Alun L Lloyd

List of Publications by Year
in descending order

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111

papers

10,744

citations

71004

43

h-index

39744

98

g-index

128

all docs

128

docs citations

128

times ranked

11677

citing authors

#	ARTICLE	IF	CITATIONS
1	Geographic disparities and predictors of COVID-19 hospitalization risks in the St. Louis Area, Missouri (USA). BMC Public Health, 2022, 22, 321.	1.2	6
2	Embracing Dynamic Models for Gene Drive Management. Trends in Biotechnology, 2021, 39, 211-214.	4.9	10
3	Population genomics of invasive rodents on islands: Genetic consequences of colonization and prospects for localized synthetic gene drive. Evolutionary Applications, 2021, 14, 1421-1435.	1.5	18
4	Mathematical modeling of genetic pest management through femaleâ€•specific lethality: Is one locus better than two?. Evolutionary Applications, 2021, 14, 1612-1622.	1.5	7
5	Rapid evolution of knockdown resistance haplotypes in response to pyrethroid selection in <i>Aedes aegypti</i>. Evolutionary Applications, 2021, 14, 2098-2113.	1.5	14
6	Bidirectional contact tracing could dramatically improve COVID-19 control. Nature Communications, 2021, 12, 232.	5.8	100
7	Disease-driven reduction in human mobility influences human-mosquito contacts and dengue transmission dynamics. PLoS Computational Biology, 2021, 17, e1008627.	1.5	19
8	The basic reproductive number for disease systems with multiple coupled heterogeneities. Mathematical Biosciences, 2020, 321, 108294.	0.9	3
9	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	1.2	106
10	Gene Drive Dynamics in Natural Populations: The Importance of Density Dependence, Space, and Sex. Annual Review of Ecology, Evolution, and Systematics, 2020, 51, 505-531.	3.8	44
11	Optimizing the deployment of ultra-low volume and targeted indoor residual spraying for dengue outbreak response. PLoS Computational Biology, 2020, 16, e1007743.	1.5	27
12	Disease control across urbanâ€“rural gradients. Journal of the Royal Society Interface, 2020, 17, 20200775.	1.5	16
13	After the honeymoon, the divorce: Unexpected outcomes of disease control measures against endemic infections. PLoS Computational Biology, 2020, 16, e1008292.	1.5	8
14	Title is missing!. , 2020, 16, e1007743.		0
15	Title is missing!. , 2020, 16, e1007743.		0
16	Title is missing!. , 2020, 16, e1007743.		0
17	Title is missing!. , 2020, 16, e1007743.		0
18	Rodent gene drives for conservation: opportunities and data needs. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191606.	1.2	38

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19	Tethered homing gene drives: A new design for spatially restricted population replacement and suppression. Evolutionary Applications, 2019, 12, 1688-1702.	1.5	49
20	Pest management by genetic addiction. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5849-5851.	3.3	1
21	Locally Fixed Alleles: A method to localize gene drive to island populations. Scientific Reports, 2019, 9, 15821.	1.6	52
22	Invasion and migration of spatially selfâ€limiting gene drives: A comparative analysis. Evolutionary Applications, 2018, 11, 794-808.	1.5	91
23	Plasmodium knowlesi invasion following spread by infected mosquitoes, macaques and humans. Parasitology, 2018, 145, 101-110.	0.7	17
24	Efficacy of Aedes aegypti control by indoor Ultra Low Volume (ULV) insecticide spraying in Iquitos, Peru. PLoS Neglected Tropical Diseases, 2018, 12, e0006378.	1.3	46
25	An approach to periodic, time-varying parameter estimation using nonlinear filtering. Inverse Problems, 2018, 34, 105005.	1.0	11
26	Contributions from the silent majority dominate dengue virus transmission. PLoS Pathogens, 2018, 14, e1006965.	2.1	118
27	Dynamical behavior of an epidemiological model with a demographic Allee effect. Mathematics and Computers in Simulation, 2017, 133, 311-325.	2.4	5
28	Evaluating strategies for reversing CRISPR-Cas9 gene drives. Scientific Reports, 2017, 7, 11038.	1.6	73
29	Adaptive filtering for hidden node detection and tracking in networks. Chaos, 2017, 27, 073106.	1.0	5
30	Hybrid modeling and prediction of dynamical systems. PLoS Computational Biology, 2017, 13, e1005655.	1.5	37
31	Computational model of the fathead minnow hypothalamicâ€"pituitaryâ€"gonadal axis: Incorporating protein synthesis in improving predictability of responses to endocrine active chemicals. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2016, 183-184, 36-45.	1.3	3
32	Comparison of two detailed models of <i>Aedes aegypti</i> population dynamics. Ecosphere, 2016, 7, e01515.	1.0	22
33	Coupled Heterogeneities and Their Impact on Parasite Transmission and Control. Trends in Parasitology, 2016, 32, 356-367.	1.5	41
34	On the Seasonal Occurrence and Abundance of the Zika Virus Vector Mosquito Aedes Aegypti in the Contiguous United States. PLOS Currents, 2016, 8, .	1.4	106
35	Integrating Transgenic Vector Manipulation with Clinical Interventions to Manage Vector-Borne Diseases. PLoS Computational Biology, 2016, 12, e1004695.	1.5	12
36	Nine challenges for deterministic epidemic models. Epidemics, 2015, 10, 49-53.	1.5	112

