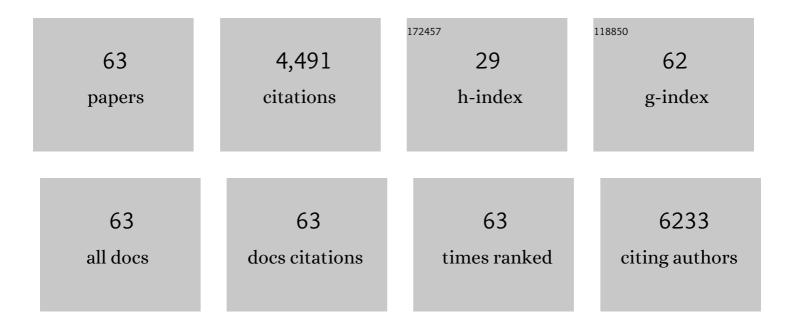
Daniel T Haydon

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2988913/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Rabies shows how scale of transmission can enable acute infections to persist at low prevalence. Science, 2022, 376, 512-516.	12.6	17
2	Integration of mark–recapture and acoustic detections for unbiased population estimation in animal communities. Ecology, 2022, 103, .	3.2	4
3	Molecular detection of <i>Coxiella burnetii</i> infection in small mammals from Moshi Rural and Urban Districts, northern Tanzania. Veterinary Medicine and Science, 2021, 7, 960-967.	1.6	3
4	Reservoir dynamics of rabies in southâ€east Tanzania and the roles of crossâ€species transmission and domestic dog vaccination. Journal of Applied Ecology, 2021, 58, 2673-2685.	4.0	10
5	Latent class evaluation of the performance of serological tests for exposure to Brucella spp. in cattle, sheep, and goats in Tanzania. PLoS Neglected Tropical Diseases, 2021, 15, e0009630.	3.0	7
6	Persistent pathogens and wildlife reservoirs. Science, 2021, 374, 35-36.	12.6	3
7	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
8	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
9	Farm-Level Risk Factors of Increased Abortion and Mortality in Domestic Ruminants during the 2010 Rift Valley Fever Outbreak in Central South Africa. Pathogens, 2020, 9, 914.	2.8	2
10	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
11	Socially vs. Privately Optimal Control of Livestock Diseases: A Case for Integration of Epidemiology and Economics. Frontiers in Veterinary Science, 2020, 7, 558409.	2.2	6
12	One Health in Practice: Using Integrated Bite Case Management to Increase Detection of Rabid Animals in Tanzania. Frontiers in Public Health, 2020, 8, 13.	2.7	35
13	Prevalence and speciation of brucellosis in febrile patients from a pastoralist community of Tanzania. Scientific Reports, 2020, 10, 7081.	3.3	30
14	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
15	Low topotype diversity of recent foot-and-mouth disease virus serotypes O and A from districts located along the Uganda and Tanzania border. Journal of Veterinary Science, 2019, 20, e4.	1.3	4
16	Transmission ecology of canine parvovirus in a multi-host, multi-pathogen system. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182772.	2.6	26
17	Venezuela's humanitarian crisis, resurgence of vector-borne diseases, and implications for spillover in the region. Lancet Infectious Diseases, The, 2019, 19, e149-e161.	9.1	138
18	Deep Sequencing of Foot-and-Mouth Disease Virus Reveals RNA Sequences Involved in Genome Packaging. Journal of Virology, 2018, 92, .	3.4	19

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19	A method for the direct detection of airborne dispersal in lichens. Molecular Ecology Resources, 2018, 18, 240-250.	4.8	8
20	The impact of passive case detection on the transmission dynamics of gambiense Human African Trypanosomiasis. PLoS Neglected Tropical Diseases, 2018, 12, e0006276.	3.0	7
21	Waves of endemic foot-and-mouth disease in eastern Africa suggest feasibility of proactive vaccination approaches. Nature Ecology and Evolution, 2018, 2, 1449-1457.	7.8	66
22	Driving improvements in emerging disease surveillance through locally relevant capacity strengthening. Science, 2017, 357, 146-148.	12.6	60
23	One Health Research in Northern Tanzania – Challenges and Progress. The East African Health Research Journal, 2017, 1, 8-18.	0.4	11
24	Integrating serological and genetic data to quantify cross-species transmission: brucellosis as a case study. Parasitology, 2016, 143, 821-834.	1.5	24
25	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
26	Efficient generation of vesicular stomatitis virus (VSV)-pseudotypes bearing morbilliviral glycoproteins and their use in quantifying virus neutralising antibodies. Vaccine, 2016, 34, 814-822.	3.8	25
27	Mobile Phones As Surveillance Tools: Implementing and Evaluating a Large-Scale Intersectoral Surveillance System for Rabies in Tanzania. PLoS Medicine, 2016, 13, e1002002.	8.4	85
28	Identification of Low- and High-Impact Hemagglutinin Amino Acid Substitutions That Drive Antigenic Drift of Influenza A(H1N1) Viruses. PLoS Pathogens, 2016, 12, e1005526.	4.7	58
29	Heterogeneity in the spread and control of infectious disease: consequences for the elimination of canine rabies. Scientific Reports, 2015, 5, 18232.	3.3	45
30	Conservation and economic benefits of a road around the Serengeti. Conservation Biology, 2015, 29, 932-936.	4.7	17
31	Updated estimate of the duration of the meningo-encephalitic stage in gambiense human African trypanosomiasis. BMC Research Notes, 2015, 8, 292.	1.4	22
32	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
33	Establishing the link between habitat selection and animal population dynamics. Ecological Monographs, 2015, 85, 413-436.	5.4	111
34	Dynamics of a morbillivirus at the domestic–wildlife interface: Canine distemper virus in domestic dogs and lions. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1464-1469.	7.1	128
35	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
36	Distinguishing low frequency mutations from RT-PCR and sequence errors in viral deep sequencing data. BMC Genomics, 2015, 16, 229.	2.8	44

