

Samuel Alizon

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

4,858
citations

147801

31
h-index

114465

63
g-index

137
all docs

137
docs citations

137
times ranked

5365
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysing different exposures identifies that wearing masks and establishing COVID-19 areas reduce secondary-attack risk in aged-care facilities. <i>International Journal of Epidemiology</i> , 2022, 50, 1788-1794.	1.9	2
2	Epidemiological and clinical insights from SARS-CoV-2 RT-PCR crossing threshold values, France, January to November 2020. <i>Eurosurveillance</i> , 2022, 27, .	7.0	6
3	Non-Markovian modelling highlights the importance of age structure on Covid-19 epidemiological dynamics. <i>Mathematical Modelling of Natural Phenomena</i> , 2022, 17, 7.	2.4	9
4	Challenges for mathematical epidemiological modelling. <i>Anaesthesia, Critical Care & Pain Medicine</i> , 2022, 41, 101053.	1.4	5
5	Variant-specific SARS-CoV-2 within-host kinetics. <i>Journal of Medical Virology</i> , 2022, 94, 3625-3633.	5.0	11
6	The source of individual heterogeneity shapes infectious disease outbreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220232.	2.6	3
7	Analyzing and Modeling the Spread of SARS-CoV-2 Omicron Lineages BA.1 and BA.2, France, September 2021–February 2022. <i>Emerging Infectious Diseases</i> , 2022, 28, 1355-1365.	4.3	18
8	Superspreading genomes. <i>Science</i> , 2021, 371, 574-575.	12.6	9
9	Within-host bacterial growth dynamics with both mutation and horizontal gene transfer. <i>Journal of Mathematical Biology</i> , 2021, 82, 16.	1.9	4
10	Age-structured non-pharmaceutical interventions for optimal control of COVID-19 epidemic. <i>PLoS Computational Biology</i> , 2021, 17, e1008776.	3.2	38
11	Cytokine response following perturbation of the cervicovaginal milieu during HPV genital infection. <i>Immunologic Research</i> , 2021, 69, 255-263.	2.9	5
12	Detecting Rapid Spread of SARS-CoV-2 Variants, France, January 26–February 16, 2021. <i>Emerging Infectious Diseases</i> , 2021, 27, 1496-1499.	4.3	32
13	Two waves and a high tide: the COVID-19 epidemic in France. <i>Anaesthesia, Critical Care & Pain Medicine</i> , 2021, 40, 100881.	1.4	6
14	Memory is key in capturing COVID-19 epidemiological dynamics. <i>Epidemics</i> , 2021, 35, 100459.	3.0	43
15	The SARS-CoV-2 B.1.351 lineage (VOC \hat{I}^2) is outgrowing the B.1.1.7 lineage (VOC \hat{I}^{\pm}) in some French regions in April 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	24
16	SARS-CoV-2 virulence evolution: Avirulence theory, immunity and trade-offs. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1867-1877.	1.7	29
17	Rapid spread of the SARS-CoV-2 Delta variant in some French regions, June 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	83
18	Anticipating COVID-19 intensive care unit capacity strain: A look back at epidemiological projections in France. <i>Anaesthesia, Critical Care & Pain Medicine</i> , 2021, 40, 100943.	1.4	10

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19	Quantifying transmission dynamics of acute hepatitis C virus infections in a heterogeneous population using sequence data. <i>PLoS Pathogens</i> , 2021, 17, e1009916.	4.7	6
20	Reconstructing contact network structure and cross-immunity patterns from multiple infection histories. <i>PLoS Computational Biology</i> , 2021, 17, e1009375.	3.2	1
21	Episome partitioning and symmetric cell divisions: Quantifying the role of random events in the persistence of HPV infections. <i>PLoS Computational Biology</i> , 2021, 17, e1009352.	3.2	2
22	SARS-CoV-2 viral RNA levels are not 'viral load'. <i>Trends in Microbiology</i> , 2021, 29, 970-972.	7.7	26
23	Predicting COVID-19 incidence in French hospitals using human contact network analytics. <i>International Journal of Infectious Diseases</i> , 2021, 111, 100-107.	3.3	9
24	SARS-CoV-2 variants of concern are associated with lower RT-PCR amplification cycles between January and March 2021 in France. <i>International Journal of Infectious Diseases</i> , 2021, 113, 12-14.	3.3	13
25	Emerging dynamics from high-resolution spatial numerical epidemics. <i>ELife</i> , 2021, 10, .	6.0	7
26	«Avec le Covid-19, la modélisation des épidémies s'ouvre aux données massives». <i>Pour la science</i> Fr, 2021, N° 529 - novembre, 22-27.	0.0	0
27	Can we eradicate viral pathogens?. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1851-1854.	1.7	0
28	HPV cervical infections and serological status in vaccinated and unvaccinated women. <i>Vaccine</i> , 2020, 38, 8167-8174.	3.8	9
29	Detecting within-host interactions from genotype combination prevalence data. <i>Epidemics</i> , 2019, 29, 100349.	3.0	9
30	Epithelial stratification shapes infection dynamics. <i>PLoS Computational Biology</i> , 2019, 15, e1006646.	3.2	13
31	Natural history, dynamics, and ecology of human papillomaviruses in genital infections of young women: protocol of the PAPCLEAR cohort study. <i>BMJ Open</i> , 2019, 9, e025129.	1.9	17
32	Towards a multi-level and a multi-disciplinary approach to DNA oncovirus virulence. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190041.	4.0	5
33	Modelling the evolution of viral oncogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180302.	4.0	1
34	COUSIN (COdon Usage Similarity INdex): A Normalized Measure of Codon Usage Preferences. <i>Genome Biology and Evolution</i> , 2019, 11, 3523-3528.	2.5	51
35	Coevolution of virulence and immunosuppression in multiple infections. <i>Journal of Evolutionary Biology</i> , 2018, 31, 995-1005.	1.7	19
36	Inexpensive Research in the Golden Open-Access Era. <i>Trends in Ecology and Evolution</i> , 2018, 33, 301-303.	8.7	32

