

Daniel G Streicker

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

5,295
citations

100601

38
h-index

111975

67
g-index

89
all docs

89
docs citations

89
times ranked

6391
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.	3.9	22
2	Self-spreading vaccines: Base policy on evidence. <i>Science</i> , 2022, 375, 1362-1363.	6.0	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.	3.3	22
4	Longitudinal deep sequencing informs vector selection and future deployment strategies for transmissible vaccines. <i>PLoS Biology</i> , 2022, 20, e3001580.	2.6	10
5	Divergent Rabies Virus Variant of Probable Bat Origin in 2 Gray Foxes, New Mexico, USA. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	2
6	Temporal patterns of vampire bat rabies and host connectivity in Belize. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 870-879.	1.3	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.	1.3	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, .	3.3	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.	1.0	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.	0.9	15
11	Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. <i>Viruses</i> , 2021, 13, 252.	1.5	35
12	Knowledge and use of antibiotics among low-income small-scale farmers of Peru. <i>Preventive Veterinary Medicine</i> , 2021, 189, 105287.	0.7	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.	2.6	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.	1.1	2
15	Identifying and prioritizing potential human-infecting viruses from their genome sequences. <i>PLoS Biology</i> , 2021, 19, e3001390.	2.6	54
16	Demographic and environmental drivers of metagenomic viral diversity in vampire bats. <i>Molecular Ecology</i> , 2020, 29, 26-39.	2.0	66
17	Contextualizing bats as viral reservoirs. <i>Science</i> , 2020, 370, 172-173.	6.0	24
18	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	5.8	18

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19	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.	3.3	41
20	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.	2.1	127
21	Complete Genome Sequence of an Alphacoronavirus from Common Vampire Bats in Peru. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	14
22	Defining New Pathways to Manage the Ongoing Emergence of Bat Rabies in Latin America. <i>Viruses</i> , 2020, 12, 1002.	1.5	38
23	Evolution of rabies virus. , 2020, , 83-101.		4
24	Knowledge gaps about rabies transmission from vampire bats to humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 517-518.	3.4	19
25	Abortive vampire bat rabies infections in Peruvian peridomestic livestock. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008194.	1.3	18
26	Ecological and evolutionary drivers of haemoplasma infection and bacterial genotype sharing in a Neotropical bat community. <i>Molecular Ecology</i> , 2020, 29, 1534-1549.	2.0	27
27	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.	3.3	234
28	Using host traits to predict reservoir host species of rabies virus. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008940.	1.3	29
29	Phylodynamics 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.	1.2	19
30	Leukocyte Profiles Reflect Geographic Range Limits in a Widespread Neotropical Bat. <i>Integrative and Comparative Biology</i> , 2019, 59, 1176-1189.	0.9	24
31	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.	4.6	138
32	Fluorescent biomarkers demonstrate prospects for spreadable vaccines to control disease transmission in wild bats. <i>Nature Ecology and Evolution</i> , 2019, 3, 1697-1704.	3.4	42
33	Using noninvasive metagenomics to characterize viral communities from wildlife. <i>Molecular Ecology Resources</i> , 2019, 19, 128-143.	2.2	53
34	The spread and evolution of rabies virus: conquering new frontiers. <i>Nature Reviews Microbiology</i> , 2018, 16, 241-255.	13.6	191
35	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.	2.2	70
36	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	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.	1.8	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.	1.8	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.	1.3	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.	1.3	46
41	Predicting reservoir hosts and arthropod vectors from evolutionary signatures in RNA virus genomes. <i>Science</i> , 2018, 362, 577-580.	6.0	140
42	Predictors and immunological correlates of sublethal mercury exposure in vampire bats. <i>Royal Society Open Science</i> , 2017, 4, 170073.	1.1	45
43	The history of rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 146, 221-232.	1.9	77
44	Successful strategies implemented towards the elimination of canine rabies in the Western Hemisphere. <i>Antiviral Research</i> , 2017, 143, 1-12.	1.9	94
45	Novel hemotropic mycoplasmas are widespread and genetically diverse in vampire bats. <i>Epidemiology and Infection</i> , 2017, 145, 3154-3167.	1.0	54
46	Quantifying the burden of vampire bat rabies in Peruvian livestock. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006105.	1.3	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.	1.3	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.	1.3	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.	1.2	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.	3.3	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.	1.9	66
52	Multiple mortality events in bats: a global review. <i>Mammal Review</i> , 2016, 46, 175-190.	2.2	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.	1.0	82
54	Linking anthropogenic resources to wildlife-pathogen dynamics: a review and meta-analysis. <i>Ecology Letters</i> , 2015, 18, 483-495.	3.0	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.	1.3	52
56	New records of pigmentation disorders in molossid and phyllostomid (Chiroptera) bats from Peru. <i>Mammalia</i> , 2014, 78, .	0.3	13
57	Anthropogenic Land Use Change and Infectious Diseases: A Review of the Evidence. <i>EcoHealth</i> , 2014, 11, 619-632.	0.9	288
58	The role of viral evolution in rabies host shifts and emergence. <i>Current Opinion in Virology</i> , 2014, 8, 68-72.	2.6	83
59	Differential sources of host species heterogeneity influence the transmission and control of multihost parasites. <i>Ecology Letters</i> , 2013, 16, 975-984.	3.0	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.	0.6	21
61	Enzootic and Epizootic Rabies Associated with Vampire Bats, Peru. <i>Emerging Infectious Diseases</i> , 2013, 19, 1463-69.	2.0	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.	1.8	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.	3.3	149
64	From Persistence to Cross-Species Emergence of a Viral Zoonosis. <i>Science</i> , 2013, 342, 1185-1186.	6.0	8
65	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.	2.1	160
66	Rates of Viral Evolution Are Linked to Host Geography in Bat Rabies. <i>PLoS Pathogens</i> , 2012, 8, e1002720.	2.1	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.	3.3	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.	1.2	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.	0.5	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.	0.3	4
71	Host Phylogeny Constrains Cross-Species Emergence and Establishment of Rabies Virus in Bats. <i>Science</i> , 2010, 329, 676-679.	6.0	407
72	Six new species of coccidia (Apicomplexa: Eimeriidae) from endangered <i>Phelsuma</i> spp. geckoes (Sauria: Tj ETQq0 0,0 rgBT /Qverlock 10	0,7	9

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73	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. <i>Emerging Infectious Diseases</i> , 2007, 13, 1526-1532.	2.0	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	1.3	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.	0.5	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