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37	Competition, predation, and migration: individual choice patterns of Serengeti migrants captured by hierarchical models. Ecological Monographs, 2014, 84, 355-372.	5.4	87
38	Genetic and antigenic characterisation of serotype A FMD viruses from East Africa to select new vaccine strains. Vaccine, 2014, 32, 5794-5800.	3.8	39
39	Supersize me: how whole-genome sequencing and big data are transforming epidemiology. Trends in Microbiology, 2014, 22, 282-291.	7.7	115
40	Assembling evidence for identifying reservoirs of infection. Trends in Ecology and Evolution, 2014, 29, 270-279.	8.7	209
41	Revisiting the diffusion approximation to estimate evolutionary rates of gene family diversification. Journal of Theoretical Biology, 2014, 341, 111-122.	1.7	1
42	Evolution of foot-and-mouth disease virus intra-sample sequence diversity during serial transmission in bovine hosts. Veterinary Research, 2013, 44, 12.	3.0	56
43	Surveillance guidelines for disease elimination: A case study of canine rabies. Comparative Immunology, Microbiology and Infectious Diseases, 2013, 36, 249-261.	1.6	87
44	Designing Programs for Eliminating Canine Rabies from Islands: Bali, Indonesia as a Case Study. PLoS Neglected Tropical Diseases, 2013, 7, e2372.	3.0	128
45	Observing micro-evolutionary processes of viral populations at multiple scales. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120203.	4.0	29
46	A Bayesian Inference Framework to Reconstruct Transmission Trees Using Epidemiological and Genetic Data. PLoS Computational Biology, 2012, 8, e1002768.	3.2	104
47	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
48	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
49	Metapopulation dynamics of rabies and the efficacy of vaccination. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2182-2190.	2.6	47
50	Response of endemic afroalpine rodents to the removal of livestock grazing pressure. Environmental Epigenetics, 2011, 57, 741-750.	1.8	14
51	Beyond the Consensus: Dissecting Within-Host Viral Population Diversity of Foot-and-Mouth Disease Virus by Using Next-Generation Genome Sequencing. Journal of Virology, 2011, 85, 2266-2275.	3.4	127
52	Culling wildlife hosts to control disease: mountain hares, red grouse and louping ill virus. Journal of Applied Ecology, 2010, 47, 926-930.	4.0	45
53	Transmission Dynamics and Prospects for the Elimination of Canine Rabies. PLoS Biology, 2009, 7, e1000053.	5.6	374
54	Exploring reservoir dynamics: a case study of rabies in the Serengeti ecosystem. Journal of Applied Ecology, 2008, 45, 1246-1257.	4.0	166

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#	Article	IF	CITATIONS
55	Transmission Pathways of Foot-and-Mouth Disease Virus in the United Kingdom in 2007. PLoS Pathogens, 2008, 4, e1000050.	4.7	178
56	Emerging pathogens: the epidemiology and evolution of species jumps. Trends in Ecology and Evolution, 2005, 20, 238-244.	8.7	597
57	The shape of red grouse cycles. Journal of Animal Ecology, 2004, 73, 767-776.	2.8	21
58	Analysing noisy time–series: describing regional variation in the cyclic dynamics of red grouse. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 1609-1617.	2.6	41
59	Identifying Reservoirs of Infection: A Conceptual and Practical Challenge. Emerging Infectious Diseases, 2002, 8, 1468-1473.	4.3	630
60	Serial passage of foot-and-mouth disease virus in sheep reveals declining levels of viraemia over time. Journal of General Virology, 2002, 83, 1907-1914.	2.9	33
61	Effect of fire on northern bettong (Bettongia tropica) foraging behaviour. Austral Ecology, 2001, 26, 649-659.	1.5	39
62	Evidence for Positive Selection in Foot-and-Mouth Disease Virus Capsid Genes From Field Isolates. Genetics, 2001, 157, 7-15.	2.9	126
63	Sperm-limited fecundity and polyandry-induced mortality in female nematodes Caenorhabditis remanei. Biological Journal of the Linnean Society, 0, 99, 362-369.	1.6	44