

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	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
2	Multiple infections and the evolution of virulence. <i>Ecology Letters</i> , 2013, 16, 556-567.	6.4	348
3	Inclusive fitness theory and eusociality. <i>Nature</i> , 2011, 471, E1-E4.	27.8	339
4	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
5	Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. <i>Science</i> , 2014, 343, 1243727.	12.6	215
6	Emergence of a Convex Trade-off between Transmission and Virulence. <i>American Naturalist</i> , 2005, 165, E155-E167.	2.1	140
7	Multiple Infections, Immune Dynamics, and the Evolution of Virulence. <i>American Naturalist</i> , 2008, 172, E150-E168.	2.1	135
8	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
9	Within-host and between-host evolutionary rates across the HIV-1 genome. <i>Retrovirology</i> , 2013, 10, 49.	2.0	110
10	Adaptive virulence evolution: the good old fitness-based approach. <i>Trends in Ecology and Evolution</i> , 2015, 30, 248-254.	8.7	110
11	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. <i>PLoS Pathogens</i> , 2010, 6, e1001123.	4.7	108
12	What is a pathogen? Toward a process view of host-parasite interactions. <i>Virulence</i> , 2014, 5, 775-785.	4.4	108
13	EMPTY SITES CAN PROMOTE ALTRUISTIC BEHAVIOR. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 1335-1344.	2.3	104
14	Epidemiological and clinical consequences of within-host evolution. <i>Trends in Microbiology</i> , 2011, 19, 24-32.	7.7	91
15	Rapid spread of the SARS-CoV-2 Delta variant in some French regions, June 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	83
16	Co-infection and super-infection models in evolutionary epidemiology. <i>Interface Focus</i> , 2013, 3, 20130031.	3.0	76
17	Introducing the Outbreak Threshold in Epidemiology. <i>PLoS Pathogens</i> , 2013, 9, e1003277.	4.7	63
18	Predation and Disturbance Interact to Shape Prey Species Diversity. <i>American Naturalist</i> , 2007, 170, 143-154.	2.1	59

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19	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
20	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
21	Transmission–Recovery Trade–Offs to Study Parasite Evolution. <i>American Naturalist</i> , 2008, 172, E113-E121.	2.1	53
22	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
23	Epidemic Spread on Weighted Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003352.	3.2	51
24	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
25	Modelling the Course of an HIV Infection: Insights from Ecology and Evolution. <i>Viruses</i> , 2012, 4, 1984-2013.	3.3	50
26	Why Human Papillomavirus Acute Infections Matter. <i>Viruses</i> , 2017, 9, 293.	3.3	49
27	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
28	Memory is key in capturing COVID-19 epidemiological dynamics. <i>Epidemics</i> , 2021, 35, 100459.	3.0	43
29	PARASITE CO-TRANSMISSION AND THE EVOLUTIONARY EPIDEMIOLOGY OF VIRULENCE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 921-933.	2.3	40
30	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
31	Inferring epidemiological parameters from phylogenies using regression-ABC: A comparative study. <i>PLoS Computational Biology</i> , 2017, 13, e1005416.	3.2	39
32	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
33	Age-structured non-pharmaceutical interventions for optimal control of COVID-19 epidemic. <i>PLoS Computational Biology</i> , 2021, 17, e1008776.	3.2	38
34	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
35	Exposing the diversity of multiple infection patterns. <i>Journal of Theoretical Biology</i> , 2017, 419, 278-289.	1.7	36
36	Transmission–virulence trade-offs in vector-borne diseases. <i>Theoretical Population Biology</i> , 2008, 74, 6-15.	1.1	35

