Carlos Alberto Flores-LÃ³pez

List of Publications by Year
in descending order

15 papers	230 citations	1307594 7 h-index	1125743 13 g-index
16 all docs	16 docs citations	16 times ranked	368 citing authors

#	Article	IF	Citations
1	Analyses of 32 Loci Clarify Phylogenetic Relationships among Trypanosoma cruzi Lineages and Support a Single Hybridization prior to Human Contact. PLoS Neglected Tropical Diseases, 2011, 5, e1272.	3.0	56
2	North American import? Charting the origins of an enigmatic Trypanosoma cruzi domestic genotype. Parasites and Vectors, 2012, 5, 226.	2.5	48
3	Whole genome sequencing of Mycobacterium bovis to obtain molecular fingerprints in human and cattle isolates from Baja California, Mexico. International Journal of Infectious Diseases, 2017, 63, 48-56.	3.3	37
4	Molecular characterization of multidrug-resistant Mycobacterium tuberculosis isolates from high prevalence tuberculosis states in Mexico. Infection, Genetics and Evolution, 2017, 55, 384-391.	2.3	22
5	Genetic Diversity and Population Genetics of Mosquitoes (Diptera: Culicidae:<i>Culex</i>spp.) from the Sonoran Desert of North America. Scientific World Journal, The, 2013, 2013, 1-11.	2.1	17
6	Molecular epidemiology of Mycobacterium tuberculosis in Baja California, Mexico: A result of human migration?. Infection, Genetics and Evolution, 2017, 55, 378-383.	2.3	12
7	Cultivable Bacterial Diversity in the Gut of the Chagas Disease Vector Triatoma dimidiata: Identification of Possible Bacterial Candidates for a Paratransgenesis Approach. Frontiers in Ecology and Evolution, 2018, 5, .	2.2	8
8	Phylogenetic diversity of two common Trypanosoma cruzi lineages in the Southwestern United States. Infection, Genetics and Evolution, 2022, 99, 105251.	2.3	6
9	Aggregata polibraxiona n. sp. (Apicomplexa: Aggregatidae) from Octopus bimaculatus Verrill, 1883 (Mollusca: Cephalopoda) from the Gulf of California, Mexico. European Journal of Protistology, 2021, 81, 125825.	1.5	5
10	Ontogenetic changes in wild chagasic bugs (Dipetalogaster maximus): exploring morphological adaptations in pre-adult and adult stages. Revista Mexicana De Biodiversidad, 2019, 90, .	0.4	5
11	Differences in inferred genome-wide signals of positive selection during the evolution of Trypanosoma cruzi and Leishmania spp. lineages: A result of disparities in host and tissue infection ranges?. Infection, Genetics and Evolution, 2015, 33, 37-46.	2.3	4
12	Design of a AFLP-PCR and PCR-RFLP test that identify the majority of discrete typing units ofÂTrypanosoma cruzi. PLoS ONE, 2020, 15, e0237180.	2.5	3
13	Potential distributions of the parasite <i>Trypanosoma cruzi</i> and its vector <i>Dipetalogaster maxima</i> highlight areas at risk of Chagas disease transmission in Baja California Sur, Mexico, under climate change. Medical and Veterinary Entomology, 0, , .	1.5	3
14	Infection Rate of <i>Trypanosoma cruzi</i> (Trypanosomatida: Trypanosomatidae) in <i>Dipetalogaster maxima</i> (Hemiptera: Reduviidae). Journal of Medical Entomology, 2022, 59, 394-399.	1.8	2
15	High fungal pathogen loads and prevalence in Baja California amphibian communities: The importance of species, elevation, and historical context. Global Ecology and Conservation, 2022, 33, e01968.	2.1	2