Sebastian Bonhoeffer

List of Publications by Year
in descending order

223	25,066	10956 71	8138 148
papers	citations	h-index	g-index

260	260	260	19966
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Viral dynamics in human immunodeficiency virus type 1 infection. Nature, 1995, 373, 117-122.	13.7	3,369
2	Quantitation of HIV-1-Specific Cytotoxic T Lymphocytes and Plasma Load of Viral RNA. Science, 1998, 279, 2103-2106.	6.0	1,340
3	Cooperation and Competition in the Evolution of ATP-Producing Pathways. Science, 2001, 292, 504-507.	6.0	1,116
4	Viral dynamics in hepatitis B virus infection.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 4398-4402.	3.3	919
5	Analysis of Total Human Immunodeficiency Virus (HIV)-Specific CD4 + and CD8 + T-Cell Responses: Relationship to Viral Load in Untreated HIV Infection. Journal of Virology, 2001, 75, 11983-11991.	1.5	652
6	Global trends in antimicrobial resistance in animals in low- and middle-income countries. Science, 2019, 365, .	6.0	594
7	Virus dynamics and drug therapy. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6971-6976.	3.3	560
8	Rapid production and clearance of HIV-1 and hepatitis C virus assessed by large volume plasma apheresis. Lancet, The, 1999, 354, 1782-1785.	6.3	458
9	Birthâ€“death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 228-233.	3.3	454
10	Reducing antimicrobial use in food animals. Science, 2017, 357, 1350-1352.	6.0	448
11	Evaluating treatment protocols to prevent antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12106-12111.	3.3	441
12	Viral dynamics in vivo: limitations on estimates of intracellular delay and virus decay.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 7247-7251.	3.3	383
13	Spatial games and the maintenance of cooperation.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 4877-4881.	3.3	368
14	Rapid Turnover of T Lymphocytes in SIV-Infected Rhesus Macaques. Science, 1998, 279, 1223-1227.	6.0	343
15	Practical considerations for measuring the effective reproductive number, Rt. PLoS Computational Biology, 2020, 16, e1008409.	1.5	343
16	Decay Kinetics of Human Immunodeficiency Virus-Specific Effector Cytotoxic T Lymphocytes after Combination Antiretroviral Therapy. Journal of Virology, 1999, 73, 797-800.	1.5	331
17	Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. Journal of Experimental Medicine, 2011, 208, 273-284.	4.2	271
18	MORE SPATIAL GAMES. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 1994, 04, 33-56.	0.7	249

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19	Evidence for Positive Epistasis in HIV-1. Science, 2004, 306, 1547-1550.	6.0	247
20	Anti-viral Drug Treatment: Dynamics of Resistance in Free Virus and Infected Cell Populations. Journal of Theoretical Biology, 1997, 184, 203-217.	0.8	239
21	HIV-1 Antigenâ€“specific and â€“nonspecific B Cell Responses Are Sensitive to Combination Antiretroviral Therapy. Journal of Experimental Medicine, 1998, 188, 233-245.	4.2	234
22	Population biological principles of drug-resistance evolution in infectious diseases. Lancet Infectious Diseases, The, 2011, 11, 236-247.	4.6	220
23	Population Biology, Evolution, and Infectious Disease: Convergence and Synthesis. Science, 1999, 283, 806-809.	6.0	219
24	Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. Science, 2014, 343, 1243727.	6.0	215
25	HIV-1â€“specific immune responses in subjects who temporarily contain virus replication after discontinuation of highly active antiretroviral therapy. Journal of Clinical Investigation, 1999, 104, R13-R18.	3.9	215
26	Production of resistant HIV mutants during antiretroviral therapy. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 7681-7686.	3.3	207
27	Estimating the Basic Reproductive Number from Viral Sequence Data. Molecular Biology and Evolution, 2012, 29, 347-357.	3.5	206
28	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. Antimicrobial Agents and Chemotherapy, 2014, 58, 4573-4582.	1.4	198
29	The effect of opinion clustering on disease outbreaks. Journal of the Royal Society Interface, 2008, 5, 1505-1508.	1.5	197
30	The HIV coreceptor switch: a population dynamical perspective. Trends in Microbiology, 2005, 13, 269-277.	3.5	174
31	Experimental Tests for an Evolutionary Tradeâ€Off between Growth Rate and Yield in E. coli. American Naturalist, 2006, 168, 242-251.	1.0	173
32	Molecular Epidemiology Reveals Longâ€Term Changes in HIV Type 1 Subtype B Transmission in Switzerland. Journal of Infectious Diseases, 2010, 201, 1488-1497.	1.9	172
33	Evolution of cooperation by generalized reciprocity. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 1115-1120.	1.2	169
34	Salmonella persisters promote the spread of antibiotic resistance plasmids in the gut. Nature, 2019, 573, 276-280.	13.7	169
35	A systems analysis of mutational effects in HIV-1 protease and reverse transcriptase. Nature Genetics, 2011, 43, 487-489.	9.4	168
36	An evolutionary scenario for the transition to undifferentiated multicellularity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1095-1098.	3.3	166