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37	Modeling infectious disease dynamics in the complex landscape of global health. Science, 2015, 347, aaa4339.	6.0	492
38	Seven challenges for modelling indirect transmission: Vector-borne diseases, macroparasites and neglected tropical diseases. Epidemics, 2015, 10, 16-20.	1.5	43
39	Seven challenges for model-driven data collection in experimental and observational studies. Epidemics, 2015, 10, 78-82.	1.5	35
40	Five challenges for stochastic epidemic models involving global transmission. Epidemics, 2015, 10, 54-57.	1.5	44
41	Feasible Introgression of an Anti-pathogen Transgene into an Urban Mosquito Population without Using Gene-Drive. PLoS Neglected Tropical Diseases, 2014, 8, e2827.	1.3	18
42	Recasting the theory of mosquito-borne pathogen transmission dynamics and control. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2014, 108, 185-197.	0.7	142
43	Antipathogen genes and the replacement of diseaseâ€vectoring mosquito populations: a modelâ€based evaluation. Evolutionary Applications, 2014, 7, 1238-1251.	1.5	11
44	A global assembly of adult female mosquito mark-release-recapture data to inform the control of mosquito-borne pathogens. Parasites and Vectors, 2014, 7, 276.	1.0	116
45	Optimal two-phase vaccine allocation to geographically different regions under uncertainty. European Journal of Operational Research, 2014, 233, 208-219.	3.5	87
46	Time-varying, serotype-specific force of infection of dengue virus. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2694-702.	3.3	105
47	Viral Substitution Rate Variation Can Arise from the Interplay between Within-Host and Epidemiological Dynamics. American Naturalist, 2013, 182, 494-513.	1.0	27
48	A systematic review of mathematical models of mosquito-borne pathogen transmission: 1970â€“2010. Journal of the Royal Society Interface, 2013, 10, 20120921.	1.5	306
49	Regulation of Aedes aegypti Population Dynamics in Field Systems: Quantifying Direct and Delayed Density Dependence. American Journal of Tropical Medicine and Hygiene, 2013, 89, 68-77.	0.6	31
50	Developmental timing of mutations revealed by whole-genome sequencing of twins with acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7429-7433.	3.3	49
51	Developing Predictive Approaches to Characterize Adaptive Responses of the Reproductive Endocrine Axis to Aromatase Inhibition: II. Computational Modeling. Toxicological Sciences, 2013, 133, 234-247.	1.4	19
52	A Reduce and Replace Strategy for Suppressing Vector-Borne Diseases: Insights from a Deterministic Model. PLoS ONE, 2013, 8, e73233.	1.1	30
53	A Reduce and Replace Strategy for Suppressing Vector-Borne Diseases: Insights from a Stochastic, Spatial Model. PLoS ONE, 2013, 8, e81860.	1.1	30
54	Field Cage Studies and Progressive Evaluation of Genetically-Engineered Mosquitoes. PLoS Neglected Tropical Diseases, 2013, 7, e2001.	1.3	68

