

# François Blanquart

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7463893/publications.pdf>

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	A practical guide to measuring local adaptation. <i>Ecology Letters</i> , 2013, 16, 1195-1205.	6.4	458
2	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
3	Quantifying the relationship between SARS-CoV-2 viral load and infectiousness. <i>ELife</i> , 2021, 10, .	6.0	97
4	What drives parallel evolution?. <i>BioEssays</i> , 2017, 39, 1-9.	2.5	84
5	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
6	Evolutionary epidemiology models to predict the dynamics of antibiotic resistance. <i>Evolutionary Applications</i> , 2019, 12, 365-383.	3.1	65
7	Early assessment of diffusion and possible expansion of SARS-CoV-2 Lineage 20I/501Y.V1 (B.1.1.7, variant) Tj ETQq1 1 0.784314 rgBT (C	7.0	65
8	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
9	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , 2019, 15, e1007763.	4.7	54
10	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180040.	3.4	49
11	Time-shift experiments and patterns of adaptation across time and space. <i>Ecology Letters</i> , 2013, 16, 31-38.	6.4	46
12	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
13	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016, 5, .	6.0	46
14	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
15	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
16	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	An evolutionary model to predict the frequency of antibiotic resistance under seasonal antibiotic use, and an application to <i>Streptococcus pneumoniae</i> . Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170679.	2.6	29
20	Factors favouring the evolution of multidrug resistance in bacteria. Journal of the Royal Society Interface, 2020, 17, 20200105.	3.4	26
21	ON THE EVOLUTION OF MIGRATION IN HETEROGENEOUS ENVIRONMENTS. Evolution; International Journal of Organic Evolution, 2014, 68, 1617-1628.	2.3	19
22	Large Variations in HIV-1 Viral Load Explained by Shifting-Mosaic Metapopulation Dynamics. PLoS Biology, 2016, 14, e1002567.	5.6	17
23	SARS-CoV-2 viral dynamics in infections with Alpha and Beta variants of concern in the French community. Journal of Infection, 2021, , .	3.3	16
24	The stochastic dynamics of early epidemics: probability of establishment, initial growth rate, and infection cluster size at first detection. Journal of the Royal Society Interface, 2021, 18, 20210575.	3.4	9
25	The evolution of subtype B HIV-1 tat in the Netherlands during 1985–2012. Virus Research, 2018, 250, 51-64.	2.2	8
26	Selection for infectivity profiles in slow and fast epidemics, and the rise of SARS-CoV-2 variants. ELife, 2022, 11, .	6.0	8
27	High-risk exposure without personal protective equipment and infection with SARS-CoV-2 in-hospital workers - The CoV-CONTACT cohort. Journal of Infection, 2021, 82, 186-230.	3.3	7
28	Nosocomial transmission clusters and lineage diversity characterized by SARS-CoV-2 genomes from two large hospitals in Paris, France, in 2020. Scientific Reports, 2022, 12, 1094.	3.3	7
29	Heritability of the HIV-1 reservoir size and decay under long-term suppressive ART. Nature Communications, 2020, 11, 5542.	12.8	5
30	Estimating the global reduction in transmission and rise in detection capacity of the novel coronavirus SARS-CoV-2 in early 2020. Epidemics, 2021, 35, 100445.	3.0	5
31	The demography of a metapopulation in an environment changing in time and space. Theoretical Population Biology, 2014, 94, 1-9.	1.1	1
32	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. Virus Evolution, 2022, 8, veac022.	4.9	1
33	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. Methods in Molecular Biology, 2018, 1746, 55-61.	0.9	0