

# Daniel G Streicker

## List of Publications by Year in descending order

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76  
papers

5,295  
citations

87888

38  
h-index

98798

67  
g-index

89  
all docs

89  
docs citations

89  
times ranked

5860  
citing authors

#	ARTICLE	IF	CITATIONS
1	Host Phylogeny Constrains Cross-Species Emergence and Establishment of Rabies Virus in Bats. <i>Science</i> , 2010, 329, 676-679.	12.6	407
2	Anthropogenic Land Use Change and Infectious Diseases: A Review of the Evidence. <i>EcoHealth</i> , 2014, 11, 619-632.	2.0	288
3	Linking anthropogenic resources to wildlifeâ€“pathogen dynamics: a review and metaâ€“analysis. <i>Ecology Letters</i> , 2015, 18, 483-495.	6.4	266
4	Multiple mortality events in bats: a global review. <i>Mammal Review</i> , 2016, 46, 175-190.	4.8	240
5	Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9423-9430.	7.1	234
6	The spread and evolution of rabies virus: conquering new frontiers. <i>Nature Reviews Microbiology</i> , 2018, 16, 241-255.	28.6	191
7	Ecological and anthropogenic drivers of rabies exposure in vampire bats: implications for transmission and control. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3384-3392.	2.6	187
8	Molecular Inferences Suggest Multiple Host Shifts of Rabies Viruses from Bats to Mesocarnivores in Arizona during 2001â€“2009. <i>PLoS Pathogens</i> , 2012, 8, e1002786.	4.7	160
9	Transmission or Within-Host Dynamics Driving Pulses of Zoonotic Viruses in Reservoirâ€“Host Populations. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004796.	3.0	152
10	Resolving the roles of immunity, pathogenesis, and immigration for rabies persistence in vampire bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20837-20842.	7.1	149
11	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120196.	4.0	141
12	Predicting reservoir hosts and arthropod vectors from evolutionary signatures in RNA virus genomes. <i>Science</i> , 2018, 362, 577-580.	12.6	140
13	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
14	Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. <i>PLoS Pathogens</i> , 2020, 16, e1008758.	4.7	127
15	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
16	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. <i>Emerging Infectious Diseases</i> , 2007, 13, 1526-1532.	4.3	123
17	Hostâ€“pathogen evolutionary signatures reveal dynamics and future invasions of vampire bat rabies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10926-10931.	7.1	108
18	Differential sources of host species heterogeneity influence the transmission and control of multihost parasites. <i>Ecology Letters</i> , 2013, 16, 975-984.	6.4	100

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19	Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 143, 1-12.	4.1	94
20	The role of viral evolution in rabies host shifts and emergence. <i>Current Opinion in Virology</i> , 2014, 8, 68-72.	5.4	83
21	Are All Hosts Created Equal? Partitioning Host Species Contributions to Parasite Persistence in Multihost Communities. <i>American Naturalist</i> , 2015, 186, 610-622.	2.1	82
22	Rates of Viral Evolution Are Linked to Host Geography in Bat Rabies. <i>PLoS Pathogens</i> , 2012, 8, e1002720.	4.7	79
23	The history of rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 146, 221-232.	4.1	77
24	Variable evolutionary routes to host establishment across repeated rabies virus host shifts among bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19715-19720.	7.1	70
25	Using <scp>DNA</scp> metabarcoding for simultaneous inference of common vampire bat diet and population structure. <i>Molecular Ecology Resources</i> , 2018, 18, 1050-1063.	4.8	70
26	Livestock abundance predicts vampire bat demography, immune profiles and bacterial infection risk. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170089.	4.0	68
27	Foraging choices of vampire bats in diverse landscapes: potential implications for land-use change and disease transmission. <i>Journal of Applied Ecology</i> , 2016, 53, 1280-1288.	4.0	66
28	Demographic and environmental drivers of metagenomic viral diversity in vampire bats. <i>Molecular Ecology</i> , 2020, 29, 26-39.	3.9	66
29	Novel hemotropic mycoplasmas are widespread and genetically diverse in vampire bats. <i>Epidemiology and Infection</i> , 2017, 145, 3154-3167.	2.1	54
30	Food for contagion: synthesis and future directions for studying host-parasite responses to resource shifts in anthropogenic environments. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170102.	4.0	54
31	Identifying and prioritizing potential human-infecting viruses from their genome sequences. <i>PLoS Biology</i> , 2021, 19, e3001390.	5.6	54
32	Using host species traits to understand the consequences of resource provisioning for host-parasite interactions. <i>Journal of Animal Ecology</i> , 2018, 87, 511-525.	2.8	53
33	Using noninvasive metagenomics to characterize viral communities from wildlife. <i>Molecular Ecology Resources</i> , 2019, 19, 128-143.	4.8	53
34	Vampire Bats and Rabies: Toward an Ecological Solution to a Public Health Problem. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2867.	3.0	52
35	Enzootic and Epizootic Rabies Associated with Vampire Bats, Peru. <i>Emerging Infectious Diseases</i> , 2013, 19, 1463-69.	4.3	48
36	Spatial expansions and travelling waves of rabies in vampire bats. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160328.	2.6	48

