

Alun L Lloyd

List of Publications by Year in descending order

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112
papers

10,744
citations

61984

43
h-index

34986

98
g-index

128
all docs

128
docs citations

128
times ranked

10522
citing authors

#	ARTICLE	IF	CITATIONS
1	Presence of an inducible HIV-1 latent reservoir during highly active antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 13193-13197.	7.1	1,786
2	The wMel Wolbachia strain blocks dengue and invades caged <i>Aedes aegypti</i> populations. <i>Nature</i> , 2011, 476, 450-453.	27.8	1,092
3	Infection dynamics on scale-free networks. <i>Physical Review E</i> , 2001, 64, 066112.	2.1	603
4	EPIDEMIOLOGY: How Viruses Spread Among Computers and People. <i>Science</i> , 2001, 292, 1316-1317.	12.6	558
5	Modeling infectious disease dynamics in the complex landscape of global health. <i>Science</i> , 2015, 347, aaa4339.	12.6	492
6	HLA alleles determine human T-lymphotropic virus-I (HTLV-I) proviral load and the risk of HTLV-I-associated myelopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 3848-3853.	7.1	393
7	Realistic Distributions of Infectious Periods in Epidemic Models: Changing Patterns of Persistence and Dynamics. <i>Theoretical Population Biology</i> , 2001, 60, 59-71.	1.1	314
8	A systematic review of mathematical models of mosquito-borne pathogen transmission: 1970–2010. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20120921.	3.4	306
9	Spatial Heterogeneity in Epidemic Models. <i>Journal of Theoretical Biology</i> , 1996, 179, 1-11.	1.7	269
10	Viral dynamics of primary viremia and antiretroviral therapy in simian immunodeficiency virus infection. <i>Journal of Virology</i> , 1997, 71, 7518-7525.	3.4	263
11	The Influence of HLA Class I Alleles and Heterozygosity on the Outcome of Human T Cell Lymphotropic Virus Type I Infection. <i>Journal of Immunology</i> , 2000, 165, 7278-7284.	0.8	199
12	The coupled logistic map: a simple model for the effects of spatial heterogeneity on population dynamics. <i>Journal of Theoretical Biology</i> , 1995, 173, 217-230.	1.7	144
13	Recasting the theory of mosquito-borne pathogen transmission dynamics and control. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2014, 108, 185-197.	1.8	142
14	Skeeter Buster: A Stochastic, Spatially Explicit Modeling Tool for Studying <i>Aedes aegypti</i> Population Replacement and Population Suppression Strategies. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e508.	3.0	141
15	Graph fission in an evolving voter model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3682-3687.	7.1	123
16	Contributions from the silent majority dominate dengue virus transmission. <i>PLoS Pathogens</i> , 2018, 14, e1006965.	4.7	118
17	Spatiotemporal dynamics of epidemics: synchrony in metapopulation models. <i>Mathematical Biosciences</i> , 2004, 188, 1-16.	1.9	116
18	A global assembly of adult female mosquito mark-release-recapture data to inform the control of mosquito-borne pathogens. <i>Parasites and Vectors</i> , 2014, 7, 276.	2.5	116

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19	Nine challenges for deterministic epidemic models. <i>Epidemics</i> , 2015, 10, 49-53.	3.0	112
20	Key questions for modelling COVID-19 exit strategies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201405.	2.6	106
21	On the Seasonal Occurrence and Abundance of the Zika Virus Vector Mosquito <i>Aedes Aegypti</i> in the Contiguous United States. <i>PLOS Currents</i> , 2016, 8, .	1.4	106
22	Time-varying, serotype-specific force of infection of dengue virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2694-702.	7.1	105
23	Density-Dependent Intraspecific Competition in the Larval Stage of <i>Aedes aegypti</i> (Diptera: Tj ETQq1 1 0.784314 rgBT/Overload	1.8	102
24	Bidirectional contact tracing could dramatically improve COVID-19 control. <i>Nature Communications</i> , 2021, 12, 232.	12.8	100
25	The estimation of the effective reproductive number from disease outbreak data. <i>Mathematical Biosciences and Engineering</i> , 2009, 6, 261-282.	1.9	98
26	Local stability analysis of spatially homogeneous solutions of multi-patch systems. <i>Journal of Mathematical Biology</i> , 2000, 41, 232-252.	1.9	95
27	Invasion and migration of spatially self-limiting gene drives: A comparative analysis. <i>Evolutionary Applications</i> , 2018, 11, 794-808.	3.1	91
28	A Killer "Rescue system for self-limiting gene drive of anti-pathogen constructs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 2823-2829.	2.6	89
29	Optimal two-phase vaccine allocation to geographically different regions under uncertainty. <i>European Journal of Operational Research</i> , 2014, 233, 208-219.	5.7	87
30	Polygenic Control of Human T Lymphotropic Virus Type I (HTLV-1) Provirus Load and the Risk of HTLV-1 Associated Myelopathy/Tropical Spastic Paraparesis. <i>Journal of Infectious Diseases</i> , 2002, 186, 932-939.	4.0	85
31	Direct quantitation of rapid elimination of viral antigen-positive lymphocytes by antiviral CD8+ T cells in vivo. <i>European Journal of Immunology</i> , 2000, 30, 1356-1363.	2.9	78
32	Stochasticity and heterogeneity in host-vector models. <i>Journal of the Royal Society Interface</i> , 2007, 4, 851-863.	3.4	76
33	Dynamics of Macrophage and T Cell Infection by HIV. <i>Journal of Theoretical Biology</i> , 1999, 196, 101-113.	1.7	74
34	A sensitivity matrix based methodology for inverse problem formulation. <i>Journal of Inverse and Ill-Posed Problems</i> , 2009, 17, .	1.0	73
35	Evaluating strategies for reversing CRISPR-Cas9 gene drives. <i>Scientific Reports</i> , 2017, 7, 11038.	3.3	73
36	Field Cage Studies and Progressive Evaluation of Genetically-Engineered Mosquitoes. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2001.	3.0	68

