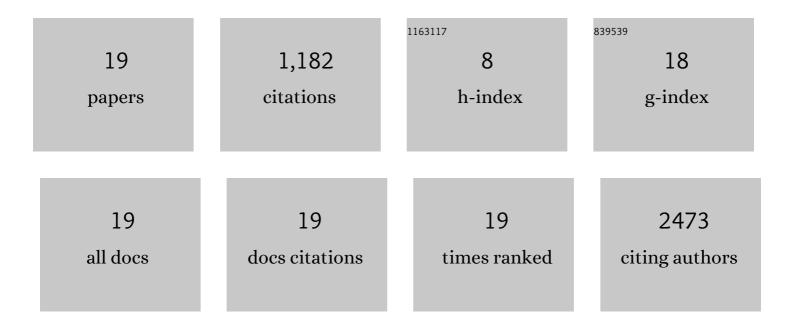
## **Rafael Ojeda-Flores**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5804338/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Strategy To Estimate Unknown Viral Diversity in Mammals. MBio, 2013, 4, e00598-13.	4.1	320
2	Global patterns in coronavirus diversity. Virus Evolution, 2017, 3, vex012.	4.9	310
3	Bats are a major natural reservoir for hepaciviruses and pegiviruses. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8194-8199.	7.1	251
4	One Health proof of concept: Bringing a transdisciplinary approach to surveillance for zoonotic viruses at the human-wild animal interface. Preventive Veterinary Medicine, 2017, 137, 112-118.	1.9	112
5	Non-random patterns in viral diversity. Nature Communications, 2015, 6, 8147.	12.8	65
6	Dengue Virus in Bats from Southeastern Mexico. American Journal of Tropical Medicine and Hygiene, 2014, 91, 129-131.	1.4	40
7	Quantitative evaluation of MPTP-treated nonhuman parkinsonian primates in the HALLWAY task. Journal of Neuroscience Methods, 2009, 177, 361-368.	2.5	24
8	Potential Sympatric Vectors and Mammalian Hosts of Venezuelan Equine Encephalitis Virus in Southern Mexico. Journal of Wildlife Diseases, 2017, 53, 657.	0.8	16
9	Effects of landscape anthropization on sylvatic mosquito assemblages in a rainforest in Chiapas, Mexico. Acta Tropica, 2021, 216, 105849.	2.0	8
10	Viral diversity of bat communities in human-dominated landscapes in Mexico. Veterinaria México OA, 2015, 2, .	0.2	7
11	Eco-Epidemiological Evidence of the Transmission of Avian and Human Influenza A Viruses in Wild Pigs in Campeche, Mexico. Viruses, 2020, 12, 528.	3.3	6
12	Molecular detection of Rickettsia amblyommatis and Rickettsia parkeri in ticks collected from wild pigs in Campeche, Mexico. Ticks and Tick-borne Diseases, 2022, 13, 101844.	2.7	6
13	Assemblage variation of mosquitoes (Diptera: Culicidae) in different land use and activity periods within a lowland tropical forest matrix in Campeche, Mexico. Journal of Vector Ecology, 2020, 45, 188-196.	1.0	5
14	Simulation modeling of influenza transmission through backyard pig trade networks in a wildlife/livestock interface area. Tropical Animal Health and Production, 2019, 51, 2019-2024.	1.4	3
15	Global subtype diversity, spatial distribution patterns, and phylogenetic analysis of avian influenza virus in water. Transboundary and Emerging Diseases, 2021, , .	3.0	3
16	Molecular identification and phylogenetic characterization of influenza A virus at a wildlife–livestock interface in Mexico. Transboundary and Emerging Diseases, 2021, 68, 3563-3573.	3.0	3
17	Phylogenetic characterization of a reassortant H5N2 influenza A virus from a resident Mexican duck (Anas diazi). Infection, Genetics and Evolution, 2020, 84, 104475.	2.3	2
18	Composición de comunidades y filoespecificidad de ectoparásitos de murciélagos en paisajes agropecuarios de Veracruz, México Ecosistemas Y Recursos Agropecuarios, 2019, 7, .	0.2	1

#	Article	IF	CITATIONS
19	A transdisciplinary approach to disease ecology: Emerging coronaviruses. Veterinaria México OA, 0, 8, .	0.2	о