Sarah A Tishkoff

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3036648/publications.pdf

Version: 2024-02-01

114 papers 19,110 citations

59 h-index 21540 114 g-index

122 all docs $\begin{array}{c} 122 \\ \\ \text{docs citations} \end{array}$

times ranked

122

22832 citing authors

#	Article	IF	CITATIONS
1	Convergent adaptation of human lactase persistence in Africa and Europe. Nature Genetics, 2007, 39, 31-40.	21.4	1,375
2	The Genetic Structure and History of Africans and African Americans. Science, 2009, 324, 1035-1044.	12.6	1,267
3	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
4	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
5	The Missing Diversity in Human Genetic Studies. Cell, 2019, 177, 26-31.	28.9	838
6	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
7	African Genetic Diversity: Implications for Human Demographic History, Modern Human Origins, and Complex Disease Mapping. Annual Review of Genomics and Human Genetics, 2008, 9, 403-433.	6.2	625
8	Tracing the peopling of the world through genomics. Nature, 2017, 541, 302-310.	27.8	562
9	Taking race out of human genetics. Science, 2016, 351, 564-565.	12.6	474
10	<i>Microcephalin</i> $$, a Gene Regulating Brain Size, Continues to Evolve Adaptively in Humans. Science, 2005, 309, 1717-1720.	12.6	447
11	Ongoing Adaptive Evolution of <i>ASPM</i> , a Brain Size Determinant in <i>Homo sapiens</i> . Science, 2005, 309, 1720-1722.	12.6	445
12	Genome-wide patterns of population structure and admixture in West Africans and African Americans. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 786-791.	7.1	430
13	A High-Density Admixture Map for Disease Gene Discovery in African Americans. American Journal of Human Genetics, 2004, 74, 1001-1013.	6.2	416
14	Implications of biogeography of human populations for 'race' and medicine. Nature Genetics, 2004, 36, S21-S27.	21.4	403
15	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	27.8	360
16	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
17	Genetic adaptation to high altitude in the Ethiopian highlands. Genome Biology, 2012, 13, R1.	9.6	327
18	Genetic analysis of African populations: human evolution and complex disease. Nature Reviews Genetics, 2002, 3, 611-621.	16.3	310

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19	Patterns of Human Genetic Diversity: Implications for Human Evolutionary History and Disease. Annual Review of Genomics and Human Genetics, 2003, 4, 293-340.	6.2	302
20	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
21	Evolutionary History and Adaptation from High-Coverage Whole-Genome Sequences of Diverse African Hunter-Gatherers. Cell, 2012, 150, 457-469.	28.9	289
22	SNP ascertainment bias in population genetic analyses: Why it is important, and how to correct it. BioEssays, 2013, 35, 780-786.	2.5	283
23	The genetic prehistory of southern Africa. Nature Communications, 2012, 3, 1143.	12.8	271
24	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
25	Going global by adapting local: A review of recent human adaptation. Science, 2016, 354, 54-59.	12.6	254
26	Whole-mtDNA Genome Sequence Analysis of Ancient African Lineages. Molecular Biology and Evolution, 2007, 24, 757-768.	8.9	234
27	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. Human Molecular Genetics, 2012, 21, 5385-5394.	2.9	210
28	History of Click-Speaking Populations of Africa Inferred from mtDNA and Y Chromosome Genetic Variation. Molecular Biology and Evolution, 2007, 24, 2180-2195.	8.9	202
29	Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. American Journal of Human Genetics, 2014, 94, 496-510.	6.2	174
30	The Evolution of Human Genetic and Phenotypic Variation in Africa. Current Biology, 2010, 20, R166-R173.	3.9	169
31	Molecular haplotyping of genetic markers 10 kb apart by allele-specific long-range PCR. Nucleic Acids Research, 1996, 24, 4841-4843.	14.5	137
32	Evidence for Balancing Selection from Nucleotide Sequence Analyses of Human G6PD. American Journal of Human Genetics, 2002, 71, 1112-1128.	6.2	136
33	Y-chromosomal evidence of a pastoralist migration through Tanzania to southern Africa. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10693-10698.	7.1	133
34	Structural diversity and African origin of the 17q21.31 inversion polymorphism. Nature Genetics, 2012, 44, 872-880.	21,4	129
35	Patterns of Ancestry, Signatures of Natural Selection, and Genetic Association with Stature in Western African Pygmies. PLoS Genetics, 2012, 8, e1002641.	3.5	118
36	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	16.3	118

