

Rowland R Kao

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

2,827
citations

172207

29
h-index

189595

50
g-index

72
all docs

72
docs citations

72
times ranked

2490
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic analysis of an emergent <i>Mycobacterium bovis</i> outbreak in an area with no previously known wildlife infections. <i>Journal of Applied Ecology</i> , 2022, 59, 210-222.	1.9	19
2	Multi-species temporal network of livestock movements for disease spread. <i>Applied Network Science</i> , 2021, 6, .	0.8	7
3	Phylogenetic Structure and Sequential Dominance of Sub-Lineages of PRRSV Type-2 Lineage 1 in the United States. <i>Vaccines</i> , 2021, 9, 608.	2.1	38
4	A new phylodynamic model of <i>Mycobacterium bovis</i> transmission in a multi-host system uncovers the role of the unobserved reservoir. <i>PLoS Computational Biology</i> , 2021, 17, e1009005.	1.5	3
5	Assessing potential routes of <i>Streptococcus agalactiae</i> transmission between dairy herds using national surveillance, animal movement and molecular typing data. <i>Preventive Veterinary Medicine</i> , 2021, 197, 105501.	0.7	3
6	Site Specific Relationships between COVID-19 Cases and SARS-CoV-2 Viral Load in Wastewater Treatment Plant Influent. <i>Environmental Science & Technology</i> , 2021, 55, 15276-15286.	4.6	38
7	Spontaneous divergence of disease status in an economic epidemiological game. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2020, 476, 20190837.	1.0	0
8	Disease control across urban-rural gradients. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200775.	1.5	16
9	<i>Mycobacterium bovis</i> genomics reveals transmission of infection between cattle and deer in Ireland. <i>Microbial Genomics</i> , 2020, 6, .	1.0	39
10	Identifying likely transmissions in <i>Mycobacterium bovis</i> infected populations of cattle and badgers using the Kolmogorov Forward Equations. <i>Scientific Reports</i> , 2020, 10, 21980.	1.6	2
11	Analysing livestock network data for infectious disease control: an argument for routine data collection in emerging economies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180264.	1.8	49
12	Predictive analysis across spatial scales links zoonotic malaria to deforestation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182351.	1.2	51
13	Disease management at the wildlife-livestock interface: Using whole-genome sequencing to study the role of elk in <i>Mycobacterium bovis</i> transmission in Michigan, USA. <i>Molecular Ecology</i> , 2019, 28, 2192-2205.	2.0	51
14	Combining genomics and epidemiology to analyse bi-directional transmission of <i>Mycobacterium bovis</i> in a multi-host system. <i>ELife</i> , 2019, 8, .	2.8	63
15	Genome epidemiology of <i>Mycobacterium bovis</i> infection in contemporaneous, sympatric badger and cattle populations in Northern Ireland. <i>Access Microbiology</i> , 2019, 1, .	0.2	1
16	Identifying genotype specific elevated-risk areas and associated herd risk factors for bovine tuberculosis spread in British cattle. <i>Epidemics</i> , 2018, 24, 34-42.	1.5	9
17	Manipulation of contact network structure and the impact on foot-and-mouth disease transmission. <i>Preventive Veterinary Medicine</i> , 2018, 157, 8-18.	0.7	29
18	<i>Plasmodium knowlesi</i> invasion following spread by infected mosquitoes, macaques and humans. <i>Parasitology</i> , 2018, 145, 101-110.	0.7	17

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19	Whole Genome Sequencing for Determining the Source of Mycobacterium bovis Infections in Livestock Herds and Wildlife in New Zealand. <i>Frontiers in Veterinary Science</i> , 2018, 5, 272.	0.9	44
20	Using whole genome sequencing to investigate transmission in a multi-host system: bovine tuberculosis in New Zealand. <i>BMC Genomics</i> , 2017, 18, 180.	1.2	86
21	An Integrated Framework for Process-Driven Model Construction in Disease Ecology and Animal Health. <i>Frontiers in Veterinary Science</i> , 2017, 4, 155.	0.9	8
22	Quantifying the roles of host movement and vector dispersal in the transmission of vector-borne diseases of livestock. <i>PLoS Computational Biology</i> , 2017, 13, e1005470.	1.5	30
23	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. <i>Epidemics</i> , 2016, 17, 27-34.	1.5	13
24	A fast algorithm for calculating an expected outbreak size on dynamic contagion networks. <i>Epidemics</i> , 2016, 16, 56-62.	1.5	2
25	Broadwick: a framework for computational epidemiology. <i>BMC Bioinformatics</i> , 2016, 17, 65.	1.2	15
26	A descriptive analysis of the growth of unrecorded interactions amongst cattle-raising premises in Scotland and their implications for disease spread. <i>BMC Veterinary Research</i> , 2016, 12, 37.	0.7	4
27	Use of bacterial whole-genome sequencing to investigate local persistence and spread in bovine tuberculosis. <i>Epidemics</i> , 2016, 14, 26-35.	1.5	70
28	Use of genomics to track bovine tuberculosis transmission. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 241-268.	0.5	35
29	Herd-level bovine tuberculosis risk factors: assessing the role of low-level badger population disturbance. <i>Scientific Reports</i> , 2015, 5, 13062.	1.6	32
30	Limitations of variable number of tandem repeat typing identified through whole genome sequencing of Mycobacterium avium subsp. paratuberculosis on a national and herd level. <i>BMC Genomics</i> , 2015, 16, 161.	1.2	71
31	Determining the impact of badger culling on the incidence of TB in cattle. <i>Veterinary Record</i> , 2015, 177, 415-416.	0.2	0
32	A Few Bad Apples: A Model of Disease Influenced Agent Behaviour in a Heterogeneous Contact Environment. <i>PLoS ONE</i> , 2015, 10, e0118127.	1.1	12
33	Supersize me: how whole-genome sequencing and big data are transforming epidemiology. <i>Trends in Microbiology</i> , 2014, 22, 282-291.	3.5	115
34	A restatement of the natural science evidence base relevant to the control of bovine tuberculosis in Great Britain ^{â€}. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131634.	1.2	118
35	Whole Genome Sequencing Reveals Local Transmission Patterns of Mycobacterium bovis in Sympatric Cattle and Badger Populations. <i>PLoS Pathogens</i> , 2012, 8, e1003008.	2.1	173
36	Simulating the impact of badger culling on bovine tuberculosis in cattle. <i>Veterinary Record</i> , 2012, 170, 175-176.	0.2	0

