

Daniel G Streicker

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	Self-spreading vaccines: Base policy on evidence. <i>Science</i> , 2022, 375, 1362-1363.	12.6	3
3	Bats host the most virulent "but not the most dangerous" zoonotic viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113628119.	7.1	22
4	Longitudinal deep sequencing informs vector selection and future deployment strategies for transmissible vaccines. <i>PLoS Biology</i> , 2022, 20, e3001580.	5.6	10
5	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
6	Temporal patterns of vampire bat rabies and host connectivity in Belize. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 870-879.	3.0	14
7	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
8	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
9	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
10	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
11	Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. <i>Viruses</i> , 2021, 13, 252.	3.3	35
12	Knowledge and use of antibiotics among low-income small-scale farmers of Peru. <i>Preventive Veterinary Medicine</i> , 2021, 189, 105287.	1.9	18
13	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
14	Global high-risk clone of extended-spectrum β -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
15	Identifying and prioritizing potential human-infecting viruses from their genome sequences. <i>PLoS Biology</i> , 2021, 19, e3001390.	5.6	54
16	Demographic and environmental drivers of metagenomic viral diversity in vampire bats. <i>Molecular Ecology</i> , 2020, 29, 26-39.	3.9	66
17	Contextualizing bats as viral reservoirs. <i>Science</i> , 2020, 370, 172-173.	12.6	24
18	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	12.8	18

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19	Virulence mismatches in index hosts shape the outcomes of cross-species transmission. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28859-28866.	7.1	41
20	Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. PLoS Pathogens, 2020, 16, e1008758.	4.7	127
21	Complete Genome Sequence of an Alphacoronavirus from Common Vampire Bats in Peru. Microbiology Resource Announcements, 2020, 9, .	0.6	14
22	Defining New Pathways to Manage the Ongoing Emergence of Bat Rabies in Latin America. Viruses, 2020, 12, 1002.	3.3	38
23	Evolution of rabies virus. , 2020, , 83-101.		4
24	Knowledge gaps about rabies transmission from vampire bats to humans. Nature Ecology and Evolution, 2020, 4, 517-518.	7.8	19
25	Abortive vampire bat rabies infections in Peruvian peridomestic livestock. PLoS Neglected Tropical Diseases, 2020, 14, e0008194.	3.0	18
26	Ecological and evolutionary drivers of haemoplasma infection and bacterial genotype sharing in a Neotropical bat community. Molecular Ecology, 2020, 29, 1534-1549.	3.9	27
27	Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9423-9430.	7.1	234
28	Using host traits to predict reservoir host species of rabies virus. PLoS Neglected Tropical Diseases, 2020, 14, e0008940.	3.0	29
29	Phylodynamics reveals extinctionâ€“recolonization dynamics underpin apparently endemic vampire bat rabies in Costa Rica. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191527.	2.6	19
30	Leukocyte Profiles Reflect Geographic Range Limits in a Widespread Neotropical Bat. Integrative and Comparative Biology, 2019, 59, 1176-1189.	2.0	24
31	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
32	Fluorescent biomarkers demonstrate prospects for spreadable vaccines to control disease transmission in wild bats. Nature Ecology and Evolution, 2019, 3, 1697-1704.	7.8	42
33	Using noninvasive metagenomics to characterize viral communities from wildlife. Molecular Ecology Resources, 2019, 19, 128-143.	4.8	53
34	The spread and evolution of rabies virus: conquering new frontiers. Nature Reviews Microbiology, 2018, 16, 241-255.	28.6	191
35	Using <scp>DNA</scp> metabarcoding for simultaneous inference of common vampire bat diet and population structure. Molecular Ecology Resources, 2018, 18, 1050-1063.	4.8	70
36	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. Nature Ecology and Evolution, 2018, 2, 659-668.	7.8	124

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37	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
38	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
39	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
40	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
41	Predicting reservoir hosts and arthropod vectors from evolutionary signatures in RNA virus genomes. <i>Science</i> , 2018, 362, 577-580.	12.6	140
42	Predictors and immunological correlates of sublethal mercury exposure in vampire bats. <i>Royal Society Open Science</i> , 2017, 4, 170073.	2.4	45
43	The history of rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 146, 221-232.	4.1	77
44	Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 143, 1-12.	4.1	94
45	Novel hemotropic mycoplasmas are widespread and genetically diverse in vampire bats. <i>Epidemiology and Infection</i> , 2017, 145, 3154-3167.	2.1	54
46	Quantifying the burden of vampire bat rabies in Peruvian livestock. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006105.	3.0	46
47	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
48	Transmission or Within-Host Dynamics Driving Pulses of Zoonotic Viruses in Reservoir-Host Populations. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004796.	3.0	152
49	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
50	Host-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
51	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
52	Multiple mortality events in bats: a global review. <i>Mammal Review</i> , 2016, 46, 175-190.	4.8	240
53	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
54	Linking anthropogenic resources to wildlife-pathogen dynamics: a review and meta-analysis. <i>Ecology Letters</i> , 2015, 18, 483-495.	6.4	266

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55	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
56	New records of pigmentation disorders in molossid and phyllostomid (Chiroptera) bats from Peru. <i>Mammalia</i> , 2014, 78, .	0.7	13
57	Anthropogenic Land Use Change and Infectious Diseases: A Review of the Evidence. <i>EcoHealth</i> , 2014, 11, 619-632.	2.0	288
58	The role of viral evolution in rabies host shifts and emergence. <i>Current Opinion in Virology</i> , 2014, 8, 68-72.	5.4	83
59	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
60	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
61	Enzootic and Epizootic Rabies Associated with Vampire Bats, Peru. <i>Emerging Infectious Diseases</i> , 2013, 19, 1463-69.	4.3	48
62	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
63	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
64	From Persistence to Cross-Species Emergence of a Viral Zoonosis. <i>Science</i> , 2013, 342, 1185-1186.	12.6	8
65	Molecular Inferences Suggest Multiple Host Shifts of Rabies Viruses from Bats to Mesocarnivores in Arizona during 2001-2009. <i>PLoS Pathogens</i> , 2012, 8, e1002786.	4.7	160
66	Rates of Viral Evolution Are Linked to Host Geography in Bat Rabies. <i>PLoS Pathogens</i> , 2012, 8, e1002720.	4.7	79
67	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
68	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
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	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
71	Host Phylogeny Constrains Cross-Species Emergence and Establishment of Rabies Virus in Bats. <i>Science</i> , 2010, 329, 676-679.	12.6	407
72	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

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73	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. <i>Emerging Infectious Diseases</i> , 2007, 13, 1526-1532.	4.3	123
74	A new phylogenetic lineage of Rabies virus associated with western pipistrelle bats (<i>Pipistrellus</i>) Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50 70	2.9	28
75	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
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