

Stephen F Schaffner

List of Publications by Year in Descending Order

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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	Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering.. <i>Scientific Reports</i> , 2022 , 12, 938	4.9	0
80	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. 2022 ,		14
79	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak.. <i>Cell</i> , 2021 ,	56.2	8
78	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
77	Adam, Eve, and the evolution of humankind Eerdmans, 2021. 439 pp. <i>Science</i> , 2021 , 374, 162	33.3	0
76	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> , 2021 , 118,	11.5	4
75	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> , 2021 , 74, 496-503	3.9	2
74	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Microscopy and Microanalysis</i> , 2021 , 27, 3260-3262	0.5	0
73	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021 , 371,	33.3	111
72	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021 , 73, e3939-e3948	11.6	3
71	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020 , 183, 1383-1401, e319	36.4	59
70	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020 , 18, e3000611	9.7	20
69	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> , 2020 , 12,	6.2	3
68	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> , 2020 , 103, 66-73	3.2	6
67	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant 2020 ,		44
66	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 2020 ,		3
65	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020 , 183, 739-751, e28	56.2	566

64	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020 , 19, 276	3.6	2
63	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020 , 19, 342	3.6	2
62	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020 , 11, 4131	17.4	34
61	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
60	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
59	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
58	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
57	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
56	Combining genomics and epidemiology to track mumps virus transmission in the United States 2020 , 18, e3000611		
55	Development of a SNP barcode to genotype Babesia microti infections. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007194	4.8	2
54	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> , 2018 , 18, 684-695	25.5	64
53	Plasmepsin II-III copy number accounts for bimodal piperazine resistance among Cambodian Plasmodium falciparum. <i>Nature Communications</i> , 2018 , 9, 1769	17.4	58
52	hmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , 2018 , 17, 196	3.6	44
51	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018 , 379, 1745-1753	59.2	82
50	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
49	Artemisinin resistance without pfkclch13 mutations in Plasmodium falciparum isolates from Cambodia. <i>Malaria Journal</i> , 2017 , 16, 195	3.6	71
48	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
47	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017 , 546, 411-415	50.4	253

46	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thié, Senegal. <i>Genome Medicine</i> , 2017 , 9, 5	14.4	29
45	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. <i>PLoS Genetics</i> , 2017 , 13, e1007065	6	49
44	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016 , 167, 1088-1098.e6	56.2	135
43	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016 , 165, 1519-1529	56.2	228
42	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016 , 214, S102-S109	7	14
41	Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , 2016 , 3, 173-195	14.6	33
40	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015 , 161, 1516-26	56.2	210
39	Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003631	4.8	36
38	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> , 2015 , 112, 7067-72	11.5	114
37	Development of a single nucleotide polymorphism barcode to genotype <i>Plasmodium vivax</i> infections. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003539	4.8	62
36	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
35	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015 , 162, 738-50	56.2	176
34	Data sharing: Make outbreak research open access. <i>Nature</i> , 2015 , 518, 477-9	50.4	96
33	Clinical illness and outcomes in patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , 2014 , 371, 2092-100	59.2	392
32	Cos2: an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , 2014 , 30, 3427-9	7.2	22
31	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014 , 345, 1369-72	33.3	847
30	Searching for missing heritability: designing rare variant association studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E455-64	11.5	437
29	Identifying recent adaptations in large-scale genomic data. <i>Cell</i> , 2013 , 152, 703-13	56.2	259

28	Natural selection in a bangladeshi population from the cholera-endemic ganges river delta. <i>Science Translational Medicine</i> , 2013 , 5, 192ra86	17.5	57
27	Genetic surveillance detects both clonal and epidemic transmission of malaria following enhanced intervention in Senegal. <i>PLoS ONE</i> , 2013 , 8, e60780	3.7	71
26	Epidemiology. Emerging disease or diagnosis?. <i>Science</i> , 2012 , 338, 750-2	33.3	23
25	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012 , 13, 315-28	30.1	70
24	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> , 2012 , 29, 3249-53	8.3	27
23	Sequence-based association and selection scans identify drug resistance loci in the <i>Plasmodium falciparum</i> malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13052-7	11.5	85
22	Genomic sequencing of <i>Plasmodium falciparum</i> malaria parasites from Senegal reveals the demographic history of the population. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3427-39	8.3	46
21	Identification and functional validation of the novel antimalarial resistance locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011 , 7, e1001383	6	71
20	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010 , 467, 52-8	50.4	2135
19	A composite of multiple signals distinguishes causal variants in regions of positive selection. <i>Science</i> , 2010 , 327, 883-6	33.3	365
18	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007 , 39, 113-9	36.3	265
17	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
16	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
15	Comment on "Ongoing adaptive evolution of ASPM, a brain size determinant in Homo sapiens". <i>Science</i> , 2007 , 316, 370	33.3	19
14	Searching for signals of evolutionary selection in 168 genes related to immune function. <i>Human Genetics</i> , 2006 , 119, 92-102	6.3	62
13	Calibrating a coalescent simulation of human genome sequence variation. <i>Genome Research</i> , 2005 , 15, 1576-83	9.7	493
12	The X chromosome in population genetics. <i>Nature Reviews Genetics</i> , 2004 , 5, 43-51	30.1	175
11	An integrated haplotype map of the human major histocompatibility complex. <i>American Journal of Human Genetics</i> , 2003 , 73, 580-90	11	138

10	Detecting recent positive selection in the human genome from haplotype structure. <i>Nature</i> , 2002 , 419, 832-7	50.4	1451
9	Human genome sequence variation and the influence of gene history, mutation and recombination. <i>Nature Genetics</i> , 2002 , 32, 135-42	36.3	236
8	The structure of haplotype blocks in the human genome. <i>Science</i> , 2002 , 296, 2225-9	33.3	4660
7	Association analysis of NOTCH4 loci in schizophrenia using family and population-based controls. <i>Nature Genetics</i> , 2001 , 28, 126-8	36.3	57
6	High-resolution haplotype structure in the human genome. <i>Nature Genetics</i> , 2001 , 29, 229-32	36.3	1398
5	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> , 2001 , 69, 106-16	11	153
4	The common PPARgamma Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. <i>Nature Genetics</i> , 2000 , 26, 76-80	36.3	1486
3	hmmIBD: software to infer pairwise identity by descent between haploid genotypes		5
2	Co-circulating mumps lineages at multiple geographic scales		3
1	Genome sequencing reveals Zika virus diversity and spread in the Americas		1