

Alan S Perelson

List of Publications by Year in descending order

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Version: 2024-02-01

501
papers

56,821
citations

1368

108
h-index

1627

215
g-index

522
all docs

522
docs citations

522
times ranked

25413
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex decay dynamics of HIV virions, intact and defective proviruses, and 2LTR circles following initiation of antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	46
2	Antithetic effect of interferon- λ on cell-free and cell-to-cell HIV-1 infection. <i>PLoS Computational Biology</i> , 2022, 18, e1010053.	1.5	1
3	Disrupting autorepression circuitry generates "open-loop lethality" to yield escape-resistant antiviral agents. <i>Cell</i> , 2022, 185, 2086-2102.e22.	13.5	7
4	HIV influences clustering and intracellular replication of hepatitis C virus. <i>Journal of Viral Hepatitis</i> , 2021, 28, 334-344.	1.0	6
5	Suppression of hepatitis B virus through therapeutic activation of RIG-I and IRF3 signaling in hepatocytes. <i>Science</i> , 2021, 24, 101969.	1.9	17
6	Zika virus dynamics: Effects of inoculum dose, the innate immune response and viral interference. <i>PLoS Computational Biology</i> , 2021, 17, e1008564.	1.5	10
7	CD8 Lymphocyte Depletion Enhances the Latency Reversal Activity of the SMAC Mimetic AZD5582 in ART-Suppressed Simian Immunodeficiency Virus-Infected Rhesus Macaques. <i>Journal of Virology</i> , 2021, 95, .	1.5	17
8	Mechanistic Modeling of SARS-CoV-2 and Other Infectious Diseases and the Effects of Therapeutics. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 109, 829-840.	2.3	70
9	A quantitative model used to compare within-host SARS-CoV-2, MERS-CoV, and SARS-CoV dynamics provides insights into the pathogenesis and treatment of SARS-CoV-2. <i>PLoS Biology</i> , 2021, 19, e3001128.	2.6	99
10	Success of prophylactic antiviral therapy for SARS-CoV-2: Predicted critical efficacies and impact of different drug-specific mechanisms of action. <i>PLoS Computational Biology</i> , 2021, 17, e1008752.	1.5	41
11	Unified model of short- and long-term HIV viral rebound for clinical trial planning. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20201015.	1.5	6
12	Viral Load Kinetics of Severe Acute Respiratory Syndrome Coronavirus 2 in Hospitalized Individuals With Coronavirus Disease 2019. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab153.	0.4	20
13	A participant-derived xenograft model of HIV enables long-term evaluation of autologous immunotherapies. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	9
14	Understanding Hepatitis B Virus Dynamics and the Antiviral Effect of Interferon Alpha Treatment in Humanized Chimeric Mice. <i>Journal of Virology</i> , 2021, 95, e0049220.	1.5	14
15	Immunological Correlates of the HIV-1 Replication-Competent Reservoir Size. <i>Clinical Infectious Diseases</i> , 2021, 73, 1528-1531.	2.9	4
16	Mechanistic basis of post-treatment control of SIV after anti- λ 4 ²⁷ antibody therapy. <i>PLoS Computational Biology</i> , 2021, 17, e1009031.	1.5	4
17	Detection of significant antiviral drug effects on COVID-19 with reasonable sample sizes in randomized controlled trials: A modeling study. <i>PLoS Medicine</i> , 2021, 18, e1003660.	3.9	32
18	Modeling HIV-1 Within-Host Dynamics After Passive Infusion of the Broadly Neutralizing Antibody VRC01. <i>Frontiers in Immunology</i> , 2021, 12, 710012.	2.2	6

