

Richard Reeve

List of Publications by Year in descending order

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53
papers

4,442
citations

304368

22
h-index

182168

51
g-index

58
all docs

58
docs citations

58
times ranked

7705
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex model calibration through emulation, a worked example for a stochastic epidemic model. <i>Epidemics</i> , 2022, , 100574.	1.5	1
2	The pitfalls and virtues of population genetic summary statistics: Detecting selective sweeps in recent divergences. <i>Journal of Evolutionary Biology</i> , 2021, 34, 893-909.	0.8	6
3	Genetic Determinants of Receptor-Binding Preference and Zoonotic Potential of H9N2 Avian Influenza Viruses. <i>Journal of Virology</i> , 2021, 95, .	1.5	14
4	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	13.6	2,650
5	Solving the fourthâ€“corner problem: forecasting ecosystem primary production from spatial multispecies traitâ€“based models. <i>Ecological Monographs</i> , 2021, 91, e01454.	2.4	16
6	Livestock movement informs the risk of disease spread in traditional production systems in East Africa. <i>Scientific Reports</i> , 2021, 11, 16375.	1.6	14
7	Distemper, extinction, and vaccination of the Amur tiger. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31954-31962.	3.3	33
8	Genetic Basis of Antigenic Variation of SAT3 Foot-And-Mouth Disease Viruses in Southern Africa. <i>Frontiers in Veterinary Science</i> , 2020, 7, 568.	0.9	1
9	Reply to Kloepfer and Gern: Independent studies suggest an arms race between influenza and rhinovirus: What next?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6988-6989.	3.3	0
10	Uptake of Diagnostic Tests by Livestock Farmers: A Stochastic Game Theory Approach. <i>Frontiers in Veterinary Science</i> , 2020, 7, 36.	0.9	7
11	Improving the identification of antigenic sites in the H1N1 influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2019, 68, 859-885.	0.5	5
12	Estimating the protection afforded by foot-and-mouth disease vaccines in the laboratory. <i>Vaccine</i> , 2019, 37, 5515-5524.	1.7	33
13	1980sâ€“2010s: The world's largest mangrove ecosystem is becoming homogeneous. <i>Biological Conservation</i> , 2019, 236, 79-91.	1.9	41
14	Divergent Allele Advantage Provides a Quantitative Model for Maintaining Alleles with a Wide Range of Intrinsic Merits. <i>Genetics</i> , 2019, 212, 553-564.	1.2	12
15	Are orchid bees useful indicators of the impacts of human disturbance?. <i>Ecological Indicators</i> , 2019, 103, 745-755.	2.6	15
16	Application of long read sequencing to determine expressed antigen diversity in <i>Trypanosoma brucei</i> infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007262.	1.3	25
17	Modelling spatial biodiversity in the worldâ€™s largest mangrove ecosystemâ€“The Bangladesh Sundarbans: A baseline for conservation. <i>Diversity and Distributions</i> , 2019, 25, 729-742.	1.9	27
18	Opportunities for enhanced surveillance of footâ€“andâ€“mouth disease in endemic settings using milk samples. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1405-1410.	1.3	14

