

David G Bonsall

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.

64
papers

3,955
citations

26
h-index

62
g-index

71
ext. papers

5,743
ext. citations

14.2
avg, IF

5.77
L-index

#	Paper	IF	Citations
64	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020 , 368,	33.3	1366
63	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
62	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7): an exploratory analysis of a randomised controlled trial. <i>Lancet, The</i> , 2021 , 397, 1351-1362	40	316
61	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health, The</i> , 2021 , 6, e335-e345	22.4	146
60	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing		132
59	A one-step SYBR Green I-based product-enhanced reverse transcriptase assay for the quantitation of retroviruses in cell culture supernatants. <i>Journal of Virological Methods</i> , 2009 , 156, 1-7	2.6	126
58	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021 , 372,	33.3	110
57	Ethics of instantaneous contact tracing using mobile phone apps in the control of the COVID-19 pandemic. <i>Journal of Medical Ethics</i> , 2020 , 46, 427-431	2.5	99
56	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017 , 49, 666-673	36.3	81
55	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 2470-84	9.7	78
54	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 719-733	8.3	68
53	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018 , 23, 855-864.e7	23.4	60
52	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021 , 594, 408-412	50.4	57
51	B-cell depletion reveals a role for antibodies in the control of chronic HIV-1 infection. <i>Nature Communications</i> , 2010 , 1, 102	17.4	55
50	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019 , 69, 1861-1872	11.2	43
49	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019 , 9, 7081	4.9	41
48	ve-SEQ: Robust, unbiased enrichment for streamlined detection and whole-genome sequencing of HCV and other highly diverse pathogens. <i>F1000Research</i> , 2015 , 4, 1062	3.6	39

47	Epidemiological changes on the Isle of Wight after the launch of the NHS Test and Trace programme: a preliminary analysis. <i>The Lancet Digital Health</i> , 2020 , 2, e658-e666	14.4	34
46	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016 , 22, 671-8	10.2	34
45	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021 , 27, 361-362	50.5	32
44	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
43	Within-host genomics of SARS-CoV-2		29
42	Characterization of the Specificity, Functionality, and Durability of Host T-Cell Responses Against the Full-Length Hepatitis E Virus. <i>Hepatology</i> , 2016 , 64, 1934-1950	11.2	28
41	OpenABM-Covid19-An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021 , 17, e1009146	5	28
40	Modeling the effect of exposure notification and non-pharmaceutical interventions on COVID-19 transmission in Washington state. <i>Npj Digital Medicine</i> , 2021 , 4, 49	15.7	27
39	Highly-Immunogenic Virally-Vectored T-cell Vaccines Cannot Overcome Subversion of the T-cell Response by HCV during Chronic Infection. <i>Vaccines</i> , 2016 , 4,	5.3	27
38	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26
37	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV,the</i> , 2020 , 7, e173-e183	7.8	26
36	Modeling the combined effect of digital exposure notification and non-pharmaceutical interventions on the COVID-19 epidemic in Washington state		26
35	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3155-64	9.7	25
34	OpenABM-Covid19 - an agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing		22
33	Early analysis of a potential link between viral load and the N501Y mutation in the SARS-COV-2 spike protein		22
32	Detection and Characterization of Homologues of Human Hepatitis Viruses and Pegiviruses in Rodents and Bats in Vietnam. <i>Viruses</i> , 2018 , 10,	6.2	21
31	Phylogenetic analysis consistent with a clinical history of sexual transmission of HIV-1 from a single donor reveals transmission of highly distinct variants. <i>Retrovirology</i> , 2011 , 8, 54	3.6	18
30	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019 , 8,	8.9	17

29	Restriction of V3 region sequence divergence in the HIV-1 envelope gene during antiretroviral treatment in a cohort of recent seroconverters. <i>Retrovirology</i> , 2013 , 10, 8	3.6	15
28	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	15
27	Virological Characterization of Critically Ill Patients With COVID-19 in the United Kingdom: Interactions of Viral Load, Antibody Status, and B.1.1.7 Infection. <i>Journal of Infectious Diseases</i> , 2021 , 224, 595-605	7	14
26	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021 , 12, 5861	17.4	11
25	HIGH-FREQUENCY failure of combination antiretroviral therapy in paediatric HIV infection is associated with unmet maternal needs causing maternal NON-ADHERENCE. <i>EClinicalMedicine</i> , 2020 , 22, 100344	11.3	9
24	Virological and serological characterization of critically ill patients with COVID-19 in the UK: a special focus on variant detection		9
23	High prevalence of integrase mutation L74I in West African HIV-1 subtypes prior to integrase inhibitor treatment. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 1575-1579	5.1	8
22	Targeted metagenomic sequencing enhances the identification of pathogens associated with acute infection		7
21	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019 , 25, 1598-1600	10.2	6
20	Symptoms and SARS-CoV-2 positivity in the general population in the UK. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	6
19	Characterization of hepatitis C virus resistance to grazoprevir reveals complex patterns of mutations following on-treatment breakthrough that are not observed at relapse. <i>Infection and Drug Resistance</i> , 2018 , 11, 1119-1135	4.2	5
18	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
17	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 3510-3516	5.1	5
16	Simultaneous Viral Whole-Genome Sequencing and Differential Expression Profiling in Respiratory Syncytial Virus Infection of Infants. <i>Journal of Infectious Diseases</i> , 2020 , 222, S666-S671	7	4
15	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020 , 222, 1670-1680 ⁷		3
14	COVID-19 incidence and R decreased on the Isle of Wight after the launch of the Test, Trace, Isolate programme		
13	A comprehensive genomics solution for HIV surveillance and clinical monitoring in a global health setting		3
12	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil; an exploratory analysis of a randomised controlled trial		3

11	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021 , 12, 5125	17.4	3
10	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV)		2
9	Evidence of tenofovir resistance in chronic hepatitis B virus (HBV) infection: An observational case series of South African adults. <i>Journal of Clinical Virology</i> , 2020 , 129, 104548	14.5	2
8	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012	17.4	2
7	Recombination Analysis of Near Full-Length HIV-1 Sequences and the Identification of a Potential New Circulating Recombinant Form from Rakai, Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020 , 36, 467-474	1.6	1
6	Lineage replacement and evolution captured by the United Kingdom Covid Infection Survey		1
5	Evidence of Tenofovir Resistance in Chronic Hepatitis B Virus (HBV) Infection: An Observational Case Series of South African Adults		1
4	Transfusion-transmitted hepatitis C: A cluster of cases in transfusion-dependent thalassaemia patients in Sri Lanka. <i>Transfusion Medicine</i> , 2020 , 30, 377-383	1.3	1
3	Two distinct mechanisms leading to loss of virological control in the rare group of antiretroviral therapy-naïve, transiently aviraemic children living with HIV. <i>Journal of Virology</i> , 2021 , JVI0153521	6.6	0
2	Second-generation mother-to-child HIV transmission in South Africa is characterized by poor outcomes. <i>Aids</i> , 2021 , 35, 1597-1604	3.5	0
1	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR.. <i>Journal of Clinical Microbiology</i> , 2022 , e0228321	9.7	0