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19	Modeling Within-Host Dynamics of SARS-CoV-2 Infection: A Case Study in Ferrets. <i>Viruses</i> , 2021, 13, 1635.	1.5	24
20	Safety, pharmacokinetics and antiviral activity of PGT121, a broadly neutralizing monoclonal antibody against HIV-1: a randomized, placebo-controlled, phase 1 clinical trial. <i>Nature Medicine</i> , 2021, 27, 1718-1724.	15.2	39
21	Modeling hepatitis C virus kinetics during liver transplantation reveals the role of the liver in virus clearance. <i>ELife</i> , 2021, 10, .	2.8	4
22	In vivo kinetics of SARS-CoV-2 infection and its relationship with a person's infectiousness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	108
23	Disentangling the lifespans of hepatitis C virus-infected cells and intracellular vRNA replication-complexes during direct-acting anti-viral therapy. <i>Journal of Viral Hepatitis</i> , 2020, 27, 261-269.	1.0	3
24	Accumulated mutations by 6 months of infection collectively render transmitted/founder HIV-1 significantly less fit. <i>Journal of Infection</i> , 2020, 80, 210-218.	1.7	5
25	Models of SIV rebound after treatment interruption that involve multiple reactivation events. <i>PLoS Computational Biology</i> , 2020, 16, e1008241.	1.5	3
26	Fc-mediated effector function contributes to the in vivo antiviral effect of an HIV neutralizing antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18754-18763.	3.3	53
27	Quantifying the contribution of Fc-mediated effector functions to the antiviral activity of anti-HIV-1 IgG1 antibodies in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18002-18009.	3.3	44
28	A Coupled Mathematical Model of the Intracellular Replication of Dengue Virus and the Host Cell Immune Response to Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 725.	1.5	28
29	Continuous and discrete modeling of HIV-1 decline on therapy. <i>Journal of Mathematical Biology</i> , 2020, 81, 1-24.	0.8	6
30	Timing of Antiviral Treatment Initiation is Critical to Reduce SARS-CoV-2 Viral Load. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2020, 9, 509-514.	1.3	170
31	A direct-acting antiviral drug abrogates viremia in Zika virus-infected rhesus macaques. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	21
32	Single hepatocytes show persistence and transcriptional inactivity of hepatitis B. <i>JCI Insight</i> , 2020, 5, .	2.3	17
33	Quantification of Ebola virus replication kinetics in vitro. <i>PLoS Computational Biology</i> , 2020, 16, e1008375.	1.5	10
34	Mathematical modeling of hepatitis C RNA replication, exosome secretion and virus release. <i>PLoS Computational Biology</i> , 2020, 16, e1008421.	1.5	7
35	Predictions of time to HIV viral rebound following ART suspension that incorporate personal biomarkers. <i>PLoS Computational Biology</i> , 2019, 15, e1007229.	1.5	30
36	Within-host mathematical models of hepatitis B virus infection: Past, present, and future. <i>Current Opinion in Systems Biology</i> , 2019, 18, 27-35.	1.3	28