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19	Enhancing livestock vaccination decision-making through rapid diagnostic testing. <i>World Development Perspectives</i> , 2019, 16, 100144.	0.8	8
20	Virus-virus interactions impact the population dynamics of influenza and the common cold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27142-27150.	3.3	338
21	Estimation of temporal covariances in pathogen dynamics using Bayesian multivariate autoregressive models. <i>PLoS Computational Biology</i> , 2019, 15, e1007492.	1.5	9
22	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	24
23	Waves of endemic foot-and-mouth disease in eastern Africa suggest feasibility of proactive vaccination approaches. <i>Nature Ecology and Evolution</i> , 2018, 2, 1449-1457.	3.4	66
24	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017, 1, 176.	3.4	156
25	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. <i>Computational Statistics</i> , 2017, 32, 803-843.	0.8	8
26	Detection of Rare Antimicrobial Resistance Profiles by Active and Passive Surveillance Approaches. <i>PLoS ONE</i> , 2016, 11, e0158515.	1.1	19
27	Are we failing to protect threatened mangroves in the Sundarbans world heritage ecosystem?. <i>Scientific Reports</i> , 2016, 6, 21234.	1.6	73
28	Selecting Random Effect Components in a Sparse Hierarchical Bayesian Model for Identifying Antigenic Variability. <i>Lecture Notes in Computer Science</i> , 2016, , 14-27.	1.0	1
29	Tracking the Antigenic Evolution of Foot-and-Mouth Disease Virus. <i>PLoS ONE</i> , 2016, 11, e0159360.	1.1	32
30	Identification of Low- and High-Impact Hemagglutinin Amino Acid Substitutions That Drive Antigenic Drift of Influenza A(H1N1) Viruses. <i>PLoS Pathogens</i> , 2016, 12, e1005526.	2.1	58
31	Prediction and characterization of novel epitopes of serotype A foot-and-mouth disease viruses circulating in East Africa using site-directed mutagenesis. <i>Journal of General Virology</i> , 2015, 96, 1033-1041.	1.3	19
32	Genetic and antigenic characterisation of serotype A FMD viruses from East Africa to select new vaccine strains. <i>Vaccine</i> , 2014, 32, 5794-5800.	1.7	39
33	Estimating the Potential Impact of Canine Distemper Virus on the Amur Tiger Population (<i>Panthera tigris</i>) in the Amur River Basin. <i>PLoS ONE</i> , 2014, 9, e0100001.	1.1	48
34	The impact of host species and vector control measures on the fitness of African malaria vectors. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20122823.	1.2	28
35	Predicting the public health benefit of vaccinating cattle against <i>Escherichia coli</i> O157. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16265-16270.	3.3	106
36	The diversity of antimicrobial resistance is different in <i>Salmonella</i> Typhimurium DT104 from co-located animals and humans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2924-2925.	1.2	2

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37	An ecological approach to assessing the epidemiology of antimicrobial resistance in animal and human populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1630-1639.	1.2	60
38	Assessing the impact of marine wind farms on birds through movement modelling. <i>Journal of the Royal Society Interface</i> , 2012, 9, 2120-2130.	1.5	23
39	The fitness of African malaria vectors in the presence and limitation of host behaviour. <i>Malaria Journal</i> , 2012, 11, 425.	0.8	9
40	Selective forces shaping diversity in the class I region of the major histocompatibility complex in dairy cattle. <i>Animal Genetics</i> , 2012, 43, 239-249.	0.6	29
41	Reducing animal experimentation in foot-and-mouth disease vaccine potency tests. <i>Vaccine</i> , 2011, 29, 5467-5473.	1.7	11
42	Bayesian salamanders: analysing the demography of an underground population of the European plethodontid <i>Speleomantes strinatii</i> with state-space modelling. <i>BMC Ecology</i> , 2010, 10, 4.	3.0	20
43	Inheritance in tetraploid yeast revisited: segregation patterns and statistical power under different inheritance models. <i>Journal of Evolutionary Biology</i> , 2010, 23, 1570-1578.	0.8	20
44	Sequence-Based Prediction for Vaccine Strain Selection and Identification of Antigenic Variability in Foot-and-Mouth Disease Virus. <i>PLoS Computational Biology</i> , 2010, 6, e1001027.	1.5	63
45	Exploiting strain diversity to expose transmission heterogeneities and predict the impact of targeting supershedding. <i>Epidemics</i> , 2009, 1, 221-229.	1.5	20
46	Directional hearing in a silicon cricket. <i>BioSystems</i> , 2007, 87, 307-313.	0.9	4
47	New technologies for testing a model of cricket phonotaxis on an outdoor robot. <i>Robotics and Autonomous Systems</i> , 2005, 51, 41-54.	3.0	50
48	An Analysis of Neural Models for Walking Control. <i>IEEE Transactions on Neural Networks</i> , 2005, 16, 733-742.	4.8	20
49	New Ears for a Robot Cricket. <i>Lecture Notes in Computer Science</i> , 2005, , 297-304.	1.0	3
50	Robot phonotaxis in the wild: a biologically inspired approach to outdoor sound localization. <i>Advanced Robotics</i> , 2004, 18, 801-816.	1.1	50
51	New neural circuits for robot phonotaxis. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2003, 361, 2245-2266.	1.6	49
52	Talking to Godot: dialogue with a mobile robot. , 0, , .		25
53	A cricket-inspired Neural Network For FeedForward Compensation and Multisensory Integration. , 0, , .		9