

Sebastian Bonhoeffer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Test-trace-isolate-quarantine (TTIQ) intervention strategies after symptomatic COVID-19 case identification.. <i>PLoS ONE</i> , 2022 , 17, e0263597	3.7	1
230	Plasmid co-infection: linking biological mechanisms to ecological and evolutionary dynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022 , 377, 20200478	5.8	2
229	Constrained optimization of divisional load in hierarchically organized tissues during homeostasis.. <i>Journal of the Royal Society Interface</i> , 2022 , 19, 20210784	4.1	
228	Estimating plasmid conjugation rates: A new computational tool and a critical comparison of methods.. <i>Plasmid</i> , 2022 , 102627	3.3	2
227	Applying mixture model methods to SARS-CoV-2 serosurvey data from Geneva.. <i>Epidemics</i> , 2022 , 39, 100572	5.1	
226	Multidrug Resistance Dynamics in Salmonella in Food Animals in the United States: An Analysis of Genomes from Public Databases. <i>Microbiology Spectrum</i> , 2021 , 9, e0049521	8.9	2
225	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
224	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids. <i>Evolution Letters</i> , 2021 , 5, 290-301	5.3	6
223	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
222	Estimating the cumulative incidence of SARS-CoV-2 with imperfect serological tests: Exploiting cutoff-free approaches. <i>PLoS Computational Biology</i> , 2021 , 17, e1008728	5	4
221	ARC: An Open Web-Platform for Request/Supply Matching for a Prioritized and Controlled COVID-19 Response. <i>Frontiers in Public Health</i> , 2021 , 9, 607677	6	0
220	Quantifying the impact of quarantine duration on COVID-19 transmission. <i>ELife</i> , 2021 , 10,	8.9	32
219	Antibiotic treatment protocols revisited: the challenges of a conclusive assessment by mathematical modelling. <i>Journal of the Royal Society Interface</i> , 2021 , 18, 20210308	4.1	3
218	The search for universality in evolutionary landscapes: Comment on "From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics" by Susanna Manrubia, Jos[A. Cuesta, et al. <i>Physics of Life Reviews</i> , 2021 , 39, 76-78	2.1	1
217	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
216	Pathogen invasion-dependent tissue reservoirs and plasmid-encoded antibiotic degradation boost plasmid spread in the gut. <i>ELife</i> , 2021 , 10,	8.9	3
215	Metabolically cohesive microbial consortia and ecosystem functioning. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190245	5.8	21

214	Cancer-induced immunosuppression can enable effectiveness of immunotherapy through bistability generation: A mathematical and computational examination. <i>Journal of Theoretical Biology</i> , 2020 , 492, 110185	2.3	2
213	Practical considerations for measuring the effective reproductive number, Rt. <i>PLoS Computational Biology</i> , 2020 , 16, e1008409	5	140
212	A research agenda for digital proximity tracing apps. <i>Swiss Medical Weekly</i> , 2020 , 150, w20324	3.1	29
211	COVID-19 infectivity profile correction. <i>Swiss Medical Weekly</i> , 2020 , 150, w20336	3.1	50
210	Practical considerations for measuring the effective reproductive number, 2020 ,		46
209	MPN patients with low mutant JAK2 allele burden show late expansion restricted to erythroid and megakaryocytic lineages. <i>Blood</i> , 2020 , 136, 2591-2595	2.2	3
208	Is antimicrobial resistance evolution accelerating?. <i>PLoS Pathogens</i> , 2020 , 16, e1008905	7.6	8
207	Stochastic Gene Expression Influences the Selection of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 58-70	8.3	3
206	Salmonella persisters promote the spread of antibiotic resistance plasmids in the gut. <i>Nature</i> , 2019 , 573, 276-280	50.4	85
205	Global trends in antimicrobial resistance in animals in low- and middle-income countries. <i>Science</i> , 2019 , 365,	33.3	301
204	Quantifying the impact of treatment history on plasmid-mediated resistance evolution in human gut microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23106-23116	11.5	7
203	Hematopoietic Stem Cells Increase Quiescence during Aging. <i>Blood</i> , 2019 , 134, 2484-2484	2.2	1
202	An evolutionary perspective on the systems of adaptive immunity. <i>Biological Reviews</i> , 2018 , 93, 505-528	13.5	40
201	Death and population dynamics affect mutation rate estimates and evolvability under stress in bacteria. <i>PLoS Biology</i> , 2018 , 16, e2005056	9.7	41
200	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018 , 14, e1006895	7.6	30
199	Antibacterial effects of antiretrovirals, potential implications for microbiome studies in HIV. <i>Antiviral Therapy</i> , 2018 , 23, 91-94	1.6	13
198	Effective polyploidy causes phenotypic delay and influences bacterial evolvability. <i>PLoS Biology</i> , 2018 , 16, e2004644	9.7	22
197	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