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37	Regulation of T cell expansion by antigen presentation dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5914-5919.	3.3	67
38	Modeling the Effects of Morphine-Altered Virus Specific Antibody Responses on HIV/SIV Dynamics. Scientific Reports, 2019, 9, 5423.	1.6	12
39	Mathematical modelling identifies the role of adaptive immunity as a key controller of respiratory syncytial virus in cotton rats. Journal of the Royal Society Interface, 2019, 16, 20190389.	1.5	19
40	Principles Governing Establishment versus Collapse of HIV-1 Cellular Spread. Cell Host and Microbe, 2019, 26, 748-763.e20.	5.1	30
41	Acute hepatitis B virus infection in humanized chimeric mice has multiphasic viral kinetics. Hepatology, 2018, 68, 473-484.	3.6	30
42	A Pharmacokinetic/Viral Kinetic Model to Evaluate Treatment of Chronic HCV Infection with a Non-Nucleoside Polymerase Inhibitor. Antiviral Therapy, 2018, 23, 353-361.	0.6	3
43	Intracellular Hepatitis C Virus Modeling Predicts Infection Dynamics and Viral Protein Mechanisms. Journal of Virology, 2018, 92, .	1.5	21
44	Probabilistic control of HIV latency and transactivation by the Tat gene circuit. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12453-12458.	3.3	23
45	Determinants of the efficacy of HIV latency-reversing agents and implications for drug and treatment design. JCI Insight, 2018, 3, .	2.3	14
46	Variation in cell-associated unspliced HIV RNA on antiretroviral therapy is associated with the circadian regulator brain-and-muscle-ARNT-like-1. Aids, 2018, 32, 2119-2128.	1.0	28
47	CD8+ lymphocyte control of SIV infection during antiretroviral therapy. PLoS Pathogens, 2018, 14, e1007350.	2.1	20
48	Early HIV Infection Predictions: Role of Viral Replication Errors. SIAM Journal on Applied Mathematics, 2018, 78, 1863-1890.	0.8	7
49	A New Age-Structured Multiscale Model of the Hepatitis C Virus Life-Cycle During Infection and Therapy With Direct-Acting Antiviral Agents. Frontiers in Microbiology, 2018, 9, 601.	1.5	16
50	Correlation Between Anti-gp41 Antibodies and Virus Infectivity Decay During Primary HIV-1 Infection. Frontiers in Microbiology, 2018, 9, 1326.	1.5	13
51	Superinfection and cure of infected cells as mechanisms for hepatitis C virus adaptation and persistence. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7139-E7148.	3.3	16
52	Mathematical modeling of within-host Zika virus dynamics. Immunological Reviews, 2018, 285, 81-96.	2.8	40
53	Introduction to modeling viral infections and immunity. Immunological Reviews, 2018, 285, 5-8.	2.8	22
54	No recovery of replication-competent HIV-1 from human liver macrophages. Journal of Clinical Investigation, 2018, 128, 4501-4509.	3.9	41

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55	Population dynamics of host and pathogens. , 2018, , 265-278.		3
56	Quantifying antiviral activity optimizes drug combinations against hepatitis C virus infection. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1922-1927.	3.3	50
57	Zika Virus Persistence in the Central Nervous System and Lymph Nodes of Rhesus Monkeys. Cell, 2017, 169, 610-620.e14.	13.5	191
58	Reply to Padmanabhan and Dixit: Hepatitis C virus entry inhibitors for optimally boosting direct-acting antiviral-based treatments. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4527-E4529.	3.3	9
59	Prevalence of end of treatment RNA-positive/sustained viral response in HCV patients treated with sofosbuvir combination therapies. Therapeutic Advances in Gastroenterology, 2017, 10, 68-73.	1.4	15
60	The paradox of highly effective sofosbuvir-based combination therapy despite slow viral decline: can we still rely on viral kinetics?. Scientific Reports, 2017, 7, 10233.	1.6	20
61	How Germinal Centers Evolve Broadly Neutralizing Antibodies: the Breadth of the Follicular Helper T Cell Response. Journal of Virology, 2017, 91, .	1.5	32
62	Zika plasma viral dynamics in nonhuman primates provides insights into early infection and antiviral strategies. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8847-8852.	3.3	89
63	Modelling the effects of phylogeny and body size on within-host pathogen replication and immune response. Journal of the Royal Society Interface, 2017, 14, 20170479.	1.5	23
64	On the Death Rate of Abortively Infected Cells: Estimation from Simian-Human Immunodeficiency Virus Infection. Journal of Virology, 2017, 91, .	1.5	11
65	The Role of Infected Cell Proliferation in the Clearance of Acute HBV Infection in Humans. Viruses, 2017, 9, 350.	1.5	25
66	Editorial: Transplant Rejection and Tolerance—Advancing the Field through Integration of Computational and Experimental Investigation. Frontiers in Immunology, 2017, 8, 616.	2.2	1
67	A strongly selected mutation in the HIV-1 genome is independent of T cell responses and neutralizing antibodies. Retrovirology, 2017, 14, 46.	0.9	2
68	Nonlatching positive feedback enables robust bimodality by decoupling expression noise from the mean. PLoS Biology, 2017, 15, e2000841.	2.6	19
69	NS5A inhibitors unmask differences in functional replicase complex half-life between different hepatitis C virus strains. PLoS Pathogens, 2017, 13, e1006343.	2.1	12
70	Treatment with integrase inhibitor suggests a new interpretation of HIV RNA decay curves that reveals a subset of cells with slow integration. PLoS Pathogens, 2017, 13, e1006478.	2.1	45
71	Modelling the Interaction between Danoprevir and Mericitabine in the Treatment of Chronic HCV Infection. Antiviral Therapy, 2016, 21, 297-306.	0.6	2
72	Mathematical Modeling. , 2016, , 199-211.		1

