

# David G Bonsall

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

6,755  
citations

186209

28  
h-index

175177

52  
g-index

71  
all docs

71  
docs citations

71  
times ranked

13088  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .	6.0	2,048
2	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
3	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.	6.3	540
4	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
5	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.	4.7	269
6	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021, 594, 408-412.	13.7	188
7	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.	1.0	177
8	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.	1.0	156
9	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.	9.4	129
10	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	3.5	122
11	OpenABM-Covid19 – An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021, 17, e1009146.	1.5	118
12	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	1.8	112
13	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	6.0	111
14	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.	5.1	82
15	Illumina and Nanopore methods for whole genome sequencing of hepatitis B virus (HBV). <i>Scientific Reports</i> , 2019, 9, 7081.	1.6	75
16	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.	5.9	74
17	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	15.2	71
18	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019, 69, 1861-1872.	3.6	68

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19	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.	0.8	66
20	B-cell depletion reveals a role for antibodies in the control of chronic HIV-1 infection. <i>Nature Communications</i> , 2010, 1, 102.	5.8	62
21	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183.	2.1	59
22	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.	5.7	59
23	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	5.8	50
24	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016, 22, 671-678.	2.0	46
25	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.	3.6	42
26	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	39
27	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
28	COVID-19 due to the B.1.617.2 (Delta) variant compared to B.1.1.7 (Alpha) variant of SARS-CoV-2: a prospective observational cohort study. <i>Scientific Reports</i> , 2022, 12, .	1.6	39
29	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021, 12, 5861.	5.8	38
30	Detection and Characterization of Homologues of Human Hepatitis Viruses and Pegiviruses in Rodents and Bats in Vietnam. <i>Viruses</i> , 2018, 10, 102.	1.5	37
31	Highly-Immunogenic Virologically-Vectored T-cell Vaccines Cannot Overcome Subversion of the T-cell Response by HCV during Chronic Infection. <i>Vaccines</i> , 2016, 4, 27.	2.1	35
32	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3155-3164.	1.8	28
33	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. <i>ELife</i> , 2019, 8, .	2.8	28
34	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.	3.2	23
35	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.	1.9	20
36	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. <i>Clinical Infectious Diseases</i> , 2022, 75, e329-e337.	2.9	20

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37	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.	0.9	18
38	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.	0.9	17
39	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.	1.6	16
40	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. <i>Nature Communications</i> , 2021, 12, 5125.	5.8	16
41	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.	1.3	13
42	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.	1.9	12
43	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.	1.3	12
44	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.	1.9	11
45	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
46	Prolonged Zika Virus RNA Detection in Semen of Immunosuppressed Patient. <i>Emerging Infectious Diseases</i> , 2019, 25, 1598-1600.	2.0	8
47	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, Volume 11, 1119-1135.	1.1	6
48	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0228321.	1.8	5
49	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.	0.5	4
50	Two Distinct Mechanisms Leading to Loss of Virological Control in the Rare Group of Antiretroviral Therapy-Naive, Transiently Aviremic Children Living with HIV. <i>Journal of Virology</i> , 2022, 96, JVI0153521.	1.5	3
51	Transfusion-transmitted hepatitis C: A cluster of cases in transfusion-dependent thalassaemia patients in Sri Lanka. <i>Transfusion Medicine</i> , 2020, 30, 377-383.	0.5	2
52	Second-generation mother-to-child HIV transmission in South Africa is characterized by poor outcomes. <i>Aids</i> , 2021, 35, 1597-1604.	1.0	2