

Katrina A Lythgoe

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,261
citations

361045

20
h-index

433756

31
g-index

48
all docs

48
docs citations

48
times ranked

4392
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant. <i>Nature Communications</i> , 2022, 13, 460.	5.8	304
2	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
3	Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. <i>Science</i> , 2014, 343, 1243727.	6.0	215
4	OpenABM-Covid19â€”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
5	Challenges in control of COVID-19: short doubling time and long delay to effect of interventions. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200264.	1.8	93
6	Possible future waves of SARS-CoV-2 infection generated by variants of concern with a range of characteristics. <i>Nature Communications</i> , 2021, 12, 5730.	5.8	90
7	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	15.2	71
8	New insights into the evolutionary rate of HIV-1 at the within-host and epidemiological levels. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3367-3375.	1.2	69
9	Mechanisms of coexistence of a bacteria and a bacteriophage in a spatially homogeneous environment. <i>Ecology Letters</i> , 2003, 6, 326-334.	3.0	66
10	Parasite-intrinsic factors can explain ordered progression of trypanosome antigenic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8095-8100.	3.3	62
11	Preexposure prophylaxis will have a limited impact on HIV-1 drug resistance in sub-Saharan Africa. <i>Aids</i> , 2013, 27, 2943-2951.	1.0	61
12	Short-Sighted Virus Evolution and a Germline Hypothesis for Chronic Viral Infections. <i>Trends in Microbiology</i> , 2017, 25, 336-348.	3.5	50
13	IS HIV SHORTâ€”SIGHTED? INSIGHTS FROM A MULTISTRAIN NESTED MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2769-2782.	1.1	49
14	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016, 5, .	2.8	46
15	On the diverse and opposing effects of nutrition on pathogen virulence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191220.	1.2	44
16	Hepatitis B Virus Adaptation to the CD8+ T Cell Response: Consequences for Host and Pathogen. <i>Frontiers in Immunology</i> , 2018, 9, 1561.	2.2	33
17	THE COEVOLUTION OF PARASITES WITH HOST-ACQUIRED IMMUNITY AND THE EVOLUTION OF SEX. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1142-1156.	1.1	32
18	Catching the Red Queen? The advice of the Rose. <i>Trends in Ecology and Evolution</i> , 1998, 13, 473-474.	4.2	29

#	ARTICLE	IF	CITATIONS
19	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. <i>PLoS Pathogens</i> , 2018, 14, e1007167.	2.1	27
20	Effect of the Latent Reservoir on the Evolution of HIV at the Within- and Between-Host Levels. <i>PLoS Computational Biology</i> , 2017, 13, e1005228.	1.5	26
21	Consequences of gene flow in spatially structured populations. <i>Genetical Research</i> , 1997, 69, 49-60.	0.3	24
22	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
23	Estimating hepatitis B virus cccDNA persistence in chronic infection. <i>Virus Evolution</i> , 2021, 7, veaa063.	2.2	18
24	Large Variations in HIV-1 Viral Load Explained by Shifting-Mosaic Metapopulation Dynamics. <i>PLoS Biology</i> , 2016, 14, e1002567.	2.6	17
25	Effects of Acquired Immunity and Mating Strategy on the Genetic Structure of Parasite Populations. <i>American Naturalist</i> , 2002, 159, 519-529.	1.0	13
26	Link between the numbers of particles and variants founding new HIV-1 infections depends on the timing of transmission. <i>Virus Evolution</i> , 2019, 5, vey038.	2.2	13
27	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2019, 219, 1722-1729.	1.9	11
28	Number of HIV-1 founder variants is determined by the recency of the source partner infection. <i>Science</i> , 2020, 369, 103-108.	6.0	11
29	Coronavirus: full peer review in hours. <i>Nature</i> , 2020, 584, 192-192.	13.7	5
30	Bimodal distribution and set point HBV DNA viral loads in chronic infection: retrospective analysis of cohorts from the UK and South Africa. <i>Wellcome Open Research</i> , 2020, 5, 113.	0.9	5
31	A de novo approach to inferring within-host fitness effects during untreated HIV-1 infection. <i>PLoS Pathogens</i> , 2020, 16, e1008171.	2.1	4
32	Invisible foes. <i>Current Biology</i> , 2013, 23, R548-R549.	1.8	0