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73	Molecular clock of HIV-1 envelope genes under early immune selection. <i>Retrovirology</i> , 2016, 13, 38.	0.9	11
74	Hepatitis C virus dynamics and cellular gene expression in <uPA>â€</uPA>SCID</uPA> chimeric mice with humanized livers during intravenous silibinin monotherapy. <i>Journal of Viral Hepatitis</i> , 2016, 23, 708-717.	1.0	14
75	Transmission of Multiple HIV-1 Subtype C Transmitted/founder Viruses into the Same Recipients Was not Determined by Modest Phenotypic Differences. <i>Scientific Reports</i> , 2016, 6, 38130.	1.6	18
76	Estimating biologically relevant parameters under uncertainty for experimental within-host murine West Nile virus infection. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160130.	1.5	39
77	Modeling Viral Spread. <i>Annual Review of Virology</i> , 2016, 3, 555-572.	3.0	79
78	Zika viral dynamics and shedding in rhesus and cynomolgus macaques. <i>Nature Medicine</i> , 2016, 22, 1448-1455.	15.2	270
79	Efficacy and safety of 3-week response-guided triple direct-acting antiviral therapy for chronic hepatitis C infection: a phase 2, open-label, proof-of-concept study. <i>The Lancet Gastroenterology and Hepatology</i> , 2016, 1, 97-104.	3.7	80
80	Authors' response: Danoprevir pharmacokinetic/viral kinetic model for treating chronic HCV â€“ some considerations. <i>Antiviral Therapy</i> , 2016, 21, 648-649.	0.6	0
81	Viral dynamic modelling of Hepatitis C and resistanceâ€“associated variants in haemophiliacs. <i>Haemophilia</i> , 2016, 22, 543-548.	1.0	1
82	Single-Genome Sequencing of Hepatitis C Virus in Donor-Recipient Pairs Distinguishes Modes and Models of Virus Transmission and Early Diversification. <i>Journal of Virology</i> , 2016, 90, 152-166.	1.5	17
83	SPMM: estimating infection duration of multivariant HIV-1 infections. <i>Bioinformatics</i> , 2016, 32, 1308-1315.	1.8	13
84	Residual Viremia in Treated HIV+ Individuals. <i>PLoS Computational Biology</i> , 2016, 12, e1004677.	1.5	58
85	Modeling the Effects of Morphine on Simian Immunodeficiency Virus Dynamics. <i>PLoS Computational Biology</i> , 2016, 12, e1005127.	1.5	19
86	Severity of Liver Disease Affects HCV Kinetics in Patients Treated with Intravenous Silibinin Monotherapy. <i>Antiviral Therapy</i> , 2015, 20, 149-155.	0.6	14
87	A Pharmacokinetic/Viral Kinetic Model to Evaluate the Treatment Effectiveness of Danoprevir against Chronic HCV. <i>Antiviral Therapy</i> , 2015, 20, 469-477.	0.6	7
88	Early HIV RNA decay during raltegravir-containing regimens exhibits two distinct subphases (1a and 1b). <i>Aids</i> , 2015, 29, 2419-2426.	1.0	18
89	Recombination Enhances HIV-1 Envelope Diversity by Facilitating the Survival of Latent Genomic Fragments in the Plasma Virus Population. <i>PLoS Computational Biology</i> , 2015, 11, e1004625.	1.5	19
90	Modeling the Effects of Vorinostat In Vivo Reveals both Transient and Delayed HIV Transcriptional Activation and Minimal Killing of Latently Infected Cells. <i>PLoS Pathogens</i> , 2015, 11, e1005237.	2.1	46

