

Christian T Happi

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

4,156
citations

236925

25
h-index

168389

53
g-index

59
all docs

59
docs citations

59
times ranked

6195
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	12.6	1,083
2	Clinical Illness and Outcomes in Patients with Ebola in Sierra Leone. <i>New England Journal of Medicine</i> , 2014, 371, 2092-2100.	27.0	471
3	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
4	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
5	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	28.9	230
6	Lassa Fever in Post-Conflict Sierra Leone. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2748.	3.0	172
7	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544.	12.8	148
8	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.	27.0	135
9	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020, 11, 4131.	12.8	101
10	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.	9.1	100
11	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168.	17.5	96
12	Genome-wide scans provide evidence for positive selection of genes implicated in Lassa fever. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 868-877.	4.0	93
13	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014, 6, 4760-4799.	3.3	83
14	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003631.	3.0	56
15	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	3.3	49
16	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8.	28.9	48
17	Lassa fever diagnostics: past, present, and future. <i>Current Opinion in Virology</i> , 2019, 37, 132-138.	5.4	47
18	Quadrivalent VesiculoVax vaccine protects nonhuman primates from viral-induced hemorrhagic fever and death. <i>Journal of Clinical Investigation</i> , 2019, 130, 539-551.	8.2	40

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19	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018, 8, 5939.	3.3	39
20	Potential contribution of prescription practices to the emergence and spread of chloroquine resistance in south-west Nigeria: caution in the use of artemisinin combination therapy. <i>Malaria Journal</i> , 2009, 8, 313.	2.3	34
21	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	4.0	34
22	Caseload and Case Fatality of Lassa Fever in Nigeria, 2001â€“2018: A Specialist Center's Experience and Its Implications. <i>Frontiers in Public Health</i> , 2019, 7, 170.	2.7	34
23	Retrospective Cohort Study of Lassa Fever in Pregnancy, Southern Nigeria. <i>Emerging Infectious Diseases</i> , 2019, 25, 1494-1500.	4.3	34
24	Emerging Disease or Diagnosis?. <i>Science</i> , 2012, 338, 750-752.	12.6	29
25	Empowering African genomics for infectious disease control. <i>Genome Biology</i> , 2014, 15, 515.	8.8	28
26	Accelerating genomics-based surveillance for COVID-19 response in Africa. <i>Lancet Microbe</i> , The, 2020, 1, e227-e228.	7.3	28
27	Tracking the emergence of new SARS-CoV-2 variants in South Africa. <i>Nature Medicine</i> , 2021, 27, 372-373.	30.7	28
28	Efficacy of Artemisinin-Based Combination Treatments of Uncomplicated <i>Falciparum</i> Malaria in Under-Five-Year-Old Nigerian Children Ten Years Following Adoption as First-Line Antimalarials. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 649-664.	1.4	25
29	In Vitro-Reduced Susceptibility to Artemether in <i>P. falciparum</i> and Its Association With Polymorphisms on Transporter Genes. <i>Journal of Infectious Diseases</i> , 2012, 206, 324-332.	4.0	24
30	Real-time Metagenomic Analysis of Undiagnosed Fever Cases Unveils a Yellow Fever Outbreak in Edo State, Nigeria. <i>Scientific Reports</i> , 2020, 10, 3180.	3.3	23
31	High crossreactivity of human T cell responses between Lassa virus lineages. <i>PLoS Pathogens</i> , 2020, 16, e1008352.	4.7	22
32	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	4.0	19
33	Antibodies from Sierra Leonean and Nigerian Lassa fever survivors cross-react with recombinant proteins representing Lassa viruses of divergent lineages. <i>Scientific Reports</i> , 2020, 10, 16030.	3.3	15
34	Identification of Common CD8 ⁺ T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020, 94, .	3.4	15
35	Declining responsiveness of childhood <i>Plasmodium falciparum</i> infections to artemisinin-based combination treatments ten years following deployment as first-line antimalarials in Nigeria. <i>Infectious Diseases of Poverty</i> , 2019, 8, 69.	3.7	14
36	Field evaluation of a Pan-Lassa rapid diagnostic test during the 2018 Nigerian Lassa fever outbreak. <i>Scientific Reports</i> , 2020, 10, 8724.	3.3	14

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37	Characterization of Plasmodium falciparum structure in Nigeria with malaria SNPs barcode. Malaria Journal, 2018, 17, 472.	2.3	12
38	Metagenomic sequencing characterizes a wide diversity of viruses in field mosquito samples in Nigeria. Scientific Reports, 2022, 12, 7616.	3.3	12
39	Polymorphisms in Plasmodium falciparum dihydropteroate synthetase and dihydrofolate reductase genes in Nigerian children with uncomplicated malaria using high-resolution melting technique. Scientific Reports, 2021, 11, 471.	3.3	9
40	Genetic diversity and population structure of Plasmodium falciparum in Nigeria: insights from microsatellite loci analysis. Malaria Journal, 2021, 20, 236.	2.3	8
41	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. Viruses, 2021, 13, 1605.	3.3	8
42	Whole genome sequencing of clinical samples reveals extensively drug resistant tuberculosis (XDR) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.3	8
43	The Bacteria Genome Pipeline (BAGEP): an automated, scalable workflow for bacteria genomes with Snakemake. PeerJ, 2020, 8, e10121.	2.0	8
44	Molecular profiling of the artemisinin resistance Kelch 13 gene in Plasmodium falciparum from Nigeria. PLoS ONE, 2022, 17, e0264548.	2.5	8
45	Early rising asexual parasitaemia in Nigerian children following a first dose of artemisinin-based combination treatments of falciparum malaria. BMC Infectious Diseases, 2017, 17, 110.	2.9	7
46	Polymorphisms in Plasmodium falciparum chloroquine resistance transporter (Pfcrt) and multidrug-resistant gene 1 (Pfmdr-1) in Nigerian children 10 years post-adoption of artemisinin-based combination treatments. International Journal for Parasitology, 2021, 51, 301-310.	3.1	7
47	52 Years of Lassa Fever Outbreaks in Nigeria, 1969–2020: An Epidemiologic Analysis of the Temporal and Spatial Trends. American Journal of Tropical Medicine and Hygiene, 2021, 105, 974-985.	1.4	6
48	Biosafety level-2 laboratory diagnosis of Zaire Ebola virus disease imported from Liberia to Nigeria. African Journal of Laboratory Medicine, 2016, 5, 468.	0.6	5
49	Parasite reduction ratio one day after initiation of artemisinin-based combination therapies and its relationship with parasite clearance time in acutely malarious children. Infectious Diseases of Poverty, 2018, 7, 122.	3.7	5
50	Microbial metagenomic approach uncovers the first rabbit haemorrhagic disease virus genome in Sub-Saharan Africa. Scientific Reports, 2021, 11, 13689.	3.3	5
51	Detection of Antibody and Antigen for Lassa Virus Nucleoprotein in Monkeys from Southern Nigeria. Journal of Epidemiology and Global Health, 2019, 9, 125-127.	2.9	5
52	Lassa Virus Genetics. Current Topics in Microbiology and Immunology, 2020, , 1.	1.1	4
53	VGEA: an RNA viral assembly toolkit. PeerJ, 2021, 9, e12129.	2.0	2
54	Preparing for the next Ebola outbreak: in-country genomic capacity in Africa. Lancet Infectious Diseases, The, 2019, 19, 569-570.	9.1	0