196	Assessing the public health impact of tolerance-based therapies with mathematical models. <i>PLoS Computational Biology</i> , 2018 , 14, e1006119	5	7
195	Emergence of Resistance to Fungicides: The Role of Fungicide Dose. <i>Phytopathology</i> , 2017 , 107, 545-560	3.8	20
194	Modeling antimicrobial cycling and mixing: Differences arising from an individual-based versus a population-based perspective. <i>Mathematical Biosciences</i> , 2017 , 294, 85-91	3.9	10
193	Reversing resistance: different routes and common themes across pathogens. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	13
192	Reducing antimicrobial use in food animals. <i>Science</i> , 2017 , 357, 1350-1352	33.3	236
191	Short-term activity cycles impede information transmission in ant colonies. <i>PLoS Computational Biology</i> , 2017 , 13, e1005527	5	11
190	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
189	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
188	Host population structure impedes reversion to drug sensitivity after discontinuation of treatment. <i>PLoS Computational Biology</i> , 2017 , 13, e1005704	5	2
187	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
186	Clonal dominance and transplantation dynamics in hematopoietic stem cell compartments. <i>PLoS Computational Biology</i> , 2017 , 13, e1005803	5	14
185	How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2454-68	8.3	19
184	The Role of Adherence and Retreatment in De Novo Emergence of MDR-TB. <i>PLoS Computational Biology</i> , 2016 , 12, e1004749	5	12
183	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
182	Invasiveness of plant pathogens depends on the spatial scale of host distribution 2016 , 26, 1238-48		9
181	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
180	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
179	Potential Pitfalls in Estimating Viral Load Heritability. <i>Trends in Microbiology</i> , 2016 , 24, 687-698	12.4	7

178	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
177	Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015 , 10, 88-92	5.1	83
176	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
175	Spatial heterogeneity in drug concentrations can facilitate the emergence of resistance to cancer therapy. <i>PLoS Computational Biology</i> , 2015 , 11, e1004142	5	69
174	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
173	Contribution of recombination to the evolutionary history of HIV. <i>Current Opinion in HIV and AIDS</i> , 2015 , 10, 84-9	4.2	28
172	Evolution and emergence of infectious diseases in theoretical and real-world networks. <i>Nature Communications</i> , 2015 , 6, 6101	17.4	75
171	Developing smarter host mixtures to control plant disease. <i>Plant Pathology</i> , 2015 , 64, 996-1004	2.8	26
170	Why There Are No Essential Genes on Plasmids. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3079-88	8.3	19
169	Plasmids and evolutionary rescue by drug resistance. <i>Evolution; International Journal of Organic Evolution</i> , 2014 , 68, 2066-78	3.8	14
168	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
167	Virus-induced target cell activation reconciles set-point viral load heritability and within-host evolution. <i>Epidemics</i> , 2014 , 7, 36-42	5.1	0
166	Antagonism between bacteriostatic and bactericidal antibiotics is prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 4573-82	5.9	143
165	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
164	Cycling empirical antibiotic therapy in hospitals: meta-analysis and models. <i>PLoS Pathogens</i> , 2014 , 10, e1004225	7.6	60
163	Recombination accelerates adaptation on a large-scale empirical fitness landscape in HIV-1. <i>PLoS Genetics</i> , 2014 , 10, e1004439	6	28
162	Inference of epidemiological dynamics based on simulated phylogenies using birth-death and coalescent models. <i>PLoS Computational Biology</i> , 2014 , 10, e1003913	5	30
161	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