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91	Transmitted Virus Fitness and Host T Cell Responses Collectively Define Divergent Infection Outcomes in Two HIV-1 Recipients. <i>PLoS Pathogens</i> , 2015, 11, e1004565.	2.1	44
92	Modelling hepatitis C therapyâ€”predicting effects of treatment. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2015, 12, 437-445.	8.2	72
93	Post-treatment control of HIV infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5467-5472.	3.3	166
94	Proof-of-Principle for Immune Control of Global HIV-1 Reactivation In Vivo. <i>Clinical Infectious Diseases</i> , 2015, 61, 120-128.	2.9	17
95	Quantification of Hepatitis C Virus Cell-to-Cell Spread Using a Stochastic Modeling Approach. <i>Journal of Virology</i> , 2015, 89, 6551-6561.	1.5	32
96	The challenges of modelling antibody repertoire dynamics in HIV infection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140247.	1.8	9
97	Competitive exclusion by autologous antibodies can prevent broad HIV-1 antibodies from arising. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11654-11659.	3.3	58
98	Reversion and T Cell Escape Mutations Compensate the Fitness Loss of a CD8+ T Cell Escape Mutant in Their Cognate Transmitted/Founder Virus. <i>PLoS ONE</i> , 2014, 9, e102734.	1.1	8
99	Preexisting compensatory amino acids compromise fitness costs of a HIV-1Â T cell escape mutation. <i>Retrovirology</i> , 2014, 11, 101.	0.9	12
100	Persistent HIV-1 replication is associated with lower antiretroviral drug concentrations in lymphatic tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2307-2312.	3.3	579
101	Antibody Responses during Hepatitis B Viral Infection. <i>PLoS Computational Biology</i> , 2014, 10, e1003730.	1.5	60
102	A Hepatitis C Virus Infection Model with Time-Varying Drug Effectiveness: Solution and Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003769.	1.5	15
103	Inferring Viral Dynamics in Chronically HCV Infected Patients from the Spatial Distribution of Infected Hepatocytes. <i>PLoS Computational Biology</i> , 2014, 10, e1003934.	1.5	45
104	Impact of Different Oseltamivir Regimens on Treating Influenza A Virus Infection and Resistance Emergence: Insights from a Modelling Study. <i>PLoS Computational Biology</i> , 2014, 10, e1003568.	1.5	60
105	Quantifying the Turnover of Transcriptional Subclasses of HIV-1-Infected Cells. <i>PLoS Computational Biology</i> , 2014, 10, e1003871.	1.5	19
106	Effects of Aging on Influenza Virus Infection Dynamics. <i>Journal of Virology</i> , 2014, 88, 4123-4131.	1.5	114
107	Modulation of HCV replication after combination antiretroviral therapy in HCV/HIV co-infected patients. <i>Science Translational Medicine</i> , 2014, 6, 246ra98.	5.8	19
108	Effect of ribavirin on viral kinetics and liver gene expression in chronic hepatitis C. <i>Gut</i> , 2014, 63, 161-169.	6.1	51

