

Sebastian Bonhoeffer

List of Publications by Year in descending order

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Version: 2024-02-01

223
papers

25,066
citations

10956

71
h-index

8138

148
g-index

260
all docs

260
docs citations

260
times ranked

19966
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | 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. | 1.8 | 9 |
| 2 | Test-trace-isolate-quarantine (TTIQ) intervention strategies after symptomatic COVID-19 case identification. <i>PLoS ONE</i> , 2022, 17, e0263597. | 1.1 | 17 |
| 3 | Constrained optimization of divisional load in hierarchically organized tissues during homeostasis. <i>Journal of the Royal Society Interface</i> , 2022, 19, 20210784. | 1.5 | 0 |
| 4 | Estimating plasmid conjugation rates: A new computational tool and a critical comparison of methods. <i>Plasmid</i> , 2022, 121, 102627. | 0.4 | 19 |
| 5 | Increase in antimicrobial resistance in <i>Escherichia coli</i> in food animals between 1980 and 2018 assessed using genomes from public databases. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 646-655. | 1.3 | 10 |
| 6 | Applying mixture model methods to SARS-CoV-2 serosurvey data from Geneva. <i>Epidemics</i> , 2022, 39, 100572. | 1.5 | 2 |
| 7 | Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. <i>ISME Journal</i> , 2021, 15, 862-878. | 4.4 | 66 |
| 8 | Estimating the cumulative incidence of SARS-CoV-2 with imperfect serological tests: Exploiting cutoff-free approaches. <i>PLoS Computational Biology</i> , 2021, 17, e1008728. | 1.5 | 16 |
| 9 | 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. | 1.3 | 1 |
| 10 | Quantifying the impact of quarantine duration on COVID-19 transmission. <i>ELife</i> , 2021, 10, . | 2.8 | 66 |
| 11 | 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, . | 3.3 | 38 |
| 12 | Evolutionary mechanisms that determine which bacterial genes are carried on plasmids. <i>Evolution Letters</i> , 2021, 5, 290-301. | 1.6 | 23 |
| 13 | Antibiotic treatment protocols revisited: the challenges of a conclusive assessment by mathematical modelling. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210308. | 1.5 | 8 |
| 14 | The search for universality in evolutionary landscapes. <i>Physics of Life Reviews</i> , 2021, 39, 76-78. | 1.5 | 1 |
| 15 | On the relationship between serial interval, infectiousness profile and generation time. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200756. | 1.5 | 54 |
| 16 | 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. | 1.2 | 11 |
| 17 | Pathogen invasion-dependent tissue reservoirs and plasmid-encoded antibiotic degradation boost plasmid spread in the gut. <i>ELife</i> , 2021, 10, . | 2.8 | 15 |
| 18 | Stochastic Gene Expression Influences the Selection of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2020, 37, 58-70. | 3.5 | 8 |