160	Evolutionary rescue: linking theory for conservation and medicine. <i>Evolutionary Applications</i> , 2014 , 7, 1161-79	4.8	66
159	Can high-risk fungicides be used in mixtures without selecting for fungicide resistance?. <i>Phytopathology</i> , 2014 , 104, 324-31	3.8	30
158	Virulence and pathogenesis of HIV-1 infection: an evolutionary perspective. <i>Science</i> , 2014 , 343, 1243727333	33.3	163
157	On the role of resonance in drug failure under HIV treatment interruption. <i>Theoretical Biology and Medical Modelling</i> , 2013 , 10, 44	2.3	1
156	Nested model reveals potential amplification of an HIV epidemic due to drug resistance. <i>Epidemics</i> , 2013 , 5, 34-43	5.1	13
155	Virus-induced target cell activation reconciles set-point viral load heritability and within-host evolution. <i>Epidemics</i> , 2013 , 5, 174-80	5.1	6
154	Fixation probability of mobile genetic elements such as plasmids. <i>Theoretical Population Biology</i> , 2013 , 90, 49-55	1.2	8
153	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
152	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	295
151	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
150	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
149	Weighting for sex acts to understand the spread of STI on networks. <i>Journal of Theoretical Biology</i> , 2012 , 311, 46-53	2.3	9
148	Estimating the basic reproductive number from viral sequence data. <i>Molecular Biology and Evolution</i> , 2012 , 29, 347-57	8.3	136
147	Inferring epidemic contact structure from phylogenetic trees. <i>PLoS Computational Biology</i> , 2012 , 8, e1002413	3	67
146	Estimating the fitness cost of escape from HLA presentation in HIV-1 protease and reverse transcriptase. <i>PLoS Computational Biology</i> , 2012 , 8, e1002525	5	10
145	Exploring the complexity of the HIV-1 fitness landscape. <i>PLoS Genetics</i> , 2012 , 8, e1002551	6	77
144	Evolution of stress response in the face of unreliable environmental signals. <i>PLoS Computational Biology</i> , 2012 , 8, e1002627	5	44
143	Population biological principles of drug-resistance evolution in infectious diseases. <i>Lancet Infectious Diseases</i> , 2011 , 11, 236-47	25.5	150

142	A systems analysis of mutational effects in HIV-1 protease and reverse transcriptase. <i>Nature Genetics</i> , 2011 , 43, 487-9	36.3	139
141	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
140	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
139	Assessing predicted HIV-1 replicative capacity in a clinical setting. <i>PLoS Pathogens</i> , 2011 , 7, e1002321	7.6	32
138	Informed switching strongly decreases the prevalence of antibiotic resistance in hospital wards. <i>PLoS Computational Biology</i> , 2011 , 7, e1001094	5	35
137	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
136	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
135	The role of recombination for the coevolutionary dynamics of HIV and the immune response. <i>PLoS ONE</i> , 2011 , 6, e16052	3.7	24
134	Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. <i>Journal of Cell Biology</i> , 2011 , 192, i3-i3	7.3	
133	On the evolution of sexual reproduction in hosts coevolving with multiple parasites. <i>Evolution; International Journal of Organic Evolution</i> , 2010 , 64, 1644-56	3.8	7
132	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
131	Phylogenetic approach reveals that virus genotype largely determines HIV set-point viral load. <i>PLoS Pathogens</i> , 2010 , 6, e1001123	7.6	91
130	Principal component analysis of general patterns of HIV-1 replicative fitness in different drug environments. <i>Epidemics</i> , 2010 , 2, 85-91	5.1	5
129	Compensation of fitness costs and reversibility of antibiotic resistance mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 2085-95	5.9	103
128	Rotating antibiotics does not minimize selection for resistance. <i>Mathematical Biosciences and Engineering</i> , 2010 , 7, 919-22	2.1	16
127	Hematopoietic Stem Cell Cycling Dynamics In Steady State and Upon Hematopoietic Challenge. <i>Blood</i> , 2010 , 116, 572-572	2.2	
126	Estimating the stoichiometry of human immunodeficiency virus entry. <i>Journal of Virology</i> , 2009 , 83, 1523-31	3.1	86
125	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

