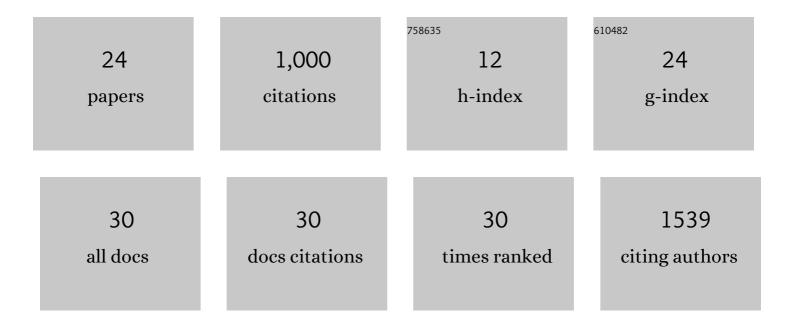
Rachel J Sippy

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8912599/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Thermal biology of mosquitoâ€borne disease. Ecology Letters, 2019, 22, 1690-1708.	3.0	349
2	Time to reality check the promises of machine learning-powered precision medicine. The Lancet Digital Health, 2020, 2, e677-e680.	5.9	126
3	Molecular Evidence for Zoonotic Transmission of an Emergent, Highly Pathogenic Campylobacter jejuni Clone in the United States. Journal of Clinical Microbiology, 2012, 50, 680-687.	1.8	98
4	Climate predicts geographic and temporal variation in mosquito-borne disease dynamics on two continents. Nature Communications, 2021, 12, 1233.	5.8	49
5	Effects of Political Instability in Venezuela on Malaria Resurgence at Ecuador–Peru Border, 2018. Emerging Infectious Diseases, 2019, 25, 834-836.	2.0	47
6	Occurrence and molecular analysis of Campylobacter in wildlife on livestock farms. Veterinary Microbiology, 2012, 157, 369-375.	0.8	45
7	Recommended reporting items for epidemic forecasting and prediction research: The EPIFORGE 2020 guidelines. PLoS Medicine, 2021, 18, e1003793.	3.9	42
8	Genetic Diversity and Antimicrobial Susceptibility of Campylobacter jejuni Isolates Associated with Sheep Abortion in the United States and Great Britain. Journal of Clinical Microbiology, 2014, 52, 1853-1861.	1.8	41
9	Critical Role of LuxS in the Virulence of Campylobacter jejuni in a Guinea Pig Model of Abortion. Infection and Immunity, 2012, 80, 585-593.	1.0	38
10	Assessing critical gaps in COVID-19 testing capacity: the case of delayed results in Ecuador. BMC Public Health, 2021, 21, 637.	1.2	32
11	Seasonal and geographic variation in insecticide resistance in Aedes aegypti in southern Ecuador. PLoS Neglected Tropical Diseases, 2019, 13, e0007448.	1.3	21
12	Severity Index for Suspected Arbovirus (SISA): Machine learning for accurate prediction of hospitalization in subjects suspected of arboviral infection. PLoS Neglected Tropical Diseases, 2020, 14, e0007969.	1.3	16
13	The origins of dengue and chikungunya viruses in Ecuador following increased migration from Venezuela and Colombia. BMC Evolutionary Biology, 2020, 20, 31.	3.2	15
14	Development of a Loop-Mediated Isothermal Amplification Assay for Rapid, Sensitive and Specific Detection of a <i>Campylobacter jejuni</i> Clone. Journal of Veterinary Medical Science, 2012, 74, 591-596.	0.3	13
15	Seasonal patterns of dengue fever in rural Ecuador: 2009-2016. PLoS Neglected Tropical Diseases, 2019, 13, e0007360.	1.3	12
16	Identification and evaluation of epidemic prediction and forecasting reporting guidelines: A systematic review and a call for action. Epidemics, 2020, 33, 100400.	1.5	10
17	The 2018–2019 weak El Niño: Predicting the risk of a dengue outbreak in Machala, Ecuador. International Journal of Climatology, 2021, 41, 3813-3823.	1.5	9
18	Genetics of critical contacts and clashes in the DNA packaging specificities of bacteriophages λ and 21. Virology, 2015, 476, 115-123.	1.1	8

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#	Article	IF	CITATIONS
19	A decade of arbovirus emergence in the temperate southern cone of South America: dengue, Aedes aegypti and climate dynamics in Córdoba, Argentina. Heliyon, 2020, 6, e04858.	1.4	8
20	Household and climate factors influence Aedes aegypti presence in the arid city of Huaquillas, Ecuador. PLoS Neglected Tropical Diseases, 2021, 15, e0009931.	1.3	7
21	Chronic kidney disease in Ecuador: An epidemiological and health system analysis of an emerging public health crisis. PLoS ONE, 2022, 17, e0265395.	1.1	3
22	Key Findings and Comparisons From Analogous Case-Cluster Studies for Dengue Virus Infection Conducted in Machala, Ecuador, and Kamphaeng Phet, Thailand. Frontiers in Public Health, 2020, 8, 2.	1.3	2
23	Prioritization of family member sequencing for the detection of rare variants. BMC Proceedings, 2016, 10, 227-231.	1.8	1
24	DNA Topology and the Initiation of Virus DNA Packaging. PLoS ONE, 2016, 11, e0154785.	1.1	1