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37	MEDEA SELFISH GENETIC ELEMENTS AS TOOLS FOR ALTERING TRAITS OF WILD POPULATIONS: A THEORETICAL ANALYSIS. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1149-1162.	2.3	66
38	Parameter estimation and uncertainty quantification for an epidemic model. <i>Mathematical Biosciences and Engineering</i> , 2012, 9, 553-576.	1.9	64
39	Estimating variability in models for recurrent epidemics: assessing the use of moment closure techniques. <i>Theoretical Population Biology</i> , 2004, 65, 49-65.	1.1	61
40	Hypothesis: the central oscillator of the circadian clock is a controlled chaotic attractor. <i>BioSystems</i> , 1993, 29, 77-85.	2.0	59
41	Chaos : Its significance and detection in biology. <i>Biological Rhythm Research</i> , 1995, 26, 233-252.	0.9	56
42	Gene drive into insect populations with age and spatial structure: a theoretical assessment. <i>Evolutionary Applications</i> , 2011, 4, 415-428.	3.1	55
43	Polymorphism in the Interleukin-10 Promoter Affects Both Provirus Load and the Risk of Human T Lymphotropic Virus Type 1-Associated Myelopathy/Tropical Spastic Paraparesis. <i>Journal of Infectious Diseases</i> , 2004, 190, 1279-1285.	4.0	52
44	Locally Fixed Alleles: A method to localize gene drive to island populations. <i>Scientific Reports</i> , 2019, 9, 15821.	3.3	52
45	A simple relationship between viral load and survival time in HIV-1 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11549-11553.	7.1	49
46	Developmental timing of mutations revealed by whole-genome sequencing of twins with acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7429-7433.	7.1	49
47	Tethered homing gene drives: A new design for spatially restricted population replacement and suppression. <i>Evolutionary Applications</i> , 2019, 12, 1688-1702.	3.1	49
48	Resolving the impact of waiting time distributions on the persistence of measles. <i>Journal of the Royal Society Interface</i> , 2010, 7, 623-640.	3.4	48
49	Efficacy of <i>Aedes aegypti</i> control by indoor Ultra Low Volume (ULV) insecticide spraying in Iquitos, Peru. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006378.	3.0	46
50	Five challenges for stochastic epidemic models involving global transmission. <i>Epidemics</i> , 2015, 10, 54-57.	3.0	44
51	Gene Drive Dynamics in Natural Populations: The Importance of Density Dependence, Space, and Sex. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2020, 51, 505-531.	8.3	44
52	A Model for Estimating Total Parasite Load in <i>Falciparum Malaria</i> Patients. <i>Journal of Theoretical Biology</i> , 2002, 217, 137-148.	1.7	43
53	Seven challenges for modelling indirect transmission: Vector-borne diseases, macroparasites and neglected tropical diseases. <i>Epidemics</i> , 2015, 10, 16-20.	3.0	43
54	Quantitative Models for Germination and Infection of <i>Pseudoperonospora cubensis</i> in Response to Temperature and Duration of Leaf Wetness. <i>Phytopathology</i> , 2010, 100, 959-967.	2.2	42

