

Rowland R Kao

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

2,827
citations

172386

29
h-index

189801

50
g-index

72
all docs

72
docs citations

72
times ranked

2490
citing authors

#	ARTICLE	IF	CITATIONS
1	Demographic structure and pathogen dynamics on the network of livestock movements in Great Britain. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1999-2007.	1.2	198
2	The network of sheep movements within Great Britain: network properties and their implications for infectious disease spread. <i>Journal of the Royal Society Interface</i> , 2006, 3, 669-677.	1.5	195
3	Whole Genome Sequencing Reveals Local Transmission Patterns of <i>Mycobacterium bovis</i> in Sympatric Cattle and Badger Populations. <i>PLoS Pathogens</i> , 2012, 8, e1003008.	2.1	173
4	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
5	Disease dynamics over very different time-scales: foot-and-mouth disease and scrapie on the network of livestock movements in the UK. <i>Journal of the Royal Society Interface</i> , 2007, 4, 907-916.	1.5	143
6	Modelling the initial spread of foot-and-mouth disease through animal movements. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 2729-2735.	1.2	131
7	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
8	Supersize me: how whole-genome sequencing and big data are transforming epidemiology. <i>Trends in Microbiology</i> , 2014, 22, 282-291.	3.5	115
9	Estimates for local and movement-based transmission of bovine tuberculosis in British cattle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 1001-1005.	1.2	110
10	Infectious disease control using contact tracing in random and scale-free networks. <i>Journal of the Royal Society Interface</i> , 2006, 3, 55-62.	1.5	96
11	The effect of contact heterogeneity and multiple routes of transmission on final epidemic size. <i>Mathematical Biosciences</i> , 2006, 203, 124-136.	0.9	94
12	The UK foot-and-mouth disease outbreak â€” the aftermath. <i>Nature Reviews Microbiology</i> , 2004, 2, 675-681.	13.6	92
13	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
14	Limitations of variable number of tandem repeat typing identified through whole genome sequencing of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> on a national and herd level. <i>BMC Genomics</i> , 2015, 16, 161.	1.2	71
15	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
16	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
17	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
18	Disease management at the wildlifeâ€”livestock interface: Using wholeâ€”genome sequencing to study the role of elk in <i> <i>Mycobacterium bovis</i> Molecular Ecology, 2019, 28, 2192-2205.	2.0	51

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19	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
20	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
21	Risk factors for bovine Tuberculosis at the national level in Great Britain. <i>BMC Veterinary Research</i> , 2012, 8, 51.	0.7	46
22	Whole Genome Sequencing for Determining the Source of <i>Mycobacterium bovis</i> Infections in Livestock Herds and Wildlife in New Zealand. <i>Frontiers in Veterinary Science</i> , 2018, 5, 272.	0.9	44
23	BSE – a wolf in sheep's clothing?. <i>Trends in Microbiology</i> , 2002, 10, 563-570.	3.5	40
24	<i>Mycobacterium bovis</i> genomics reveals transmission of infection between cattle and deer in Ireland. <i>Microbial Genomics</i> , 2020, 6, .	1.0	39
25	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
26	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
27	Modelling the national scrapie eradication programme in the UK. <i>Mathematical Biosciences</i> , 2001, 174, 61-76.	0.9	36
28	Demographic risk factors for classical and atypical scrapie in Great Britain. <i>Journal of General Virology</i> , 2007, 88, 3486-3492.	1.3	35
29	Use of genomics to track bovine tuberculosis transmission. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 241-268.	0.5	35
30	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
31	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
32	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
33	An ecological and comparative perspective on the control of bovine tuberculosis in Great Britain and the Republic of Ireland. <i>Preventive Veterinary Medicine</i> , 2012, 104, 185-197.	0.7	24
34	Entrepreneurism. , 2002, , .		19
35	Phylodynamic 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
36	Searching for BSE in sheep: interpreting the results so far. <i>Veterinary Record</i> , 2003, 152, 298-299.	0.2	18

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37	Plasmodium knowlesi invasion following spread by infected mosquitoes, macaques and humans. Parasitology, 2018, 145, 101-110.	0.7	17
38	Evolution of pathogens towards low R0 in heterogeneous populations. Journal of Theoretical Biology, 2006, 242, 634-642.	0.8	16
39	Disease control across urban-rural gradients. Journal of the Royal Society Interface, 2020, 17, 20200775.	1.5	16
40	Broadwick: a framework for computational epidemiology. BMC Bioinformatics, 2016, 17, 65.	1.2	15
41	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. Epidemics, 2016, 17, 27-34.	1.5	13
42	A Few Bad Apples: A Model of Disease Influenced Agent Behaviour in a Heterogeneous Contact Environment. PLoS ONE, 2015, 10, e0118127.	1.1	12
43	Identifying genotype specific elevated-risk areas and associated herd risk factors for bovine tuberculosis spread in British cattle. Epidemics, 2018, 24, 34-42.	1.5	9
44	An Integrated Framework for Process-Driven Model Construction in Disease Ecology and Animal Health. Frontiers in Veterinary Science, 2017, 4, 155.	0.9	8
45	Multi-species temporal network of livestock movements for disease spread. Applied Network Science, 2021, 6, .	0.8	7
46	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
47	An Entrepreneurial Approach to Stewardship Accountability. , 2004, , .		5
48	A descriptive analysis of the growth of unrecorded interactions amongst cattle-raising premises in Scotland and their implications for disease spread. BMC Veterinary Research, 2016, 12, 37.	0.7	4
49	A new phylodynamic model of Mycobacterium bovis transmission in a multi-host system uncovers the role of the unobserved reservoir. PLoS Computational Biology, 2021, 17, e1009005.	1.5	3
50	Assessing potential routes of Streptococcus agalactiae transmission between dairy herds using national surveillance, animal movement and molecular typing data. Preventive Veterinary Medicine, 2021, 197, 105501.	0.7	3
51	SCoVMod - a spatially explicit mobility and deprivation adjusted model of first wave COVID-19 transmission dynamics. Wellcome Open Research, 0, 7, 161.	0.9	3
52	Parasite strain coexistence in a heterogeneous host population. Oikos, 2006, 115, 495-503.	1.2	2
53	A fast algorithm for calculating an expected outbreak size on dynamic contagion networks. Epidemics, 2016, 16, 56-62.	1.5	2
54	Identifying likely transmissions in Mycobacterium bovis infected populations of cattle and badgers using the Kolmogorov Forward Equations. Scientific Reports, 2020, 10, 21980.	1.6	2

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55	Evolution of Entrepreneurship: Toward Stewardship-based Economics. , 2011, , .		1
56	Genome epidemiology of Mycobacterium bovis infection in contemporaneous, sympatric badger and cattle populations in Northern Ireland. Access Microbiology, 2019, 1, .	0.2	1
57	Simulating the impact of badger culling on bovine tuberculosis in cattle. Veterinary Record, 2012, 170, 175-176.	0.2	0
58	Determining the impact of badger culling on the incidence of TB in cattle. Veterinary Record, 2015, 177, 415-416.	0.2	0
59	Spontaneous divergence of disease status in an economic epidemiological game. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2020, 476, 20190837.	1.0	0
60	Network Concepts and Epidemiological Models. , 2009, , 85-112.		0
61	FROM ENTREPRENEURSHIP TO STEWARDSHIP-BASED ECONOMICS. , 2010, , 291-310.		0