

# Daniel T Haydon

## List of Publications by Year in descending order

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63  
papers

4,491  
citations

172457

29  
h-index

118850

62  
g-index

63  
all docs

63  
docs citations

63  
times ranked

6233  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying Reservoirs of Infection: A Conceptual and Practical Challenge. <i>Emerging Infectious Diseases</i> , 2002, 8, 1468-1473.	4.3	630
2	Emerging pathogens: the epidemiology and evolution of species jumps. <i>Trends in Ecology and Evolution</i> , 2005, 20, 238-244.	8.7	597
3	Transmission Dynamics and Prospects for the Elimination of Canine Rabies. <i>PLoS Biology</i> , 2009, 7, e1000053.	5.6	374
4	Assembling evidence for identifying reservoirs of infection. <i>Trends in Ecology and Evolution</i> , 2014, 29, 270-279.	8.7	209
5	Transmission Pathways of Foot-and-Mouth Disease Virus in the United Kingdom in 2007. <i>PLoS Pathogens</i> , 2008, 4, e1000050.	4.7	178
6	Exploring reservoir dynamics: a case study of rabies in the Serengeti ecosystem. <i>Journal of Applied Ecology</i> , 2008, 45, 1246-1257.	4.0	166
7	Venezuela's humanitarian crisis, resurgence of vector-borne diseases, and implications for spillover in the region. <i>Lancet Infectious Diseases</i> , The, 2019, 19, e149-e161.	9.1	138
8	Designing Programs for Eliminating Canine Rabies from Islands: Bali, Indonesia as a Case Study. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2372.	3.0	128
9	Dynamics of a morbillivirus at the domestic-wildlife interface: Canine distemper virus in domestic dogs and lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1464-1469.	7.1	128
10	Beyond the Consensus: Dissecting Within-Host Viral Population Diversity of Foot-and-Mouth Disease Virus by Using Next-Generation Genome Sequencing. <i>Journal of Virology</i> , 2011, 85, 2266-2275.	3.4	127
11	Evidence for Positive Selection in Foot-and-Mouth Disease Virus Capsid Genes From Field Isolates. <i>Genetics</i> , 2001, 157, 7-15.	2.9	126
12	Supersize me: how whole-genome sequencing and big data are transforming epidemiology. <i>Trends in Microbiology</i> , 2014, 22, 282-291.	7.7	115
13	Establishing the link between habitat selection and animal population dynamics. <i>Ecological Monographs</i> , 2015, 85, 413-436.	5.4	111
14	A Bayesian Inference Framework to Reconstruct Transmission Trees Using Epidemiological and Genetic Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002768.	3.2	104
15	Surveillance guidelines for disease elimination: A case study of canine rabies. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2013, 36, 249-261.	1.6	87
16	Competition, predation, and migration: individual choice patterns of Serengeti migrants captured by hierarchical models. <i>Ecological Monographs</i> , 2014, 84, 355-372.	5.4	87
17	Mobile Phones As Surveillance Tools: Implementing and Evaluating a Large-Scale Intersectoral Surveillance System for Rabies in Tanzania. <i>PLoS Medicine</i> , 2016, 13, e1002002.	8.4	85
18	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.	7.8	66

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19	Driving improvements in emerging disease surveillance through locally relevant capacity strengthening. <i>Science</i> , 2017, 357, 146-148.	12.6	60
20	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.	4.7	58
21	Evolution of foot-and-mouth disease virus intra-sample sequence diversity during serial transmission in bovine hosts. <i>Veterinary Research</i> , 2013, 44, 12.	3.0	56
22	Metapopulation dynamics of rabies and the efficacy of vaccination. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2182-2190.	2.6	47
23	Culling wildlife hosts to control disease: mountain hares, red grouse and louping ill virus. <i>Journal of Applied Ecology</i> , 2010, 47, 926-930.	4.0	45
24	Heterogeneity in the spread and control of infectious disease: consequences for the elimination of canine rabies. <i>Scientific Reports</i> , 2015, 5, 18232.	3.3	45
25	Sperm-limited fecundity and polyandry-induced mortality in female nematodes <i>Caenorhabditis remanei</i> . <i>Biological Journal of the Linnean Society</i> , 0, 99, 362-369.	1.6	44
26	Distinguishing low frequency mutations from RT-PCR and sequence errors in viral deep sequencing data. <i>BMC Genomics</i> , 2015, 16, 229.	2.8	44
27	Analysing noisy time-series: describing regional variation in the cyclic dynamics of red grouse. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1609-1617.	2.6	41
28	Effect of fire on northern bettong ( <i>Bettongia tropica</i> ) foraging behaviour. <i>Austral Ecology</i> , 2001, 26, 649-659.	1.5	39
29	Genetic and antigenic characterisation of serotype A FMD viruses from East Africa to select new vaccine strains. <i>Vaccine</i> , 2014, 32, 5794-5800.	3.8	39
30	One Health in Practice: Using Integrated Bite Case Management to Increase Detection of Rabid Animals in Tanzania. <i>Frontiers in Public Health</i> , 2020, 8, 13.	2.7	35
31	Serial passage of foot-and-mouth disease virus in sheep reveals declining levels of viraemia over time. <i>Journal of General Virology</i> , 2002, 83, 1907-1914.	2.9	33
32	Prevalence and speciation of brucellosis in febrile patients from a pastoralist community of Tanzania. <i>Scientific Reports</i> , 2020, 10, 7081.	3.3	30
33	Observing micro-evolutionary processes of viral populations at multiple scales. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120203.	4.0	29
34	Transmission ecology of canine parvovirus in a multi-host, multi-pathogen system. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182772.	2.6	26
35	Efficient generation of vesicular stomatitis virus (VSV)-pseudotypes bearing morbilliviral glycoproteins and their use in quantifying virus neutralising antibodies. <i>Vaccine</i> , 2016, 34, 814-822.	3.8	25
36	Integrating serological and genetic data to quantify cross-species transmission: brucellosis as a case study. <i>Parasitology</i> , 2016, 143, 821-834.	1.5	24

