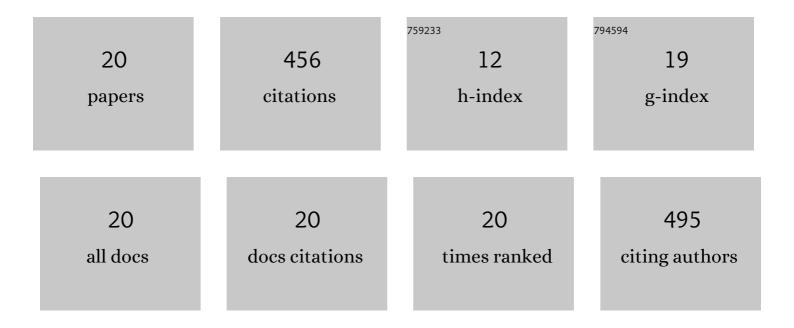
Juan Jose Lauthier

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6034470/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	MLSTest: Novel software for multi-locus sequence data analysis in eukaryotic organisms. Infection, Genetics and Evolution, 2013, 20, 188-196.	2.3	74
2	Candidate targets for Multilocus Sequence Typing of Trypanosoma cruzi: Validation using parasite stocks from the Chaco Region and a set of reference strains. Infection, Genetics and Evolution, 2012, 12, 350-358.	2.3	54
3	Trypanosoma cruzi diversity in the Gran Chaco: Mixed infections and differential host distribution of TcV and TcVI. Infection, Genetics and Evolution, 2015, 29, 53-59.	2.3	54
4	Reassessment of MLST schemes for Leptospira spp. typing worldwide. Infection, Genetics and Evolution, 2014, 22, 216-222.	2.3	50
5	Interest and limitations of Spliced Leader Intergenic Region sequences for analyzing Trypanosoma cruzi I phylogenetic diversity in the Argentinean Chaco. Infection, Genetics and Evolution, 2011, 11, 300-307.	2.3	38
6	Optimized Multilocus Sequence Typing (MLST) Scheme for Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2014, 8, e3117.	3.0	31
7	How Often Do They Have Sex? A Comparative Analysis of the Population Structure of Seven Eukaryotic Microbial Pathogens. PLoS ONE, 2014, 9, e103131.	2.5	30
8	Multilocus sequence typing approach for a broader range of species of Leishmania genus: Describing parasite diversity in Argentina. Infection, Genetics and Evolution, 2015, 30, 308-317.	2.3	23
9	Benznidazole treatment in chronic children infected with Trypanosoma cruzi: Serological and molecular follow-up of patients and identification of Discrete Typing Units. Acta Tropica, 2013, 128, 130-136.	2.0	20
10	Biological behavior of different Trypanosoma cruzi isolates circulating in an endemic area for Chagas disease in the Gran Chaco region of Argentina. Acta Tropica, 2012, 123, 196-201.	2.0	17
11	Experimental Evidence of Biological Interactions among Different Isolates of Trypanosoma cruzi from the Chaco Region. PLoS ONE, 2015, 10, e0119866.	2.5	16
12	Preponderant clonal evolution of Trypanosoma cruzi I from Argentinean Chaco revealed by Multilocus Sequence Typing (MLST). Infection, Genetics and Evolution, 2014, 27, 348-354.	2.3	15
13	The TcTASV proteins are novel promising antigens to detect active <i>Trypanosoma cruzi</i> infection in dogs. Parasitology, 2016, 143, 1382-1389.	1.5	7
14	Development of a Multilocus sequence typing (MLST) scheme for Pan-Leishmania. Acta Tropica, 2020, 201, 105189.	2.0	7
15	Morphological and ITS2 Molecular Characterization ofRibeiroiaCercariae (Digenea: Psilostomidae) fromBiomphalariaspp. (Gastropoda: Planorbidae) in Northern Argentina. Journal of Parasitology, 2015, 101, 549-555.	0.7	6
16	Sand fly typing: a simple and morphologically-supported method based on polymorphism of 18S rRNA gene in a Leishmaniasis endemic area of Argentina. Acta Tropica, 2020, 211, 105609.	2.0	5
17	Evaluation of recombinant antigens of <i><scp>T</scp>rypanosoma cruzi</i> to diagnose infection in naturally infected dogs from Chaco region, Argentina. Parasite Immunology, 2014, 36, 694-699.	1.5	4
18	The life cycle of Magnivitellinum saltaensis n. sp. (Digenea: Alloglossidiidae) in Salta Province, Argentina. Parasitology Research, 2021, 120, 1233-1245.	1.6	4

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#	Article	IF	CITATIONS
19	Two Cases with Creeping Disease due to <i>Gnathostomia doloresi</i> . Nishinihon Journal of Dermatology, 2017, 79, 264-268.	0.0	1

20 Immunological and Immunopathological Aspects. , 2018, , 107-125.