

# Stephen F Schaffner

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81  
papers

32,251  
citations

44  
h-index

85  
g-index

85  
ext. papers

39,486  
ext. citations

25.4  
avg, IF

5.76  
L-index

#	Paper	IF	Citations
81	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
80	The structure of haplotype blocks in the human genome. <i>Science</i> , <b>2002</b> , 296, 2225-9	33.3	4660
79	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , <b>2007</b> , 449, 851-61	50.4	3647
78	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , <b>2010</b> , 467, 52-8	50.4	2135
77	The common PPARgamma Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. <i>Nature Genetics</i> , <b>2000</b> , 26, 76-80	36.3	1486
76	Detecting recent positive selection in the human genome from haplotype structure. <i>Nature</i> , <b>2002</b> , 419, 832-7	50.4	1451
75	High-resolution haplotype structure in the human genome. <i>Nature Genetics</i> , <b>2001</b> , 29, 229-32	36.3	1398
74	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , <b>2007</b> , 449, 913-8	50.4	1367
73	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , <b>2014</b> , 345, 1369-72	33.3	847
72	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , <b>2020</b> , 183, 739-751	56.2	566
71	Calibrating a coalescent simulation of human genome sequence variation. <i>Genome Research</i> , <b>2005</b> , 15, 1576-83	9.7	493
70	Searching for missing heritability: designing rare variant association studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E455-64	11.5	437
69	Clinical illness and outcomes in patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , <b>2014</b> , 371, 2092-100	59.2	392
68	A composite of multiple signals distinguishes causal variants in regions of positive selection. <i>Science</i> , <b>2010</b> , 327, 883-6	33.3	365
67	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , <b>2007</b> , 39, 113-9	36.3	265
66	Identifying recent adaptations in large-scale genomic data. <i>Cell</i> , <b>2013</b> , 152, 703-13	56.2	259
65	Zika virus evolution and spread in the Americas. <i>Nature</i> , <b>2017</b> , 546, 411-415	50.4	253

64	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , <b>2017</b> , 544, 309-315	50.4	238
63	Human genome sequence variation and the influence of gene history, mutation and recombination. <i>Nature Genetics</i> , <b>2002</b> , 32, 135-42	36.3	236
62	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , <b>2017</b> , 546, 401-405	50.4	235
61	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , <b>2016</b> , 165, 1519-1529	56.2	228
60	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , <b>2015</b> , 161, 1516-26	56.2	210
59	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , <b>2015</b> , 162, 738-50	56.2	176
58	The X chromosome in population genetics. <i>Nature Reviews Genetics</i> , <b>2004</b> , 5, 43-51	30.1	175
57	Genomewide linkage analysis of stature in multiple populations reveals several regions with evidence of linkage to adult height. <i>American Journal of Human Genetics</i> , <b>2001</b> , 69, 106-16	11	153
56	An integrated haplotype map of the human major histocompatibility complex. <i>American Journal of Human Genetics</i> , <b>2003</b> , 73, 580-90	11	138
55	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , <b>2016</b> , 167, 1088-1098.e6	56.2	135
54	Modeling malaria genomics reveals transmission decline and rebound in Senegal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 7067-72	11.5	114
53	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , <b>2021</b> , 371,	33.3	111
52	Data sharing: Make outbreak research open access. <i>Nature</i> , <b>2015</b> , 518, 477-9	50.4	96
51	Sequence-based association and selection scans identify drug resistance loci in the Plasmodium falciparum malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 13052-7	11.5	85
50	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , <b>2018</b> , 379, 1745-1753	59.2	82
49	Artemisinin resistance without pfkclch13 mutations in Plasmodium falciparum isolates from Cambodia. <i>Malaria Journal</i> , <b>2017</b> , 16, 195	3.6	71
48	Genetic surveillance detects both clonal and epidemic transmission of malaria following enhanced intervention in Senegal. <i>PLoS ONE</i> , <b>2013</b> , 8, e60780	3.7	71
47	Identification and functional validation of the novel antimalarial resistance locus PF10_0355 in Plasmodium falciparum. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001383	6	71

