

François Blanquart

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,664
citations

361413

20
h-index

414414

32
g-index

46
all docs

46
docs citations

46
times ranked

2866
citing authors

#	ARTICLE	IF	CITATIONS
1	Nosocomial transmission clusters and lineage diversity characterized by SARS-CoV-2 genomes from two large hospitals in Paris, France, in 2020. <i>Scientific Reports</i> , 2022, 12, 1094.	3.3	7
2	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
3	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	4.9	1
4	Selection for infectivity profiles in slow and fast epidemics, and the rise of SARS-CoV-2 variants. <i>ELife</i> , 2022, 11, .	6.0	8
5	Early assessment of diffusion and possible expansion of SARS-CoV-2 Lineage 20I/501Y.V1 (B.1.1.7, variant) Tj ETQq] 0.784314 rgBT	7.0	65
6	Success of prophylactic antiviral therapy for SARS-CoV-2: Predicted critical efficacies and impact of different drug-specific mechanisms of action. <i>PLoS Computational Biology</i> , 2021, 17, e1008752.	3.2	41
7	High-risk exposure without personal protective equipment and infection with SARS-CoV-2 in-hospital workers - The CoV-CONTACT cohort. <i>Journal of Infection</i> , 2021, 82, 186-230.	3.3	7
8	Estimating the global reduction in transmission and rise in detection capacity of the novel coronavirus SARS-CoV-2 in early 2020. <i>Epidemics</i> , 2021, 35, 100445.	3.0	5
9	SARS-CoV-2 viral dynamics in infections with Alpha and Beta variants of concern in the French community. <i>Journal of Infection</i> , 2021, , .	3.3	16
10	Quantifying the relationship between SARS-CoV-2 viral load and infectiousness. <i>ELife</i> , 2021, 10, .	6.0	97
11	Characterisation of vaccine breakthrough infections of SARS-CoV-2 Delta and Alpha variants and within-host viral load dynamics in the community, France, June to July 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	46
12	The stochastic dynamics of early epidemics: probability of establishment, initial growth rate, and infection cluster size at first detection. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210575.	3.4	9
13	Factors favouring the evolution of multidrug resistance in bacteria. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200105.	3.4	26
14	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. <i>Nature Communications</i> , 2020, 11, 5542.	12.8	5
15	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , 2019, 15, e1007763.	4.7	54
16	Evolutionary epidemiology models to predict the dynamics of antibiotic resistance. <i>Evolutionary Applications</i> , 2019, 12, 365-383.	3.1	65
17	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018, 1746, 55-61.	0.9	0
18	The evolution of subtype B HIV-1 tat in the Netherlands during 1985â€“2012. <i>Virus Research</i> , 2018, 250, 51-64.	2.2	8

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19	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	4.9	64
20	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180040.	3.4	49
21	Evolution of antibiotic resistance is linked to any genetic mechanism affecting bacterial duration of carriage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1075-1080.	7.1	133
22	An evolutionary model to predict the frequency of antibiotic resistance under seasonal antibiotic use, and an application to <i>Streptococcus pneumoniae</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170679.	2.6	29
23	What drives parallel evolution?. <i>BioEssays</i> , 2017, 39, 1-9.	2.5	84
24	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017, 15, e2001855.	5.6	38
25	Epistasis and the Structure of Fitness Landscapes: Are Experimental Fitness Landscapes Compatible with Fisher's Geometric Model?. <i>Genetics</i> , 2016, 203, 847-862.	2.9	42
26	Evidence for parasite-mediated selection during short-lasting toxic algal blooms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161870.	2.6	38
27	Large Variations in HIV-1 Viral Load Explained by Shifting-Mosaic Metapopulation Dynamics. <i>PLoS Biology</i> , 2016, 14, e1002567.	5.6	17
28	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016, 5, .	6.0	46
29	Properties of selected mutations and genotypic landscapes under Fisher's geometric model. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3537-3554.	2.3	73
30	ON THE EVOLUTION OF MIGRATION IN HETEROGENEOUS ENVIRONMENTS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1617-1628.	2.3	19
31	The demography of a metapopulation in an environment changing in time and space. <i>Theoretical Population Biology</i> , 2014, 94, 1-9.	1.1	1
32	A practical guide to measuring local adaptation. <i>Ecology Letters</i> , 2013, 16, 1195-1205.	6.4	458
33	Time-shift experiments and patterns of adaptation across time and space. <i>Ecology Letters</i> , 2013, 16, 31-38.	6.4	46