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37	Risk factors for bovine Tuberculosis at the national level in Great Britain. BMC Veterinary Research, 2012, 8, 51.	0.7	46
38	An ecological and comparative perspective on the control of bovine tuberculosis in Great Britain and the Republic of Ireland. Preventive Veterinary Medicine, 2012, 104, 185-197.	0.7	24
39	An Economic Evaluation of Preclinical Testing Strategies Compared to the Compulsory Scrapie Flock Scheme in the Control of Classical Scrapie. PLoS ONE, 2012, 7, e32884.	1.1	5
40	Evolution of Entrepreneurship: Toward Stewardship-based Economics. , 2011, , .		1
41	FROM ENTREPRENEURSHIP TO STEWARDSHIP-BASED ECONOMICS. , 2010, , 291-310.		0
42	Network Concepts and Epidemiological Models. , 2009, , 85-112.		0
43	Estimates for local and movement-based transmission of bovine tuberculosis in British cattle. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 1001-1005.	1.2	110
44	Disease dynamics over very different time-scales: foot-and-mouth disease and scrapie on the network of livestock movements in the UK. Journal of the Royal Society Interface, 2007, 4, 907-916.	1.5	143
45	Demographic risk factors for classical and atypical scrapie in Great Britain. Journal of General Virology, 2007, 88, 3486-3492.	1.3	35
46	Parasite strain coexistence in a heterogeneous host population. Oikos, 2006, 115, 495-503.	1.2	2
47	Infectious disease control using contact tracing in random and scale-free networks. Journal of the Royal Society Interface, 2006, 3, 55-62.	1.5	96
48	The network of sheep movements within Great Britain: network properties and their implications for infectious disease spread. Journal of the Royal Society Interface, 2006, 3, 669-677.	1.5	195
49	The effect of contact heterogeneity and multiple routes of transmission on final epidemic size. Mathematical Biosciences, 2006, 203, 124-136.	0.9	94
50	Evolution of pathogens towards low R0 in heterogeneous populations. Journal of Theoretical Biology, 2006, 242, 634-642.	0.8	16
51	Demographic structure and pathogen dynamics on the network of livestock movements in Great Britain. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 1999-2007.	1.2	198
52	Modelling the initial spread of foot-and-mouth disease through animal movements. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 2729-2735.	1.2	131
53	The UK foot-and-mouth disease outbreak " the aftermath. Nature Reviews Microbiology, 2004, 2, 675-681.	13.6	92
54	An Entrepreneurial Approach to Stewardship Accountability. , 2004, , .		5

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55	The impact of local heterogeneity on alternative control strategies for foot-and-mouth disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 2557-2564.	1.2	50
56	Searching for BSE in sheep: interpreting the results so far. <i>Veterinary Record</i> , 2003, 152, 298-299.	0.2	18
57	The role of mathematical modelling in the control of the 2001 FMD epidemic in the UK. <i>Trends in Microbiology</i> , 2002, 10, 279-286.	3.5	162
58	BSE – a wolf in sheep's clothing?. <i>Trends in Microbiology</i> , 2002, 10, 563-570.	3.5	40
59	Entrepreneurism. , 2002, , .		19
60	Modelling the national scrapie eradication programme in the UK. <i>Mathematical Biosciences</i> , 2001, 174, 61-76.	0.9	36
61	SCoVMod – a spatially explicit mobility and deprivation adjusted model of first wave COVID-19 transmission dynamics. <i>Wellcome Open Research</i> , 0, 7, 161.	0.9	3