive protein (CRP) promoter polymorphisms influence circulating CRP levels in a genome-wide association study of African Americans. Human Molecular Genetics, 2012, 21, 3063-3072.	1.4	32
49	Genome-wide associated loci influencing interleukin (IL)-10, IL-1Ra, and IL-6 levels in African Americans. Immunogenetics, 2012, 64, 351-359.	1.2	31
50	Genomeâ€wide analysis identifies an africanâ€specific variant in <i>SEMA4D</i> associated with body mass index. Obesity, 2017, 25, 794-800.	1.5	30
51	Evolution of intrahost HIV-1 genetic diversity during chronic infection. Evolution; International Journal of Organic Evolution, 2006, 60, 1165-76.	1.1	30
52	EVOLUTION OF INTRAHOST HIV - 1 GENETIC DIVERSITY DURING CHRONIC INFECTION. Evolution; International Journal of Organic Evolution, 2006, 60, 1165-1176.	1.1	28
53	Variation in <i>APOL1</i> Contributes to Ancestry-Level Differences in HDLc-Kidney Function Association. International Journal of Nephrology, 2012, 2012, 1-10.	0.7	28
54	Accounting for Linkage Disequilibrium in Association Analysis of Diverse Populations. Genetic Epidemiology, 2014, 38, 265-273.	0.6	25

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55	Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies â€. Nucleic Acids Research, 2008, 36, e26-e26.	6.5	24
56	Deviance information criterion (DIC) in Bayesian multiple QTL mapping. Computational Statistics and Data Analysis, 2009, 53, 1850-1860.	0.7	22
57	Genetic modifiers of longâ€term survival in sickle cell anemia. Clinical and Translational Medicine, 2020, 10, e152.	1.7	21
58	Molecular clock-like evolution of human immunodeficiency virus type 1. Virology, 2004, 329, 101-108.	1.1	15
59	EVOLUTION OF INTRAHOST HIV-1 GENETIC DIVERSITY DURING CHRONIC INFECTION. Evolution; International Journal of Organic Evolution, 2006, 60, 1165.	1.1	15
60	Development of admixture mapping panels for African Americans from commercial high-density SNP arrays. BMC Genomics, 2010, 11, 417.	1.2	15
61	Ancient Human Migration after Out-of-Africa. Scientific Reports, 2016, 6, 26565.	1.6	15
62	Genome science and health disparities: a growing success story?. Genome Medicine, 2013, 5, 61.	3.6	14
63	Phenotypic variance explained by local ancestry in admixed African Americans. Frontiers in Genetics, 2015, 6, 324.	1.1	13
64	Trans-ethnic meta-analysis identifies new loci associated with longitudinal blood pressure traits. Scientific Reports, 2021, 11, 4075.	1.6	13
65	Approximate and exact tests of Hardy-Weinberg equilibrium using uncertain genotypes. Genetic Epidemiology, 2011, 35, 632-637.	0.6	12
66	Identifying a major locus that regulates spontaneous arthritis in IL-1ra-deficient mice and analysis of potential candidates. Genetical Research, 2011, 93, 95-103.	0.3	12
67	Admixture mapping identifies genetic regions associated with blood pressure phenotypes in African Americans. PLoS ONE, 2020, 15, e0232048.	1.1	12
68	Improved Eigenanalysis of Discrete Subpopulations and Admixture Using the Minimum Average Partial Test. Human Heredity, 2012, 73, 73-83.	0.4	11
69	Transferability of genome-wide associated loci for asthma in African Americans. Journal of Asthma, 2017, 54, 1-8.	0.9	11
70	A unified framework for multi-locus association analysis of both common and rare variants. BMC Genomics, 2011, 12, 89.	1.2	10
71	Genetic history of Chad. American Journal of Physical Anthropology, 2018, 167, 804-812.	2.1	10
72	Brief Report: Wholeâ€Exome Sequencing to Identify Rare Variants and Gene Networks That Increase Susceptibility to Scleroderma in African Americans. Arthritis and Rheumatology, 2018, 70, 1654-1660.	2.9	10

