

Sebastian Bonhoeffer

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231
papers

19,812
citations

68
h-index

137
g-index

260
ext. papers

22,788
ext. citations

9
avg, IF

6.69
L-index

#	Paper	IF	Citations
231	Viral dynamics in human immunodeficiency virus type 1 infection. <i>Nature</i> , 1995 , 373, 117-22	50.4	2863
230	Quantitation of HIV-1-specific cytotoxic T lymphocytes and plasma load of viral RNA. <i>Science</i> , 1998 , 279, 2103-6	33.3	1247
229	Cooperation and competition in the evolution of ATP-producing pathways. <i>Science</i> , 2001 , 292, 504-7	33.3	901
228	Viral dynamics in hepatitis B virus infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 4398-402	11.5	739
227	Analysis of total human immunodeficiency virus (HIV)-specific CD4(+) and CD8(+) T-cell responses: relationship to viral load in untreated HIV infection. <i>Journal of Virology</i> , 2001 , 75, 11983-91	6.6	616
226	Virus dynamics and drug therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 6971-6	11.5	468
225	Rapid production and clearance of HIV-1 and hepatitis C virus assessed by large volume plasma apheresis. <i>Lancet, The</i> , 1999 , 354, 1782-5	40	397
224	Evaluating treatment protocols to prevent antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 12106-11	11.5	368
223	Viral dynamics in vivo: limitations on estimates of intracellular delay and virus decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 7247-51	11.5	324
222	Spatial games and the maintenance of cooperation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 4877-81	11.5	310
221	Rapid turnover of T lymphocytes in SIV-infected rhesus macaques. <i>Science</i> , 1998 , 279, 1223-7	33.3	308
220	Global trends in antimicrobial resistance in animals in low- and middle-income countries. <i>Science</i> , 2019 , 365,	33.3	301
219	Birth-death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 228-33 ^{11.5}	11.5	295
218	Decay kinetics of human immunodeficiency virus-specific effector cytotoxic T lymphocytes after combination antiretroviral therapy. <i>Journal of Virology</i> , 1999 , 73, 797-800	6.6	289
217	Reducing antimicrobial use in food animals. <i>Science</i> , 2017 , 357, 1350-1352	33.3	236
216	HIV-1 antigen-specific and -nonspecific B cell responses are sensitive to combination antiretroviral therapy. <i>Journal of Experimental Medicine</i> , 1998 , 188, 233-45	16.6	219
215	Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. <i>Journal of Experimental Medicine</i> , 2011 , 208, 273-84	16.6	210

214	Evidence for positive epistasis in HIV-1. <i>Science</i> , 2004 , 306, 1547-50	33.3	209
213	MORE SPATIAL GAMES. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 1994 , 04, 33-56	2	209
212	Anti-viral drug treatment: dynamics of resistance in free virus and infected cell populations. <i>Journal of Theoretical Biology</i> , 1997 , 184, 203-17	2.3	203
211	Population biology, evolution, and infectious disease: convergence and synthesis. <i>Science</i> , 1999 , 283, 806-9	33.3	191
210	HIV-1-specific immune responses in subjects who temporarily contain virus replication after discontinuation of highly active antiretroviral therapy. <i>Journal of Clinical Investigation</i> , 1999 , 104, R13-8	15.9	179
209	Production of resistant HIV mutants during antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 7681-6	11.5	171
208	Virulence and pathogenesis of HIV-1 infection: an evolutionary perspective. <i>Science</i> , 2014 , 343, 1243727	33.3	163
207	Population biological principles of drug-resistance evolution in infectious diseases. <i>Lancet Infectious Diseases</i> , 2011 , 11, 236-47	25.5	150
206	The HIV coreceptor switch: a population dynamical perspective. <i>Trends in Microbiology</i> , 2005 , 13, 269-77	12.4	150
205	Molecular epidemiology reveals long-term changes in HIV type 1 subtype B transmission in Switzerland. <i>Journal of Infectious Diseases</i> , 2010 , 201, 1488-97	7	145
204	Antagonism between bacteriostatic and bactericidal antibiotics is prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 4573-82	5.9	143
203	Evolution of cooperation by generalized reciprocity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005 , 272, 1115-20	4.4	142
202	Emergence of drug-resistant influenza virus: population dynamical considerations. <i>Science</i> , 2006 , 312, 389-91	33.3	140
201	Practical considerations for measuring the effective reproductive number, Rt. <i>PLoS Computational Biology</i> , 2020 , 16, e1008409	5	140
200	A systems analysis of mutational effects in HIV-1 protease and reverse transcriptase. <i>Nature Genetics</i> , 2011 , 43, 487-9	36.3	139
199	The effect of opinion clustering on disease outbreaks. <i>Journal of the Royal Society Interface</i> , 2008 , 5, 1505-8	4.1	138
198	The virological and immunological consequences of structured treatment interruptions in chronic HIV-1 infection. <i>Aids</i> , 2001 , 15, F29-40	3.5	138
197	Experimental tests for an evolutionary trade-off between growth rate and yield in <i>E. coli</i> . <i>American Naturalist</i> , 2006 , 168, 242-51	3.7	137