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|----|--|------|-----------|
| 19 | MPN patients with low mutant <i>JAK2</i> allele burden show late expansion restricted to erythroid and megakaryocytic lineages. <i>Blood</i> , 2020, 136, 2591-2595. | 0.6 | 12 |
| 20 | Is antimicrobial resistance evolution accelerating?. <i>PLoS Pathogens</i> , 2020, 16, e1008905. | 2.1 | 18 |
| 21 | Metabolically cohesive microbial consortia and ecosystem functioning. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190245. | 1.8 | 37 |
| 22 | 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. | 0.8 | 10 |
| 23 | Practical considerations for measuring the effective reproductive number, R_t . <i>PLoS Computational Biology</i> , 2020, 16, e1008409. | 1.5 | 343 |
| 24 | A research agenda for digital proximity tracing apps. <i>Swiss Medical Weekly</i> , 2020, 150, w20324. | 0.8 | 49 |
| 25 | COVID-19 infectivity profile correction. <i>Swiss Medical Weekly</i> , 2020, 150, w20336. | 0.8 | 77 |
| 26 | 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. | 3.3 | 19 |
| 27 | <i>Salmonella</i> persists promote the spread of antibiotic resistance plasmids in the gut. <i>Nature</i> , 2019, 573, 276-280. | 13.7 | 169 |
| 28 | Global trends in antimicrobial resistance in animals in low- and middle-income countries. <i>Science</i> , 2019, 365, . | 6.0 | 594 |
| 29 | Hematopoietic Stem Cells Increase Quiescence during Aging. <i>Blood</i> , 2019, 134, 2484-2484. | 0.6 | 3 |
| 30 | Antibacterial Effects of Antiretrovirals, Potential Implications for Microbiome Studies in HIV. <i>Antiviral Therapy</i> , 2018, 23, 91-94. | 0.6 | 28 |
| 31 | An evolutionary perspective on the systems of adaptive immunity. <i>Biological Reviews</i> , 2018, 93, 505-528. | 4.7 | 76 |
| 32 | 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. | 3.5 | 37 |
| 33 | Assessing the public health impact of tolerance-based therapies with mathematical models. <i>PLoS Computational Biology</i> , 2018, 14, e1006119. | 1.5 | 8 |
| 34 | Death and population dynamics affect mutation rate estimates and evolvability under stress in bacteria. <i>PLoS Biology</i> , 2018, 16, e2005056. | 2.6 | 70 |
| 35 | Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018, 14, e1006895. | 2.1 | 53 |
| 36 | Effective polyploidy causes phenotypic delay and influences bacterial evolvability. <i>PLoS Biology</i> , 2018, 16, e2004644. | 2.6 | 37 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | 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, msw244. | 3.5 | 28 |
| 38 | Emergence of Resistance to Fungicides: The Role of Fungicide Dose. <i>Phytopathology</i> , 2017, 107, 545-560. | 1.1 | 44 |
| 39 | Modeling antimicrobial cycling and mixing: Differences arising from an individual-based versus a population-based perspective. <i>Mathematical Biosciences</i> , 2017, 294, 85-91. | 0.9 | 12 |
| 40 | Reversing resistance: different routes and common themes across pathogens. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171619. | 1.2 | 22 |
| 41 | Reducing antimicrobial use in food animals. <i>Science</i> , 2017, 357, 1350-1352. | 6.0 | 448 |
| 42 | Short-term activity cycles impede information transmission in ant colonies. <i>PLoS Computational Biology</i> , 2017, 13, e1005527. | 1.5 | 17 |
| 43 | Detection of antibiotic resistance is essential for gonorrhoea point-of-care testing: a mathematical modelling study. <i>BMC Medicine</i> , 2017, 15, 142. | 2.3 | 30 |
| 44 | Host population structure impedes reversion to drug sensitivity after discontinuation of treatment. <i>PLoS Computational Biology</i> , 2017, 13, e1005704. | 1.5 | 3 |
| 45 | 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. | 1.5 | 51 |
| 46 | Clonal dominance and transplantation dynamics in hematopoietic stem cell compartments. <i>PLoS Computational Biology</i> , 2017, 13, e1005803. | 1.5 | 26 |
| 47 | Invasiveness of plant pathogens depends on the spatial scale of host distribution. <i>Ecological Applications</i> , 2016, 26, 1238-1248. | 1.8 | 19 |
| 48 | 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, 20160148. | 1.5 | 41 |
| 49 | Influence of recombination on acquisition and reversion of immune escape and compensatory mutations in HIV-1. <i>Epidemics</i> , 2016, 14, 11-25. | 1.5 | 17 |
| 50 | Potential Pitfalls in Estimating Viral Load Heritability. <i>Trends in Microbiology</i> , 2016, 24, 687-698. | 3.5 | 14 |
| 51 | 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. | 3.5 | 14 |
| 52 | How Good Are Statistical Models at Approximating Complex Fitness Landscapes?. <i>Molecular Biology and Evolution</i> , 2016, 33, 2454-2468. | 3.5 | 28 |
| 53 | The Role of Adherence and Retreatment in De Novo Emergence of MDR-TB. <i>PLoS Computational Biology</i> , 2016, 12, e1004749. | 1.5 | 21 |
| 54 | Antibiotic-Resistant <i>Neisseria gonorrhoeae</i> Spread Faster with More Treatment, Not More Sexual Partners. <i>PLoS Pathogens</i> , 2016, 12, e1005611. | 2.1 | 84 |