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37	Evolution of Crossâ€Feeding in Microbial Populations. American Naturalist, 2004, 163, E126-E135.	1.0	166
38	Causes of HIV diversity. Nature, 1995, 376, 125-125.	13.7	164
39	The virological and immunological consequences of structured treatment interruptions in chronic HIV-1 infection. Aids, 2001, 15, F29-F40.	1.0	160
40	Emergence of Drug-Resistant Influenza Virus: Population Dynamical Considerations. Science, 2006, 312, 389-391.	6.0	155
41	The frequency of resistant mutant virus before antiviral therapy. Aids, 1998, 12, 461-465.	1.0	151
42	Temporal Analyses of Virus Replication, Immune Responses, and Efficacy in Rhesus Macaques Immunized with a Live, Attenuated Simian Immunodeficiency Virus Vaccine. Journal of Virology, 1998, 72, 7501-7509.	1.5	151
43	HIV-1 Evolution and Disease Progression. Science, 1996, 274, 1008-1011.	6.0	150
44	Structured antiretroviral treatment interruptions in chronically HIV-1-infected subjects. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13288-13293.	3.3	150
45	Compensation of Fitness Costs and Reversibility of Antibiotic Resistance Mutations. Antimicrobial Agents and Chemotherapy, 2010, 54, 2085-2095.	1.4	144
46	Epistasis between deleterious mutations and the evolution of recombination. Trends in Ecology and Evolution, 2007, 22, 308-315.	4.2	143
47	EVOLUTION OF VIRULENCE IN A HETEROGENEOUS HOST POPULATION. Evolution; International Journal of Organic Evolution, 2000, 54, 64-71.	1.1	137
48	The state of affairs in the kingdom of the Red Queen. Trends in Ecology and Evolution, 2008, 23, 439-445.	4.2	135
49	Preâ€“existence and emergence of drug resistance in HIVâ€“1 infection. Proceedings of the Royal Society B: Biological Sciences, 1997, 264, 631-637.	1.2	134
50	Eight challenges in phylodynamic inference. Epidemics, 2015, 10, 88-92.	1.5	131
51	Ambiguous Nucleotide Calls From Population-based Sequencing of HIV-1 are a Marker for Viral Diversity and the Age of Infection. Clinical Infectious Diseases, 2011, 52, 532-539.	2.9	127
52	Doseâ€“dependent infection rates of parasites produce the Allee effect in epidemiology. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 271-279.	1.2	122
53	Emergence of Minor Populations of Human Immunodeficiency Virus Type 1 Carrying the M184V and L90M Mutations in Subjects Undergoing Structured Treatment Interruptions. Journal of Infectious Diseases, 2003, 188, 1433-1443.	1.9	121
54	Risks and benefits of structured antiretroviral drug therapy interruptions in HIV-1 infection. Aids, 2000, 14, 2313-2322.	1.0	117