196	Estimating the basic reproductive number from viral sequence data. <i>Molecular Biology and Evolution</i> , 2012 , 29, 347-57	8.3	136
195	Structured antiretroviral treatment interruptions in chronically HIV-1-infected subjects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 13288-93	11.5	135
194	An evolutionary scenario for the transition to undifferentiated multicellularity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 1095-8	11.5	134
193	Evolution of cross-feeding in microbial populations. <i>American Naturalist</i> , 2004 , 163, E126-35	3.7	130
192	Temporal analyses of virus replication, immune responses, and efficacy in rhesus macaques immunized with a live, attenuated simian immunodeficiency virus vaccine. <i>Journal of Virology</i> , 1998 , 72, 7501-9	6.6	130
191	Epistasis between deleterious mutations and the evolution of recombination. <i>Trends in Ecology and Evolution</i> , 2007 , 22, 308-15	10.9	124
190	Causes of HIV diversity. <i>Nature</i> , 1995 , 376, 125	50.4	122
189	HIV-1 evolution and disease progression. <i>Science</i> , 1996 , 274, 1008-11	33.3	121
188	The state of affairs in the kingdom of the Red Queen. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 439-45	10.9	119
187	The frequency of resistant mutant virus before antiviral therapy. <i>Aids</i> , 1998 , 12, 461-5	3.5	118
186	Pre-existence and emergence of drug resistance in HIV-1 infection. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997 , 264, 631-7	4.4	114
185	Emergence of minor populations of human immunodeficiency virus type 1 carrying the M184V and L90M mutations in subjects undergoing structured treatment interruptions. <i>Journal of Infectious Diseases</i> , 2003 , 188, 1433-43	7	114
184	Evolution of virulence in a heterogeneous host population. <i>Evolution; International Journal of Organic Evolution</i> , 2000 , 54, 64-71	3.8	110
183	Compensation of fitness costs and reversibility of antibiotic resistance mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 2085-95	5.9	103
182	Dose-dependent infection rates of parasites produce the Allee effect in epidemiology. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002 , 269, 271-9	4.4	102
181	Ambiguous nucleotide calls from population-based sequencing of HIV-1 are a marker for viral diversity and the age of infection. <i>Clinical Infectious Diseases</i> , 2011 , 52, 532-9	11.6	99
180	Risks and benefits of structured antiretroviral drug therapy interruptions in HIV-1 infection. <i>Aids</i> , 2000 , 14, 2313-22	3.5	93
179	Phylogenetic approach reveals that virus genotype largely determines HIV set-point viral load. <i>PLoS Pathogens</i> , 2010 , 6, e1001123	7.6	91