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|----|---|-----|-----------|
| 55 | Developing smarter host mixtures to control plant disease. <i>Plant Pathology</i> , 2015, 64, 996-1004. | 1.2 | 44 |
| 56 | Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015, 10, 88-92. | 1.5 | 131 |
| 57 | Persistence of Transmitted HIV-1 Drug Resistance Mutations Associated with Fitness Costs and Viral Genetic Backgrounds. <i>PLoS Pathogens</i> , 2015, 11, e1004722. | 2.1 | 68 |
| 58 | Spatial Heterogeneity in Drug Concentrations Can Facilitate the Emergence of Resistance to Cancer Therapy. <i>PLoS Computational Biology</i> , 2015, 11, e1004142. | 1.5 | 100 |
| 59 | High Heritability Is Compatible with the Broad Distribution of Set Point Viral Load in HIV Carriers. <i>PLoS Pathogens</i> , 2015, 11, e1004634. | 2.1 | 29 |
| 60 | Contribution of recombination to the evolutionary history of HIV. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 84-89. | 1.5 | 40 |
| 61 | Evolution and emergence of infectious diseases in theoretical and real-world networks. <i>Nature Communications</i> , 2015, 6, 6101. | 5.8 | 102 |
| 62 | From "What Is?" to "What Isn't?" <i>Computational Biology</i> . <i>PLoS Computational Biology</i> , 2015, 11, e1004318. | 1.5 | 5 |
| 63 | The path of least resistance: aggressive or moderate treatment?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140566. | 1.2 | 79 |
| 64 | Cycling Empirical Antibiotic Therapy in Hospitals: Meta-Analysis and Models. <i>PLoS Pathogens</i> , 2014, 10, e1004225. | 2.1 | 87 |
| 65 | Recombination Accelerates Adaptation on a Large-Scale Empirical Fitness Landscape in HIV-1. <i>PLoS Genetics</i> , 2014, 10, e1004439. | 1.5 | 41 |
| 66 | Inference of Epidemiological Dynamics Based on Simulated Phylogenies Using Birth-Death and Coalescent Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003913. | 1.5 | 58 |
| 67 | Using an Epidemiological Model for Phylogenetic Inference Reveals Density Dependence in HIV Transmission. <i>Molecular Biology and Evolution</i> , 2014, 31, 6-17. | 3.5 | 55 |
| 68 | Why There Are No Essential Genes on Plasmids. <i>Molecular Biology and Evolution</i> , 2014, 32, msu293. | 3.5 | 29 |
| 69 | Evolutionary rescue: linking theory for conservation and medicine. <i>Evolutionary Applications</i> , 2014, 7, 1161-1179. | 1.5 | 104 |
| 70 | Can High-Risk Fungicides be Used in Mixtures Without Selecting for Fungicide Resistance?. <i>Phytopathology</i> , 2014, 104, 324-331. | 1.1 | 44 |
| 71 | Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. <i>Science</i> , 2014, 343, 1243727. | 6.0 | 215 |
| 72 | PLASMIDS AND EVOLUTIONARY RESCUE BY DRUG RESISTANCE. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2066-2078. | 1.1 | 20 |