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55	Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120198.	1.8	117
56	The Evolution of Connectivity in Metabolic Networks. PLoS Biology, 2005, 3, e228.	2.6	109
57	Recombination in HIV and the evolution of drug resistance: for better or for worse?. BioEssays, 2004, 26, 180-188.	1.2	108
58	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. PLoS Pathogens, 2010, 6, e1001123.	2.1	108
59	Spatial models of virus-immune dynamics. Journal of Theoretical Biology, 2005, 233, 221-236.	0.8	104
60	Evolutionary rescue: linking theory for conservation and medicine. Evolutionary Applications, 2014, 7, 1161-1179.	1.5	104
61	Intra-host versus inter-host selection: viral strategies of immune function impairment.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 8062-8066.	3.3	102
62	Evolution and emergence of infectious diseases in theoretical and real-world networks. Nature Communications, 2015, 6, 6101.	5.8	102
63	Exploring the Complexity of the HIV-1 Fitness Landscape. PLoS Genetics, 2012, 8, e1002551.	1.5	100
64	Spatial Heterogeneity in Drug Concentrations Can Facilitate the Emergence of Resistance to Cancer Therapy. PLoS Computational Biology, 2015, 11, e1004142.	1.5	100
65	Quantification of Cell Turnover Kinetics Using 5-Bromo-2â€²-deoxyuridine1. Journal of Immunology, 2000, 164, 5049-5054.	0.4	95
66	Estimating the Stoichiometry of Human Immunodeficiency Virus Entry. Journal of Virology, 2009, 83, 1523-1531.	1.5	95
67	Stochastic or deterministic: what is the effective population size of HIV-1?. Trends in Microbiology, 2006, 14, 507-511.	3.5	90
68	Cycling Empirical Antibiotic Therapy in Hospitals: Meta-Analysis and Models. PLoS Pathogens, 2014, 10, e1004225.	2.1	87
69	Stochastic Interplay between Mutation and Recombination during the Acquisition of Drug Resistance Mutations in Human Immunodeficiency Virus Type 1. Journal of Virology, 2005, 79, 13572-13578.	1.5	85
70	Inferring Epidemic Contact Structure from Phylogenetic Trees. PLoS Computational Biology, 2012, 8, e1002413.	1.5	85
71	Rapid Clearance of Simian Immunodeficiency Virus Particles from Plasma of Rhesus Macaques. Journal of Virology, 1999, 73, 855-860.	1.5	84
72	Antibiotic-Resistant Neisseria gonorrhoeae Spread Faster with More Treatment, Not More Sexual Partners. PLoS Pathogens, 2016, 12, e1005611.	2.1	84

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73	Evolution of complexity in signaling pathways. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16337-16342.	3.3	79
74	The path of least resistance: aggressive or moderate treatment?. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140566.	1.2	79
75	COVID-19 infectivity profile correction. Swiss Medical Weekly, 2020, 150, w20336.	0.8	77
76	Quantification of infectious HIV-1 plasma viral load using a boosted in vitro infection protocol. Virology, 2004, 326, 113-129.	1.1	76
77	An evolutionary perspective on the systems of adaptive immunity. Biological Reviews, 2018, 93, 505-528.	4.7	76
78	The Role of Migration and Domestic Transmission in the Spread of HIV-1 Non-B Subtypes in Switzerland. Journal of Infectious Diseases, 2011, 204, 1095-1103.	1.9	74
79	Interchromatid and Interhomolog Recombination in Arabidopsis thaliana. Plant Cell, 2004, 16, 342-352.	3.1	72
80	The importance of being erroneous. Nature, 2002, 420, 367-369.	13.7	70
81	Death and population dynamics affect mutation rate estimates and evolvability under stress in bacteria. PLoS Biology, 2018, 16, e2005056.	2.6	70
82	Persistence of Transmitted HIV-1 Drug Resistance Mutations Associated with Fitness Costs and Viral Genetic Backgrounds. PLoS Pathogens, 2015, 11, e1004722.	2.1	68
83	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. ISME Journal, 2021, 15, 862-878.	4.4	66
84	Quantifying the impact of quarantine duration on COVID-19 transmission. ELife, 2021, 10, .	2.8	66
85	RNA multi-structure landscapes. European Biophysics Journal, 1993, 22, 13-24.	1.2	65
86	High Frequency of Cytomegalovirusâ€Specific Cytotoxic Tâ€Effector Cells in HLAâ€A*0201â€“Positive Subjects during Multiple Viral Coinfections. Journal of Infectious Diseases, 2000, 181, 165-175.	1.9	65
87	RAPID PARASITE ADAPTATION DRIVES SELECTION FOR HIGH RECOMBINATION RATES. Evolution; International Journal of Organic Evolution, 2008, 62, 295-300.	1.1	65
88	The evolution of groups of cooperating bacteria and the growth rate versus yield trade-off. Microbiology (United Kingdom), 2005, 151, 637-641.	0.7	63
89	Evolution of Stress Response in the Face of Unreliable Environmental Signals. PLoS Computational Biology, 2012, 8, e1002627.	1.5	59
90	Inference of Epidemiological Dynamics Based on Simulated Phylogenies Using Birth-Death and Coalescent Models. PLoS Computational Biology, 2014, 10, e1003913.	1.5	58