178	The evolution of connectivity in metabolic networks. <i>PLoS Biology</i> , 2005 , 3, e228	9.7	90
177	Quantification of cell turnover kinetics using 5-bromo-2Pdeoxyuridine. <i>Journal of Immunology</i> , 2000 , 164, 5049-54	5.3	90
176	Estimating the stoichiometry of human immunodeficiency virus entry. <i>Journal of Virology</i> , 2009 , 83, 1523-31	3.1	86
175	Recombination in HIV and the evolution of drug resistance: for better or for worse?. <i>BioEssays</i> , 2004 , 26, 180-8	4.1	86
174	Spatial models of virus-immune dynamics. <i>Journal of Theoretical Biology</i> , 2005 , 233, 221-36	2.3	86
173	Intra-host versus inter-host selection: viral strategies of immune function impairment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 8062-6	11.5	86
172	Salmonella persisters promote the spread of antibiotic resistance plasmids in the gut. <i>Nature</i> , 2019 , 573, 276-280	50.4	85
171	Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015 , 10, 88-92	5.1	83
170	Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120198	5.8	81
169	Stochastic or deterministic: what is the effective population size of HIV-1?. <i>Trends in Microbiology</i> , 2006 , 14, 507-11	12.4	78
168	Exploring the complexity of the HIV-1 fitness landscape. <i>PLoS Genetics</i> , 2012 , 8, e1002551	6	77
167	Evolution and emergence of infectious diseases in theoretical and real-world networks. <i>Nature Communications</i> , 2015 , 6, 6101	17.4	75
166	Stochastic interplay between mutation and recombination during the acquisition of drug resistance mutations in human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2005 , 79, 13572-8	6.6	72
165	Rapid clearance of simian immunodeficiency virus particles from plasma of rhesus macaques. <i>Journal of Virology</i> , 1999 , 73, 855-60	6.6	71
164	Spatial heterogeneity in drug concentrations can facilitate the emergence of resistance to cancer therapy. <i>PLoS Computational Biology</i> , 2015 , 11, e1004142	5	69
163	Inferring epidemic contact structure from phylogenetic trees. <i>PLoS Computational Biology</i> , 2012 , 8, e1002413	3.1	67
162	Evolutionary rescue: linking theory for conservation and medicine. <i>Evolutionary Applications</i> , 2014 , 7, 1161-79	4.8	66
161	Quantification of infectious HIV-1 plasma viral load using a boosted in vitro infection protocol. <i>Virology</i> , 2004 , 326, 113-29	3.6	66

160	Evolution of complexity in signaling pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16337-42	11.5	65
159	Interchromatid and interhomolog recombination in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2004 , 16, 342-52	11.6	64
158	The path of least resistance: aggressive or moderate treatment?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20140566	4.4	63
157	Antibiotic-Resistant <i>Neisseria gonorrhoeae</i> Spread Faster with More Treatment, Not More Sexual Partners. <i>PLoS Pathogens</i> , 2016 , 12, e1005611	7.6	63
156	Cycling empirical antibiotic therapy in hospitals: meta-analysis and models. <i>PLoS Pathogens</i> , 2014 , 10, e1004225	7.6	60
155	The role of migration and domestic transmission in the spread of HIV-1 non-B subtypes in Switzerland. <i>Journal of Infectious Diseases</i> , 2011 , 204, 1095-103	7	60
154	High frequency of cytomegalovirus-specific cytotoxic T-effector cells in HLA-A*0201-positive subjects during multiple viral coinfections. <i>Journal of Infectious Diseases</i> , 2000 , 181, 165-75	7	60
153	Rapid parasite adaptation drives selection for high recombination rates. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 295-300	3.8	58
152	The evolution of groups of cooperating bacteria and the growth rate versus yield trade-off. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 637-641	2.9	55
151	Persistence of transmitted HIV-1 drug resistance mutations associated with fitness costs and viral genetic backgrounds. <i>PLoS Pathogens</i> , 2015 , 11, e1004722	7.6	52
150	Glancing behind virus load variation in HIV-1 infection. <i>Trends in Microbiology</i> , 2003 , 11, 499-504	12.4	51
149	RNA multi-structure landscapes. A study based on temperature dependent partition functions. <i>European Biophysics Journal</i> , 1993 , 22, 13-24	1.9	51
148	Human immunodeficiency virus type 1 fitness is a determining factor in viral rebound and set point in chronic infection. <i>Journal of Virology</i> , 2003 , 77, 13146-55	6.6	50
147	COVID-19 infectivity profile correction. <i>Swiss Medical Weekly</i> , 2020 , 150, w20336	3.1	50
146	The effect of multifunctionality on the rate of evolution in yeast. <i>Molecular Biology and Evolution</i> , 2006 , 23, 721-2	8.3	46
145	Practical considerations for measuring the effective reproductive number, 2020 ,		46
144	Stable virulence levels in the HIV epidemic of Switzerland over two decades. <i>Aids</i> , 2006 , 20, 889-94	3.5	45
143	Evolution of stress response in the face of unreliable environmental signals. <i>PLoS Computational Biology</i> , 2012 , 8, e1002627	5	44

