Carrie A Manore

List of Publications by Year
in descending order

34 papers	763 citations	759233 12 h-index	552781 26 g-index
43 all docs	43 docs citations	43 times ranked	992 citing authors

#	Article	IF	Citations
1	Comparing dengue and chikungunya emergence and endemic transmission in A. aegypti and A. albopictus. Journal of Theoretical Biology, 2014, 356, 174-191.	1.7	139
2	Forecasting Zoonotic Infectious Disease Response to Climate Change: Mosquito Vectors and a Changing Environment. Veterinary Sciences, 2019, 6, 40.	1.7	85
3	Modelling vertical transmission in vector-borne diseases with applications to Rift Valley fever. Journal of Biological Dynamics, 2013, 7, 11-40.	1.7	67
4	Defining the Risk of Zika and Chikungunya Virus Transmission in Human Population Centers of the Eastern United States. PLoS Neglected Tropical Diseases, 2017, 11, e0005255.	3.0	54
5	Two-sex mosquito model for the persistence ofWolbachia. Journal of Biological Dynamics, 2017, 11, 216-237.	1.7	46
6	Modeling Virus Coinfection to Inform Management of Maize Lethal Necrosis in Kenya. Phytopathology, 2017, 107, 1095-1108.	2.2	41
7	Updated distribution maps of predominant Culex mosquitoes across the Americas. Parasites and Vectors, 2021, 14, 547.	2.5	40
8	A network-patch methodology for adapting agent-based models for directly transmitted disease to mosquito-borne disease. Journal of Biological Dynamics, 2015, 9, 52-72.	1.7	37
9	Estimating the reproductive number, total outbreak size, and reporting rates for Zika epidemics in South and Central America. Epidemics, 2017, 21, 63-79.	3.0	33
10	Towards an Early Warning System for Forecasting Human West Nile Virus Incidence. PLOS Currents, 2014, 6, .	1.4	32
11	Spatiotemporal incidence of Zika and associated environmental drivers for the 2015-2016 epidemic in Colombia. Scientific Data, 2018, 5, 180073.	5.3	29
12	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. PLoS Biology, 2019, 17, e3000551.	5.6	26
13	Trade-offs between individual and ensemble forecasts of an emerging infectious disease. Nature Communications, 2021, 12, 5379.	12.8	16
14	Distinguishing viruses responsible for influenza-like illness. Journal of Theoretical Biology, 2022, 545, 111145.	1.7	14
15	Disease properties, geography, and mitigation strategies in a simulation spread of rinderpest across the United States. Veterinary Research, 2011, 42, 55.	3.0	12
16	Google Health Trends performance reflecting dengue incidence for the Brazilian states. BMC Infectious Diseases, 2020, 20, 252.	2.9	11
17	Using heterogeneous data to identify signatures of dengue outbreaks at fine spatio-temporal scales across Brazil. PLoS Neglected Tropical Diseases, 2021, 15, e0009392.	3.0	10
18	Heterogeneous local dynamics revealed by classification analysis of spatially disaggregated time series data. Epidemics, 2019, 29, 100357.	3.0	9

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19	Modeling and Cost Benefit Analysis to Guide Deployment of POC Diagnostics for Non-typhoidal Salmonella Infections with Antimicrobial Resistance. Scientific Reports, 2019, 9, 11245.	3.3	8
20	Intermittent Preventive Treatment (IPT): Its Role in Averting Disease-Induced Mortality in Children and in Promoting the Spread of Antimalarial Drug Resistance. Bulletin of Mathematical Biology, 2019, 81, 193-234.	1.9	8
21	How New Mexico Leveraged a COVID-19 Case Forecasting Model to Preemptively Address the Health Care Needs of the State: Quantitative Analysis. JMIR Public Health and Surveillance, 2021, 7, e27888.	2.6	8
22	Constructing Rigorous and Broad Biosurveillance Networks for Detecting Emerging Zoonotic Outbreaks. PLoS ONE, 2015, 10, e0124037.	2.5	7
23	Predicting Dengue Incidence in Brazil Using Broad-Scale Spectral Remote Sensing Imagery. , 2018, , .		5
24	Bayesian time-varying occupancy model for West Nile virus in Ontario, Canada. Stochastic Environmental Research and Risk Assessment, 2022, 36, 2337-2352.	4.0	5
25	A time-varying vulnerability index for COVID-19 in New Mexico, USA using generalized propensity scores. Health Policy OPEN, 2021, 2, 100052.	1.5	4
26	Agent-based hantavirus transmission model incorporating host behavior and viral shedding heterogeneities derived from field transmission experiments. Letters in Biomathematics, 2016, 3, 209-228.	0.1	3
27	Intermittent Preventive Treatment (IPT) and the Spread of Drug Resistant Malaria. The IMA Volumes in Mathematics and Its Applications, 2015, , 197-233.	0.5	3
28	A Flexible Spatial Framework for Modeling Spread of Pathogens in Animals with Biosurveillance and Disease Control Applications. ISPRS International Journal of Geo-Information, 2014, 3, 638-661.	2.9	2
29	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0
30	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0
31	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0
32	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0
33	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0
34	Coinfections by noninteracting pathogens are not independent and require new tests of interaction. , 2019, 17, e3000551.		0