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91	Glancing behind virus load variation in HIV-1 infection. Trends in Microbiology, 2003, 11, 499-504.	3.5	55
92	Using an Epidemiological Model for Phylogenetic Inference Reveals Density Dependence in HIV Transmission. Molecular Biology and Evolution, 2014, 31, 6-17.	3.5	55
93	HumanImmunodeficiency Virus Type 1 Fitness Is a Determining Factor in ViralRebound and Set Point in ChronicInfection. Journal of Virology, 2003, 77, 13146-13155.	1.5	54
94	The effect of population structure on the emergence of drug resistance during influenza pandemics. Journal of the Royal Society Interface, 2007, 4, 893-906.	1.5	54
95	On the relationship between serial interval, infectiousness profile and generation time. Journal of the Royal Society Interface, 2021, 18, 20200756.	1.5	54
96	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. PLoS Pathogens, 2018, 14, e1006895.	2.1	53
97	Stable virulence levels in the HIV epidemic of Switzerland over two decades. Aids, 2006, 20, 889-894.	1.0	52
98	The Effect of Multifunctionality on the Rate of Evolution in Yeast. Molecular Biology and Evolution, 2006, 23, 721-722.	3.5	52
99	Modeling antibiotic treatment in hospitals: A systematic approach shows benefits of combination therapy over cycling, mixing, and mono-drug therapies. PLoS Computational Biology, 2017, 13, e1005745.	1.5	51
100	HIV results in the frame. Nature, 1995, 375, 193-193.	13.7	50
101	Phenotypic Changes in Drug Susceptibility Associated with Failure of Human Immunodeficiency Virus Type 1 (HIVâ€1) Triple Combination Therapy. Journal of Infectious Diseases, 1999, 180, 865-870.	1.9	50
102	A research agenda for digital proximity tracing apps. Swiss Medical Weekly, 2020, 150, w20324.	0.8	49
103	Effect of Varying Epistasis on the Evolution of Recombination. Genetics, 2006, 173, 589-597.	1.2	48
104	Procedures for reliable estimation of viral fitness from time-series data. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 1887-1893.	1.2	47
105	Quantification of In Vivo Replicative Capacity of HIV-1 in Different Compartments of Infected Cells. Journal of Acquired Immune Deficiency Syndromes (1999), 2001, 26, 397-404.	0.9	46
106	Entry and Transcription as Key Determinants of Differences in CD4 T-Cell Permissiveness to Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2004, 78, 10747-10754.	1.5	46
107	Humoral immunity to HIV-1: kinetics of antibody responses in chronic infection reflects capacity of immune system to improve viral set point. Blood, 2004, 104, 1784-1792.	0.6	46
108	Informed Switching Strongly Decreases the Prevalence of Antibiotic Resistance in Hospital Wards. PLoS Computational Biology, 2011, 7, e1001094.	1.5	45

