Kathryn A Hanley

List of Publications by Year
in descending order

48 papers	2,043 citations	257450 24 h-index	254184 43 g-index
49 all docs	49 docs citations	49 times ranked	3350 citing authors

#	Article	IF	Citations
1	Zika Virus Emergence in Mosquitoes in Southeastern Senegal, 2011. PLoS ONE, 2014, 9, e109442.	2.5	275
2	Fever versus fever: The role of host and vector susceptibility and interspecific competition in shaping the current and future distributions of the sylvatic cycles of dengue virus and yellow fever virus. Infection, Genetics and Evolution, 2013, 19, 292-311.	2.3	152
3	Mosquitoes Put the Brake on Arbovirus Evolution: Experimental Evolution Reveals Slower Mutation Accumulation in Mosquito Than Vertebrate Cells. PLoS Pathogens, 2009, 5, e1000467.	4.7	146
4	Congenital Zika virus infection as a silent pathology with loss of neurogenic output in the fetal brain. Nature Medicine, 2018, 24, 368-374.	30.7	117
5	Superior infectivity for mosquito vectors contributes to competitive displacement among strains of dengue virus. BMC Ecology, 2008, 8, 1.	3.0	103
6	Potential for Zika Virus to Establish a Sylvatic Transmission Cycle in the Americas. PLoS Neglected Tropical Diseases, 2016, 10, e0005055.	3.0	89
7	The Double-Edged Sword: How Evolution Can Make or Break a Live-Attenuated Virus Vaccine. Evolution: Education and Outreach, 2011, 4, 635-643.	0.8	88
8	Impact of Climate and Mosquito Vector Abundance on Sylvatic Arbovirus Circulation Dynamics in Senegal. American Journal of Tropical Medicine and Hygiene, 2015, 92, 88-97.	1.4	80
9	Differential Vector Competency of Aedes albopictus Populations from the Americas for Zika Virus. American Journal of Tropical Medicine and Hygiene, 2017, 97, 330-339.	1.4	72
10	A trade-off in replication in mosquito versus mammalian systems conferred by a point mutation in the NS4B protein of dengue virus type 4. Virology, 2003, 312, 222-232.	2.4	69
11	Role of monkeys in the sylvatic cycle of chikungunya virus in Senegal. Nature Communications, 2018, 9, 1046.	12.8	56
12	Lineage II of Southeast Asian/American DENV-2 is Associated with a Severe Dengue Outbreak in the Peruvian Amazon. American Journal of Tropical Medicine and Hygiene, 2014, 91, 611-620.	1.4	50
13	PacBio-Based Mitochondrial Genome Assembly of Leucaena trichandra (Leguminosae) and an Intrageneric Assessment of Mitochondrial RNA Editing. Genome Biology and Evolution, 2018, 10, 2501-2517.	2.5	49
14	The tortoise or the hare? Impacts of within-host dynamics on transmission success of arthropod-borne viruses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140299.	4.0	46
15	Characterization of Three New Insect-Specific Flaviviruses: Their Relationship to the Mosquito-Borne Flavivirus Pathogens. American Journal of Tropical Medicine and Hygiene, 2018, 98, 410-419.	1.4	45
16	Abundance and distribution of sylvatic dengue virus vectors in three different land cover types in Sarawak, Malaysian Borneo. Parasites and Vectors, 2017, 10, 406.	2.5	42
17	Secondary structure of dengue virus type 4 3â€² untranslated region: impact of deletion and substitution mutations. Journal of General Virology, 2006, 87, 3291-3296.	2.9	40
18	Widespread insecticide resistance in Aedes aegypti L. from New Mexico, U.S.A.. PLoS ONE, 2019, 14, e0212693.	2.5	39