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|----|---|-----|-----------|
| 73 | Social Meets Molecular: Combining Phylogenetic and Latent Class Analyses to Understand HIV-1 Transmission in Switzerland. <i>American Journal of Epidemiology</i> , 2014, 179, 1514-1525. | 1.6 | 25 |
| 74 | Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4573-4582. | 1.4 | 198 |
| 75 | On the role of resonance in drug failure under HIV treatment interruption. <i>Theoretical Biology and Medical Modelling</i> , 2013, 10, 44. | 2.1 | 1 |
| 76 | Nested model reveals potential amplification of an HIV epidemic due to drug resistance. <i>Epidemics</i> , 2013, 5, 34-43. | 1.5 | 19 |
| 77 | Virus-induced target cell activation reconciles set-point viral load heritability and within-host evolution. <i>Epidemics</i> , 2013, 5, 174-180. | 1.5 | 7 |
| 78 | Fixation probability of mobile genetic elements such as plasmids. <i>Theoretical Population Biology</i> , 2013, 90, 49-55. | 0.5 | 17 |
| 79 | Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120198. | 1.8 | 117 |
| 80 | 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, 228-233. | 3.3 | 454 |
| 81 | Estimating the Basic Reproductive Number from Viral Sequence Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 347-357. | 3.5 | 206 |
| 82 | Inferring Epidemic Contact Structure from Phylogenetic Trees. <i>PLoS Computational Biology</i> , 2012, 8, e1002413. | 1.5 | 85 |
| 83 | Estimating the Fitness Cost of Escape from HLA Presentation in HIV-1 Protease and Reverse Transcriptase. <i>PLoS Computational Biology</i> , 2012, 8, e1002525. | 1.5 | 13 |
| 84 | Exploring the Complexity of the HIV-1 Fitness Landscape. <i>PLoS Genetics</i> , 2012, 8, e1002551. | 1.5 | 100 |
| 85 | 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, 2309-2320. | 1.5 | 26 |
| 86 | Pre-existence and emergence of drug resistance in a generalized model of intra-host viral dynamics. <i>Epidemics</i> , 2012, 4, 187-202. | 1.5 | 43 |
| 87 | Weighting for sex acts to understand the spread of STI on networks. <i>Journal of Theoretical Biology</i> , 2012, 311, 46-53. | 0.8 | 11 |
| 88 | Evolution of Stress Response in the Face of Unreliable Environmental Signals. <i>PLoS Computational Biology</i> , 2012, 8, e1002627. | 1.5 | 59 |
| 89 | Population biological principles of drug-resistance evolution in infectious diseases. <i>Lancet Infectious Diseases</i> , 2011, 11, 236-247. | 4.6 | 220 |
| 90 | A systems analysis of mutational effects in HIV-1 protease and reverse transcriptase. <i>Nature Genetics</i> , 2011, 43, 487-489. | 9.4 | 168 |

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|-----|--|-----|-----------|
| 91 | Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. <i>Journal of Experimental Medicine</i> , 2011, 208, 273-284. | 4.2 | 271 |
| 92 | 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, 1095-1103. | 1.9 | 74 |
| 93 | Assessing Predicted HIV-1 Replicative Capacity in a Clinical Setting. <i>PLoS Pathogens</i> , 2011, 7, e1002321. | 2.1 | 37 |
| 94 | Informed Switching Strongly Decreases the Prevalence of Antibiotic Resistance in Hospital Wards. <i>PLoS Computational Biology</i> , 2011, 7, e1001094. | 1.5 | 45 |
| 95 | 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. | 2.1 | 35 |
| 96 | 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, 532-539. | 2.9 | 127 |
| 97 | The Role of Recombination for the Coevolutionary Dynamics of HIV and the Immune Response. <i>PLoS ONE</i> , 2011, 6, e16052. | 1.1 | 27 |
| 98 | Dynamic variation in cycling of hematopoietic stem cells in steady state and inflammation. <i>Journal of Cell Biology</i> , 2011, 192, i3-i3. | 2.3 | 0 |
| 99 | ON THE EVOLUTION OF SEXUAL REPRODUCTION IN HOSTS COEVOLVING WITH MULTIPLE PARASITES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 1644-1656. | 1.1 | 7 |
| 100 | Molecular Epidemiology Reveals Long-Term Changes in HIV Type 1 Subtype B Transmission in Switzerland. <i>Journal of Infectious Diseases</i> , 2010, 201, 1488-1497. | 1.9 | 172 |
| 101 | Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. <i>PLoS Pathogens</i> , 2010, 6, e1001123. | 2.1 | 108 |
| 102 | Principal component analysis of general patterns of HIV-1 replicative fitness in different drug environments. <i>Epidemics</i> , 2010, 2, 85-91. | 1.5 | 5 |
| 103 | Compensation of Fitness Costs and Reversibility of Antibiotic Resistance Mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 2085-2095. | 1.4 | 144 |
| 104 | Rotating antibiotics does not minimize selection for resistance. <i>Mathematical Biosciences and Engineering</i> , 2010, 7, 919-922. | 1.0 | 18 |
| 105 | Hematopoietic Stem Cell Cycling Dynamics In Steady State and Upon Hematopoietic Challenge. <i>Blood</i> , 2010, 116, 572-572. | 0.6 | 0 |
| 106 | Estimating the Stoichiometry of Human Immunodeficiency Virus Entry. <i>Journal of Virology</i> , 2009, 83, 1523-1531. | 1.5 | 95 |
| 107 | On the Causes of Selection for Recombination Underlying the Red Queen Hypothesis. <i>American Naturalist</i> , 2009, 174, S31-S42. | 1.0 | 25 |
| 108 | Red Queen Dynamics with Non-Standard Fitness Interactions. <i>PLoS Computational Biology</i> , 2009, 5, e1000469. | 1.5 | 30 |