124	Red Queen dynamics with non-standard fitness interactions. <i>PLoS Computational Biology</i> , 2009 , 5, e1000469	4.69	28
123	Predicting the evolution of sex on complex fitness landscapes. <i>PLoS Computational Biology</i> , 2009 , 5, e1000510	13	
122	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
121	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
120	Bacterial growth properties at low optical densities. <i>Antonie Van Leeuwenhoek</i> , 2009 , 96, 267-74	2.1	8
119	Recombination and drug resistance in HIV: population dynamics and stochasticity. <i>Epidemics</i> , 2009 , 1, 58-69	5.1	20
118	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
117	Evolutionary Origin and Consequences of Design Properties of Metabolic Networks 2009 , 113-126		
116	The effect of opinion clustering on disease outbreaks. <i>Journal of the Royal Society Interface</i> , 2008 , 5, 1505-8	4.1	138
115	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
114	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
113	Intra-host Dynamics and Evolution of HIV Infection 2008 , 279-301		4
112	Rapid parasite adaptation drives selection for high recombination rates. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 295-300	3.8	58
111	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
110	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
109	Epistasis between deleterious mutations and the evolution of recombination. <i>Trends in Ecology and Evolution</i> , 2007 , 22, 308-15	10.9	124
108	Signal transduction networks: topology, response and biochemical processes. <i>Journal of Theoretical Biology</i> , 2006 , 238, 416-25	2.3	33
107	Simulating the evolution of signal transduction pathways. <i>Journal of Theoretical Biology</i> , 2006 , 241, 223-32	35	

106	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
105	The effect of multifunctionality on the rate of evolution in yeast. <i>Molecular Biology and Evolution</i> , 2006 , 23, 721-2	8.3	46
104	High epitope expression levels increase competition between T cells. <i>PLoS Computational Biology</i> , 2006 , 2, e109	5	20
103	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
102	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
101	Effect of varying epistasis on the evolution of recombination. <i>Genetics</i> , 2006 , 173, 589-97	4	42
100	Emergence of drug-resistant influenza virus: population dynamical considerations. <i>Science</i> , 2006 , 312, 389-91	33.3	140
99	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
98	Experimental tests for an evolutionary trade-off between growth rate and yield in E. coli. <i>American Naturalist</i> , 2006 , 168, 242-51	3.7	137
97	Stochastic or deterministic: what is the effective population size of HIV-1?. <i>Trends in Microbiology</i> , 2006 , 14, 507-11	12.4	78
96	Stable virulence levels in the HIV epidemic of Switzerland over two decades. <i>Aids</i> , 2006 , 20, 889-94	3.5	45
95	Mutation accumulation in space and the maintenance of sexual reproduction. <i>Ecology Letters</i> , 2006 , 9, 941-6	10	27
94	Evolution of cooperation by generalized reciprocity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005 , 272, 1115-20	4.4	142
93	The HIV coreceptor switch: a population dynamical perspective. <i>Trends in Microbiology</i> , 2005 , 13, 269-77	12.4	150
92	The evolution of network topology by selective removal. <i>Journal of the Royal Society Interface</i> , 2005 , 2, 533-6	4.1	23
91	Spatial models of virus-immune dynamics. <i>Journal of Theoretical Biology</i> , 2005 , 233, 221-36	2.3	86
90	Epitope down-modulation as a mechanism for the coexistence of competing T-cells. <i>Journal of Theoretical Biology</i> , 2005 , 233, 379-90	2.3	9
89	Neutral drift and polymorphism in gene-for-gene systems. <i>Ecology Letters</i> , 2005 , 8, 925-932	10	38

