Richard Reeve

List of Publications by Year
in descending order

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	SARS-CoV-2 variants, spike mutations and immune escape. Nature Reviews Microbiology, 2021, 19, 409-424.	13.6	2,650
2	Virus–virus interactions impact the population dynamics of influenza and the common cold. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 27142-27150.	3.3	338
3	Connecting Earth observation to high-throughput biodiversity data. Nature Ecology and Evolution, 2017, 1, 176.	3.4	156
4	Predicting the public health benefit of vaccinating cattle against <i>Escherichia</i> <i>coli</i> O157. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16265-16270.	3.3	106
5	Are we failing to protect threatened mangroves in the Sundarbans world heritage ecosystem?. Scientific Reports, 2016, 6, 21234.	1.6	73
6	Waves of endemic foot-and-mouth disease in eastern Africa suggest feasibility of proactive vaccination approaches. Nature Ecology and Evolution, 2018, 2, 1449-1457.	3.4	66
7	Sequence-Based Prediction for Vaccine Strain Selection and Identification of Antigenic Variability in Foot-and-Mouth Disease Virus. PLoS Computational Biology, 2010, 6, e1001027.	1.5	63
8	An ecological approach to assessing the epidemiology of antimicrobial resistance in animal and human populations. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1630-1639.	1.2	60
9	Identification of Low- and High-Impact Hemagglutinin Amino Acid Substitutions That Drive Antigenic Drift of Influenza A(H1N1) Viruses. PLoS Pathogens, 2016, 12, e1005526.	2.1	58
10	Robot phonotaxis in the wild: a biologically inspired approach to outdoor sound localization. Advanced Robotics, 2004, 18, 801-816.	1.1	50
11	New technologies for testing a model of cricket phonotaxis on an outdoor robot. Robotics and Autonomous Systems, 2005, 51, 41-54.	3.0	50
12	New neural circuits for robot phonotaxis. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2003, 361, 2245-2266.	1.6	49
13	Estimating the Potential Impact of Canine Distemper Virus on the Amur Tiger Population (Panthera) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	48
14	1980s–2010s: The world's largest mangrove ecosystem is becoming homogeneous. Biological Conservation, 2019, 236, 79-91.	1.9	41
15	Genetic and antigenic characterisation of serotype A FMD viruses from East Africa to select new vaccine strains. Vaccine, 2014, 32, 5794-5800.	1.7	39
16	Estimating the protection afforded by foot-and-mouth disease vaccines in the laboratory. Vaccine, 2019, 37, 5515-5524.	1.7	33
17	Distemper, extinction, and vaccination of the Amur tiger. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31954-31962.	3.3	33
18	Tracking the Antigenic Evolution of Foot-and-Mouth Disease Virus. PLoS ONE, 2016, 11, e0159360.	1.1	32