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55	Understanding Uncertainties in Model-Based Predictions of <i>Aedes aegypti</i> Population Dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e830.	3.0	41
56	Coupled Heterogeneities and Their Impact on Parasite Transmission and Control. <i>Trends in Parasitology</i> , 2016, 32, 356-367.	3.3	41
57	Synchronicity, chaos and population cycles: spatial coherence in an uncertain world. <i>Trends in Ecology and Evolution</i> , 1999, 14, 417-418.	8.7	39
58	INTRODUCING DESIRABLE TRANSGENES INTO INSECT POPULATIONS USING Y-LINKED MEIOTIC DRIVE? A THEORETICAL ASSESSMENT. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 717-726.	2.3	39
59	Rodent gene drives for conservation: opportunities and data needs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191606.	2.6	38
60	Hybrid modeling and prediction of dynamical systems. <i>PLoS Computational Biology</i> , 2017, 13, e1005655.	3.2	37
61	Seven challenges for model-driven data collection in experimental and observational studies. <i>Epidemics</i> , 2015, 10, 78-82.	3.0	35
62	Immune responses and the emergence of drug-resistant virus strains <i>in vivo</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 1101-1109.	2.6	32
63	Computing Bouts of the Prisoner's Dilemma. <i>Scientific American</i> , 1995, 272, 110-115.	1.0	31
64	Regulation of <i>Aedes aegypti</i> Population Dynamics in Field Systems: Quantifying Direct and Delayed Density Dependence. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 68-77.	1.4	31
65	Assessing the Feasibility of Controlling <i>Aedes aegypti</i> with Transgenic Methods: A Model-Based Evaluation. <i>PLoS ONE</i> , 2012, 7, e52235.	2.5	30
66	A Reduce and Replace Strategy for Suppressing Vector-Borne Diseases: Insights from a Deterministic Model. <i>PLoS ONE</i> , 2013, 8, e73233.	2.5	30
67	A Reduce and Replace Strategy for Suppressing Vector-Borne Diseases: Insights from a Stochastic, Spatial Model. <i>PLoS ONE</i> , 2013, 8, e81860.	2.5	30
68	Stochastic and deterministic models for agricultural production networks. <i>Mathematical Biosciences and Engineering</i> , 2007, 4, 373-402.	1.9	28
69	The cell division cycle: a physiologically plausible dynamic model can exhibit chaotic solutions. <i>BioSystems</i> , 1992, 27, 17-24.	2.0	27
70	Reply to: Models for the in-host dynamics of malaria revisited: errors in some basic models lead to large over-estimates of growth rates. <i>Parasitology</i> , 1998, 117, 409-410.	1.5	27
71	Viral Substitution Rate Variation Can Arise from the Interplay between Within-Host and Epidemiological Dynamics. <i>American Naturalist</i> , 2013, 182, 494-513.	2.1	27
72	Optimizing the deployment of ultra-low volume and targeted indoor residual spraying for dengue outbreak response. <i>PLoS Computational Biology</i> , 2020, 16, e1007743.	3.2	27

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73	Gene-drive in age-structured insect populations. <i>Evolutionary Applications</i> , 2009, 2, 143-159.	3.1	26
74	Introducing transgenes into insect populations using combined gene-drive strategies: Modeling and analysis. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 1054-1063.	2.7	24
75	Evaluation of Location-Specific Predictions by a Detailed Simulation Model of <i>Aedes aegypti</i> Populations. <i>PLoS ONE</i> , 2011, 6, e22701.	2.5	24
76	Comparison of two detailed models of <i>Aedes aegypti</i> population dynamics. <i>Ecosphere</i> , 2016, 7, e01515.	2.2	22
77	Developing Predictive Approaches to Characterize Adaptive Responses of the Reproductive Endocrine Axis to Aromatase Inhibition: II. Computational Modeling. <i>Toxicological Sciences</i> , 2013, 133, 234-247.	3.1	19
78	Disease-driven reduction in human mobility influences human-mosquito contacts and dengue transmission dynamics. <i>PLoS Computational Biology</i> , 2021, 17, e1008627.	3.2	19
79	Feasible Introgression of an Anti-pathogen Transgene into an Urban Mosquito Population without Using Gene-Drive. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2827.	3.0	18
80	Population genomics of invasive rodents on islands: Genetic consequences of colonization and prospects for localized synthetic gene drive. <i>Evolutionary Applications</i> , 2021, 14, 1421-1435.	3.1	18
81	Modeling the Dynamics of a Non-Limited and a Self-Limited Gene Drive System in Structured <i>Aedes aegypti</i> Populations. <i>PLoS ONE</i> , 2013, 8, e83354.	2.5	18
82	<i>Plasmodium knowlesi</i> invasion following spread by infected mosquitoes, macaques and humans. <i>Parasitology</i> , 2018, 145, 101-110.	1.5	17
83	Disease control across urban-rural gradients. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200775.	3.4	16
84	Network models in epidemiology: an overview. <i>World Scientific Lecture Notes in Complex Systems</i> , 2007, , 189-214.	0.1	16
85	Rapid evolution of knockdown resistance haplotypes in response to pyrethroid selection in <i>Aedes aegypti</i> . <i>Evolutionary Applications</i> , 2021, 14, 2098-2113.	3.1	14
86	Integrating Transgenic Vector Manipulation with Clinical Interventions to Manage Vector-Borne Diseases. <i>PLoS Computational Biology</i> , 2016, 12, e1004695.	3.2	12
87	Mechanistic Computational Model of Steroidogenesis in H295R Cells: Role of Oxysterols and Cell Proliferation to Improve Predictability of Biochemical Response to Endocrine Active Chemical-Metyrapone. <i>Toxicological Sciences</i> , 2011, 123, 80-93.	3.1	11
88	Antipathogen genes and the replacement of disease-vectoring mosquito populations: a model-based evaluation. <i>Evolutionary Applications</i> , 2014, 7, 1238-1251.	3.1	11
89	An approach to periodic, time-varying parameter estimation using nonlinear filtering. <i>Inverse Problems</i> , 2018, 34, 105005.	2.0	11
90	Fluctuations in HIV-1 Viral Load Are Correlated to CD4+ T-Lymphocyte Count During the Natural Course of Infection. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2000, 23, 375-379.	2.1	10