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37	Recent human adaptation: genomic approaches, interpretation and insights. Nature Reviews Genetics, 2013, 14, 692-702.	16.3	105
38	Evidence from Cameroon reveals differences in the genetic structure and histories of chimpanzee populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4766-4771.	7.1	103
39	Genetic Structure of the Ancestral Population of Modern Humans. Journal of Molecular Evolution, 1998, 47, 146-155.	1.8	100
40	African human diversity, origins and migrations. Current Opinion in Genetics and Development, 2006, 16, 597-605.	3.3	98
41	Working toward a synthesis of archaeological, linguistic, and genetic data for inferring African population history. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8931-8938.	7.1	98
42	Signatures of Selection and Gene Conversion Associated with Human Color Vision Variation. American Journal of Human Genetics, 2004, 75, 363-375.	6.2	91
43	Identifying Darwinian Selection Acting on Different Human APOL1 Variants among Diverse African Populations. American Journal of Human Genetics, 2013, 93, 54-66.	6.2	91
44	Nuclear DNA diversity in worldwide distributed human populations. Gene, 1997, 205, 161-171.	2.2	90
45	Phylogeny Estimation by Integration over Isolation with Migration Models. Molecular Biology and Evolution, 2018, 35, 2805-2818.	8.9	89
46	Genetic Variation and Adaptation in Africa: Implications for Human Evolution and Disease. Cold Spring Harbor Perspectives in Biology, 2014, 6, a008524-a008524.	5 . 5	87
47	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. Genome Research, 2016, 26, 291-300.	5.5	87
48	Shorter telomere length in Europeans than in Africans due to polygenetic adaptation. Human Molecular Genetics, 2016, 25, 2324-2330.	2.9	86
49	Elevated male European and female African contributions to the genomes of African American individuals. Human Genetics, 2006, 120, 713-722.	3.8	84
50	African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. Genome Biology, 2019, 20, 82.	8.8	84
51	Population Genomics of Human Adaptation. Annual Review of Ecology, Evolution, and Systematics, 2013, 44, 123-143.	8.3	81
52	Evolution of Functionally Diverse Alleles Associated with PTC Bitter Taste Sensitivity in Africa. Molecular Biology and Evolution, 2012, 29, 1141-1153.	8.9	80
53	Genetic studies of African populations: an overview on disease susceptibility and response to vaccines and therapeutics. Human Genetics, 2008, 123, 557-598.	3.8	79
54	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. American Journal of Human Genetics, 2016, 98, 514-524.	6.2	78