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55	Modeling the Dynamics of a Non-Limited and a Self-Limited Gene Drive System in Structured Aedes aegypti Populations. PLoS ONE, 2013, 8, e83354.	1.1	18
56	Mathematical Models as Aids for Design and Development of Experiments: The Case of Transgenic Mosquitoes. Journal of Medical Entomology, 2012, 49, 1177-1188.	0.9	10
57	Graph fission in an evolving voter model. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3682-3687.	3.3	123
58	Assessing the Feasibility of Controlling Aedes aegypti with Transgenic Methods: A Model-Based Evaluation. PLoS ONE, 2012, 7, e52235.	1.1	30
59	Parameter estimation and uncertainty quantification for an epidemic model. Mathematical Biosciences and Engineering, 2012, 9, 553-576.	1.0	64
60	Evaluation of Location-Specific Predictions by a Detailed Simulation Model of Aedes aegypti Populations. PLoS ONE, 2011, 6, e22701.	1.1	24
61	MEDEA SELFISH GENETIC ELEMENTS AS TOOLS FOR ALTERING TRAITS OF WILD POPULATIONS: A THEORETICAL ANALYSIS. Evolution; International Journal of Organic Evolution, 2011, 65, 1149-1162.	1.1	66
62	Geneâ€drive into insect populations with age and spatial structure: a theoretical assessment. Evolutionary Applications, 2011, 4, 415-428.	1.5	55
63	The wMel Wolbachia strain blocks dengue and invades caged Aedes aegypti populations. Nature, 2011, 476, 450-453.	13.7	1,092
64	Mechanistic Computational Model of Steroidogenesis in H295R Cells: Role of Oxysterols and Cell Proliferation to Improve Predictability of Biochemical Response to Endocrine Active Chemicalâ€"Metyrapone. Toxicological Sciences, 2011, 123, 80-93.	1.4	11
65	Quantitative Models for Germination and Infection of Pseudoperonospora cubensis in Response to Temperature and Duration of Leaf Wetness. Phytopathology, 2010, 100, 959-967.	1.1	42
66	Resolving the impact of waiting time distributions on the persistence of measles. Journal of the Royal Society Interface, 2010, 7, 623-640.	1.5	48
67	Understanding Uncertainties in Model-Based Predictions of Aedes aegypti Population Dynamics. PLoS Neglected Tropical Diseases, 2010, 4, e830.	1.3	41
68	A sensitivity matrix based methodology for inverse problem formulation. Journal of Inverse and Ill-Posed Problems, 2009, 17, .	0.5	73
69	Density-Dependent Intraspecific Competition in the Larval Stage of<i>Aedes aegypti</i>(Diptera:) Tj ETQq1 1 0.784314 rgBT /Overloc	0.9	102
70	Skeeter Buster: A Stochastic, Spatially Explicit Modeling Tool for Studying Aedes aegypti Population Replacement and Population Suppression Strategies. PLoS Neglected Tropical Diseases, 2009, 3, e508.	1.3	141
71	Geneâ€drive in ageâ€structured insect populations. Evolutionary Applications, 2009, 2, 143-159.	1.5	26
72	The estimation of the effective reproductive number from disease outbreak data. Mathematical Biosciences and Engineering, 2009, 6, 261-282.	1.0	98

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73	A Killerâ€“Rescue system for self-limiting gene drive of anti-pathogen constructs. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 2823-2829.	1.2	89
74	Introducing transgenes into insect populations using combined gene-drive strategies: Modeling and analysis. Insect Biochemistry and Molecular Biology, 2007, 37, 1054-1063.	1.2	24
75	Stochasticity and heterogeneity in hostâ€“vector models. Journal of the Royal Society Interface, 2007, 4, 851-863.	1.5	76
76	INTRODUCING DESIRABLE TRANSGENES INTO INSECT POPULATIONS USING Y-LINKED MEIOTIC DRIVE?A THEORETICAL ASSESSMENT. Evolution; International Journal of Organic Evolution, 2007, 61, 717-726.	1.1	39
77	Network models in epidemiology: an overview. World Scientific Lecture Notes in Complex Systems, 2007, , 189-214.	0.1	16
78	Stochastic and deterministic models for agricultural production networks. Mathematical Biosciences and Engineering, 2007, 4, 373-402.	1.0	28
79	Drug resistance in acute viral infections: Rhinovirus as a case study. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 2006, , 193-212.	0.0	2
80	Immune responses and the emergence of drugâ€“resistant virus strainsin vivo. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 1101-1109.	1.2	32
81	Polymorphism in the Interleukinâ€10 Promoter Affects Both Provirus Load and the Risk of Human T Lymphotropic Virus Type Iâ€“Associated Myelopathy/Tropical Spastic Paraparesis. Journal of Infectious Diseases, 2004, 190, 1279-1285.	1.9	52
82	Estimating variability in models for recurrent epidemics: assessing the use of moment closure techniques. Theoretical Population Biology, 2004, 65, 49-65.	0.5	61
83	Spatiotemporal dynamics of epidemics: synchrony in metapopulation models. Mathematical Biosciences, 2004, 188, 1-16.	0.9	116
84	Polygenic Control of Human T Lymphotropic Virus Type I (HTLVâ€I) Provirus Load and the Risk of HTLVâ€Iâ€“Associated Myelopathy/Tropical Spastic Paraparesis. Journal of Infectious Diseases, 2002, 186, 932-939.	1.9	85
85	A Model for Estimating Total Parasite Load in Falciparum Malaria Patients. Journal of Theoretical Biology, 2002, 217, 137-148.	0.8	43
86	Infection dynamics on scale-free networks. Physical Review E, 2001, 64, 066112.	0.8	603
87	Realistic Distributions of Infectious Periods in Epidemic Models: Changing Patterns of Persistence and Dynamics. Theoretical Population Biology, 2001, 60, 59-71.	0.5	314
88	EPIDEMIOLOGY: How Viruses Spread Among Computers and People. Science, 2001, 292, 1316-1317.	6.0	558
89	Fluctuations in HIV-1 Viral Load Are Correlated to CD4+ T-Lymphocyte Count During the Natural Course of Infection. Journal of Acquired Immune Deficiency Syndromes (1999), 2000, 23, 375-379.	0.9	3
90	Fluctuations in HIV-1 Viral Load Are Correlated to CD4+ T-Lymphocyte Count During the Natural Course of Infection. Journal of Acquired Immune Deficiency Syndromes (1999), 2000, 23, 375-379.	0.9	10