142	Using an epidemiological model for phylogenetic inference reveals density dependence in HIV transmission. <i>Molecular Biology and Evolution</i> , 2014 , 31, 6-17	8.3	43
141	Quantification of in vivo replicative capacity of HIV-1 in different compartments of infected cells. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 26, 397-404	3.1	43
140	Phenotypic changes in drug susceptibility associated with failure of human immunodeficiency virus type 1 (HIV-1) triple combination therapy. <i>Journal of Infectious Diseases</i> , 1999 , 180, 865-70	7	43
139	Effect of varying epistasis on the evolution of recombination. <i>Genetics</i> , 2006 , 173, 589-97	4	42
138	Humoral immunity to HIV-1: kinetics of antibody responses in chronic infection reflects capacity of immune system to improve viral set point. <i>Blood</i> , 2004 , 104, 1784-92	2.2	42
137	HIV results in the frame. Results confirmed. <i>Nature</i> , 1995 , 375, 193	50.4	42
136	Death and population dynamics affect mutation rate estimates and evolvability under stress in bacteria. <i>PLoS Biology</i> , 2018 , 16, e2005056	9.7	41
135	Long-term trends of HIV type 1 drug resistance prevalence among antiretroviral treatment-experienced patients in Switzerland. <i>Clinical Infectious Diseases</i> , 2009 , 48, 979-87	11.6	41
134	Entry and transcription as key determinants of differences in CD4 T-cell permissiveness to human immunodeficiency virus type 1 infection. <i>Journal of Virology</i> , 2004 , 78, 10747-54	6.6	41
133	Procedures for reliable estimation of viral fitness from time-series data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002 , 269, 1887-93	4.4	41
132	An evolutionary perspective on the systems of adaptive immunity. <i>Biological Reviews</i> , 2018 , 93, 505-528	13.5	40
131	Neutral drift and polymorphism in gene-for-gene systems. <i>Ecology Letters</i> , 2005 , 8, 925-932	10	38
130	Error Thresholds on Correlated Fitness Landscapes. <i>Journal of Theoretical Biology</i> , 1993 , 164, 359-372	2.3	38
129	Passive infusion of immune serum into simian immunodeficiency virus-infected rhesus macaques undergoing a rapid disease course has minimal effect on plasma viremia. <i>Virology</i> , 2000 , 270, 237-49	3.6	36
128	Informed switching strongly decreases the prevalence of antibiotic resistance in hospital wards. <i>PLoS Computational Biology</i> , 2011 , 7, e1001094	5	35
127	Simulating the evolution of signal transduction pathways. <i>Journal of Theoretical Biology</i> , 2006 , 241, 223-32	3	35
126	Signal transduction networks: topology, response and biochemical processes. <i>Journal of Theoretical Biology</i> , 2006 , 238, 416-25	2.3	33
125	Pre-existence and emergence of drug resistance in a generalized model of intra-host viral dynamics. <i>Epidemics</i> , 2012 , 4, 187-202	5.1	32

124	Assessing predicted HIV-1 replicative capacity in a clinical setting. <i>PLoS Pathogens</i> , 2011 , 7, e1002321	7.6	32
123	The Red Queen and the persistence of linkage-disequilibrium oscillations in finite and infinite populations. <i>BMC Evolutionary Biology</i> , 2007 , 7, 211	3	32
122	Quantifying the impact of quarantine duration on COVID-19 transmission. <i>ELife</i> , 2021 , 10,	8.9	32
121	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018 , 14, e1006895	7.6	30
120	Inference of epidemiological dynamics based on simulated phylogenies using birth-death and coalescent models. <i>PLoS Computational Biology</i> , 2014 , 10, e1003913	5	30
119	Can high-risk fungicides be used in mixtures without selecting for fungicide resistance?. <i>Phytopathology</i> , 2014 , 104, 324-31	3.8	30
118	Rapid viral decay in simian immunodeficiency virus-infected macaques receiving quadruple antiretroviral therapy. <i>Journal of Virology</i> , 2006 , 80, 9861-4	6.6	29
117	Decelerating decay of latently infected cells during prolonged therapy for human immunodeficiency virus type 1 infection. <i>Journal of Virology</i> , 2002 , 76, 8963-5	6.6	29
116	Modeling antibiotic treatment in hospitals: A systematic approach shows benefits of combination therapy over cycling, mixing, and mono-drug therapies. <i>PLoS Computational Biology</i> , 2017 , 13, e1005745 ⁵		29
115	A research agenda for digital proximity tracing apps. <i>Swiss Medical Weekly</i> , 2020 , 150, w20324	3.1	29
114	Contribution of recombination to the evolutionary history of HIV. <i>Current Opinion in HIV and AIDS</i> , 2015 , 10, 84-9	4.2	28
113	Recombination accelerates adaptation on a large-scale empirical fitness landscape in HIV-1. <i>PLoS Genetics</i> , 2014 , 10, e1004439	6	28
112	Red Queen dynamics with non-standard fitness interactions. <i>PLoS Computational Biology</i> , 2009 , 5, e1000469	3.6	28
111	A stochastic model for primary HIV infection: optimal timing of therapy. <i>Aids</i> , 1999 , 13, 351-7	3.5	28
110	African descent is associated with slower CD4 cell count decline in treatment-naive patients of the Swiss HIV Cohort Study. <i>Aids</i> , 2009 , 23, 1269-76	3.5	27
109	The effect of population structure on the emergence of drug resistance during influenza pandemics. <i>Journal of the Royal Society Interface</i> , 2007 , 4, 893-906	4.1	27
108	Mutation accumulation in space and the maintenance of sexual reproduction. <i>Ecology Letters</i> , 2006 , 9, 941-6	10	27
107	No signs of hidden language in noncoding DNA. <i>Physical Review Letters</i> , 1996 , 76, 1977	7.4	27