88	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
87	The evolution of connectivity in metabolic networks. <i>PLoS Biology</i> , 2005 , 3, e228	9.7	90
86	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
85	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
84	Short communication: HIV type 2 dynamics. <i>AIDS Research and Human Retroviruses</i> , 2005 , 21, 608-10	1.6	2
83	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
82	Interchromatid and interhomolog recombination in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2004 , 16, 342-52	11.6	64
81	CCTTT-repeat polymorphism of the inducible nitric oxide synthase is not associated with HIV pathogenesis. <i>Clinical and Experimental Immunology</i> , 2004 , 137, 566-9	6.2	8
80	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
79	Recombination in HIV and the evolution of drug resistance: for better or for worse?. <i>BioEssays</i> , 2004 , 26, 180-8	4.1	86
78	Evidence for positive epistasis in HIV-1. <i>Science</i> , 2004 , 306, 1547-50	33.3	209
77	Evolution of cross-feeding in microbial populations. <i>American Naturalist</i> , 2004 , 163, E126-35	3.7	130
76	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
75	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
74	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
73	Glancing behind virus load variation in HIV-1 infection. <i>Trends in Microbiology</i> , 2003 , 11, 499-504	12.4	51
72	Quantitative constraints on the scope of negative selection. <i>Trends in Immunology</i> , 2003 , 24, 132-5	14.4	26
71	Response to Bandeira and Faro: Closing the circle of constraints. <i>Trends in Immunology</i> , 2003 , 24, 173-5	14.4	1

70	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
69	HIV coreceptor usage and drug treatment. <i>Journal of Theoretical Biology</i> , 2002 , 217, 443-57	2.3	10
68	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
67	Contribution of peaks of virus load to simian immunodeficiency virus pathogenesis. <i>Journal of Virology</i> , 2002 , 76, 2573-8	6.6	11
66	Evolutionary Consequences of Tradeoffs between Yield and Rate of ATP Production. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002 , 216,	3.1	18
65	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
64	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
63	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
62	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
61	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
60	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
59	Cooperation and competition in the evolution of ATP-producing pathways. <i>Science</i> , 2001 , 292, 504-7	33.3	901
58	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
57	The virological and immunological consequences of structured treatment interruptions in chronic HIV-1 infection. <i>Aids</i> , 2001 , 15, F29-40	3.5	138
56	Risks and benefits of structured antiretroviral drug therapy interruptions in HIV-1 infection. <i>Aids</i> , 2000 , 14, 2313-22	3.5	93
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12	Antibiotic treatment protocols revisited: The challenges of a conclusive assessment by mathematical modeling		1
11	Microbial metabolically cohesive consortia and ecosystem functioning		1
10	Quantifying the impact of test-trace-isolate-quarantine (TTIQ) strategies on COVID-19 transmission		2
9	Contact patterns reveal a stable dynamic community structure with fission-fusion dynamics in wild house mice		1
8	Estimating plasmid conjugation rates: a new computational tool and a critical comparison of methods		2
7	Estimating cumulative incidence of SARS-CoV-2 with imperfect serological tests: exploiting cutoff-free approaches		3
6	Ecological effects of stress drive bacterial evolvability under sub-inhibitory antibiotic treatments		2
5	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids		2
4	On the relationship between serial interval, infectiousness profile and generation time		3
3	Quantifying the impact of quarantine duration on COVID-19 transmission		8
2	Clinical extended-spectrum beta-lactamase antibiotic resistance plasmids have diverse transfer rates and can spread in the absence of antibiotic selection		5
1	Potential pitfalls in estimating viral load heritability		1