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37	Can Ebola virus evolve to be less virulent in humans?. <i>Journal of Evolutionary Biology</i> , 2018, 31, 382-392.	1.7	8
38	Reconciling Pasteur and Darwin to control infectious diseases. <i>PLoS Biology</i> , 2018, 16, e2003815.	5.6	15
39	Modelling the evolution of how vector-borne parasites manipulate the vector's host choice. <i>Peer Community in Evolutionary Biology</i> , 2018, , 100023.	0.0	0
40	Exposing the diversity of multiple infection patterns. <i>Journal of Theoretical Biology</i> , 2017, 419, 278-289.	1.7	36
41	Why Human Papillomavirus Acute Infections Matter. <i>Viruses</i> , 2017, 9, 293.	3.3	49
42	Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study. <i>PLoS Computational Biology</i> , 2017, 13, e1005416.	3.2	39
43	Invasions of Host-Associated Microbiome Networks. <i>Advances in Ecological Research</i> , 2017, , 201-281.	2.7	19
44	Phylodynamique des infections virales. <i>Virologie</i> , 2017, 21, 119-129.	0.1	1
45	A Visionary Pioneer of Parasite Ecology and Evolution. <i>American Naturalist</i> , 2016, 187, ii-iii.	2.1	2
46	From within-host interactions to epidemiological competition: a general model for multiple infections. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140303.	4.0	34
47	Within-Host Stochastic Emergence Dynamics of Immune-Escape Mutants. <i>PLoS Computational Biology</i> , 2015, 11, e1004149.	3.2	10
48	Adaptive virulence evolution: the good old fitness-based approach. <i>Trends in Ecology and Evolution</i> , 2015, 30, 248-254.	8.7	110
49	Emerging Disease and the Evolution of Virulence: The Case of the 1918-1919 Influenza Pandemic. <i>History, Philosophy and Theory of the Life Sciences</i> , 2015, , 93-130.	0.4	7
50	Parasite evolution in response to sex-based host heterogeneity in resistance and tolerance. <i>Journal of Evolutionary Biology</i> , 2014, 27, 2753-2766.	1.7	37
51	Quantifying the epidemic spread of Ebola virus (EBOV) in Sierra Leone using phylodynamics. <i>Virulence</i> , 2014, 5, 825-827.	4.4	25
52	What is a pathogen? Toward a process view of host-parasite interactions. <i>Virulence</i> , 2014, 5, 775-785.	4.4	108
53	Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. <i>Science</i> , 2014, 343, 1243727.	12.6	215
54	Evidence that hepatitis C virus genome partly controls infection outcome. <i>Evolutionary Applications</i> , 2014, 7, 533-547.	3.1	4