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109	Error Thresholds on Correlated Fitness Landscapes. Journal of Theoretical Biology, 1993, 164, 359-372.	0.8	44
110	Can High-Risk Fungicides be Used in Mixtures Without Selecting for Fungicide Resistance?. Phytopathology, 2014, 104, 324-331.	1.1	44
111	Developing smarter host mixtures to control plant disease. Plant Pathology, 2015, 64, 996-1004.	1.2	44
112	Emergence of Resistance to Fungicides: The Role of Fungicide Dose. Phytopathology, 2017, 107, 545-560.	1.1	44
113	Neutral drift and polymorphism in gene-for-gene systems. Ecology Letters, 2005, 8, 925-932.	3.0	43
114	Longâ€Term Trends of HIV Type 1 Drug Resistance Prevalence among Antiretroviral Treatmentâ€“Experienced Patients in Switzerland. Clinical Infectious Diseases, 2009, 48, 979-987.	2.9	43
115	Pre-existence and emergence of drug resistance in a generalized model of intra-host viral dynamics. Epidemics, 2012, 4, 187-202.	1.5	43
116	Recombination Accelerates Adaptation on a Large-Scale Empirical Fitness Landscape in HIV-1. PLoS Genetics, 2014, 10, e1004439.	1.5	41
117	A combined within-host and between-hosts modelling framework for the evolution of resistance to antimalarial drugs. Journal of the Royal Society Interface, 2016, 13, 20160148.	1.5	41
118	Simulating the evolution of signal transduction pathways. Journal of Theoretical Biology, 2006, 241, 223-232.	0.8	40
119	Contribution of recombination to the evolutionary history of HIV. Current Opinion in HIV and AIDS, 2015, 10, 84-89.	1.5	40
120	Passive Infusion of Immune Serum into Simian Immunodeficiency Virus-Infected Rhesus Macaques Undergoing a Rapid Disease Course Has Minimal Effect on Plasma Viremia. Virology, 2000, 270, 237-249.	1.1	39
121	Comparing treatment strategies to reduce antibiotic resistance in an in vitro epidemiological setting. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
122	Signal transduction networks: Topology, response and biochemical processes. Journal of Theoretical Biology, 2006, 238, 416-425.	0.8	37
123	Assessing Predicted HIV-1 Replicative Capacity in a Clinical Setting. PLoS Pathogens, 2011, 7, e1002321.	2.1	37
124	Dissecting HIV Virulence: Heritability of Setpoint Viral Load, CD4+ T-Cell Decline, and Per-Parasite Pathogenicity. Molecular Biology and Evolution, 2018, 35, 27-37.	3.5	37
125	Metabolically cohesive microbial consortia and ecosystem functioning. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190245.	1.8	37
126	Effective polyploidy causes phenotypic delay and influences bacterial evolvability. PLoS Biology, 2018, 16, e2004644.	2.6	37

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127	The Red Queen and the persistence of linkage-disequilibrium oscillations in finite and infinite populations. BMC Evolutionary Biology, 2007, 7, 211.	3.2	36
128	On Being the Right Size: The Impact of Population Size and Stochastic Effects on the Evolution of Drug Resistance in Hospitals and the Community. PLoS Pathogens, 2011, 7, e1001334.	2.1	35
129	Decelerating Decay of Latently Infected Cells during Prolonged Therapy for Human Immunodeficiency Virus Type 1 Infection. Journal of Virology, 2002, 76, 8963-8965.	1.5	34
130	A stochastic model for primary HIV infection: optimal timing of therapy. Aids, 1999, 13, 351-357.	1.0	33
131	Rapid Viral Decay in Simian Immunodeficiency Virus-Infected Macaques Receiving Quadruple Antiretroviral Therapy. Journal of Virology, 2006, 80, 9861-9864.	1.5	32
132	No Signs of Hidden Language in Noncoding DNA. Physical Review Letters, 1996, 76, 1977-1977.	2.9	31
133	Mutation accumulation in space and the maintenance of sexual reproduction. Ecology Letters, 2006, 9, 941-946.	3.0	30
134	Red Queen Dynamics with Non-Standard Fitness Interactions. PLoS Computational Biology, 2009, 5, e1000469.	1.5	30
135	Detection of antibiotic resistance is essential for gonorrhoea point-of-care testing: a mathematical modelling study. BMC Medicine, 2017, 15, 142.	2.3	30
136	Why There Are No Essential Genes on Plasmids. Molecular Biology and Evolution, 2014, 32, msu293.	3.5	29
137	High Heritability Is Compatible with the Broad Distribution of Set Point Viral Load in HIV Carriers. PLoS Pathogens, 2015, 11, e1004634.	2.1	29
138	Quantitative constraints on the scope of negative selection. Trends in Immunology, 2003, 24, 132-135.	2.9	28
139	The evolution of network topology by selective removal. Journal of the Royal Society Interface, 2005, 2, 533-536.	1.5	28
140	Recombination and drug resistance in HIV: Population dynamics and stochasticity. Epidemics, 2009, 1, 58-69.	1.5	28
141	African descent is associated with slower CD4 cell count decline in treatment-naive patients of the Swiss HIV Cohort Study. Aids, 2009, 23, 1269-1276.	1.0	28
142	Population Heterogeneity in Mutation Rate Increases the Frequency of Higher-Order Mutants and Reduces Long-Term Mutational Load. Molecular Biology and Evolution, 2017, 34, msw244.	3.5	28
143	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. Molecular Biology and Evolution, 2016, 33, 2454-2468.	3.5	28
144	Antibacterial Effects of Antiretrovirals, Potential Implications for Microbiome Studies in HIV. Antiviral Therapy, 2018, 23, 91-94.	0.6	28