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37	Quantifying the burden of vampire bat rabies in Peruvian livestock. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006105.	3.0	46
38	Genetic diversity, infection prevalence, and possible transmission routes of <i>Bartonella</i> spp. in vampire bats. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006786.	3.0	46
39	Predictors and immunological correlates of sublethal mercury exposure in vampire bats. <i>Royal Society Open Science</i> , 2017, 4, 170073.	2.4	45
40	Fluorescent biomarkers demonstrate prospects for spreadable vaccines to control disease transmission in wild bats. <i>Nature Ecology and Evolution</i> , 2019, 3, 1697-1704.	7.8	42
41	Virulence mismatches in index hosts shape the outcomes of cross-species transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28859-28866.	7.1	41
42	Diversification of mammalian deltaviruses by host shifting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
43	Defining New Pathways to Manage the Ongoing Emergence of Bat Rabies in Latin America. <i>Viruses</i> , 2020, 12, 1002.	3.3	38
44	Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. <i>Viruses</i> , 2021, 13, 252.	3.3	35
45	Serologic survey of <i>Eptesicus fuscus</i> from Georgia, U.S.A. for <i>Rickettsia</i> and <i>Borrelia</i> and laboratory transmission of a <i>Rickettsia</i> by bat ticks. <i>Journal of Vector Ecology</i> , 2006, 31, 386-389.	1.0	33
46	Using host traits to predict reservoir host species of rabies virus. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008940.	3.0	29
47	A new phylogenetic lineage of Rabies virus associated with western pipistrelle bats ( <i>Pipistrellus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.9	28
48	Ecological and evolutionary drivers of haemoplasma infection and bacterial genotype sharing in a Neotropical bat community. <i>Molecular Ecology</i> , 2020, 29, 1534-1549.	3.9	27
49	Leukocyte Profiles Reflect Geographic Range Limits in a Widespread Neotropical Bat. <i>Integrative and Comparative Biology</i> , 2019, 59, 1176-1189.	2.0	24
50	Contextualizing bats as viral reservoirs. <i>Science</i> , 2020, 370, 172-173.	12.6	24
51	Long-term maintenance of multidrug-resistant <i>Escherichia coli</i> carried by vampire bats and shared with livestock in Peru. <i>Science of the Total Environment</i> , 2022, 810, 152045.	8.0	22
52	Bats host the most virulentâ€”but not the most dangerousâ€”zoonotic viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113628119.	7.1	22
53	Anthropogenic Roost Switching and Rabies Virus Dynamics in House-Roosting Big Brown Bats. <i>Vector-Borne and Zoonotic Diseases</i> , 2013, 13, 498-504.	1.5	21
54	Phylogenetics reveals extinctionâ€”recolonization dynamics underpin apparently endemic vampire bat rabies in Costa Rica. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191527.	2.6	19