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91	Mathematical Models as Aids for Design and Development of Experiments: The Case of Transgenic Mosquitoes. <i>Journal of Medical Entomology</i> , 2012, 49, 1177-1188.	1.8	10
92	Embracing Dynamic Models for Gene Drive Management. <i>Trends in Biotechnology</i> , 2021, 39, 211-214.	9.3	10
93	After the honeymoon, the divorce: Unexpected outcomes of disease control measures against endemic infections. <i>PLoS Computational Biology</i> , 2020, 16, e1008292.	3.2	8
94	Mathematical modeling of genetic pest management through female-specific lethality: Is one locus better than two?. <i>Evolutionary Applications</i> , 2021, 14, 1612-1622.	3.1	7
95	Chaos and forecasting. <i>Trends in Ecology and Evolution</i> , 1994, 9, 244-245.	8.7	6
96	Geographic disparities and predictors of COVID-19 hospitalization risks in the St. Louis Area, Missouri (USA). <i>BMC Public Health</i> , 2022, 22, 321.	2.9	6
97	Dynamical behavior of an epidemiological model with a demographic Allee effect. <i>Mathematics and Computers in Simulation</i> , 2017, 133, 311-325.	4.4	5
98	Adaptive filtering for hidden node detection and tracking in networks. <i>Chaos</i> , 2017, 27, 073106.	2.5	5
99	Hypothesis: a controlled chaotic attractor constitutes the central oscillator of the circadian clock. <i>Biochemical Society Transactions</i> , 1994, 22, 322S-322S.	3.4	3
100	Fluctuations in HIV-1 Viral Load Are Correlated to CD4+ T-Lymphocyte Count During the Natural Course of Infection. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2000, 23, 375-379.	2.1	3
101	Computational model of the fathead minnow hypothalamic-pituitary-gonadal axis: Incorporating protein synthesis in improving predictability of responses to endocrine active chemicals. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2016, 183-184, 36-45.	2.6	3
102	The basic reproductive number for disease systems with multiple coupled heterogeneities. <i>Mathematical Biosciences</i> , 2020, 321, 108294.	1.9	3
103	Linear filters and nonlinear forecasting. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1994, 256, 157-161.	2.6	2
104	Drug resistance in acute viral infections: Rhinovirus as a case study. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2006, , 193-212.	0.0	2
105	Pest management by genetic addiction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5849-5851.	7.1	1
106	The feasibility of targeted test-trace-isolate for the control of SARS-CoV-2 variants. <i>F1000Research</i> , 0, 10, 291.	1.6	1
107	An inexpensive infrared growth sensor array for detection of bacterial antibiotic susceptibility. <i>FEMS Microbiology Letters</i> , 1993, 111, 251-254.	1.8	0
108	Title is missing!. , 2020, 16, e1007743.		0

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109	Title is missing!. , 2020, 16, e1007743.		0
110	Title is missing!. , 2020, 16, e1007743.		0
111	Title is missing!. , 2020, 16, e1007743.		0
112	An inexpensive infrared growth sensor array for detection of bacterial antibiotic susceptibility. FEMS Microbiology Letters, 1993, 111, 251-254.	1.8	0