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145	The Role of Recombination for the Coevolutionary Dynamics of HIV and the Immune Response. PLoS ONE, 2011, 6, e16052.	1.1	27
146	Evolutionary Consequences of Tradeoffs between Yield and Rate of ATP Production. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	26
147	Assessing the impact of adherence to anti-retroviral therapy on treatment failure and resistance evolution in HIV. Journal of the Royal Society Interface, 2012, 9, 2309-2320.	1.5	26
148	Clonal dominance and transplantation dynamics in hematopoietic stem cell compartments. PLoS Computational Biology, 2017, 13, e1005803.	1.5	26
149	Residual Viral Replication during Antiretroviral Therapy Boosts Human Immunodeficiency Virus Type 1-Specific CD8 + T-Cell Responses in Subjects Treated Early after Infection. Journal of Virology, 2002, 76, 411-415.	1.5	25
150	On the Causes of Selection for Recombination Underlying the Red Queen Hypothesis. American Naturalist, 2009, 174, S31-S42.	1.0	25
151	Social Meets Molecular: Combining Phylogenetic and Latent Class Analyses to Understand HIV-1 Transmission in Switzerland. American Journal of Epidemiology, 2014, 179, 1514-1525.	1.6	25
152	Robustness of cooperation. Nature, 1996, 379, 126-126.	13.7	24
153	The role of epistasis on the evolution of recombination in hostâ€“parasite coevolution. Theoretical Population Biology, 2009, 75, 1-13.	0.5	23
154	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids. Evolution Letters, 2021, 5, 290-301.	1.6	23
155	Reversing resistance: different routes and common themes across pathogens. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20171619.	1.2	22
156	Resistance to Antimicrobial Chemotherapy: A Prescription for Research and Action. American Journal of the Medical Sciences, 1998, 315, 87-94.	0.4	22
157	High Epitope Expression Levels Increase Competition between T Cells. PLoS Computational Biology, 2006, 2, e109.	1.5	21
158	The Role of Adherence and Retreatment in De Novo Emergence of MDR-TB. PLoS Computational Biology, 2016, 12, e1004749.	1.5	21
159	Viral Dynamics and In Vivo Fitness of HIV-1 in the Presence and Absence of Enfuvirtide. Journal of Acquired Immune Deficiency Syndromes (1999), 2008, 48, 572-576.	0.9	20
160	PLASMIDS AND EVOLUTIONARY RESCUE BY DRUG RESISTANCE. Evolution; International Journal of Organic Evolution, 2014, 68, 2066-2078.	1.1	20
161	Nested model reveals potential amplification of an HIV epidemic due to drug resistance. Epidemics, 2013, 5, 34-43.	1.5	19
162	Invasiveness of plant pathogens depends on the spatial scale of host distribution. Ecological Applications, 2016, 26, 1238-1248.	1.8	19