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37	Molecular detection and genetic characterization of Bartonella species from rodents and their associated ectoparasites from northern Tanzania. PLoS ONE, 2019, 14, e0223667.	2.5	24
38	Updated estimate of the duration of the meningo-encephalitic stage in gambiense human African trypanosomiasis. BMC Research Notes, 2015, 8, 292.	1.4	22
39	The shape of red grouse cycles. Journal of Animal Ecology, 2004, 73, 767-776.	2.8	21
40	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.	2.9	19
41	Deep Sequencing of Foot-and-Mouth Disease Virus Reveals RNA Sequences Involved in Genome Packaging. Journal of Virology, 2018, 92, .	3.4	19
42	Conservation and economic benefits of a road around the Serengeti. Conservation Biology, 2015, 29, 932-936.	4.7	17
43	Investigating intra-host and intra-herd sequence diversity of foot-and-mouth disease virus. Infection, Genetics and Evolution, 2016, 44, 286-292.	2.3	17
44	Rabies shows how scale of transmission can enable acute infections to persist at low prevalence. Science, 2022, 376, 512-516.	12.6	17
45	Estimating viral bottleneck sizes for FMDV transmission within and between hosts and implications for the rate of viral evolution. Interface Focus, 2020, 10, 20190066.	3.0	16
46	An analysis of long-term trends in the abundance of domestic livestock and free-roaming dogs in the Bale Mountains National Park, Ethiopia. African Journal of Ecology, 2011, 49, 91-102.	0.9	15
47	Response of endemic afroalpine rodents to the removal of livestock grazing pressure. Environmental Epigenetics, 2011, 57, 741-750.	1.8	14
48	The impact of within-herd genetic variation upon inferred transmission trees for foot-and-mouth disease virus. Infection, Genetics and Evolution, 2015, 32, 440-448.	2.3	14
49	Tracking animal movements using biomarkers in tail hairs: a novel approach for animal geolocating from sulfur isoscapes. Movement Ecology, 2020, 8, 37.	2.8	13
50	Limits to exploitation: dynamic food web models predict the impact of livestock grazing on Ethiopian wolves <i>Canis simensis</i> and their prey. Journal of Applied Ecology, 2011, 48, 340-347.	4.0	12
51	One Health Research in Northern Tanzania – Challenges and Progress. The East African Health Research Journal, 2017, 1, 8-18.	0.4	11
52	Reservoir dynamics of rabies in south-east Tanzania and the roles of cross-species transmission and domestic dog vaccination. Journal of Applied Ecology, 2021, 58, 2673-2685.	4.0	10
53	Towards the elimination of dog-mediated rabies: development and application of an evidence-based management tool. BMC Infectious Diseases, 2020, 20, 778.	2.9	9
54	A method for the direct detection of airborne dispersal in lichens. Molecular Ecology Resources, 2018, 18, 240-250.	4.8	8

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55	The impact of passive case detection on the transmission dynamics of gambiense Human African Trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006276.	3.0	7
56	Latent class evaluation of the performance of serological tests for exposure to <i>Brucella</i> spp. in cattle, sheep, and goats in Tanzania. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009630.	3.0	7
57	Socially vs. Privately Optimal Control of Livestock Diseases: A Case for Integration of Epidemiology and Economics. <i>Frontiers in Veterinary Science</i> , 2020, 7, 558409.	2.2	6
58	Low topotype diversity of recent foot-and-mouth disease virus serotypes O and A from districts located along the Uganda and Tanzania border. <i>Journal of Veterinary Science</i> , 2019, 20, e4.	1.3	4
59	Integration of mark-recapture and acoustic detections for unbiased population estimation in animal communities. <i>Ecology</i> , 2022, 103, .	3.2	4
60	Molecular detection of <i>Coxiella burnetii</i> infection in small mammals from Moshi Rural and Urban Districts, northern Tanzania. <i>Veterinary Medicine and Science</i> , 2021, 7, 960-967.	1.6	3
61	Persistent pathogens and wildlife reservoirs. <i>Science</i> , 2021, 374, 35-36.	12.6	3
62	Farm-Level Risk Factors of Increased Abortion and Mortality in Domestic Ruminants during the 2010 Rift Valley Fever Outbreak in Central South Africa. <i>Pathogens</i> , 2020, 9, 914.	2.8	2
63	Revisiting the diffusion approximation to estimate evolutionary rates of gene family diversification. <i>Journal of Theoretical Biology</i> , 2014, 341, 111-122.	1.7	1