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|-----|--|-----|-----------|
| 109 | Predicting the Evolution of Sex on Complex Fitness Landscapes. <i>PLoS Computational Biology</i> , 2009, 5, e1000510. | 1.5 | 16 |
| 110 | Long-Term Trends of HIV Type 1 Drug Resistance Prevalence among Antiretroviral Treatment-Experienced Patients in Switzerland. <i>Clinical Infectious Diseases</i> , 2009, 48, 979-987. | 2.9 | 43 |
| 111 | The role of epistasis on the evolution of recombination in host-parasite coevolution. <i>Theoretical Population Biology</i> , 2009, 75, 1-13. | 0.5 | 23 |
| 112 | Bacterial growth properties at low optical densities. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 267-274. | 0.7 | 10 |
| 113 | Recombination and drug resistance in HIV: Population dynamics and stochasticity. <i>Epidemics</i> , 2009, 1, 58-69. | 1.5 | 28 |
| 114 | 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, 1269-1276. | 1.0 | 28 |
| 115 | Evolutionary Origin and Consequences of Design Properties of Metabolic Networks. , 2009, , 113-126. | | 0 |
| 116 | Research on infectious disease dynamics. Introduction. <i>Epidemics</i> , 2009, 1, 1. | 1.5 | 0 |
| 117 | RAPID PARASITE ADAPTATION DRIVES SELECTION FOR HIGH RECOMBINATION RATES. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 295-300. | 1.1 | 65 |
| 118 | The effect of opinion clustering on disease outbreaks. <i>Journal of the Royal Society Interface</i> , 2008, 5, 1505-1508. | 1.5 | 197 |
| 119 | The state of affairs in the kingdom of the Red Queen. <i>Trends in Ecology and Evolution</i> , 2008, 23, 439-445. | 4.2 | 135 |
| 120 | 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, 572-576. | 0.9 | 20 |
| 121 | Intra-host Dynamics and Evolution of HIV Infection. , 2008, , 279-301. | | 5 |
| 122 | Epistasis between deleterious mutations and the evolution of recombination. <i>Trends in Ecology and Evolution</i> , 2007, 22, 308-315. | 4.2 | 143 |
| 123 | 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. | 1.5 | 54 |
| 124 | The Red Queen and the persistence of linkage-disequilibrium oscillations in finite and infinite populations. <i>BMC Evolutionary Biology</i> , 2007, 7, 211. | 3.2 | 36 |
| 125 | Evolution of complexity in signaling pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16337-16342. | 3.3 | 79 |
| 126 | Experimental Tests for an Evolutionary Trade-Off between Growth Rate and Yield in <i>E. coli</i> . <i>American Naturalist</i> , 2006, 168, 242-251. | 1.0 | 173 |

