

Roland R Regoes

List of Publications by Year in descending order

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Version: 2024-02-01

100
papers

6,481
citations

81743

39
h-index

76769

74
g-index

119
all docs

119
docs citations

119
times ranked

8692
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of evolution in the emergence of infectious diseases. <i>Nature</i> , 2003, 426, 658-661.	13.7	473
2	High-avidity IgA protects the intestine by enchaining growing bacteria. <i>Nature</i> , 2017, 544, 498-502.	13.7	307
3	Pharmacodynamic Functions: a Multiparameter Approach to the Design of Antibiotic Treatment Regimens. <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 3670-3676.	1.4	298
4	Stabilization of cooperative virulence by the expression of an avirulent phenotype. <i>Nature</i> , 2013, 494, 353-356.	13.7	289
5	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
6	Population biological principles of drug-resistance evolution in infectious diseases. <i>Lancet Infectious Diseases</i> , 2011, 11, 236-247.	4.6	220
7	Investigating the Consequences of Interference between Multiple CD8+ T Cell Escape Mutations in Early HIV Infection. <i>PLoS Computational Biology</i> , 2016, 12, e1004721.	1.5	219
8	Combination Effects of Antimicrobial Peptides. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 1717-1724.	1.4	190
9	Phenotypic Tolerance: Antibiotic Enrichment of Noninherited Resistance in Bacterial Populations. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 1483-1494.	1.4	178
10	The HIV coreceptor switch: a population dynamical perspective. <i>Trends in Microbiology</i> , 2005, 13, 269-277.	3.5	174
11	Salmonella persisters promote the spread of antibiotic resistance plasmids in the gut. <i>Nature</i> , 2019, 573, 276-280.	13.7	169
12	Emergence of Drug-Resistant Influenza Virus: Population Dynamical Considerations. <i>Science</i> , 2006, 312, 389-391.	6.0	155
13	Cecum Lymph Node Dendritic Cells Harbor Slow-Growing Bacteria Phenotypically Tolerant to Antibiotic Treatment. <i>PLoS Biology</i> , 2014, 12, e1001793.	2.6	139
14	Predicting drug resistance evolution: insights from antimicrobial peptides and antibiotics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172687.	1.2	139
15	EVOLUTION OF VIRULENCE IN A HETEROGENEOUS HOST POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 64-71.	1.1	137
16	Insect antimicrobial peptides show potentiating functional interactions against Gram-negative bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150293.	1.2	134
17	Determinants of HIV-1 broadly neutralizing antibody induction. <i>Nature Medicine</i> , 2016, 22, 1260-1267.	15.2	133
18	Dose-dependent infection rates of parasites produce the Allee effect in epidemiology. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 271-279.	1.2	122

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19	The Role of Compensatory Mutations in the Emergence of Drug Resistance. <i>PLoS Computational Biology</i> , 2006, 2, e137.	1.5	110
20	Estimating the Stoichiometry of Human Immunodeficiency Virus Entry. <i>Journal of Virology</i> , 2009, 83, 1523-1531.	1.5	95
21	MPER-specific antibodies induce gp120 shedding and irreversibly neutralize HIV-1. <i>Journal of Experimental Medicine</i> , 2011, 208, 439-454.	4.2	95
22	Intestinal epithelial NAIP/NLRC4 restricts systemic dissemination of the adapted pathogen <i>Salmonella Typhimurium</i> due to site-specific bacterial PAMP expression. <i>Mucosal Immunology</i> , 2020, 13, 530-544.	2.7	94
23	Interaction of the gp120 V1V2 loop with a neighboring gp120 unit shields the HIV envelope trimer against cross-neutralizing antibodies. <i>Journal of Experimental Medicine</i> , 2011, 208, 1419-1433.	4.2	92
24	Epidemiological and clinical consequences of within-host evolution. <i>Trends in Microbiology</i> , 2011, 19, 24-32.	3.5	91
25	Virus Dynamics: the Effect of Target Cell Limitation and Immune Responses on Virus Evolution. <i>Journal of Theoretical Biology</i> , 1998, 191, 451-462.	0.8	88
26	Different Infectivity of HIV-1 Strains Is Linked to Number of Envelope Trimers Required for Entry. <i>PLoS Pathogens</i> , 2015, 11, e1004595.	2.1	81
27	A quantitative test of the relationship between parasite dose and infection probability across different host-parasite combinations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 853-859.	1.2	78
28	COVID-19 infectivity profile correction. <i>Swiss Medical Weekly</i> , 2020, 150, w20336.	0.8	77
29	Pathogen Dose Infectivity Curves as a Method to Analyze the Distribution of Host Susceptibility: A Quantitative Assessment of Maternal Effects after Food Stress and Pathogen Exposure. <i>American Naturalist</i> , 2010, 175, 106-115.	1.0	73
30	Granulocytes Impose a Tight Bottleneck upon the Gut Luminal Pathogen Population during <i>Salmonella Typhimurium</i> Colitis. <i>PLoS Pathogens</i> , 2014, 10, e1004557.	2.1	73
31	How do pathogen evolution and host heterogeneity interact in disease emergence?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 3075-3083.	1.2	72
32	Lymph Node Colonization Dynamics after Oral <i>Salmonella Typhimurium</i> Infection in Mice. <i>PLoS Pathogens</i> , 2013, 9, e1003532.	2.1	70
33	Estimation of the rate of killing by cytotoxic T lymphocytes in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1599-1603.	3.3	68
34	Antimicrobial combinations: Bliss independence and Loewe additivity derived from mechanistic multi-hit models. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150294.	1.8	66
35	RAPID PARASITE ADAPTATION DRIVES SELECTION FOR HIGH RECOMBINATION RATES. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 295-300.	1.1	65
36	Preclinical Assessment of HIV Vaccines and Microbicides by Repeated Low-Dose Virus Challenges. <i>PLoS Medicine</i> , 2005, 2, e249.	3.9	61