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163	Quantifying the impact of treatment history on plasmid-mediated resistance evolution in human gut microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23106-23116.	3.3	19
164	Estimating plasmid conjugation rates: A new computational tool and a critical comparison of methods. Plasmid, 2022, 121, 102627.	0.4	19
165	Can live attenuated virus work as post-exposure treatment?. Trends in Immunology, 1995, 16, 131-135.	7.5	18
166	Is antimicrobial resistance evolution accelerating?. PLoS Pathogens, 2020, 16, e1008905.	2.1	18
167	Rotating antibiotics does not minimize selection for resistance. Mathematical Biosciences and Engineering, 2010, 7, 919-922.	1.0	18
168	Fixation probability of mobile genetic elements such as plasmids. Theoretical Population Biology, 2013, 90, 49-55.	0.5	17
169	Influence of recombination on acquisition and reversion of immune escape and compensatory mutations in HIV-1. Epidemics, 2016, 14, 11-25.	1.5	17
170	Short-term activity cycles impede information transmission in ant colonies. PLoS Computational Biology, 2017, 13, e1005527.	1.5	17
171	Test-trace-isolate-quarantine (TTIQ) intervention strategies after symptomatic COVID-19 case identification. PLoS ONE, 2022, 17, e0263597.	1.1	17
172	Models of Viral Kinetics and Drug Resistance in HIV-1 Infection. AIDS Patient Care and STDs, 1998, 12, 769-774.	1.1	16
173	Guanineâ€“adenine bias: a general property of retroid viruses that is unrelated to host-induced hypermutation. Trends in Genetics, 2005, 21, 264-268.	2.9	16
174	Predicting the Evolution of Sex on Complex Fitness Landscapes. PLoS Computational Biology, 2009, 5, e1000510.	1.5	16
175	Estimating the cumulative incidence of SARS-CoV-2 with imperfect serological tests: Exploiting cutoff-free approaches. PLoS Computational Biology, 2021, 17, e1008728.	1.5	16
176	Molecular tracking of an Human Immunodeficiency Virus nef specific cytotoxic T-cell clone shows persistence of clone-specific T-cell receptor DNA but not mRNA following early combination antiretroviral therapy. Immunology Letters, 1999, 66, 219-228.	1.1	15
177	Pathogen invasion-dependent tissue reservoirs and plasmid-encoded antibiotic degradation boost plasmid spread in the gut. ELife, 2021, 10, .	2.8	15
178	Modelling cytomegalovirus replication patterns in the human host: factors important for pathogenesis. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 1961-1967.	1.2	14
179	Potential Pitfalls in Estimating Viral Load Heritability. Trends in Microbiology, 2016, 24, 687-698.	3.5	14
180	Epistasis and Pleiotropy Affect the Modularity of the Genotypeâ€“Phenotype Map of Cross-Resistance in HIV-1. Molecular Biology and Evolution, 2016, 33, 3213-3225.	3.5	14

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181	Estimating the Fitness Cost of Escape from HLA Presentation in HIV-1 Protease and Reverse Transcriptase. PLoS Computational Biology, 2012, 8, e1002525.	1.5	13
182	Quantification of In Vivo Replicative Capacity of HIV-1 in Different Compartments of Infected Cells. Journal of Acquired Immune Deficiency Syndromes (1999), 2001, 26, 397-404.	0.9	12
183	Contribution of Peaks of Virus Load to Simian Immunodeficiency Virus Pathogenesis. Journal of Virology, 2002, 76, 2573-2578.	1.5	12
184	HIV replication elicits little cytopathic effects in vivo: Analysis of surrogate markers for virus production, cytotoxic T cell response and infected cell death. Journal of Medical Virology, 2006, 78, 1141-1146.	2.5	12
185	Modeling antimicrobial cycling and mixing: Differences arising from an individual-based versus a population-based perspective. Mathematical Biosciences, 2017, 294, 85-91.	0.9	12
186	MPN patients with low mutant JAK2 allele burden show late expansion restricted to erythroid and megakaryocytic lineages. Blood, 2020, 136, 2591-2595.	0.6	12
187	Virus load and antigenic diversity. Bulletin of Mathematical Biology, 1997, 59, 881-896.	0.9	11
188	Weighting for sex acts to understand the spread of STI on networks. Journal of Theoretical Biology, 2012, 311, 46-53.	0.8	11
189	Multidrug Resistance Dynamics in Salmonella in Food Animals in the United States: An Analysis of Genomes from Public Databases. Microbiology Spectrum, 2021, 9, e0049521.	1.2	11
190	HIV Coreceptor Usage and Drug Treatment. Journal of Theoretical Biology, 2002, 217, 443-457.	0.8	10
191	Bacterial growth properties at low optical densities. Antonie Van Leeuwenhoek, 2009, 96, 267-274.	0.7	10
192	Cancer-induced immunosuppression can enable effectiveness of immunotherapy through bistability generation: A mathematical and computational examination. Journal of Theoretical Biology, 2020, 492, 110185.	0.8	10
193	Increase in antimicrobial resistance in Escherichia coli in food animals between 1980 and 2018 assessed using genomes from public databases. Journal of Antimicrobial Chemotherapy, 2022, 77, 646-655.	1.3	10
194	CCTTT-repeat polymorphism of the inducible nitric oxide synthase is not associated with HIV pathogenesis. Clinical and Experimental Immunology, 2004, 137, 566-569.	1.1	9
195	Epitope down-modulation as a mechanism for the coexistence of competing T-cells. Journal of Theoretical Biology, 2005, 233, 379-390.	0.8	9
196	Plasmid co-infection: linking biological mechanisms to ecological and evolutionary dynamics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200478.	1.8	9
197	Assessing the public health impact of tolerance-based therapies with mathematical models. PLoS Computational Biology, 2018, 14, e1006119.	1.5	8
198	Stochastic Gene Expression Influences the Selection of Antibiotic Resistance Mutations. Molecular Biology and Evolution, 2020, 37, 58-70.	3.5	8