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73	Common and rare exonic MUC5B variants associated with type 2 diabetes in Han Chinese. PLoS ONE, 2017, 12, e0173784.	1.1	10
74	APOL1 G1 genotype modifies the association between HDLC and kidney function in African Americans. BMC Genomics, 2015, 16, 421.	1.2	9
75	Impact of Type 2 Diabetes on Impaired Kidney Function in Sub-Saharan African Populations. Frontiers in Endocrinology, 2016, 7, 50.	1.5	9
76	Impact of Hardy–Weinberg disequilibrium on post-imputation quality control. Human Genetics, 2013, 132, 1073-1075.	1.8	7
77	Evolutionary context for the association of γ-globin, serum uric acid, and hypertension in African Americans. BMC Medical Genetics, 2015, 16, 103.	2.1	7
78	Multiple Loci Associated with Renal Function in African Americans. PLoS ONE, 2012, 7, e45112.	1.1	7
79	An Improved Fst Estimator. PLoS ONE, 2015, 10, e0135368.	1.1	6
80	Genetic Ancestry of Hadza and Sandawe Peoples Reveals Ancient Population Structure in Africa. Genome Biology and Evolution, 2018, 10, 875-882.	1.1	6
81	Genetics of cognitive trajectory in Brazilians: 15 years of follow-up from the Bambuí-Epigen Cohort Study of Aging. Scientific Reports, 2019, 9, 18085.	1.6	6
82	Refining genome-wide associated loci for serum uric acid in individuals with African ancestry. Human Molecular Genetics, 2020, 29, 506-514.	1.4	6
83	A UGT1A1 variant is associated with serum total bilirubin levels, which are causal for hypertension in African-ancestry individuals. Npj Genomic Medicine, 2021, 6, 44.	1.7	6
84	GWAS in Africans identifies novel lipids loci and demonstrates heterogenous association within Africa. Human Molecular Genetics, 2021, 30, 2205-2214.	1.4	6
85	Re-analysis of Whole Genome Sequence Data From 279 Ancient Eurasians Reveals Substantial Ancestral Heterogeneity. Frontiers in Genetics, 2018, 9, 268.	1.1	5
86	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. Leukemia, 2021, 35, 1209-1213.	3.3	5
87	Evolutionary genetics and acclimatization in nephrology. Nature Reviews Nephrology, 2021, 17, 827-839.	4.1	5
88	Migration Route Out of Africa Unresolved by 225 Egyptian and Ethiopian Whole Genome Sequences. Frontiers in Genetics, 2016, 7, 98.	1.1	4
89	Additive genetic effect of GCKR, G6PC2, and SLC30A8 variants on fasting glucose levels and risk of type 2 diabetes. PLoS ONE, 2022, 17, e0269378.	1.1	4
90	Mixed Ancestry and Disease Risk Transferability. Current Genetic Medicine Reports, 2015, 3, 151-157.	1.9	3

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91	Mapping multiple quantitative trait loci under Bayes error control. Genetical Research, 2009, 91, 147-159.	0.3	1
92	Reconciling clinical importance and statistical significance. European Journal of Human Genetics, 2014, 22, 158-159.	1.4	1
93	Estimation of F_{ST} and the Impact of de novo Mutation. Human Heredity, 2016, 82, 37-49.	0.4	1
94	Time-to-event modeling of hypertension reveals the nonexistence of true controls. ELife, 2020, 9, .	2.8	1
95	Putting Materials and Methods in Their Place. Science, 2008, 322, 1463-1463.	6.0	0
96	Pharmacogenomics and Infectious Diseases in Africa. , 2019, , 95-127.		0
97	Statistical Methods for Multiple QTL Mapping in Experimental Crosses. , 2007, , 285-323.		0
98	Title is missing!. , 2020, 15, e0232048.		0
99	Title is missing!. , 2020, 15, e0232048.		0
100	Title is missing!. , 2020, 15, e0232048.		0
101	Title is missing!. , 2020, 15, e0232048.		0