

Stephen F Schaffner

List of Publications by Year in descending order

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77
papers

43,541
citations

41258

49
h-index

85405

71
g-index

85
all docs

85
docs citations

85
times ranked

60181
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	13
2	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	13.5	38
3	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332.	6.0	172
4	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	6.0	226
5	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021, 73, e3939-e3948.	2.9	6
6	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, .	3.3	25
7	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.	1.0	5
8	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Microscopy and Microanalysis</i> , 2021, 27, 3260-3262.	0.2	3
9	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	1.5	8
10	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
11	Adam, Eve, and the evolution of humankind In Quest of the Historical Adam: A Biblical and Scientific Exploration <i>William Lane Craig</i> Eerdmans, 2021. 439 pp.. <i>Science</i> , 2021, 374, 162-162.	6.0	2
12	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020, 183, 739-751.e8.	13.5	924
13	Genetic evidence for imported malaria and local transmission in Richard Toll, Senegal. <i>Malaria Journal</i> , 2020, 19, 276.	0.8	12
14	Use of a Plasmodium vivax genetic barcode for genomic surveillance and parasite tracking in Sri Lanka. <i>Malaria Journal</i> , 2020, 19, 342.	0.8	6
15	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020, 11, 4131.	5.8	101
16	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	13.5	79
17	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	2.6	37
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> , 2020, 12, 105.	1.5	9

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19	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.	0.6	8
20	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
21	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
22	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
23	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
24	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
25	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
26	Development of a SNP barcode to genotype <i>Babesia microti</i> infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007194.	1.3	5
27	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> , The, 2018, 18, 684-695.	4.6	100
28	Plasmepsin II copy number accounts for bimodal piperazine resistance among Cambodian <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2018, 9, 1769.	5.8	85
29	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.	13.9	135
30	hmmIBD: software to infer pairwise identity by descent between haploid genotypes. <i>Malaria Journal</i> , 2018, 17, 196.	0.8	103
31	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
32	Artemisinin resistance without pfcy5r mutations in <i>Plasmodium falciparum</i> isolates from Cambodia. <i>Malaria Journal</i> , 2017, 16, 195.	0.8	99
33	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
34	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	13.7	323
35	Genetic relatedness analysis reveals the cotransmission of genetically related <i>Plasmodium falciparum</i> parasites in Thiès, Senegal. <i>Genome Medicine</i> , 2017, 9, 5.	3.6	47
36	Quantifying connectivity between local <i>Plasmodium falciparum</i> malaria parasite populations using identity by descent. <i>PLoS Genetics</i> , 2017, 13, e1007065.	1.5	98

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37	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	1.9	19
38	Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , 2016, 3, 173-195.	3.0	61
39	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	13.5	173
40	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529.	13.5	378
41	Data sharing: Make outbreak research open access. <i>Nature</i> , 2015, 518, 477-479.	13.7	129
42	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	13.5	275
43	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003631.	1.3	56
44	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, 7067-7072.	3.3	163
45	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	1.3	90
46	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
47	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	13.5	230
48	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.	3.3	570
49	Clinical Illness and Outcomes in Patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , 2014, 371, 2092-2100.	13.9	471
50	<i>Cos2</i> : an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , 2014, 30, 3427-3429.	1.8	40
51	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	6.0	1,083
52	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
53	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. <i>Science Translational Medicine</i> , 2013, 5, 192ra86.	5.8	77
54	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. <i>PLoS ONE</i> , 2013, 8, e60780.	1.1	87

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55	SNP Genotyping Identifies New Signatures of Selection in a Deep Sample of West African Plasmodium falciparum Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2012, 29, 3249-3253.	3.5	41
56	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, 13052-13057.	3.3	99
57	Genomic Sequencing of Plasmodium falciparum Malaria Parasites from Senegal Reveals the Demographic History of the Population. <i>Molecular Biology and Evolution</i> , 2012, 29, 3427-3439.	3.5	58
58	Emerging Disease or Diagnosis?. <i>Science</i> , 2012, 338, 750-752.	6.0	29
59	Harnessing genomics and genome biology to understand malaria biology. <i>Nature Reviews Genetics</i> , 2012, 13, 315-328.	7.7	95
60	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. <i>PLoS Genetics</i> , 2011, 7, e1001383.	1.5	85
61	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	13.7	2,625
62	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. <i>Science</i> , 2010, 327, 883-886.	6.0	457
63	Corrections and Clarifications. <i>Science</i> , 2007, 316, 370a-370a.	6.0	20
64	A genome-wide map of diversity in Plasmodium falciparum. <i>Nature Genetics</i> , 2007, 39, 113-119.	9.4	320
65	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
66	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
67	Searching for signals of evolutionary selection in 168 genes related to immune function. <i>Human Genetics</i> , 2006, 119, 92-102.	1.8	67
68	Calibrating a coalescent simulation of human genome sequence variation. <i>Genome Research</i> , 2005, 15, 1576-1583.	2.4	581
69	The X chromosome in population genetics. <i>Nature Reviews Genetics</i> , 2004, 5, 43-51.	7.7	217
70	An Integrated Haplotype Map of the Human Major Histocompatibility Complex. <i>American Journal of Human Genetics</i> , 2003, 73, 580-590.	2.6	151
71	The Structure of Haplotype Blocks in the Human Genome. <i>Science</i> , 2002, 296, 2225-2229.	6.0	5,300
72	Detecting recent positive selection in the human genome from haplotype structure. <i>Nature</i> , 2002, 419, 832-837.	13.7	1,881

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73	Human genome sequence variation and the influence of gene history, mutation and recombination. Nature Genetics, 2002, 32, 135-142.	9.4	278
74	Genomewide Linkage Analysis of Stature in Multiple Populations Reveals Several Regions with Evidence of Linkage to Adult Height. American Journal of Human Genetics, 2001, 69, 106-116.	2.6	177
75	Association analysis of NOTCH4 loci in schizophrenia using family and population-based controls. Nature Genetics, 2001, 28, 126-128.	9.4	62
76	High-resolution haplotype structure in the human genome. Nature Genetics, 2001, 29, 229-232.	9.4	1,596
77	The common PPAR α Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. Nature Genetics, 2000, 26, 76-80.	9.4	1,672