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37	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
38	Inexpensive Research in the Golden Open-Access Era. <i>Trends in Ecology and Evolution</i> , 2018, 33, 301-303.	8.7	32
39	Detecting Rapid Spread of SARS-CoV-2 Variants, France, January 26â€“February 16, 2021. <i>Emerging Infectious Diseases</i> , 2021, 27, 1496-1499.	4.3	32
40	Decreased Overall Virulence in Coinfected Hosts Leads to the Persistence of Virulent Parasites. <i>American Naturalist</i> , 2008, 172, E67-E79.	2.1	30
41	SARSâ€“CoVâ€“2 virulence evolution: Avirulence theory, immunity and tradeâ€“offs. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1867-1877.	1.7	29
42	The Price equation framework to study disease withinâ€“host evolution. <i>Journal of Evolutionary Biology</i> , 2009, 22, 1123-1132.	1.7	26
43	SARS-CoV-2 viral RNA levels are not 'viral load'. <i>Trends in Microbiology</i> , 2021, 29, 970-972.	7.7	26
44	Quantifying the epidemic spread of Ebola virus (EBOV) in Sierra Leone using phylodynamics. <i>Virulence</i> , 2014, 5, 825-827.	4.4	25
45	The SARS-CoV-2 B.1.351 lineage (VOC Î²) is outgrowing the B.1.1.7 lineage (VOC Î±) in some French regions in April 2021. <i>Eurosurveillance</i> , 2021, 26, .	7.0	24
46	Epidemiological Feedbacks Affect Evolutionary Emergence of Pathogens. <i>American Naturalist</i> , 2014, 183, E105-E117.	2.1	22
47	How effectively can HIV phylogenies be used to measure heritability?. <i>Evolution, Medicine and Public Health</i> , 2013, 2013, 209-224.	2.5	21
48	Coevolution of virulence and immunosuppression in multiple infections. <i>Journal of Evolutionary Biology</i> , 2018, 31, 995-1005.	1.7	19
49	Invasions of Host-Associated Microbiome Networks. <i>Advances in Ecological Research</i> , 2017, , 201-281.	2.7	19
50	Analyzing and Modeling the Spread of SARS-CoV-2 Omicron Lineages BA.1 and BA.2, France, September 2021â€“February 2022. <i>Emerging Infectious Diseases</i> , 2022, 28, 1355-1365.	4.3	18
51	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
52	Reconciling Pasteur and Darwin to control infectious diseases. <i>PLoS Biology</i> , 2018, 16, e2003815.	5.6	15
53	Epithelial stratification shapes infection dynamics. <i>PLoS Computational Biology</i> , 2019, 15, e1006646.	3.2	13
54	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

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55	Why is HIV not vectorâ€borne?. <i>Evolutionary Applications</i> , 2008, 1, 17-27.	3.1	11
56	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
57	Variantâ€specific SARSâ€CoVâ€2 withinâ€host kinetics. <i>Journal of Medical Virology</i> , 2022, 94, 3625-3633.	5.0	11
58	Clinical applications of pathogen phylogenies. <i>Trends in Molecular Medicine</i> , 2014, 20, 394-404.	6.7	10
59	Within-Host Stochastic Emergence Dynamics of Immune-Escape Mutants. <i>PLoS Computational Biology</i> , 2015, 11, e1004149.	3.2	10
60	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
61	Withinâ€host viral evolution in a heterogeneous environment: insights into the HIV coâ€receptor switch. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2625-2635.	1.7	9
62	Detecting within-host interactions from genotype combination prevalence data. <i>Epidemics</i> , 2019, 29, 100349.	3.0	9
63	HPV cervical infections and serological status in vaccinated and unvaccinated women. <i>Vaccine</i> , 2020, 38, 8167-8174.	3.8	9
64	Superspreading genomes. <i>Science</i> , 2021, 371, 574-575.	12.6	9
65	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
66	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
67	Can Ebola virus evolve to be less virulent in humans?. <i>Journal of Evolutionary Biology</i> , 2018, 31, 382-392.	1.7	8
68	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
69	Emerging Disease and the Evolution of Virulence: The Case of the 1918â€1919 Influenza Pandemic. <i>History, Philosophy and Theory of the Life Sciences</i> , 2015, , 93-130.	0.4	7
70	Emerging dynamics from high-resolution spatial numerical epidemics. <i>ELife</i> , 2021, 10, .	6.0	7
71	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
72	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

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73	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
74	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
75	Cytokine response following perturbation of the cervicovaginal milieu during HPV genital infection. <i>Immunologic Research</i> , 2021, 69, 255-263.	2.9	5
76	Challenges for mathematical epidemiological modelling. <i>Anaesthesia, Critical Care & Pain Medicine</i> , 2022, 41, 101053.	1.4	5
77	Evidence that hepatitis C virus genome partly controls infection outcome. <i>Evolutionary Applications</i> , 2014, 7, 533-547.	3.1	4
78	Within-host bacterial growth dynamics with both mutation and horizontal gene transfer. <i>Journal of Mathematical Biology</i> , 2021, 82, 16.	1.9	4
79	Early phylodynamics analysis of the COVID-19 epidemic in France. , 0, 1, .		4
80	Estimating dates of origin and end of COVID-19 epidemics. , 0, 1, .		4
81	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
82	Treating symptomatic infections and the co-evolution of virulence and drug resistance. , 0, 1, .		3
83	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
84	A Visionary Pioneer of Parasite Ecology and Evolution. <i>American Naturalist</i> , 2016, 187, ii-iii.	2.1	2
85	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
86	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
87	Modelling the evolution of viral oncogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180302.	4.0	1
88	Reconstructing contact network structure and cross-immunity patterns from multiple infection histories. <i>PLoS Computational Biology</i> , 2021, 17, e1009375.	3.2	1
89	Phylodynamique des infections virales. <i>Virologie</i> , 2017, 21, 119-129.	0.1	1
90	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

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91	«Avec le Covid-19, la modélisation des épidémies s'ouvre aux données massives». Pour la science Fr., 2021, N° 529 - novembre, 22-27.	0.0	0
92	Can we eradicate viral pathogens?. Journal of Evolutionary Biology, 2021, 34, 1851-1854.	1.7	0