#	Article	IF	Citations
199	Antibiotic treatment protocols revisited: the challenges of a conclusive assessment by mathematical modelling. Journal of the Royal Society Interface, 2021, 18, 20210308.	1.5	8
200	ON THE EVOLUTION OF SEXUAL REPRODUCTION IN HOSTS COEVOLVING WITH MULTIPLE PARASITES. Evolution; International Journal of Organic Evolution, 2010, 64, 1644-1656.	1.1	7
201	Virus-induced target cell activation reconciles set-point viral load heritability and within-host evolution. Epidemics, 2013, 5, 174-180.	1.5	7
202	Intra-host Dynamics and Evolution of HIV Infection. , 2008, , 279-301.		5
203	Principal component analysis of general patterns of HIV-1 replicative fitness in different drug environments. Epidemics, 2010, 2, 85-91.	1.5	5
204	From â€œWhat Is?â€•to â€œWhat Isn't?â€•Computational Biology. PLoS Computational Biology, 2015, 11, e1004318.	1.5	5
205	Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. Frontiers in Microbiology, 0, 13, .	1.5	5
206	Short Communication:HIV Type 2 Dynamics. AIDS Research and Human Retroviruses, 2005, 21, 608-610.	0.5	3
207	Host population structure impedes reversion to drug sensitivity after discontinuation of treatment. PLoS Computational Biology, 2017, 13, e1005704.	1.5	3
208	Hematopoietic Stem Cells Increase Quiescence during Aging. Blood, 2019, 134, 2484-2484.	0.6	3
209	Applying mixture model methods to SARS-CoV-2 serosurvey data from Geneva. Epidemics, 2022, 39, 100572.	1.5	2
210	Virus load and antigenic diversity. Bulletin of Mathematical Biology, 1997, 59, 881-896.	0.9	1
211	A random walk from the cello to the lab. Current Biology, 1999, 9, R5.	1.8	1
212	Response to Bandeira and Faro: Closing the circle of constraints. Trends in Immunology, 2003, 24, 173-175.	2.9	1
213	On the role of resonance in drug failure under HIV treatment interruption. Theoretical Biology and Medical Modelling, 2013, 10, 44.	2.1	1
214	ARC: An Open Web-Platform for Request/Supply Matching for a Prioritized and Controlled COVID-19 Response. Frontiers in Public Health, 2021, 9, 607677.	1.3	1
215	The search for universality in evolutionary landscapes. Physics of Life Reviews, 2021, 39, 76-78.	1.5	1
216	Evolutionary Medicine. Wenda R. Trevathan , E. O. Smith , James J. McKenna. Quarterly Review of Biology, 2001, 76, 124-125.	0.0	0

#	Article	IF	Citations
217	Evolutionary Origin and Consequences of Design Properties of Metabolic Networks. , 2009, , 113-126.		0
218	Hematopoietic Stem Cell Cycling Dynamics In Steady State and Upon Hematopoietic Challenge. Blood, 2010, 116, 572-572.	0.6	0
219	Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. Journal of Cell Biology, 2011, 192, i3-i3.	2.3	0
220	Explaining "Linguistic Features" of Noncoding DNA. Science, 1996, 271, 14-15.	6.0	0
221	Explaining "Linguistic Features" of Noncoding DNA. Science, 1996, 271, 14-15.	6.0	0
222	Research on infectious disease dynamics. Introduction. Epidemics, 2009, 1, 1.	1.5	0
223	Constrained optimization of divisional load in hierarchically organized tissues during homeostasis. Journal of the Royal Society Interface, 2022, 19, 20210784.	1.5	0