106	Developing smarter host mixtures to control plant disease. <i>Plant Pathology</i> , 2015 , 64, 996-1004	2.8	26
105	On being the right size: the impact of population size and stochastic effects on the evolution of drug resistance in hospitals and the community. <i>PLoS Pathogens</i> , 2011 , 7, e1001334	7.6	26
104	Quantitative constraints on the scope of negative selection. <i>Trends in Immunology</i> , 2003 , 24, 132-5	14.4	26
103	A combined within-host and between-hosts modelling framework for the evolution of resistance to antimalarial drugs. <i>Journal of the Royal Society Interface</i> , 2016 , 13,	4.1	25
102	The role of recombination for the coevolutionary dynamics of HIV and the immune response. <i>PLoS ONE</i> , 2011 , 6, e16052	3.7	24
101	On the relationship between serial interval, infectiousness profile and generation time. <i>Journal of the Royal Society Interface</i> , 2021 , 18, 20200756	4.1	24
100	The evolution of network topology by selective removal. <i>Journal of the Royal Society Interface</i> , 2005 , 2, 533-6	4.1	23
99	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. <i>ISME Journal</i> , 2021 , 15, 862-878	11.9	23
98	Detection of antibiotic resistance is essential for gonorrhoea point-of-care testing: a mathematical modelling study. <i>BMC Medicine</i> , 2017 , 15, 142	11.4	22
97	Assessing the impact of adherence to anti-retroviral therapy on treatment failure and resistance evolution in HIV. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 2309-20	4.1	22
96	On the causes of selection for recombination underlying the red queen hypothesis. <i>American Naturalist</i> , 2009 , 174 Suppl 1, S31-42	3.7	22
95	Effective polyploidy causes phenotypic delay and influences bacterial evolvability. <i>PLoS Biology</i> , 2018 , 16, e2004644	9.7	22
94	Metabolically cohesive microbial consortia and ecosystem functioning. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190245	5.8	21
93	Social meets molecular: Combining phylogenetic and latent class analyses to understand HIV-1 transmission in Switzerland. <i>American Journal of Epidemiology</i> , 2014 , 179, 1514-25	3.8	21
92	The role of epistasis on the evolution of recombination in host-parasite coevolution. <i>Theoretical Population Biology</i> , 2009 , 75, 1-13	1.2	21
91	Residual viral replication during antiretroviral therapy boosts human immunodeficiency virus type 1-specific CD8+ T-cell responses in subjects treated early after infection. <i>Journal of Virology</i> , 2002 , 76, 411-5	6.6	21
90	Emergence of Resistance to Fungicides: The Role of Fungicide Dose. <i>Phytopathology</i> , 2017 , 107, 545-560	3.8	20
89	Recombination and drug resistance in HIV: population dynamics and stochasticity. <i>Epidemics</i> , 2009 , 1, 58-69	5.1	20