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55	Clinical applications of pathogen phylogenies. <i>Trends in Molecular Medicine</i> , 2014, 20, 394-404.	6.7	10
56	Epidemiological Feedbacks Affect Evolutionary Emergence of Pathogens. <i>American Naturalist</i> , 2014, 183, E105-E117.	2.1	22
57	Within-host and between-host evolutionary rates across the HIV-1 genome. <i>Retrovirology</i> , 2013, 10, 49.	2.0	110
58	Multiple infections and the evolution of virulence. <i>Ecology Letters</i> , 2013, 16, 556-567.	6.4	348
59	PARASITE CO-TRANSMISSION AND THE EVOLUTIONARY EPIDEMIOLOGY OF VIRULENCE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 921-933.	2.3	40
60	On the limits of interpreting some plastic responses through a cooperator/cheater prism. A comment on Harrison. <i>Journal of Evolutionary Biology</i> , 2013, 26, 2051-2056.	1.7	3
61	Epidemic Spread on Weighted Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003352.	3.2	51
62	Introducing the Outbreak Threshold in Epidemiology. <i>PLoS Pathogens</i> , 2013, 9, e1003277.	4.7	63
63	Co-infection and super-infection models in evolutionary epidemiology. <i>Interface Focus</i> , 2013, 3, 20130031.	3.0	76
64	How effectively can HIV phylogenies be used to measure heritability?. <i>Evolution, Medicine and Public Health</i> , 2013, 2013, 209-224.	2.5	21
65	Modelling the Course of an HIV Infection: Insights from Ecology and Evolution. <i>Viruses</i> , 2012, 4, 1984-2013.	3.3	50
66	Weighting for sex acts to understand the spread of STI on networks. <i>Journal of Theoretical Biology</i> , 2012, 311, 46-53.	1.7	11
67	Epidemiological and clinical consequences of within-host evolution. <i>Trends in Microbiology</i> , 2011, 19, 24-32.	7.7	91
68	Virulence evolution in response to anti-infection resistance: toxic food plants can select for virulent parasites of monarch butterflies. <i>Journal of Evolutionary Biology</i> , 2011, 24, 712-722.	1.7	38
69	BRIDGING SCALES IN THE EVOLUTION OF INFECTIOUS DISEASE LIFE HISTORIES: THEORY. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 3448-3461.	2.3	55
70	THE TRANSMISSION-VIRULENCE TRADE-OFF AND SUPERINFECTION: COMMENTS TO SMITH. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 3633-3638.	2.3	7
71	Inclusive fitness theory and eusociality. <i>Nature</i> , 2011, 471, E1-E4.	27.8	339
72	Within-host parasite cooperation and the evolution of virulence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 3738-3747.	2.6	56

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73	Within-host viral evolution in a heterogeneous environment: insights into the HIV co-receptor switch. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2625-2635.	1.7	9
74	The virulence-transmission trade-off in vector-borne plant viruses: a review of (non-)existing studies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1907-1918.	4.0	117
75	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. <i>PLoS Pathogens</i> , 2010, 6, e1001123.	4.7	108
76	The Evolutionary Dynamics of a Rapidly Mutating Virus within and between Hosts: The Case of Hepatitis C Virus. <i>PLoS Computational Biology</i> , 2009, 5, e1000565.	3.2	43
77	Virulence evolution and the trade-off hypothesis: history, current state of affairs and the future. <i>Journal of Evolutionary Biology</i> , 2009, 22, 245-259.	1.7	715
78	The Price equation framework to study disease within-host evolution. <i>Journal of Evolutionary Biology</i> , 2009, 22, 1123-1132.	1.7	26
79	EMPTY SITES CAN PROMOTE ALTRUISTIC BEHAVIOR. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 1335-1344.	2.3	104
80	Why is HIV not vector-borne?. <i>Evolutionary Applications</i> , 2008, 1, 17-27.	3.1	11
81	Transmission-virulence trade-offs in vector-borne diseases. <i>Theoretical Population Biology</i> , 2008, 74, 6-15.	1.1	35
82	Linking within- and between-host dynamics in the evolutionary epidemiology of infectious diseases. <i>Trends in Ecology and Evolution</i> , 2008, 23, 511-517.	8.7	303
83	Decreased Overall Virulence in Coinfected Hosts Leads to the Persistence of Virulent Parasites. <i>American Naturalist</i> , 2008, 172, E67-E79.	2.1	30
84	Transmission-Recovery Trade-Offs to Study Parasite Evolution. <i>American Naturalist</i> , 2008, 172, E113-E121.	2.1	53
85	Multiple Infections, Immune Dynamics, and the Evolution of Virulence. <i>American Naturalist</i> , 2008, 172, E150-E168.	2.1	135
86	Acute or Chronic? Within-Host Models with Immune Dynamics, Infection Outcome, and Parasite Evolution. <i>American Naturalist</i> , 2008, 172, E244-E256.	2.1	51
87	Competition between cryptic species explains variations in rates of lineage evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12382-12386.	7.1	39
88	Predation and Disturbance Interact to Shape Prey Species Diversity. <i>American Naturalist</i> , 2007, 170, 143-154.	2.1	59
89	Emergence of a Convex Trade-Off between Transmission and Virulence. <i>American Naturalist</i> , 2005, 165, E155-E167.	2.1	140
90	Treating symptomatic infections and the co-evolution of virulence and drug resistance. , 0, 1, .		3

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91	Early phylodynamics analysis of the COVID-19 epidemic in France. , 0, 1, .		4
92	Estimating dates of origin and end of COVID-19 epidemics. , 0, 1, .		4