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37	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
38	Disentangling Human Tolerance and Resistance Against HIV. <i>PLoS Biology</i> , 2014, 12, e1001951.	2.6	53
39	Roles of Target Cells and Virus-Specific Cellular Immunity in Primary Simian Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2004, 78, 4866-4875.	1.5	46
40	Successive range expansion promotes diversity and accelerates evolution in spatially structured microbial populations. <i>ISME Journal</i> , 2017, 11, 2112-2123.	4.4	46
41	Investigating CTL Mediated Killing with a 3D Cellular Automaton. <i>PLoS Computational Biology</i> , 2009, 5, e1000466.	1.5	44
42	Revisiting Estimates of CTL Killing Rates In Vivo. <i>PLoS ONE</i> , 2007, 2, e1301.	1.1	42
43	Estimating the Effectiveness of Simian Immunodeficiency Virus-Specific CD8 ⁺ T Cells from the Dynamics of Viral Immune Escape. <i>Journal of Virology</i> , 2007, 81, 11982-11991.	1.5	41
44	Viral mutation rates: modelling the roles of within-host viral dynamics and the trade-off between replication fidelity and speed. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20122047.	1.2	40
45	The HIV-1 Entry Process: A Stoichiometric View. <i>Trends in Microbiology</i> , 2015, 23, 763-774.	3.5	40
46	Bacteria primed by antimicrobial peptides develop tolerance and persist. <i>PLoS Pathogens</i> , 2021, 17, e1009443.	2.1	39
47	Mathematical models of cytotoxic T _H lymphocyte killing. <i>Immunology and Cell Biology</i> , 2007, 85, 274-279.	1.0	38
48	Vaccination Alters the Balance between Protective Immunity, Exhaustion, Escape, and Death in Chronic Infections. <i>Journal of Virology</i> , 2011, 85, 5565-5570.	1.5	37
49	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
50	Metabolite toxicity slows local diversity loss during expansion of a microbial cross-feeding community. <i>ISME Journal</i> , 2018, 12, 136-144.	4.4	32
51	Multi-step vs. single-step resistance evolution under different drugs, pharmacokinetics, and treatment regimens. <i>ELife</i> , 2021, 10, .	2.8	32
52	Population genetics, biofilm recalcitrance, and antibiotic resistance evolution. <i>Trends in Microbiology</i> , 2022, 30, 841-852.	3.5	32
53	Optimal Replication of Poliovirus within Cells. <i>American Naturalist</i> , 2005, 165, 364-373.	1.0	31
54	Estimating the Stoichiometry of HIV Neutralization. <i>PLoS Computational Biology</i> , 2010, 6, e1000713.	1.5	31