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109	Modeling viral kinetics and treatment outcome during alisporivir interferon-free treatment in hepatitis C virus genotype 2 and 3 patients. <i>Hepatology</i> , 2014, 59, 1706-1714.	3.6	23
110	Viral kinetic modeling: state of the art. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2014, 41, 431-443.	0.8	82
111	Treatment of hepatitis C with an interferon-based lead-in phase: a perspective from mathematical modelling. <i>Antiviral Therapy</i> , 2014, 19, 469-477.	0.6	6
112	Analysis of Hepatitis C Viral Kinetics during Administration of Two Nucleotide Analogues: Sofosbuvir (Gs-7977) and Gs-0938. <i>Antiviral Therapy</i> , 2014, 19, 211-220.	0.6	44
113	Modeling the Dynamics and Migratory Pathways of Virus-Specific Antibody-Secreting Cell Populations in Primary Influenza Infection. <i>PLoS ONE</i> , 2014, 9, e104781.	1.1	2
114	Quantifying T lymphocyte turnover. <i>Journal of Theoretical Biology</i> , 2013, 327, 45-87.	0.8	207
115	Human systems immunology: Hypothesis-based modeling and unbiased data-driven approaches. <i>Seminars in Immunology</i> , 2013, 25, 193-200.	2.7	28
116	Use of Laser Capture Microdissection to Map Hepatitis C Virus-Positive Hepatocytes in Human Liver. <i>Gastroenterology</i> , 2013, 145, 1404-1413.e10.	0.6	74
117	Modeling the within-host dynamics of HIV infection. <i>BMC Biology</i> , 2013, 11, 96.	1.7	214
118	Hepatitis C Viral Kinetics. <i>Clinics in Liver Disease</i> , 2013, 17, 13-26.	1.0	25
119	Innate Immune Tolerance and the Role of Kupffer Cells in Differential Responses to Interferon Therapy Among Patients With HCV Genotype 1 Infection. <i>Gastroenterology</i> , 2013, 144, 402-413.e12.	0.6	66
120	Understanding triphasic HCV decline during treatment in the era of IL28B polymorphisms and direct acting antiviral agents via mathematical modeling. <i>Journal of Hepatology</i> , 2013, 58, 840-842.	1.8	4
121	Spatial Aspects of HIV Infection. <i>Lecture Notes on Mathematical Modelling in the Life Sciences</i> , 2013, , 3-31.	0.1	10
122	Modeling shows that the NS5A inhibitor daclatasvir has two modes of action and yields a shorter estimate of the hepatitis C virus half-life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3991-3996.	3.3	298
123	Towards multiscale modeling of influenza infection. <i>Journal of Theoretical Biology</i> , 2013, 332, 267-290.	0.8	63
124	Modeling sequence evolution in HIV-1 infection with recombination. <i>Journal of Theoretical Biology</i> , 2013, 329, 82-93.	0.8	9
125	Mathematical modeling of escape of HIV from cytotoxic T lymphocyte responses. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013, 2013, P01010.	0.9	38
126	Mathematical analysis of multiscale models for hepatitis C virus dynamics under therapy with direct-acting antiviral agents. <i>Mathematical Biosciences</i> , 2013, 245, 22-30.	0.9	45

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127	Kinetics of Coinfection with Influenza A Virus and Streptococcus pneumoniae. PLoS Pathogens, 2013, 9, e1003238.	2.1	184
128	Inferring HIV Escape Rates from Multi-Locus Genotype Data. Frontiers in Immunology, 2013, 4, 252.	2.2	35
129	The hepatitis C virus NS5A inhibitor daclatasvir has a dual mode of action and leads to a new virus half-life estimate. Expert Review of Gastroenterology and Hepatology, 2013, 7, 397-399.	1.4	14
130	Antigen-Stimulated CD4 T Cell Expansion Can Be Limited by Their Grazing of Peptide-MHC Complexes. Journal of Immunology, 2013, 190, 5454-5458.	0.4	12
131	Modeling the Acute and Chronic Phases of Theiler Murine Encephalomyelitis Virus Infection. Journal of Virology, 2013, 87, 4052-4059.	1.5	15
132	Contribution of Follicular Dendritic Cells to Persistent HIV Viremia. Journal of Virology, 2013, 87, 7893-7901.	1.5	29
133	Vertical T cell immunodominance and epitope entropy determine HIV-1 escape. Journal of Clinical Investigation, 2013, 123, 380-93.	3.9	165
134	Analysis of Hepatitis C Virus Decline during Treatment with the Protease Inhibitor Danoprevir Using a Multiscale Model. PLoS Computational Biology, 2013, 9, e1002959.	1.5	83
135	Quantifying the Diversification of Hepatitis C Virus (HCV) during Primary Infection: Estimates of the In Vivo Mutation Rate. PLoS Pathogens, 2012, 8, e1002881.	2.1	139
136	Modeling Within-Host Dynamics of Influenza Virus Infection Including Immune Responses. PLoS Computational Biology, 2012, 8, e1002588.	1.5	223
137	Early Low-Titer Neutralizing Antibodies Impede HIV-1 Replication and Select for Virus Escape. PLoS Pathogens, 2012, 8, e1002721.	2.1	159
138	Elucidation of Hepatitis C Virus Transmission and Early Diversification by Single Genome Sequencing. PLoS Pathogens, 2012, 8, e1002880.	2.1	74
139	Modelling deuterium labelling of lymphocytes with temporal and/or kinetic heterogeneity. Journal of the Royal Society Interface, 2012, 9, 2191-2200.	1.5	22
140	Dominance of the CD4+ T helper cell response during acute resolving hepatitis A virus infection. Journal of Experimental Medicine, 2012, 209, 1481-1492.	4.2	79
141	Combination Antiviral Therapy for Influenza: Predictions From Modeling of Human Infections. Journal of Infectious Diseases, 2012, 205, 1642-1645.	1.9	59
142	Dynamics of CD4+ T Cell Responses against <i>Listeria monocytogenes</i> . Journal of Immunology, 2012, 189, 5250-5256.	0.4	7
143	Precise Determination of Time to Reach Viral Load Set Point After Acute HIV-1 Infection. Journal of Acquired Immune Deficiency Syndromes (1999), 2012, 61, 448-454.	0.9	28
144	Mathematical modelling of HCV infection: what can it teach us in the era of direct-acting antiviral agents?. Antiviral Therapy, 2012, 17, 1171-1182.	0.6	58