46	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 315-28	30.1	70
45	Clinical and laboratory predictors of Lassa fever outcome in a dedicated treatment facility in Nigeria: a retrospective, observational cohort study. <i>Lancet Infectious Diseases</i> , <b>2018</b> , 18, 684-695	25.5	64
44	Development of a single nucleotide polymorphism barcode to genotype <i>Plasmodium vivax</i> infections. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003539	4.8	62
43	Searching for signals of evolutionary selection in 168 genes related to immune function. <i>Human Genetics</i> , <b>2006</b> , 119, 92-102	6.3	62
42	Plasmeprin II-III copy number accounts for bimodal piperazine resistance among Cambodian <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 1769	17.4	58
41	Natural selection in a bangladeshi population from the cholera-endemic ganges river delta. <i>Science Translational Medicine</i> , <b>2013</b> , 5, 192ra86	17.5	57
40	Association analysis of NOTCH4 loci in schizophrenia using family and population-based controls. <i>Nature Genetics</i> , <b>2001</b> , 28, 126-8	36.3	57
39	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007065	6	49
38	Genomic sequencing of <i>Plasmodium falciparum</i> malaria parasites from Senegal reveals the demographic history of the population. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3427-39	8.3	46
37	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , <b>2018</b> , 17, 196	3.6	44
36	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant <b>2020</b> ,		44
35	Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003631	4.8	36
34	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , <b>2021</b> , 374, 423-431	33.3	35
33	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , <b>2020</b> , 11, 4131	17.4	34
32	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , <b>2020</b> , 183, 1383-1401	36.1	31
31	Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , <b>2016</b> , 3, 173-195	14.6	33
30	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. <i>Genome Medicine</i> , <b>2017</b> , 9, 5	14.4	29
29	SNP genotyping identifies new signatures of selection in a deep sample of West African <i>Plasmodium falciparum</i> malaria parasites. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3249-53	8.3	27

28	Epidemiology. Emerging disease or diagnosis?. <i>Science</i> , <b>2012</b> , 338, 750-2	33.3	23
27	Cosi2: an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , <b>2014</b> , 30, 3427-9	7.2	22
26	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000611	9.7	20
25	Comment on "Ongoing adaptive evolution of ASPM, a brain size determinant in Homo sapiens". <i>Science</i> , <b>2007</b> , 316, 370	33.3	19
24	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , <b>2016</b> , 214, S102-S109	7	14
23	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <b>2022</b> ,		14
22	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak.. <i>Cell</i> , <b>2021</b> ,	56.2	8
21	Evidence for Reduced Malaria Parasite Population after Application of Population-Level Antimalarial Drug Strategies in Southern Province, Zambia. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2020</b> , 103, 66-73	3.2	6
20	hmmIBD: software to infer pairwise identity by descent between haploid genotypes		5
19	Repeated mutation of a developmental enhancer contributed to human thermoregulatory evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	4
18	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. <i>Viruses</i> , <b>2020</b> , 12,	6.2	3
17	Development of a qualitative real-time RT-PCR assay for the detection of SARS-CoV-2: A guide and case study in setting up an emergency-use, laboratory-developed molecular assay <b>2020</b> ,		3
16	Co-circulating mumps lineages at multiple geographic scales		3
15	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e3939-e3948	11.6	3
14	Development of a SNP barcode to genotype Babesia microti infections. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007194	4.8	2
13	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , <b>2020</b> , 19, 276	3.6	2
12	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , <b>2020</b> , 19, 342	3.6	2
11	Development of a qualitative real-time RT-PCR assay for the detection of SARS-CoV-2: a guide and case study in setting up an emergency-use, laboratory-developed molecular microbiological assay. <i>Journal of Clinical Pathology</i> , <b>2021</b> , 74, 496-503	3.9	2

10	Genome sequencing reveals Zika virus diversity and spread in the Americas		1
9	Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering.. <i>Scientific Reports</i> , <b>2022</b> , 12, 938	4.9	0
8	Adam, Eve, and the evolution of humankind Eerdmans, 2021. 439 pp. <i>Science</i> , <b>2021</b> , 374, 162	33.3	0
7	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Microscopy and Microanalysis</i> , <b>2021</b> , 27, 3260-3262	0.5	0
6	Combining genomics and epidemiology to track mumps virus transmission in the United States <b>2020</b> , 18, e3000611		
5	Combining genomics and epidemiology to track mumps virus transmission in the United States <b>2020</b> , 18, e3000611		
4	Combining genomics and epidemiology to track mumps virus transmission in the United States <b>2020</b> , 18, e3000611		
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