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55	Knowledge gaps about rabies transmission from vampire bats to humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 517-518.	7.8	19
56	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	12.8	18
57	Abortive vampire bat rabies infections in Peruvian peridomestic livestock. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008194.	3.0	18
58	Knowledge and use of antibiotics among low-income small-scale farmers of Peru. <i>Preventive Veterinary Medicine</i> , 2021, 189, 105287.	1.9	18
59	The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid self-targeting. <i>PLoS Biology</i> , 2021, 19, e3001352.	5.6	18
60	Predicting spatial spread of rabies in skunk populations using surveillance data reported by the public. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005822.	3.0	17
61	Detection of <i>Trypanosoma cruzi</i> in the saliva of diverse neotropical bats. <i>Zoonoses and Public Health</i> , 2021, 68, 271-276.	2.2	15
62	Complete Genome Sequence of an Alphacoronavirus from Common Vampire Bats in Peru. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	14
63	Temporal patterns of vampire bat rabies and host connectivity in Belize. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 870-879.	3.0	14
64	New records of pigmentation disorders in molossid and phyllostomid (Chiroptera) bats from Peru. <i>Mammalia</i> , 2014, 78, .	0.7	13
65	Longitudinal deep sequencing informs vector selection and future deployment strategies for transmissible vaccines. <i>PLoS Biology</i> , 2022, 20, e3001580.	5.6	10
66	Six new species of coccidia (Apicomplexa: Eimeriidae) from endangered <i>Phelsuma</i> spp. geckoes (Sauria: Tj ETQq0 Q 0 rgBT /Qverlock 10	1.3	9
67	From Persistence to Cross-Species Emergence of a Viral Zoonosis. <i>Science</i> , 2013, 342, 1185-1186.	12.6	8
68	Predicting the presence and titre of rabies virus neutralizing antibodies from low volume serum samples in low containment facilities. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1564-1576.	3.0	7
69	A new species of <i>Caryospora</i> L�ger, 1904 (Apicomplexa: Eimeriidae) from the endangered Round Island boa <i>Casarea dussumieri</i> (Schlegel) (Serpentes: Bolyeridae) of Round Island, Mauritius: an endangered parasite?. <i>Systematic Parasitology</i> , 2011, 78, 117-122.	1.1	6
70	Management of vampire bats and rabies: a precaution for rewilding projects in the Neotropics. <i>Perspectives in Ecology and Conservation</i> , 2021, 19, 37-42.	1.9	5
71	A New Species of <i>Eimeria</i> (Apicomplexa: Eimeriidae) From the Western Hognose Snake, <i>Heterodon nasicus</i> (Serpentes: Xenodontidae), From Texas. <i>Journal of Parasitology</i> , 2011, 97, 463-465.	0.7	4
72	Evolution of rabies virus. , 2020, , 83-101.		4

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73	Self-spreading vaccines: Base policy on evidence. <i>Science</i> , 2022, 375, 1362-1363.	12.6	3
74	Global high-risk clone of extended-spectrum $\beta$ -lactamase (ESBL)-producing <i>Klebsiella pneumoniae</i> ST307 emerging in livestock in Peru. <i>International Journal of Antimicrobial Agents</i> , 2021, 58, 106389.	2.5	2
75	Divergent Rabies Virus Variant of Probable Bat Origin in 2 Gray Foxes, New Mexico, USA. <i>Emerging Infectious Diseases</i> , 2022, 28, .	4.3	2
76	A two-step metagenomics approach for the identification and mitochondrial DNA contig assembly of vertebrate prey from the blood meals of common vampire bats ( <i>Desmodus rotundus</i> ). <i>Metabarcoding and Metagenomics</i> , 0, 6, .	0.0	1