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145	Understanding silibinin's modes of action against HCV using viral kinetic modeling. <i>Journal of Hepatology</i> , 2012, 56, 1019-1024.	1.8	47
146	Impact of immune escape mutations on HIV-1 fitness in the context of the cognate transmitted/founder genome. <i>Retrovirology</i> , 2012, 9, 89.	0.9	50
147	Modeling and Simulation of Aggregation of Membrane Protein LAT with Molecular Variability in the Number of Binding Sites for Cytosolic Grb2-SOS1-Grb2. <i>PLoS ONE</i> , 2012, 7, e28758.	1.1	18
148	Spontaneous Clearance of Viral Infections by Mesoscopic Fluctuations. <i>PLoS ONE</i> , 2012, 7, e38549.	1.1	9
149	Modeling Quasispecies and Drug Resistance in Hepatitis C Patients Treated with a Protease Inhibitor. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 1789-1817.	0.9	38
150	Hepatitis C viral kinetics with the nucleoside polymerase inhibitor mericitabine (RG7128). <i>Hepatology</i> , 2012, 55, 1030-1037.	3.6	51
151	Immediate antiviral therapy appears to restrict resting CD4 ⁺ cell HIV-1 infection without accelerating the decay of latent infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9523-9528.	3.3	202
152	Evaluation of Multitype Mathematical Models for CFSE-Labeling Experiment Data. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 300-326.	0.9	28
153	Stochastic Theory of Early Viral Infection: Continuous versus Burst Production of Virions. <i>PLoS Computational Biology</i> , 2011, 7, e1001058.	1.5	114
154	On Identifiability of Nonlinear ODE Models and Applications in Viral Dynamics. <i>SIAM Review</i> , 2011, 53, 3-39.	4.2	412
155	Triple Combination Antiviral Drug (TCAD) Composed of Amantadine, Oseltamivir, and Ribavirin Impedes the Selection of Drug-Resistant Influenza A Virus. <i>PLoS ONE</i> , 2011, 6, e29778.	1.1	48
156	Designing a genome-based HIV incidence assay with high sensitivity and specificity. <i>Aids</i> , 2011, 25, F13-F19.	1.0	39
157	Hepatitis C Viral Kinetics in the Era of Direct Acting Antiviral Agents and Interleukin-28B. <i>Current Hepatitis Reports</i> , 2011, 10, 214-227.	0.3	52
158	Influenza A virus infection kinetics: quantitative data and models. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 429-445.	6.6	136
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