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55	Telomere Length and the Cancer–Atherosclerosis Trade-Off. PLoS Genetics, 2016, 12, e1006144.	3.5	72
56	Role of evolutionary history on haplotype block structure in the human genome: implications for disease mapping. Current Opinion in Genetics and Development, 2003, 13, 569-575.	3.3	69
57	<i>DCAF4</i> , a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	3.2	66
58	Population structure of human gut bacteria in a diverse cohort from rural Tanzania and Botswana. Genome Biology, 2019, 20, 16.	8.8	66
59	Ten years of genetics and genomics: what have we achieved and where are we heading?. Nature Reviews Genetics, 2010, 11, 723-733.	16.3	65
60	Specific inactivation of two immunomodulatory <i>SIGLEC</i> genes during human evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9935-9940.	7.1	64
61	The molecular epidemiology of Huntington disease is related to intermediate allele frequency and haplotype in the general population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 346-357.	1.7	60
62	Biased Gene Conversion Skews Allele Frequencies in Human Populations, Increasing the Disease Burden of Recessive Alleles. American Journal of Human Genetics, 2014, 95, 408-420.	6.2	57
63	Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. Genome Research, 2016, 26, 279-290.	5.5	54
64	Whole genome computational comparative genomics: A fruitful approach for ascertaining Alu insertion polymorphisms. Gene, 2006, 365, 11-20.	2.2	53
65	NIH must confront the use of race in science. Science, 2020, 369, 1313-1314.	12.6	53
66	Effects of Natural Selection and Gene Conversion on the Evolution of Human Glycophorins Coding for MNS Blood Polymorphisms in Malaria-Endemic African Populations. American Journal of Human Genetics, 2011, 88, 741-754.	6.2	52
67	Genetic Hitchhiking and Population Bottlenecks Contribute to Prostate Cancer Disparities in Men of African Descent. Cancer Research, 2018, 78, 2432-2443.	0.9	52
68	A founder mutation in LEPRE1 carried by 1.5% of West Africans and 0.4% of African Americans causes lethal recessive osteogenesis imperfecta. Genetics in Medicine, 2012, 14, 543-551.	2.4	49
69	Positive Selection Can Create False Hotspots of Recombination. Genetics, 2006, 172, 2011-2014.	2.9	48
70	Lifestyle and the presence of helminths is associated with gut microbiome composition in Cameroonians. Genome Biology, 2020, 21, 122.	8.8	48
71	Estimating European admixture in African Americans by using microsatellites and a microsatellite haplotype (CD4/Alu). Human Genetics, 1999, 104, 149-157.	3.8	45
72	The peopling of the African continent and the diaspora into the new world. Current Opinion in Genetics and Development, 2014, 29, 120-132.	3.3	45

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73	Origin and Differential Selection of Allelic Variation at TAS2R16 Associated with Salicin Bitter Taste Sensitivity in Africa. Molecular Biology and Evolution, 2014, 31, 288-302.	8.9	43
74	Origins, Admixture Dynamics, and Homogenization of the African Gene Pool in the Americas. Molecular Biology and Evolution, 2020, 37, 1647-1656.	8.9	43
75	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4166-4175.	7.1	40
76	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. PLoS Genetics, 2020, 16, e1008728.	3.5	40
77	Haplotype variation and genotype imputation in African populations. Genetic Epidemiology, 2011, 35, 766-780.	1.3	39
78	Characterization of genetic variation and natural selection at the arylamine <i>N</i> -acetyltransferase genes in global human populations. Pharmacogenomics, 2011, 12, 1545-1558.	1.3	38
79	Utilizing nanopore sequencing technology for the rapid and comprehensive characterization of eleven HLA loci; addressing the need for deceased donor expedited HLA typing. Human Immunology, 2020, 81, 413-422.	2.4	37
80	NNT mediates redox-dependent pigmentation via a UVB- and MITF-independent mechanism. Cell, 2021, 184, 4268-4283.e20.	28.9	35
81	Inferences of African evolutionary history from genomic data. Current Opinion in Genetics and Development, 2016, 41, 159-166.	3.3	34
82	Meta-analysis of GWA studies provides new insights on the genetic architecture of skin pigmentation in recently admixed populations. BMC Genetics, 2019, 20, 59.	2.7	32
83	Contrasting Histories of G6PD Molecular Evolution and Malarial Resistance in Humans and Chimpanzees. Molecular Biology and Evolution, 2006, 23, 1592-1601.	8.9	31
84	Apparent Variation in Neanderthal Admixture among African Populations is Consistent with Gene Flow from Non-African Populations. Genome Biology and Evolution, 2013, 5, 2075-2081.	2.5	31
85	Global variation in gene expression and the value of diverse sampling. Current Opinion in Systems Biology, 2017, 1, 102-108.	2.6	29
86	A polymorphic residue that attenuates the antiviral potential of interferon lambda 4 in hominid lineages. PLoS Pathogens, 2018, 14, e1007307.	4.7	25
87	Genetic signatures of gene flow and malaria-driven natural selection in sub-Saharan populations of the "endemic Burkitt Lymphoma belt". PLoS Genetics, 2019, 15, e1008027.	3.5	23
88	Evolutionary genetics of skin pigmentation in African populations. Human Molecular Genetics, 2021, 30, R88-R97.	2.9	23
89	Strength in small numbers. Science, 2015, 349, 1282-1283.	12.6	21
90	Molecular characterization of G6PD deficiency in Cyprus. Blood Cells, Molecules, and Diseases, 2004, 33, 25-30.	1.4	20