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19	Into the woods: Changes in mosquito community composition and presence of key vectors at increasing distances from the urban edge in urban forest parks in Manaus, Brazil. Acta Tropica, 2020, 206, 105441.	2.0	39
20	Modulation of Flavivirus Population Diversity by RNA Interference. Journal of Virology, 2015, 89, 4035-4039.	3.4	36
21	Ecological niche modeling of Aedes mosquito vectors of chikungunya virus in southeastern Senegal. Parasites and Vectors, 2018, 11, 255.	2.5	35
22	Schlafen 11 Restricts Flavivirus Replication. Journal of Virology, 2019, 93, .	3.4	34
23	Dengue virus serotype 2 infection alters midgut and carcass gene expression in the Asian tiger mosquito, Aedes albopictus. PLoS ONE, 2017, 12, e0171345.	2.5	32
24	Patterns of a Sylvatic Yellow Fever Virus Amplification in Southeastern Senegal, 2010. American Journal of Tropical Medicine and Hygiene, 2014, 90, 1003-1013.	1.4	28
25	The Effect of SkitoSnack, an Artificial Blood Meal Replacement, on Aedes aegypti Life History Traits and Gut Microbiota. Scientific Reports, 2018, 8, 11023.	3.3	28
26	The vertical stratification of potential bridge vectors of mosquito-borne viruses in a central Amazonian forest bordering Manaus, Brazil. Scientific Reports, 2020, 10, 18254.	3.3	27
27	Chikungunya Outbreak in Kedougou, Southeastern Senegal in 2009â€“2010. Open Forum Infectious Diseases, 2018, 5, ofx259.	0.9	24
28	Colonized Sabethes cyaneus, a Sylvatic New World Mosquito Species, Shows a Low Vector Competence for Zika Virus Relative to Aedes aegypti. Viruses, 2018, 10, 434.	3.3	23
29	Infection Dynamics of Sylvatic Dengue Virus in a Natural Primate Host, the African Green Monkey. American Journal of Tropical Medicine and Hygiene, 2014, 91, 672-676.	1.4	20
30	Ecological processes underlying the emergence of novel enzootic cycles: Arboviruses in the neotropics as a case study. PLoS Neglected Tropical Diseases, 2020, 14, e0008338.	3.0	19
31	Repertoire of virus-derived small RNAs produced by mosquito and mammalian cells in response to dengue virus infection. Virology, 2015, 476, 54-60.	2.4	13
32	Support for the Transmission-Clearance Trade-Off Hypothesis from a Study of Zika Virus Delivered by Mosquito Bite to Mice. Viruses, 2019, 11, 1072.	3.3	11
33	Old Drugs with New Tricks: Efficacy of Fluoroquinolones to Suppress Replication of Flaviviruses. Viruses, 2020, 12, 1022.	3.3	11
34	Shifts in mosquito diversity and abundance along a gradient from oil palm plantations to conterminous forests in Borneo. Ecosphere, 2021, 12, e03463.	2.2	11
35	ORIGINAL ARTICLE: Coinfection rates in Ï†6 bacteriophage are enhanced by virusâ€induced changes in host cells. Evolutionary Applications, 2009, 2, 24-31.	3.1	10
36	Replacement of conserved or variable sequences of the mosquito-borne dengue virus 3â€² UTR with homologous sequences from Modoc virus does not change infectivity for mosquitoes. Journal of General Virology, 2013, 94, 783-788.	2.9	10

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37	Biodiversity Pattern of Mosquitoes in Southeastern Senegal, Epidemiological Implication in Arbovirus and Malaria Transmission. Journal of Medical Entomology, 2019, 56, 453-463.	1.8	10
38	Evolution of resistance to fluoroquinolones by dengue virus serotype 4 provides insight into mechanism of action and consequences for viral fitness. Virology, 2021, 552, 94-106.	2.4	9
39	Vector Surveillance, Host Species Richness, and Demographic Factors as West Nile Disease Risk Indicators. Viruses, 2021, 13, 934.	3.3	8
40	Evolutionary consequences of feedbacks between within-host competition and disease control. Evolution, Medicine and Public Health, 2020, 2020, 30-34.	2.5	7
41	Identification of Mosquito Bloodmeals Collected in Diverse Habitats in Malaysian Borneo Using COI Barcoding. Tropical Medicine and Infectious Disease, 2020, 5, 51.	2.3	7
42	Lack of Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Spillover in Free-Living Neotropical Non-Human Primates, Brazil. Viruses, 2021, 13, 1933.	3.3	7
43	Microclimate and the vertical stratification of potential bridge vectors of mosquitoâ€‘borne viruses captured by nets and ovitraps in a central Amazonian forest bordering Manaus, Brazil. Scientific Reports, 2021, 11, 21129.	3.3	6
44	Endless Forms: Within-Host Variation in the Structure of the West Nile Virus RNA Genome during Serial Passage in Bird Hosts. MSphere, 2019, 4, .	2.9	5
45	Programmable CRISPR interference for gene silencing using Cas13a in mosquitoes. Journal of Genomics, 2020, 8, 30-36.	0.9	4
46	Surveillance along the Rio Grande during the 2020 Vesicular Stomatitis Outbreak Reveals Spatio-Temporal Dynamics of and Viral RNA Detection in Black Flies. Pathogens, 2021, 10, 1264.	2.8	4
47	Aedes aegypti Shows Increased Susceptibility to Zika Virus via Both In Vitro and In Vivo Models of Type II Diabetes. Viruses, 2022, 14, 665.	3.3	3
48	Integrating Spatiotemporal Epidemiology, Eco-Phylogenetics, and Distributional Ecology to Assess West Nile Disease Risk in Horses. Viruses, 2021, 13, 1811.	3.3	2