88	High epitope expression levels increase competition between T cells. <i>PLoS Computational Biology</i> , 2006 , 2, e109	5	20
87	Robustness of cooperation. <i>Nature</i> , 1996 , 379, 126-126	50.4	20
86	Resistance to antimicrobial chemotherapy: a prescription for research and action. <i>American Journal of the Medical Sciences</i> , 1998 , 315, 87-94	2.2	20
85	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2454-68	8.3	19
84	Why There Are No Essential Genes on Plasmids. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3079-88	8.3	19
83	Dissecting HIV Virulence: Heritability of Setpoint Viral Load, CD4+ T-Cell Decline, and Per-Parasite Pathogenicity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 27-37	8.3	19
82	High heritability is compatible with the broad distribution of set point viral load in HIV carriers. <i>PLoS Pathogens</i> , 2015 , 11, e1004634	7.6	18
81	Population Heterogeneity in Mutation Rate Increases the Frequency of Higher-Order Mutants and Reduces Long-Term Mutational Load. <i>Molecular Biology and Evolution</i> , 2017 , 34, 419-436	8.3	18
80	Viral dynamics and in vivo fitness of HIV-1 in the presence and absence of enfuvirtide. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008 , 48, 572-6	3.1	18
79	Evolutionary Consequences of Tradeoffs between Yield and Rate of ATP Production. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002 , 216,	3.1	18
78	Can live attenuated virus work as post-exposure treatment?. <i>Trends in Immunology</i> , 1995 , 16, 131-5		16
77	Rotating antibiotics does not minimize selection for resistance. <i>Mathematical Biosciences and Engineering</i> , 2010 , 7, 919-22	2.1	16
76	Models of viral kinetics and drug resistance in HIV-1 infection. <i>AIDS Patient Care and STDs</i> , 1998 , 12, 769-78	3.8	15
75	Plasmids and evolutionary rescue by drug resistance. <i>Evolution; International Journal of Organic Evolution</i> , 2014 , 68, 2066-78	3.8	14
74	Guanine-adenine bias: a general property of retroid viruses that is unrelated to host-induced hypermutation. <i>Trends in Genetics</i> , 2005 , 21, 264-8	8.5	14
73	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. <i>Immunology Letters</i> , 1999 , 66, 219-28	4.1	14
72	Clonal dominance and transplantation dynamics in hematopoietic stem cell compartments. <i>PLoS Computational Biology</i> , 2017 , 13, e1005803	5	14
71	Reversing resistance: different routes and common themes across pathogens. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	13

70	Nested model reveals potential amplification of an HIV epidemic due to drug resistance. <i>Epidemics</i> , 2013 , 5, 34-43	5.1	13
69	Antibacterial effects of antiretrovirals, potential implications for microbiome studies in HIV. <i>Antiviral Therapy</i> , 2018 , 23, 91-94	1.6	13
68	Predicting the evolution of sex on complex fitness landscapes. <i>PLoS Computational Biology</i> , 2009 , 5, e1000510	10	13
67	Comparing treatment strategies to reduce antibiotic resistance in an in vitro epidemiological setting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	13
66	HIV replication elicits little cytopathic effects in vivo: analysis of surrogate markers for virus production, cytotoxic T cell response and infected cell death. <i>Journal of Medical Virology</i> , 2006 , 78, 1141-8	19.7	12
65	Quantification of In Vivo Replicative Capacity of HIV-1 in Different Compartments of Infected Cells. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2001 , 26, 397-404	3.1	12
64	The Role of Adherence and Retreatment in De Novo Emergence of MDR-TB. <i>PLoS Computational Biology</i> , 2016 , 12, e1004749	5	12
63	Influence of recombination on acquisition and reversion of immune escape and compensatory mutations in HIV-1. <i>Epidemics</i> , 2016 , 14, 11-25	5.1	12
62	Short-term activity cycles impede information transmission in ant colonies. <i>PLoS Computational Biology</i> , 2017 , 13, e1005527	5	11
61	Modelling cytomegalovirus replication patterns in the human host: factors important for pathogenesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006 , 273, 1961-7	4.4	11
60	Contribution of peaks of virus load to simian immunodeficiency virus pathogenesis. <i>Journal of Virology</i> , 2002 , 76, 2573-8	6.6	11
59	Epistasis and Pleiotropy Affect the Modularity of the Genotype-Phenotype Map of Cross-Resistance in HIV-1. <i>Molecular Biology and Evolution</i> , 2016 , 33, 3213-3225	8.3	11
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