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91	Human evolutionary genomics: ethical and interpretive issues. Trends in Genetics, 2012, 28, 137-145.	6.7	18
92	Divergent Patterns of Mitochondrial and Nuclear Ancestry Are Associated with the Risk for Preterm Birth. Journal of Pediatrics, 2018, 194, 40-46.e4.	1.8	18
93	Race in Medicine — Genetic Variation, Social Categories, and Paths to Health Equity. New England Journal of Medicine, 2021, 385, e45.	27.0	18
94	Divergent Haplotypes and Human History as Revealed in a Worldwide Survey of X-Linked DNA Sequence Variation. Molecular Biology and Evolution, 2006, 24, 687-698.	8.9	17
95	Importance of Including Non-European Populations in Large Human Genetic Studies to Enhance Precision Medicine. Annual Review of Biomedical Data Science, 2022, 5, 321-339.	6.5	17
96	The quagmire of race, genetic ancestry, and health disparities. Journal of Clinical Investigation, 2021, 131, .	8.2	14
97	Redondovirus Diversity and Evolution on Global, Individual, and Molecular Scales. Journal of Virology, 2021, 95, e0081721.	3.4	12
98	G6PD Deficiency and Malarial Resistance in Humans: Insights from Evolutionary Genetic Analyses. , 2004, , $113-140$.		9
99	Investigating zoonotic infection barriers to ape Plasmodium parasites using faecal DNA analysis. International Journal for Parasitology, 2018, 48, 531-542.	3.1	9
100	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. Journal of Archaeological Science, 2021, 130, 105374.	2.4	9
101	FLG Variation Differs between European Americans and African Americans. Journal of Investigative Dermatology, 2021, 141, 1855-1857.	0.7	7
102	Impact of natural selection on global patterns of genetic variation and association with clinical phenotypes at genes involved in SARS-CoV-2 infection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123000119.	7.1	7
103	Genetics of cognitive trajectory in Brazilians: 15 years of follow-up from the BambuÃ-Epigen Cohort Study of Aging. Scientific Reports, 2019, 9, 18085.	3.3	6
104	Advances in integrative African genomics. Trends in Genetics, 2022, 38, 152-168.	6.7	6
105	Patterns of nucleotide and haplotype diversity at ICAM-1 across global human populations with varying levels of malaria exposure. Human Genetics, 2013, 132, 987-999.	3.8	5
106	Genetics and geography of leukocyte telomere length in sub-Saharan Africans. Human Molecular Genetics, 2020, 29, 3014-3020.	2.9	5
107	The importance of including ethnically diverse populations in studies of quantitative trait evolution. Current Opinion in Genetics and Development, 2020, 62, 30-35.	3.3	5
108	Limited evidence for adaptive evolution and functional effect of allelic variation at rs702424 in the promoter of the TAS2R16 bitter taste receptor gene in Africa. Journal of Human Genetics, 2014, 59, 349-352.	2.3	4

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109	Embracing African Genetic Diversity. Med, 2021, 2, 19-20.	4.4	4
110	Admixture/fine-mapping in Brazilians reveals a West African associated potential regulatory variant (rs114066381) with a strong female-specific effect on body mass and fat mass indexes. International Journal of Obesity, 2021, 45, 1017-1029.	3.4	4
111	Sequence Diversity of Pan troglodytes Subspecies and the Impact of WFDC6 Selective Constraints in Reproductive Immunity. Genome Biology and Evolution, 2013, 5, 2512-2523.	2.5	1
112	The Plight of Muntaser Ibrahim. PLoS Genetics, 2019, 15, e1008100.	3.5	1
113	2019 Curt Stern Award Address. American Journal of Human Genetics, 2020, 106, 297-298.	6.2	O
114	Editorial overview: Evolutionary genomics – from molecular mechanisms to phenotypes to populations. Current Opinion in Genetics and Development, 2020, 62, iii-iv.	3.3	0