#	Article	IF	Citations
19	Selective forces shaping diversity in the class I region of the major histocompatibility complex in dairy cattle. Animal Genetics, 2012, 43, 239-249.	0.6	29
20	The impact of host species and vector control measures on the fitness of African malaria vectors. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20122823.	1.2	28
21	Modelling spatial biodiversity in the world's largest mangrove ecosystem—The Bangladesh Sundarbans: A baseline for conservation. Diversity and Distributions, 2019, 25, 729-742.	1.9	27
22	Talking to Godot: dialogue with a mobile robot. , 0, , .		25
23	Application of long read sequencing to determine expressed antigen diversity in Trypanosoma brucei infections. PLoS Neglected Tropical Diseases, 2019, 13, e0007262.	1.3	25
24	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. Emerging Microbes and Infections, 2018, 7, 1-12.	3.0	24
25	Assessing the impact of marine wind farms on birds through movement modelling. Journal of the Royal Society Interface, 2012, 9, 2120-2130.	1.5	23
26	An Analysis of Neural Models for Walking Control. IEEE Transactions on Neural Networks, 2005, 16, 733-742.	4.8	20
27	Exploiting strain diversity to expose transmission heterogeneities and predict the impact of targeting supershedding. Epidemics, 2009, 1, 221-229.	1.5	20
28	Bayesian salamanders: analysing the demography of an underground population of the European plethodontid Speleomantes strinatii with state-space modelling. BMC Ecology, 2010, 10, 4.	3.0	20
29	Inheritance in tetraploid yeast revisited: segregation patterns and statistical power under different inheritance models. Journal of Evolutionary Biology, 2010, 23, 1570-1578.	0.8	20
30	Prediction and characterization of novel epitopes of serotype A foot-and-mouth disease viruses circulating in East Africa using site-directed mutagenesis. Journal of General Virology, 2015, 96, 1033-1041.	1.3	19
31	Detection of Rare Antimicrobial Resistance Profiles by Active and Passive Surveillance Approaches. PLoS ONE, 2016, 11, e0158515.	1.1	19
32	Solving the fourth-corner problem: forecasting ecosystem primary production from spatial multispecies trait-based models. Ecological Monographs, 2021, 91, e01454.	2.4	16
33	Are orchid bees useful indicators of the impacts of human disturbance?. Ecological Indicators, 2019, 103, 745-755.	2.6	15
34	Opportunities for enhanced surveillance of foot-and-mouth disease in endemic settings using milk samples. Transboundary and Emerging Diseases, 2019, 66, 1405-1410.	1.3	14
35	Genetic Determinants of Receptor-Binding Preference and Zoonotic Potential of H9N2 Avian Influenza Viruses. Journal of Virology, 2021, 95, .	1.5	14
36	Livestock movement informs the risk of disease spread in traditional production systems in East Africa. Scientific Reports, 2021, 11, 16375.	1.6	14

#	Article	IF	Citations
37	Divergent Allele Advantage Provides a Quantitative Model for Maintaining Alleles with a Wide Range of Intrinsic Merits. Genetics, 2019, 212, 553-564.	1.2	12
38	Reducing animal experimentation in foot-and-mouth disease vaccine potency tests. Vaccine, 2011, 29, 5467-5473.	1.7	11
39	A cricket-inspired Neural Network For FeedForward Compensation and Multisensory Integration. , 0, , .		9
40	The fitness of African malaria vectors in the presence and limitation of host behaviour. Malaria Journal, 2012, 11, 425.	0.8	9
41	Estimation of temporal covariances in pathogen dynamics using Bayesian multivariate autoregressive models. PLoS Computational Biology, 2019, 15, e1007492.	1.5	9
42	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. Computational Statistics, 2017, 32, 803-843.	0.8	8
43	Enhancing livestock vaccination decision-making through rapid diagnostic testing. World Development Perspectives, 2019, 16, 100144.	0.8	8
44	Uptake of Diagnostic Tests by Livestock Farmers: A Stochastic Game Theory Approach. Frontiers in Veterinary Science, 2020, 7, 36.	0.9	7
45	The pitfalls and virtues of population genetic summary statistics: Detecting selective sweeps in recent divergences. Journal of Evolutionary Biology, 2021, 34, 893-909.	0.8	6
46	Improving the identification of antigenic sites in the H1N1 influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. Journal of the Royal Statistical Society Series C: Applied Statistics, 2019, 68, 859-885.	0.5	5
47	Directional hearing in a silicon cricket. BioSystems, 2007, 87, 307-313.	0.9	4
48	New Ears for a Robot Cricket. Lecture Notes in Computer Science, 2005, , 297-304.	1.0	3
49	The diversity of antimicrobial resistance is different in <i>Salmonella</i> Typhimurium DT104 from co-located animals and humans. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2924-2925.	1.2	2
50	Genetic Basis of Antigenic Variation of SAT3 Foot-And-Mouth Disease Viruses in Southern Africa. Frontiers in Veterinary Science, 2020, 7, 568.	0.9	1
51	Selecting Random Effect Components in a Sparse Hierarchical Bayesian Model for Identifying Antigenic Variability. Lecture Notes in Computer Science, 2016, , 14-27.	1.0	1
52	Complex model calibration through emulation, a worked example for a stochastic epidemic model. Epidemics, 2022, , 100574.	1.5	1
53	Reply to Kloepfer and Gern: Independent studies suggest an arms race between influenza and rhinovirus: What next?. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6988-6989.	3.3	0