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|-----|---|-----|-----------|
| 127 | Stochastic or deterministic: what is the effective population size of HIV-1?. <i>Trends in Microbiology</i> , 2006, 14, 507-511. | 3.5 | 90 |
| 128 | Stable virulence levels in the HIV epidemic of Switzerland over two decades. <i>Aids</i> , 2006, 20, 889-894. | 1.0 | 52 |
| 129 | Mutation accumulation in space and the maintenance of sexual reproduction. <i>Ecology Letters</i> , 2006, 9, 941-946. | 3.0 | 30 |
| 130 | Signal transduction networks: Topology, response and biochemical processes. <i>Journal of Theoretical Biology</i> , 2006, 238, 416-425. | 0.8 | 37 |
| 131 | Simulating the evolution of signal transduction pathways. <i>Journal of Theoretical Biology</i> , 2006, 241, 223-232. | 0.8 | 40 |
| 132 | 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, 1141-1146. | 2.5 | 12 |
| 133 | The Effect of Multifunctionality on the Rate of Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 721-722. | 3.5 | 52 |
| 134 | High Epitope Expression Levels Increase Competition between T Cells. <i>PLoS Computational Biology</i> , 2006, 2, e109. | 1.5 | 21 |
| 135 | Rapid Viral Decay in Simian Immunodeficiency Virus-Infected Macaques Receiving Quadruple Antiretroviral Therapy. <i>Journal of Virology</i> , 2006, 80, 9861-9864. | 1.5 | 32 |
| 136 | Modelling cytomegalovirus replication patterns in the human host: factors important for pathogenesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1961-1967. | 1.2 | 14 |
| 137 | Effect of Varying Epistasis on the Evolution of Recombination. <i>Genetics</i> , 2006, 173, 589-597. | 1.2 | 48 |
| 138 | Emergence of Drug-Resistant Influenza Virus: Population Dynamical Considerations. <i>Science</i> , 2006, 312, 389-391. | 6.0 | 155 |
| 139 | Spatial models of virus-immune dynamics. <i>Journal of Theoretical Biology</i> , 2005, 233, 221-236. | 0.8 | 104 |
| 140 | Epitope down-modulation as a mechanism for the coexistence of competing T-cells. <i>Journal of Theoretical Biology</i> , 2005, 233, 379-390. | 0.8 | 9 |
| 141 | Neutral drift and polymorphism in gene-for-gene systems. <i>Ecology Letters</i> , 2005, 8, 925-932. | 3.0 | 43 |
| 142 | Guanine-adenine bias: a general property of retroid viruses that is unrelated to host-induced hypermutation. <i>Trends in Genetics</i> , 2005, 21, 264-268. | 2.9 | 16 |
| 143 | The Evolution of Connectivity in Metabolic Networks. <i>PLoS Biology</i> , 2005, 3, e228. | 2.6 | 109 |
| 144 | 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, 13572-13578. | 1.5 | 85 |

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|-----|--|-----|-----------|
| 145 | The evolution of groups of cooperating bacteria and the growth rate versus yield trade-off. <i>Microbiology</i> (United Kingdom), 2005, 151, 637-641. | 0.7 | 63 |
| 146 | Short Communication:HIV Type 2 Dynamics. <i>AIDS Research and Human Retroviruses</i> , 2005, 21, 608-610. | 0.5 | 3 |
| 147 | Evolution of cooperation by generalized reciprocity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1115-1120. | 1.2 | 169 |
| 148 | The HIV coreceptor switch: a population dynamical perspective. <i>Trends in Microbiology</i> , 2005, 13, 269-277. | 3.5 | 174 |
| 149 | The evolution of network topology by selective removal. <i>Journal of the Royal Society Interface</i> , 2005, 2, 533-536. | 1.5 | 28 |
| 150 | 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, 10747-10754. | 1.5 | 46 |
| 151 | Interchromatid and Interhomolog Recombination in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2004, 16, 342-352. | 3.1 | 72 |
| 152 | CCTTT-repeat polymorphism of the inducible nitric oxide synthase is not associated with HIV pathogenesis. <i>Clinical and Experimental Immunology</i> , 2004, 137, 566-569. | 1.1 | 9 |
| 153 | Quantification of infectious HIV-1 plasma viral load using a boosted in vitro infection protocol. <i>Virology</i> , 2004, 326, 113-129. | 1.1 | 76 |
| 154 | Recombination in HIV and the evolution of drug resistance: for better or for worse?. <i>BioEssays</i> , 2004, 26, 180-188. | 1.2 | 108 |
| 155 | Evidence for Positive Epistasis in HIV-1. <i>Science</i> , 2004, 306, 1547-1550. | 6.0 | 247 |
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