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91	Direct quantitation of rapid elimination of viral antigen-positive lymphocytes by antiviral CD8+ T cellsin vivo. European Journal of Immunology, 2000, 30, 1356-1363.	1.6	78
92	Local stability analysis of spatially homogeneous solutions of multi-patch systems. Journal of Mathematical Biology, 2000, 41, 232-252.	0.8	95
93	The Influence of HLA Class I Alleles and Heterozygosity on the Outcome of Human T Cell Lymphotropic Virus Type I Infection. Journal of Immunology, 2000, 165, 7278-7284.	0.4	199
94	HLA alleles determine human T-lymphotropic virus-I (HTLV-I) proviral load and the risk of HTLV-I-associated myelopathy. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 3848-3853.	3.3	393
95	A simple relationship between viral load and survival time in HIV-1 infection. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11549-11553.	3.3	49
96	Dynamics of Macrophage and T Cell Infection by HIV. Journal of Theoretical Biology, 1999, 196, 101-113.	0.8	74
97	Synchronicity, chaos and population cycles: spatial coherence in an uncertain world. Trends in Ecology and Evolution, 1999, 14, 417-418.	4.2	39
98	Reply to: Models for the in-host dynamics of malaria revisited: errors in some basic models lead to large over-estimates of growth rates. Parasitology, 1998, 117, 409-410.	0.7	27
99	Presence of an inducible HIV-1 latent reservoir during highly active antiretroviral therapy. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 13193-13197.	3.3	1,786
100	Viral dynamics of primary viremia and antiretroviral therapy in simian immunodeficiency virus infection. Journal of Virology, 1997, 71, 7518-7525.	1.5	263
101	Spatial Heterogeneity in Epidemic Models. Journal of Theoretical Biology, 1996, 179, 1-11.	0.8	269
102	The coupled logistic map: a simple model for the effects of spatial heterogeneity on population dynamics. Journal of Theoretical Biology, 1995, 173, 217-230.	0.8	144
103	Chaos : Its significance and detection in biology. Biological Rhythm Research, 1995, 26, 233-252.	0.4	56
104	Computing Bouts of the Prisoner's Dilemma. Scientific American, 1995, 272, 110-115.	1.0	31
105	Linear filters and nonlinear forecasting. Proceedings of the Royal Society B: Biological Sciences, 1994, 256, 157-161.	1.2	2
106	Chaos and forecasting. Trends in Ecology and Evolution, 1994, 9, 244-245.	4.2	6
107	Hypothesis: a controlled chaotic attractor constitutes the central oscillator of the circadian clock. Biochemical Society Transactions, 1994, 22, 322S-322S.	1.6	3
108	Hypothesis: the central oscillator of the circadian clock is a controlled chaotic attractor. BioSystems, 1993, 29, 77-85.	0.9	59

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109	An inexpensive infrared growth sensor array for detection of bacterial antibiotic susceptibility. FEMS Microbiology Letters, 1993, 111, 251-254.	0.7	0
110	The cell division cycle: a physiologically plausible dynamic model can exhibit chaotic solutions. BioSystems, 1992, 27, 17-24.	0.9	27
111	The feasibility of targeted test-trace-isolate for the control of SARS-CoV-2 variants. F1000Research, 0, 10, 291.	0.8	1