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55	Influence of the Fibroblastic Reticular Network on Cell-Cell Interactions in Lymphoid Organs. <i>PLoS Computational Biology</i> , 2012, 8, e1002436.	1.5	30
56	Can Non-lytic CD8+ T Cells Drive HIV-1 Escape?. <i>PLoS Pathogens</i> , 2013, 9, e1003656.	2.1	29
57	A Population Dynamics Analysis of the Interaction between Adaptive Regulatory T Cells and Antigen Presenting Cells. <i>PLoS ONE</i> , 2008, 3, e2306.	1.1	28
58	The Role of Exposure History on HIV Acquisition: Insights from Repeated Low-dose Challenge Studies. <i>PLoS Computational Biology</i> , 2012, 8, e1002767.	1.5	27
59	Pharmacodynamics of non-replicating viruses, bacteriocins and lysins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 2703-2712.	1.2	25
60	Parallel Evolution of HIV-1 in a Long-Term Experiment. <i>Molecular Biology and Evolution</i> , 2019, 36, 2400-2414.	3.5	25
61	Predicting the Impact of CD8 ⁺ T Cell Polyfunctionality on HIV Disease Progression. <i>Journal of Virology</i> , 2014, 88, 10134-10145.	1.5	23
62	Effector function does not contribute to protection from virus challenge by a highly potent HIV broadly neutralizing antibody in nonhuman primates. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	23
63	Predicting HIV-1 transmission and antibody neutralization efficacy in vivo from stoichiometric parameters. <i>PLoS Pathogens</i> , 2017, 13, e1006313.	2.1	23
64	Comparison of cytotoxic T lymphocyte efficacy in acute and persistent lymphocytic choriomeningitis virus infection. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 3395-3402.	1.2	22
65	Restricted occupancy models for neutralization of HIV virions and populations. <i>Journal of Theoretical Biology</i> , 2011, 283, 192-202.	0.8	20
66	Protective Efficacy of Individual CD8+ T Cell Specificities in Chronic Viral Infection. <i>Journal of Immunology</i> , 2015, 194, 1755-1762.	0.4	18
67	Partial rescue of V1V2 mutant infectivity by HIV-1 cell-cell transmission supports the domain's exceptional capacity for sequence variation. <i>Retrovirology</i> , 2014, 11, 75.	0.9	16
68	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
69	Analysis of the Subunit Stoichiometries in Viral Entry. <i>PLoS ONE</i> , 2012, 7, e33441.	1.1	15
70	Pathogen invasion-dependent tissue reservoirs and plasmid-encoded antibiotic degradation boost plasmid spread in the gut. <i>ELife</i> , 2021, 10, .	2.8	15
71	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
72	CpG-creating mutations are costly in many human viruses. <i>Evolutionary Ecology</i> , 2020, 34, 339-359.	0.5	14

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73	Partial rescue of V1V2 mutant infectivity by HIV-1 cell-cell transmission supports the domain's exceptional capacity for sequence variation. <i>Retrovirology</i> , 2014, 11, 75.	0.9	14
74	Estimating the In Vivo Killing Efficacy of Cytotoxic T Lymphocytes across Different Peptide-MHC Complex Densities. <i>PLoS Computational Biology</i> , 2015, 11, e1004178.	1.5	13
75	Contribution of Peaks of Virus Load to Simian Immunodeficiency Virus Pathogenesis. <i>Journal of Virology</i> , 2002, 76, 2573-2578.	1.5	12
76	Estimating the mutational fitness effects distribution during early HIV infection. <i>Virus Evolution</i> , 2018, 4, vey029.	2.2	12
77	Virus dynamics and phyloanatomy: Merging population dynamic and phylogenetic approaches. <i>Immunological Reviews</i> , 2018, 285, 134-146.	2.8	11
78	Number of HIV-1 founder variants is determined by the recency of the source partner infection. <i>Science</i> , 2020, 369, 103-108.	6.0	11
79	HIV Coreceptor Usage and Drug Treatment. <i>Journal of Theoretical Biology</i> , 2002, 217, 443-457.	0.8	10
80	Similar Impact of CD8+ T Cell Responses on Early Virus Dynamics during SIV Infections of Rhesus Macaques and Sooty Mangabeys. <i>PLoS Computational Biology</i> , 2010, 6, e1000901.	1.5	9
81	Theoretical analysis of the evolution of immune memory. <i>BMC Evolutionary Biology</i> , 2010, 10, 380.	3.2	8
82	Mathematical models: A key to understanding HIV envelope interactions?. <i>Journal of Immunological Methods</i> , 2013, 398-399, 1-18.	0.6	8
83	Assessing the public health impact of tolerance-based therapies with mathematical models. <i>PLoS Computational Biology</i> , 2018, 14, e1006119.	1.5	8
84	EVOLUTION OF VIRULENCE IN A HETEROGENEOUS HOST POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 64.	1.1	6
85	The Role of Chance in Primate Lentiviral Infectivity. <i>Progress in Molecular Biology and Translational Science</i> , 2015, 129, 327-351.	0.9	6
86	Disentangling non-specific and specific transgenerational immune priming components in host-parasite interactions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192386.	1.2	6
87	Population genetics meets cancer genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18241-18242.	3.3	5
88	Modeling Polygenic Antibiotic Resistance Evolution in Biofilms. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
89	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. <i>PLoS Biology</i> , 2020, 18, e3001010.	2.6	4
90	Population Dynamics Analysis of Ciprofloxacin-Persistent <i>S. Typhimurium</i> Cells in a Mouse Model for Salmonella Diarrhea. <i>Methods in Molecular Biology</i> , 2016, 1333, 189-203.	0.4	2

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91	Applying mixture model methods to SARS-CoV-2 serosurvey data from Geneva. <i>Epidemics</i> , 2022, 39, 100572.	1.5	2
92	More or lessâ€”On the influence of labelling strategies to infer cell population dynamics. <i>PLoS ONE</i> , 2017, 12, e0185523.	1.1	1
93	Correction: Theoretical analysis of the evolution of immune memory. <i>BMC Evolutionary Biology</i> , 2011, 11, .	3.2	0
94	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
95	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0
96	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0
97	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0
98	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0
99	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0
100	Long-term experimental evolution of HIV-1 reveals effects of environment and mutational history. , 2020, 18, e3001010.		0