Juan Jose Lauthier

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The life cycle of Magnivitellinum saltaensis n. sp. (Digenea: Alloglossidiidae) in Salta Province, Argentina. Parasitology Research, 2021, 120, 1233-1245.	1.6	4
2	Development of a Multilocus sequence typing (MLST) scheme for Pan-Leishmania. Acta Tropica, 2020, 201, 105189.	2.0	7
3	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
4	Immunological and Immunopathological Aspects. , 2018, , 107-125.		0
5	Two Cases with Creeping Disease due to <i>Gnathostomia doloresi</i> . Nishinihon Journal of Dermatology, 2017, 79, 264-268.	0.0	1
6	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
7	Experimental Evidence of Biological Interactions among Different Isolates of Trypanosoma cruzi from the Chaco Region. PLoS ONE, 2015, 10, e0119866.	2.5	16
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	Morphological and ITS2 Molecular Characterization ofRibeiroiaCercariae (Digenea: Psilostomidae) fromBiomphalariaspp. (Gastropoda: Planorbidae) in Northern Argentina. Journal of Parasitology, 2015, 101, 549-555.	0.7	6
10	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
11	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
12	Optimized Multilocus Sequence Typing (MLST) Scheme for Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2014, 8, e3117.	3.0	31
13	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
14	Reassessment of MLST schemes for Leptospira spp. typing worldwide. Infection, Genetics and Evolution, 2014, 22, 216-222.	2.3	50
15	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
16	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
17	MLSTest: Novel software for multi-locus sequence data analysis in eukaryotic organisms. Infection, Genetics and Evolution, 2013, 20, 188-196.	2.3	74
18	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

#	Article	IF	CITATIONS
19	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
20	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